Gene_ID	Skm1M_1	Skm1M_2	Skm1M_3	Skm1WT_1	Skm1WT_2	Skm1WT_3	log2FoldCh	pvalue	padj	GeneName	Chrom	Strand	Start	End	GeneLengt
ENSG0000(	974.6802	1117.579	1021.226	1381.295	1196.562	1194.315	-0.27699	0.028802	0.059995	TSPAN6	chrX	-	99883667	99894988	2206
ENSG0000(	7.250543	20.47289	5.277655	0	0	0	4.6387	8.61E-05	0.000283	TNMD	chrX	+	99839799	99854882	1339
ENSG0000(	662.9068	639.4768	430.1289	1086.909	916.7503	944.4377	-0.76221	4.81E-06	1.85E-05	DPM1	chr20	-	49551404	49575092	1161
ENSG0000(	95.29286	75.87013	104.2337	106.3687	119.6562	96.99186	-0.2277	0.3823	0.51303	SCYL3	chr1	-	1.7E+08	1.7E+08	3477
ENSG0000(	183.3352	204.7289	189.9956	599.2604	583.5539	529.3454	-1.5619	2.72E-22	3.03E-21	C1orf112	chr1	+	1.7E+08	1.7E+08	4355
ENSG0000(	1850.96	1869.055	2285.225	0	0	0	11.612	4.49E-42	9.83E-41	CFH	chr1	+	1.97E+08	1.97E+08	6985
ENSG0000(	1438.715	1454.78	1431.564	1217.248	1103.598	1071.842	0.34931	0.002822	0.007325	FUCA2	chr6	-	1.44E+08	1.44E+08	1690
ENSG0000(	321.0955	252.9004	259.9245	338.5821	357.1276	307.4149	-0.26251	0.13388	0.22272	GCLC	chr6	-	53362139	53481768	3813
ENSG0000(	790.3092	846.6143	1006.713	617.2383	778.6855	584.4171	0.41529	0.007319	0.017543	NFYA	chr6	+	41040684	41067715	3811
ENSG0000(	90.1139	104.773	67.2901	150.5642	149.11	130.6924	-0.70543	0.005309	0.013087	STPG1	chr1	-	24683489	24743424	6016
ENSG0000(	209.23	251.6961	199.2315	226.9699	242.994	188.23	0.005059	0.97958	0.98808	NIPAL3	chr1	+	24742284	24799466	5481
ENSG0000(	696.0522	691.2612	662.3457	1197.023	1212.209	1208.288	-0.81754	9.68E-12	6.16E-11	LAS1L	chrX	-	64732462	64754655	5205
ENSG0000(	7.250543	14.45145	7.916483	33.7084	53.38506	29.59074	-1.8993	0.000361	0.001084	ENPP4	chr6	+	46097730	46114436	4651
ENSG0000(	355.2766	263.739	261.2439	234.4606	250.3575	258.097	0.24701	0.18651	0.29112	SEMA3F	chr3	+	50192478	50226508	3802
ENSG0000(	2.071584	0	1.319414	53.18436	53.38506	43.56414	-4.8848	2.08E-10	1.20E-09	CFTR	chr7	+	1.17E+08	1.17E+08	6128
ENSG0000(	953.9643	977.8816	1211.222	528.0983	647.9841	490.7131	0.91225	2.87E-09	1.51E-08	ANKIB1	chr7	+	91875548	92030698	6081
ENSG0000(	93.22127	61.41867	104.2337	29.96302	34.97642	25.48091	1.4943	1.58E-05	5.73E-05	CYP51A1	chr7	-	91741465	91772266	3210
ENSG0000(	394.6367	466.0593	489.5025	421.7295	482.3064	437.2853	0.008378	0.95693	0.97456	KRIT1	chr7	-	91828283	91875480	4762
ENSG0000(	240.3037	286.6205	199.2315	217.981	255.8801	261.3848	-0.01568	0.93625	0.96165	RAD52	chr12	-	1021243	1100356	2826
ENSG0000(	3.107376	2.408575	3.958241	0	2.761296	6.575719	0.019394	0.98621	0.99155	MYH16	chr7	+	98836417	98908753	6294
ENSG0000(	101.5076	48.17151	83.12307	34.45748	43.2603	75.62077	0.594	0.11371	0.19491	BAD	chr11	-	64037302	64052176	1157
ENSG0000(	1072.045	934.5273	915.6732	1313.129	1261.912	1246.099	-0.38519	0.001765	0.004749	LAP3	chr4	+	17578815	17609595	2213
ENSG0000(	25139.71	24935.98	22172.75	6681.754	6359.265	7279.321	1.8272	9.17E-66	3.65E-64	CD99	chrX	+	2609220	2659350	1245
ENSG0000(	5.17896	0	3.958241	16.47966	23.93123	7.397684	-2.1112	0.011588	0.026537	HS3ST1	chr4	-	11394774	11431389	8031
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	ABP1	chr7	+	1.51E+08	1.51E+08	3135
ENSG0000(	164.6909	167.396	237.4945	8.239831	18.40864	7.397684	4.0175	5.35E-30	8.11E-29	WNT16	chr7	+	1.21E+08	1.21E+08	3147
ENSG0000(	54.89697	79.48299	93.67838	8.239831	4.60216	3.28786	3.6717	3.66E-14	2.74E-13	HECW1	chr7	+	43152198	43602938	6839
ENSG0000(	702.2669	609.3696	617.4856	1203.015	1172.63	1288.019	-0.92216	6.19E-13	4.29E-12	MAD1L1	chr7	-	1855429	2272878	2991
ENSG0000(	9848.309	9730.645	9770.259	8749.951	11429	11483.67	-0.10914	0.37055	0.50107	LASP1	chr17	+	37026112	37078023	4109
ENSG0000(	265.1627	263.739	244.0915	310.8664	277.9705	285.2218	-0.17641	0.30082	0.42585	SNX11	chr17	+	46180719	46200436	2733
ENSG0000(	903.2105	886.3558	1023.865	1041.215	1298.73	1229.66	-0.34266	0.010856	0.025041	M6PR	chr12	-	9092959	9102551	2756
ENSG0000(	0	0	0	157.3059	116.8949	138.9121	-7.7595	4.78E-15	3.78E-14	KLHL13	chrX	-	1.17E+08	1.17E+08	5331
ENSG0000(	50.7538	45.76293	73.88717	15.73059	27.61296	29.59074	1.198	0.003337	0.008562	CYP26B1	chr2	-	72356367	72375167	4732
ENSG0000(	4.143168	7.225726	1.319414	65.91865	76.39586	87.95025	-3.9862	1.07E-13	7.81E-13	ICA1	chr7	-	8152814	8302317	2458
ENSG0000(	84.93494	109.5902	73.88717	642.7068	624.9733	601.6783	-2.7852	6.91E-51	1.95E-49	DBNDD1	chr16	-	90071273	90086536	2889
ENSG0000(	584.1866	604.5524	711.164	1069.68	1240.742	929.6423	-0.76858	2.35E-07	1.04E-06	ALS2	chr2	-	2.03E+08	2.03E+08	6644
ENSG0000(	3.107376	12.04288	5.277655	19.47596	17.48821	9.863579	-1.1159	0.11924	0.20267	CASP10	chr2	+	2.02E+08	2.02E+08	5928
ENSG0000(	269.3059	285.4162	248.0498	481.6556	359.8889	424.1339	-0.6548	0.000159	0.000505	CFLAR	chr2	+	2.02E+08	2.02E+08	4415
ENSG0000(	420.5315	466.0593	387.9077	201.5013	154.6326	148.7757	1.3275	7.11E-13	4.92E-12	TFPI	chr2	-	1.88E+08	1.88E+08	7690
ENSG0000(	268.2701	286.6205	261.2439	263.6746	264.164	272.0704	0.02902	0.86389	0.914	NDUFAF7	chr2	+	37458774	37480546	2974
ENSG0000(	1648.981	1687.207	1892.039	1122.115	1102.678	989.6458	0.69983	8.07E-09	4.08E-08	RBM5	chr3	+	50126341	50156454	5616
ENSG0000(	25.8948	71.05298	52.77655	54.68252	24.85166	38.63235	0.3213	0.45764	0.58728	MTMR7	chr8	-	17155539	17271037	3850
ENSG0000(	489.9296	590.101	721.7193	728.8505	775.0037	588.5269	-0.2167	0.20017	0.30776	SLC7A2	chr8	+	17354597	17428082	7638

ENSG00000(	1578.547	1582.434	1246.846	2006.024	1586.825	1595.434	-0.23426	0.098386	0.17301	ARF5	chr7	+	1.27E+08	1.27E+08	1509
ENSG00000(	245.4827	217.9761	216.3839	55.43159	75.47542	54.24968	1.8685	1.57E-15	1.28E-14	SARM1	chr17	+	26691378	26728065	7304
ENSG00000(	1958.682	1642.648	1928.983	2546.108	2168.538	2408.357	-0.36452	0.00285	0.00739	POLDIP2	chr17	-	26673659	26684545	2588
ENSG00000(	2520.082	2377.264	2351.195	2353.595	3226.114	3142.372	-0.26586	0.046613	0.091322	PLXND1	chr3	-	1.29E+08	1.29E+08	7101
ENSG00000(	1982.506	2130.385	1893.359	2143.854	2055.325	2159.302	-0.08206	0.45458	0.58424	AK2	chr1	-	33473585	33546597	3586
ENSG00000(	0	2.408575	3.958241	11.23613	10.12475	6.575719	-1.8591	0.051952	0.10042	CD38	chr4	+	15779898	15851069	1884
ENSG00000(	1468.753	1389.748	1347.121	3515.412	3519.732	3889.538	-1.3745	1.04E-35	1.90E-34	FKBP4	chr12	+	2904119	2914576	2267
ENSG00000(	2435.147	2345.952	2386.82	3289.94	2928.815	2609.739	-0.30012	0.011251	0.025868	KDM1A	chr1	+	23345941	23410182	3059
ENSG00000(	1294.74	1451.167	1283.79	886.9054	1276.639	1138.421	0.28732	0.050016	0.097135	RBM6	chr3	+	49977440	50137478	4324
ENSG00000(	344.9187	417.8878	328.534	20.22504	22.09037	27.12484	3.942	3.87E-56	1.22E-54	CAMKK1	chr17	-	3763609	3798185	3898
ENSG00000(	571.7571	564.8109	664.9845	458.4342	497.9537	362.4865	0.44804	0.005577	0.013692	RECQL	chr12	-	21621845	21654603	3702
ENSG00000(	198.872	175.826	240.1333	310.8664	253.1188	240.8357	-0.38937	0.050596	0.098117	CCDC132	chr7	+	92861653	92988338	3614
ENSG00000(	145.0109	116.8159	130.622	12.73428	5.522592	12.32947	3.5929	1.76E-22	1.97E-21	HSPB6	chr19	-	36245469	36248980	1634
ENSG00000(	215.4447	244.4704	155.6908	176.0328	230.108	291.7975	-0.17681	0.44773	0.57751	ARHGAP33	chr19	+	36265434	36279724	4401
ENSG00000(	1137.3	1209.105	1021.226	1922.128	1754.343	1897.095	-0.72515	1.56E-09	8.40E-09	NDUFAB1	chr16	-	23592323	23607677	885
ENSG00000(	94.25706	85.50443	75.20659	38.20285	32.21512	18.08323	1.4999	2.40E-05	8.49E-05	PDK4	chr7	-	95212811	95225803	3576
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	SLC22A16	chr6	-	1.11E+08	1.11E+08	1987
ENSG00000(	16.57267	15.65574	17.15238	2.247227	5.522592	5.753754	1.7409	0.01428	0.032081	ZMYND10	chr3	-	50378541	50384283	2896
ENSG00000(	9.322127	3.612863	5.277655	0	0	0	3.7482	0.002724	0.007089	ABCB5	chr7	+	20654830	20816658	5811
ENSG00000(	255.8406	261.3304	275.7575	2120.633	2310.284	2026.965	-3.0199	6.36E-119	6.58E-117	SLC25A13	chr7	-	95749532	95951459	3192
ENSG00000(	190.5857	157.7617	204.5091	305.6228	278.8909	252.3432	-0.59611	0.001945	0.005195	ST7	chr7	+	1.17E+08	1.17E+08	2899
ENSG00000(	1320.635	1280.158	1508.09	1354.329	1408.261	1199.247	0.05208	0.67993	0.78073	CDC27	chr17	-	45195069	45266788	5801
ENSG00000(	0	0	0	48.68991	24.85166	25.48091	-5.8686	3.88E-08	1.85E-07	CALCR	chr7	-	93053799	93204042	3696
ENSG00000(	279.6638	226.4061	295.5487	667.4263	647.9841	699.4921	-1.3258	2.62E-17	2.34E-16	HCCS	chrX	+	11129421	11141198	2277
ENSG00000(	1394.176	1425.877	1151.848	1051.702	1008.793	1355.42	0.21731	0.13954	0.23011	DVL2	chr17	-	7128660	7137864	3018
ENSG00000(	0	0	0	35.95563	28.53339	36.16646	-5.9122	2.41E-08	1.17E-07	PRSS22	chr16	-	2902728	2908171	1386
ENSG00000(	2204.165	1985.87	2039.814	2955.852	3692.773	4101.605	-0.78481	3.67E-09	1.91E-08	UPF1	chr19	+	18942747	18979045	5348
ENSG00000(	252.7332	249.2876	328.534	122.8484	137.1444	169.3248	0.94496	6.93E-06	2.62E-05	SKAP2	chr7	-	26706681	27034858	3998
ENSG00000(	2336.747	2218.298	1990.995	5348.399	3979.948	4579.989	-1.0846	8.63E-17	7.47E-16	SLC25A5	chrX	+	1.19E+08	1.19E+08	1274
ENSG00000(	309.7018	310.7062	302.1458	828.4776	587.2356	720.0413	-1.2075	1.58E-13	1.14E-12	CCDC109B	chr4	+	1.1E+08	1.11E+08	2270
ENSG00000(	500.2875	470.8765	430.1289	1.498151	0.920432	6.575719	7.0677	8.06E-59	2.72E-57	HOXA11	chr7	-	27221129	27224842	2295
ENSG00000(	689.8374	655.1325	530.4043	751.3228	691.2444	906.6273	-0.32274	0.038823	0.07795	POLR2J	chr7	-	1.02E+08	1.02E+08	932
ENSG00000(	495.1085	487.7365	558.112	823.234	957.2493	870.4608	-0.78115	1.40E-08	6.93E-08	DHX33	chr17	-	5344232	5372380	5618
ENSG00000(	5.17896	6.021439	2.638828	0	3.681728	0	1.4563	0.2171	0.32825	MEOX1	chr17	-	41717756	41739322	2707
ENSG00000(	19.68005	9.634302	31.66593	22.47227	50.62376	55.07165	-1.0369	0.03998	0.07998	THSD7A	chr7	-	11414247	11871824	6385
ENSG00000(	287.9501	363.6949	405.06	602.2567	596.4399	580.3072	-0.75219	3.01E-06	1.18E-05	LIG3	chr17	+	33307513	33332083	4664
ENSG00000(	262.0554	266.1476	327.2146	594.0169	505.3172	450.4368	-0.85673	6.60E-07	2.79E-06	RPAP3	chr12	-	48057070	48099844	2332
ENSG00000(	2.071584	2.408575	0	5.243529	11.96562	5.753754	-1.9056	0.062815	0.11826	ACSM3	chr16	+	20621565	20808903	2845
ENSG00000(	46.61064	46.96722	38.263	73.4094	80.07758	78.08667	-0.79757	0.011582	0.026529	AC004381.	chr16	+	20817751	20860987	2719
ENSG00000(	591.4372	517.8437	500.0578	1549.837	1275.719	1347.201	-1.3699	1.62E-23	1.88E-22	CIAPIN1	chr16	-	57462081	57481440	2182
ENSG00000(	1461.502	1290.996	1179.556	1145.337	1110.041	1388.299	0.1103	0.42219	0.55266	SPPL2B	chr19	+	2328617	2355099	3811
ENSG00000(	732.3049	699.6912	712.4834	439.7073	474.9429	453.7246	0.64735	1.38E-06	5.65E-06	FAM214B	chr9	-	35104109	35116338	5771
ENSG00000(	281.7354	317.932	238.8139	16.47966	14.72691	14.79537	4.1384	9.89E-48	2.55E-46	COPZ2	chr17	-	46103533	46115392	891
ENSG00000(	98.40023	105.9773	110.8308	271.1653	283.4931	197.2716	-1.2473	2.19E-08	1.07E-07	PRKAR2B	chr7	+	1.07E+08	1.07E+08	3745

ENSG00000(	478.5359	427.5221	457.8366	515.364	411.4331	433.1755	0.003446	0.9823	0.98984	MSL3	chrX	+	11776278	11793870	3446
ENSG00000(	2576.014	2589.219	2612.439	1466.69	2290.035	1842.845	0.47322	0.001323	0.003643	CREBBP	chr16	-	3775055	3930727	10803
ENSG00000(	11.39371	15.65574	13.19414	34.45748	31.29469	35.34449	-1.2882	0.00885	0.02082	BZRAP1	chr17	-	56378592	56406152	7626
ENSG00000(	0	0	0	1.498151	2.761296	0	-1.199	0.3707	NA	PON1	chr7	-	94926988	95025673	2568
ENSG00000(	187.4783	207.1375	195.2732	251.6894	220.9037	131.5144	-0.03503	0.8831	0.92688	GCFC2	chr2	-	75879126	75938115	4440
ENSG00000(	418.4599	357.6735	296.8681	398.5082	314.7877	373.994	-0.01746	0.92237	0.953	WDR54	chr2	+	74648805	74652882	2356
ENSG00000(	161.5835	185.4603	175.482	728.8505	751.9929	687.1627	-2.0476	2.79E-39	5.66E-38	CROT	chr7	+	86974997	87029111	3175
ENSG00000(	4.143168	1.204288	5.277655	8.988907	7.363456	9.863579	-1.1532	0.18708	0.29178	ABCB4	chr7	-	87031013	87109751	4020
ENSG00000(	1146.622	1104.332	1378.787	501.8806	570.6678	439.7512	1.2595	1.38E-17	1.25E-16	MLL5	chr7	+	1.05E+08	1.05E+08	7013
ENSG00000(	1168.373	1024.849	1200.667	740.0866	588.156	703.602	0.73717	1.08E-07	4.92E-07	RHBDD2	chr7	+	75471920	75518244	1878
ENSG00000(	23.82321	26.49433	21.11062	94.38352	125.1788	128.2265	-2.2448	1.58E-11	9.94E-11	SOX8	chr16	+	1031808	1036979	4153
ENSG00000(	843.1346	816.5071	1052.892	739.3376	767.6403	668.2575	0.3167	0.02712	0.056934	IBTK	chr6	-	82879700	82957471	6054
ENSG00000(	420.5315	452.8122	418.2542	918.3666	762.1177	750.454	-0.91043	3.60E-10	2.04E-09	ZNF195	chr11	-	3360491	3400448	2970
ENSG00000(	769.5934	812.8942	1054.212	381.2795	504.3967	345.2253	1.0947	4.12E-10	2.33E-09	MYCBP2	chr13	-	77618792	77901185	15025
ENSG00000(	700.1953	644.2939	820.6754	540.0835	509.9193	384.6796	0.59069	0.000347	0.001047	FBXL3	chr13	-	77566740	77601330	3503
ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	ITGAL	chr16	+	30483979	30534506	5213
ENSG00000(	211.3015	208.3418	205.8285	76.40571	31.29469	62.46933	1.8487	4.11E-11	2.50E-10	PDK2	chr17	+	48172101	48189516	3440
ENSG00000(	985.0381	852.6357	940.742	1839.73	1474.532	1659.547	-0.83823	1.35E-10	7.90E-10	ITGA3	chr17	+	48133332	48167845	5479
ENSG00000(	513.7528	468.4679	585.8197	381.2795	436.2848	403.5848	0.35949	0.019308	0.04204	ZFX	chrX	+	24167290	24234372	7558
ENSG00000(	2784.209	2809.603	3177.148	2363.333	2278.99	2139.575	0.37003	0.000955	0.002685	LAMP2	chrX	-	1.2E+08	1.2E+08	4030
ENSG00000(	1288.525	1283.771	1376.149	1382.793	1229.697	1134.312	0.074858	0.54721	0.66898	GGNBP2	chr17	+	34900737	34946278	3497
ENSG00000(	11.39371	10.83859	15.83297	3.745378	8.283888	11.50751	0.64467	0.36201	0.49166	ITGA2B	chr17	-	42449548	42466873	3333
ENSG00000(	2.071584	0	0	6.74168	1.840864	1.64393	-1.5021	0.23332	0.3471	ASB4	chr7	+	95107756	95169544	3825
ENSG00000(	1092.76	1119.988	1106.988	1340.845	1253.628	1145.819	-0.17201	0.1544	0.24993	GDE1	chr16	-	19513015	19533467	2954
ENSG00000(	495.1085	525.0694	303.4652	680.9097	506.2376	683.0528	-0.49462	0.01254	0.02851	C19orf60	chr19	+	18699495	18703146	2465
ENSG00000(	69.39806	71.05298	73.88717	113.1104	96.64536	101.9236	-0.53722	0.043894	0.086776	CRLF1	chr19	-	18683030	18718551	1792
ENSG00000(	200.9436	211.9546	184.7179	100.3761	154.6326	129.0485	0.63775	0.004562	0.011395	OSBPL7	chr17	-	45884738	45899200	4497
ENSG00000(	1596.155	1630.606	1502.812	837.4665	612.0873	608.254	1.1961	2.36E-16	2.00E-15	TMEM98	chr17	+	31254928	31272124	4434
ENSG00000(	3.107376	0	0	1.498151	1.840864	4.93179	-0.91222	0.47107	0.6	YBX2	chr17	-	7191571	7197934	4553
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	KRT33A	chr17	-	39502344	39507064	1287
ENSG00000(	450.5695	441.9736	386.5882	240.4533	221.8241	186.586	0.97566	1.81E-08	8.92E-08	MAP3K14	chr17	-	43340488	43394414	4465
ENSG00000(	1083.438	970.6559	1161.084	662.1828	835.7523	704.4239	0.5451	9.87E-05	0.000322	SYNRG	chr17	-	35874900	35969544	8229
ENSG00000(	2033.26	2043.676	1733.71	1617.254	1631.926	1871.614	0.1824	0.1384	0.22865	TMEM132A	chr11	+	60691935	60704631	3981
ENSG00000(	6641.498	6153.91	6884.701	4807.567	4792.689	4261.888	0.50478	2.46E-06	9.78E-06	AP2B1	chr17	+	33905065	34053436	6085
ENSG00000(	7.250543	4.817151	2.638828	5.992604	10.12475	4.93179	-0.43735	0.61366	0.72703	TAC1	chr7	+	97361220	97369784	1239
ENSG00000(	760.2713	696.0783	720.3999	423.2277	532.0097	544.9627	0.53686	0.000283	0.000863	ZNF263	chr16	+	3313743	3351401	3830
ENSG00000(	0	7.225726	0	17.22874	30.37426	40.27628	-3.2682	3.37E-05	0.000117	CX3CL1	chr16	+	57406370	57418960	5796
ENSG00000(	794.4524	812.8942	684.7758	395.5119	408.6718	383.0357	0.9476	1.98E-11	1.23E-10	SPATA20	chr17	+	48620419	48633213	3539
ENSG00000(	310.7376	358.8777	312.7011	44.19546	31.29469	58.35951	2.8471	5.53E-33	9.27E-32	CACNA1G	chr17	+	48638429	48704835	7848
ENSG00000(	1559.903	1617.358	1534.478	2372.322	2108.71	2830.025	-0.63252	1.07E-06	4.44E-06	TNFRSF12A	chr16	+	3068446	3072384	1678
ENSG00000(	0	0	0	361.8035	372.775	311.5247	-8.9392	3.01E-21	3.21E-20	DLX6	chr7	+	96634860	96640351	2304
ENSG00000(	109.7939	118.0202	176.8014	265.1727	360.8093	290.9756	-1.1769	1.56E-07	7.04E-07	MAP3K9	chr14	-	71189243	71276251	11169
ENSG00000(	1243.986	1264.502	1316.775	1158.071	1205.766	1246.099	0.083254	0.46867	0.59788	RALA	chr7	+	39663082	39747723	2880
ENSG00000(	52.82539	36.12863	40.90183	606.7512	510.8398	549.8945	-3.6492	7.78E-64	2.98E-62	BAIAP2L1	chr7	-	97920963	98030380	3622

ENSG00000(	103.5792	133.6759	139.8579	72.66033	68.11197	56.71558	0.92026	0.000597	0.001734	JHDM1D	chr7	-	1.4E+08	1.4E+08	9272
ENSG00000(	1161.123	1069.407	1414.412	97.37982	119.6562	90.41614	3.5566	1.88E-97	1.37E-95	ETV1	chr7	-	13930853	14031050	6752
ENSG00000(	322.1313	410.6621	366.797	626.9762	519.1236	520.3038	-0.59978	0.000201	0.000627	AGK	chr7	+	1.41E+08	1.41E+08	3849
ENSG00000(	355.2766	358.8777	310.0622	7.490755	14.72691	25.48091	4.3831	6.70E-50	1.84E-48	ALDH3B1	chr11	+	67776048	67796744	5876
ENSG00000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	TTC22	chr1	-	55245385	55266940	3345
ENSG00000(	600.7593	670.7883	720.3999	654.692	738.1865	600.0344	-0.00133	0.99262	0.99534	PHTF2	chr7	+	77428122	77586818	5005
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	CCL26	chr7	-	75398851	75419214	703
ENSG00000(	336.6324	320.3405	423.5318	168.542	219.0628	180.0103	0.9247	1.25E-06	5.13E-06	FARP2	chr2	+	2.42E+08	2.42E+08	4051
ENSG00000(	0	0	0	0	4.60216	3.28786	-1.9836	0.14291	0.23453	USH1C	chr11	-	17515442	17565963	2700
ENSG00000(	575.9003	567.2195	519.849	1270.432	1129.37	1250.209	-1.131	1.50E-18	1.43E-17	GGCT	chr7	-	30536237	30591095	1173
ENSG00000(	195.7647	193.8903	242.7721	708.6255	613.9281	641.1326	-1.6323	1.19E-23	1.40E-22	DBF4	chr7	+	87505531	87538856	3907
ENSG00000(	142.9393	166.1917	117.4278	3.745378	5.522592	0	5.3514	2.95E-27	4.01E-26	TBXA2R	chr19	-	3594504	3606838	2608
ENSG00000(	673.2647	684.0354	729.6358	1683.922	1391.693	1249.387	-1.0494	9.01E-14	6.59E-13	IFRD1	chr7	+	1.12E+08	1.12E+08	2290
ENSG00000(	218.5521	211.9546	220.3421	262.9255	284.4135	249.8773	-0.2908	0.10218	0.17852	COX10	chr17	+	13972813	14111994	2873
ENSG00000(	588.3298	520.2523	535.682	510.8695	487.829	365.7744	0.26868	0.10081	0.17661	GTF2IRD1	chr7	+	73868120	74016931	5868
ENSG00000(	1124.87	1135.643	1133.376	1273.428	1434.953	1508.306	-0.3123	0.00976	0.022751	PAF1	chr19	-	39876492	39881835	2066
ENSG00000(	1145.586	1101.923	1316.775	915.3703	830.2297	677.2991	0.55452	0.000131	0.000419	VPS41	chr7	-	38762563	38971994	5903
ENSG00000(	16.57267	24.08575	14.51355	107.8669	154.6326	193.9837	-2.9933	2.82E-17	2.50E-16	ARHGAP44	chr17	+	12692856	12894960	4428
ENSG00000(	1093.796	988.7202	1000.116	2743.864	2280.83	2048.337	-1.195	5.41E-19	5.23E-18	ELAC2	chr17	-	12895708	12921504	3738
ENSG00000(	4.143168	6.021439	3.958241	193.2615	196.052	182.4762	-5.182	2.66E-30	4.08E-29	SCIN	chr7	+	12610203	12693228	3137
ENSG00000(	286.9144	251.6961	361.5194	126.5938	185.9273	141.378	0.98315	5.00E-06	1.92E-05	ARSD	chrX	-	2822011	2847392	5159
ENSG00000(	178.1562	128.8588	138.5384	259.1801	237.4715	212.0669	-0.66212	0.001632	0.004416	PNPLA4	chrX	-	7866288	7895780	3372
ENSG00000(	1212.912	1189.836	1469.827	1670.438	1760.786	1536.252	-0.35907	0.005189	0.012823	ADIPOR2	chr12	+	1797740	1897844	4018
ENSG00000(	45.57484	44.55865	38.263	56.92974	52.46462	36.16646	-0.17578	0.63058	0.74068	CDKL3	chr5	-	1.34E+08	1.34E+08	2160
ENSG00000(	0	3.612863	2.638828	1.498151	2.761296	0.821965	0.20192	0.87035	0.91851	UPP2	chr2	+	1.59E+08	1.59E+08	2435
ENSG00000(	1896.535	2148.449	1567.464	694.393	782.3672	896.7637	1.2386	4.50E-17	3.97E-16	MARK4	chr19	+	45582546	45808541	5209
ENSG00000(	3.107376	0	2.638828	568.5483	599.2012	439.7512	-7.6803	7.26E-42	1.58E-40	PROM1	chr4	-	15964699	16086001	4349
ENSG00000(	1796.063	1645.057	1316.775	1774.56	1534.36	2136.287	-0.19352	0.20184	0.30953	CCDC124	chr19	+	18043825	18054800	1055
ENSG00000(	0	0	0	21.72319	23.93123	35.34449	-5.604	1.92E-07	8.57E-07	CEACAM21	chr19	+	42055886	42093197	1691
ENSG00000(	2451.719	2482.037	2868.406	2401.536	2795.352	2269.445	0.063242	0.6099	0.72366	PAFAH1B1	chr17	+	2496504	2588909	5497
ENSG00000(	0	1.204288	6.597069	325.8479	365.4115	347.6912	-6.8646	8.41E-37	1.59E-35	NOS2	chr17	-	26083792	26127525	4176
ENSG00000(	3.107376	2.408575	3.958241	2.996302	0	5.753754	0.07857	0.94402	0.96648	DNAH9	chr17	+	11501748	11873485	14170
ENSG00000(	1659.339	1519.811	2035.855	1507.14	1784.718	1601.188	0.091473	0.50233	0.63035	KIAA0100	chr17	-	26941458	26972472	7407
ENSG00000(	786.1661	752.6798	802.2036	845.7063	1131.211	864.7071	-0.27792	0.056396	0.10784	GAS7	chr17	-	9813926	10101868	8181
ENSG00000(	178.1562	193.8903	145.1355	188.767	130.7013	194.8057	0.007451	0.97399	0.98483	TRAPPC6A	chr19	-	45666186	45681495	805
ENSG00000(	2.071584	7.225726	2.638828	8.239831	2.761296	22.19305	-1.3026	0.14271	0.23427	MATK	chr19	-	3777971	3802127	2133
ENSG00000(	0	0	0	8.988907	0.920432	1.64393	-2.6358	0.0455	0.089462	CD79B	chr17	-	62006100	62009714	1269
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	SCN4A	chr17	-	62015914	62050278	7805
ENSG00000(	280.6996	274.5776	270.4798	186.5198	141.7465	169.3248	0.72498	0.000145	0.000463	ST7L	chr1	-	1.13E+08	1.13E+08	4528
ENSG00000(	13.46529	16.86003	18.47179	17.22874	21.16994	12.32947	-0.05572	0.92106	0.95215	PAX6	chr11	-	31806340	31839509	6922
ENSG00000(	924.9622	845.41	713.8029	1493.657	1076.905	1315.144	-0.6428	2.46E-05	8.69E-05	RPUSD1	chr16	-	834974	838397	2159
ENSG00000(	933.2485	977.8816	828.5919	438.9583	372.775	387.1455	1.1885	5.23E-17	4.58E-16	RHBDF1	chr16	-	108058	126354	2992
ENSG00000(	1158.015	1238.008	1104.349	1246.462	1198.402	1314.322	-0.10267	0.38797	0.5188	LUC7L	chr16	-	238968	279462	2737
ENSG00000(	52.82539	63.82725	42.22124	23.22134	21.16994	27.12484	1.1271	0.004209	0.010591	CACNA2D2	chr3	-	50400233	50541675	5500

ENSG00000(	23.82321	18.06432	9.235896	9.737982	16.56778	11.50751	0.4282	0.48271	0.61194	BAIAP3	chr16	+	1383602	1399439	4678
ENSG00000(	1329.957	1141.665	928.8673	1357.325	1153.301	1360.352	-0.18542	0.20912	0.31874	TSR3	chr16	-	1399241	1401912	1243
ENSG00000(	847.2778	840.5928	688.734	1325.115	1194.721	1377.613	-0.71096	1.11E-07	5.05E-07	PIGQ	chr16	+	616995	634136	3006
ENSG00000(	324.2029	350.4477	286.3128	248.6931	281.6522	347.6912	0.13093	0.47754	0.6066	CRAMP1L	chr16	+	1662326	1727909	7772
ENSG00000(	1618.943	1649.874	1402.537	1854.711	1870.318	2108.34	-0.31934	0.008443	0.019952	TEAD3	chr6	-	35441374	35464853	2983
ENSG00000(	0	0	0	1.498151	0.920432	2.465895	-1.4807	0.27499	NA	SELE	chr1	-	1.7E+08	1.7E+08	3857
ENSG00000(	742.6628	653.9282	725.6776	956.5695	1147.779	862.2412	-0.48098	0.000866	0.002451	DNAJC11	chr1	-	6694228	6761984	3311
ENSG00000(	290.0217	262.5347	281.0351	640.4596	892.819	767.7152	-1.458	5.76E-19	5.57E-18	MYLIP	chr6	+	16129356	16148479	2796
ENSG00000(	7.250543	2.408575	3.958241	10.48706	15.64734	23.01502	-1.6779	0.024239	0.05156	NOX1	chrX	-	1E+08	1E+08	2529
ENSG00000(	8.286335	7.225726	6.597069	179.7781	185.0068	175.0785	-4.4965	8.24E-30	1.25E-28	E2F2	chr1	-	23832922	23857712	5191
ENSG00000(	2878.466	2728.916	2465.984	3748.374	3738.795	4080.234	-0.51755	3.07E-06	1.21E-05	PSMB1	chr6	-	1.71E+08	1.71E+08	1939
ENSG00000(	22.78742	31.31148	30.34652	10.48706	10.12475	20.54912	0.99157	0.059959	0.11364	SYN1	chrX	-	47431303	47479252	3203
ENSG00000(	475.4285	534.7037	587.1391	627.7253	845.877	763.6054	-0.48502	0.001914	0.005117	JARID2	chr6	+	15246527	15522252	5755
ENSG00000(	21.75163	21.67718	47.4989	2.996302	20.2495	13.9734	1.2274	0.044144	0.087167	CDKL5	chrX	+	18443703	18671749	3459
ENSG00000(	0	0	0	32.95932	46.94203	41.09825	-6.1561	4.48E-09	2.32E-08	CAMK1G	chr1	+	2.1E+08	2.1E+08	2612
ENSG00000(	4.143168	2.408575	5.277655	1.498151	6.443024	4.93179	-0.09567	0.92287	0.95327	CDK11A	chr1	-	1634169	1655766	2653
ENSG00000(	1135.228	1028.462	1100.391	1393.281	1295.048	1268.292	-0.27702	0.01967	0.042742	NADK	chr1	-	1682671	1711896	3663
ENSG00000(	2.071584	0	1.319414	593.2678	622.212	614.0078	-8.3617	2.10E-38	4.16E-37	TFAP2B	chr6	+	50786436	50815326	5797
ENSG00000(	13.46529	10.83859	2.638828	0	9.20432	10.68554	0.39828	0.66459	0.76845	DLEC1	chr3	+	38080696	38165516	6426
ENSG00000(	1989.756	1835.334	2115.02	383.5267	412.3535	366.5964	2.3488	8.70E-78	4.53E-76	CYTH3	chr7	-	6201407	6312275	4505
ENSG00000(	52.82539	31.31148	68.60952	37.45378	41.41944	23.01502	0.56952	0.16555	0.26422	ADAM22	chr7	+	87563458	87832204	9334
ENSG00000(	1083.438	1247.642	1158.445	1220.993	1201.164	1183.629	-0.04769	0.6888	0.78746	SYPL1	chr7	-	1.06E+08	1.06E+08	2151
ENSG00000(	185.4068	215.5675	184.7179	855.4443	1014.316	1144.175	-2.3548	2.51E-47	6.37E-46	CYB561	chr17	-	61509665	61523739	3200
ENSG00000(	1468.753	1427.081	2078.077	1207.51	1269.276	1032.388	0.50093	0.001319	0.00363	SPAG9	chr17	-	49039535	49198226	8273
ENSG00000(	123.2592	127.6545	137.219	125.8447	233.7897	204.6693	-0.5336	0.033468	0.068374	CELSR3	chr3	-	48673902	48700348	11971
ENSG00000(	344.9187	374.5335	406.3794	161.0512	283.4931	251.5213	0.69152	0.000883	0.002497	AASS	chr7	-	1.22E+08	1.22E+08	3233
ENSG00000(	44.53905	42.15007	40.90183	265.9218	287.1748	310.7027	-2.735	8.65E-31	1.35E-29	PLEKHG6	chr12	+	6419602	6437672	3111
ENSG00000(	178.1562	171.0089	178.1209	337.8331	310.1856	393.7212	-0.97829	8.87E-08	4.09E-07	SS18L2	chr3	+	42623332	42636606	1047
ENSG00000(	120.1519	154.1488	106.8725	108.616	101.2475	134.8022	0.14399	0.56521	0.68464	MPND	chr19	+	4343524	4360083	1611
ENSG00000(	1536.079	1394.565	1236.291	3786.577	2613.106	3068.395	-1.1803	6.93E-16	5.76E-15	MGST1	chr12	+	16500076	16762193	2152
ENSG00000(	232.0174	262.5347	265.2022	477.1611	416.9557	313.9906	-0.66771	0.000423	0.001258	CRY1	chr12	-	1.07E+08	1.07E+08	3834
ENSG00000(	5.17896	12.04288	3.958241	2.247227	2.761296	5.753754	0.84994	0.35271	0.48246	PGLYRP1	chr19	-	46522411	46526323	720
ENSG00000(	9905.278	9602.99	8879.655	3.745378	5.522592	6.575719	10.654	6.59E-232	2.67E-229	NFIX	chr19	+	13106422	13209610	5530
ENSG00000(	842.0988	946.5701	939.4226	755.8172	1190.119	1145.819	-0.17946	0.28005	0.40228	ST3GAL1	chr8	-	1.34E+08	1.35E+08	6967
ENSG00000(	41.43168	78.2787	44.86007	7.490755	15.64734	7.397684	2.3634	1.11E-06	4.59E-06	MMP25	chr16	+	3096682	3110727	3554
ENSG00000(	42.46747	50.58008	42.22124	83.14739	53.38506	52.60575	-0.47923	0.16951	0.2695	IL32	chr16	+	3115298	3131908	1381
ENSG00000(	4639.312	4610.013	3950.325	824.7322	1249.947	1408.026	1.9159	1.79E-31	2.85E-30	PKD1	chr16	-	2138711	2185899	14138
ENSG00000(	167.7983	173.4174	159.6491	68.91495	70.87326	40.27628	1.4626	4.71E-08	2.23E-07	MAPK8IP2	chr22	+	51039114	51052409	5595
ENSG00000(	1329.957	1177.793	1110.946	1977.559	1567.496	1532.143	-0.48696	0.000414	0.001232	MED24	chr17	-	38175350	38217468	3896
ENSG00000(	410.1736	349.2434	296.8681	510.1204	662.711	782.5106	-0.88134	1.80E-06	7.28E-06	RHOBTB2	chr8	+	22844930	22877712	5451
ENSG00000(	426.7463	446.7907	580.5421	315.3608	294.5382	281.934	0.70003	3.76E-05	0.00013	HEATR5B	chr2	-	37195526	37311485	6905
ENSG00000(	2078.834	2148.449	2417.166	1674.933	1537.121	1610.229	0.4609	6.38E-05	0.000213	SEC62	chr3	+	1.7E+08	1.7E+08	6568
ENSG00000(	15676.71	16249.45	11992.15	14096.85	11066.35	13249.25	0.19278	0.15652	0.25256	RPS20	chr8	-	56979854	56987069	1826
ENSG00000(	12305.21	12041.67	12826.02	10272.82	10669.65	9441.089	0.29056	0.004011	0.010133	CSDE1	chr1	-	1.15E+08	1.15E+08	4167

ENSG00000(	2096.443	1994.3	2492.373	1970.069	1845.466	1713.797	0.25057	0.045296	0.089082	UBE3C	chr7	+	1.57E+08	1.57E+08	5229
ENSG00000(	1152.836	1021.236	1484.341	549.0724	567.9065	485.7813	1.1862	2.68E-14	2.02E-13	REV3L	chr6	-	1.12E+08	1.12E+08	10964
ENSG00000(	39.36009	63.82725	52.77655	71.91125	144.5078	95.34793	-0.98453	0.00326	0.008374	TENM1	chrX	-	1.24E+08	1.24E+08	12891
ENSG00000(	1.035792	1.204288	0	70.4131	106.7701	65.75719	-5.9154	1.41E-13	1.02E-12	PAX7	chr1	+	18957500	19075360	5538
ENSG00000(	74.57702	73.46155	65.97069	140.0771	75.47542	110.1433	-0.60072	0.042192	0.083855	MASP2	chr1	-	11086580	11107290	2439
ENSG00000(	81.82756	97.54731	97.63662	176.0328	178.5638	120.0069	-0.77235	0.00224	0.005916	FAM76A	chr1	+	28052490	28089633	3567
ENSG00000(	35.21692	46.96722	62.01245	63.67142	38.65814	44.38611	-0.03567	0.92412	0.95401	TRAF3IP3	chr1	+	2.1E+08	2.1E+08	3302
ENSG00000(	692.9448	566.0152	655.7486	731.0977	700.4487	800.5938	-0.22032	0.11629	0.19871	POMT2	chr14	-	77741299	77787227	5647
ENSG00000(	840.0272	710.5298	916.9926	1397.775	1164.346	1067.732	-0.55591	0.000165	0.000522	VTA1	chr6	+	1.42E+08	1.43E+08	3287
ENSG00000(	2.071584	6.021439	0	0	0.920432	0	1.795	0.17829	0.28076	MLXIPL	chr7	-	73007524	73038873	3278
ENSG00000(	2122.338	2200.234	2396.055	2680.192	3955.096	3568.15	-0.60109	2.41E-05	8.52E-05	BAZ1B	chr7	-	72854728	72936608	6102
ENSG00000(	493.0369	562.4024	692.6922	959.5658	929.6363	981.4261	-0.7159	1.32E-06	5.40E-06	RANBP9	chr6	-	13621730	13711796	3113
ENSG00000(	3.107376	10.83859	3.958241	14.23244	14.72691	19.72716	-1.3413	0.060353	0.1142	ETV7	chr6	-	36322419	36356164	2157
ENSG00000(	211.3015	197.5032	219.0227	367.047	351.605	348.5131	-0.76296	6.45E-06	2.45E-05	SPRTN	chr1	+	2.31E+08	2.31E+08	3559
ENSG00000(	580.0435	573.241	572.6256	1103.388	960.931	971.5625	-0.81322	4.38E-10	2.47E-09	METTL13	chr1	+	1.72E+08	1.72E+08	3327
ENSG00000(	217.5163	228.8147	209.7868	194.0106	185.9273	180.8323	0.22542	0.22929	0.34272	DYRK4	chr12	+	4671370	4723325	1816
ENSG00000(	1965.933	2023.203	2021.342	3496.685	2493.45	2722.348	-0.53471	7.54E-05	0.00025	ZNF207	chr17	+	30677136	30708905	13781
ENSG00000(	3560.017	3246.76	3121.733	4524.416	3958.778	3796.656	-0.30594	0.007954	0.018905	UQCRC1	chr3	-	48636435	48648409	1985
ENSG00000(	742.6628	750.2712	720.3999	1139.344	936.9998	999.5093	-0.4741	0.000302	0.000917	STARD3NL	chr7	+	38217824	38270272	3653
ENSG00000(	678.4437	593.7138	583.1809	5362.632	4383.097	4936.721	-2.9767	1.51E-125	1.68E-123	CD9	chr12	+	6308881	6347425	1554
ENSG00000(	5.17896	0	0	0	0	0	1.5469	0.24589	NA	HHATL	chr3	-	42734155	42744319	1865
ENSG00000(	1075.152	1012.806	1122.821	3105.667	2860.703	2756.87	-1.4397	1.92E-36	3.58E-35	NCAPD2	chr12	+	6602522	6641121	5548
ENSG00000(	1220.163	1136.848	1027.823	253.9366	281.6522	301.6611	2.0114	2.47E-45	5.96E-44	IFFO1	chr12	-	6647541	6665239	3101
ENSG00000(	3.107376	8.430014	1.319414	5.992604	7.363456	4.109825	-0.37585	0.68782	0.78668	GIPR	chr19	+	46171502	46186982	3289
ENSG00000(	37.28851	39.74149	15.83297	70.4131	73.63456	71.51095	-1.1796	0.001716	0.004625	PHF7	chr3	+	52443510	52457657	2130
ENSG00000(	0	0	3.958241	1.498151	0	2.465895	-0.02846	0.98306	0.99027	SEMA3G	chr3	-	52467069	52479101	4899
ENSG00000(	3709.171	3203.405	3239.161	2001.53	2109.63	1788.596	0.78195	3.58E-11	2.19E-10	NISCH	chr3	+	52489134	52527087	5350
ENSG00000(	2.071584	1.204288	0	0.749076	0	2.465895	0.026614	0.98418	0.99091	STAB1	chr3	+	52529354	52558511	7928
ENSG00000(	207.1584	260.1261	166.2461	160.3022	203.4155	189.0519	0.19831	0.36186	0.49152	FUZ	chr19	-	50310126	50320633	1675
ENSG00000(	4.143168	1.204288	2.638828	1.498151	0	0.821965	1.1996	0.34066	0.46938	SLC6A13	chr12	-	329789	372039	2185
ENSG00000(	1621.014	1574.004	1692.808	1623.996	1529.758	1361.996	0.11372	0.33946	0.46808	IDS	chrX	-	1.49E+08	1.49E+08	7619
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	PRSS3	chr9	+	33750515	33799230	966
ENSG00000(	148.1182	146.9231	158.3297	188.767	139.9057	187.408	-0.18858	0.38649	0.51735	ZNF200	chr16	-	3272325	3286221	4308
ENSG00000(	12.4295	19.2686	3.958241	0	2.761296	1.64393	2.6067	0.00624	0.015162	CD4	chr12	+	6896024	6929974	3114
ENSG00000(	97.36444	66.23582	75.20659	36.7047	54.30549	59.18147	0.66586	0.041748	0.083092	LRRC23	chr12	+	6982733	7023407	1629
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	BTK	chrX	-	1.01E+08	1.01E+08	2579
ENSG00000(	188.5141	204.7289	234.8557	100.3761	84.67974	110.1433	1.078	1.16E-06	4.78E-06	HFE	chr6	+	26087509	26098571	5286
ENSG00000(	707.4459	741.8412	616.1662	480.1574	417.8761	392.8992	0.67592	6.36E-06	2.42E-05	SCMH1	chr1	-	41492872	41707826	3346
ENSG00000(	1193.232	1358.437	1163.723	2335.618	2191.549	2073.817	-0.82764	4.05E-12	2.66E-11	FYN	chr6	-	1.12E+08	1.12E+08	3628
ENSG00000(	686.73	612.9824	1000.116	127.3428	152.7917	124.1167	2.4956	1.15E-36	2.16E-35	HIVEP2	chr6	-	1.43E+08	1.43E+08	9723
ENSG00000(	5.17896	0	2.638828	0.749076	0	0	1.8265	0.17243	0.27352	FMO1	chr1	+	1.71E+08	1.71E+08	3130
ENSG00000(	748.8775	708.1212	819.356	1348.336	1234.299	1057.047	-0.67604	8.66E-07	3.62E-06	TCEB3	chr1	+	24069645	24088549	5154
ENSG00000(	1534.008	1372.888	1312.817	2449.477	2068.211	2428.906	-0.71726	6.11E-09	3.13E-08	LYPLA2	chr1	+	24117460	24122029	1810
ENSG00000(	849.3494	821.3242	853.6607	453.1907	566.0657	528.5234	0.70506	3.97E-07	1.72E-06	CLCN6	chr1	+	11866207	11903201	5583

ENSG00000(	19948.32	19975.52	17594.38	1628.49	2249.536	2412.467	3.1847	7.37E-115	7.18E-113	MRC2	chr17	+	60704762	60770958	5988
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	SLC6A7	chr5	+	1.5E+08	1.5E+08	3739
ENSG00000(	1272.988	1103.128	1224.416	909.3777	1267.435	1488.578	-0.02505	0.87858	0.92417	TSPAN9	chr12	+	3186521	3395730	4323
ENSG00000(	976.7518	846.6143	1316.775	651.6957	834.8318	653.4621	0.55086	0.001284	0.003541	BTBD7	chr14	-	93703896	93799438	8430
ENSG00000(	292.0933	286.6205	174.1626	419.4823	275.2092	318.9224	-0.42438	0.056475	0.10798	APBA3	chr19	-	3750817	3761697	4250
ENSG00000(	96.32865	167.396	126.6637	268.169	214.4607	263.0288	-0.9315	5.41E-05	0.000183	MKS1	chr17	-	56282803	56296966	2392
ENSG00000(	166.7625	122.8373	176.8014	260.6783	201.5746	266.3166	-0.64098	0.003025	0.007811	ABHD5	chr3	+	43731605	43775863	1690
ENSG00000(	41.43168	65.03154	36.94359	173.0365	196.9724	129.8705	-1.7792	1.24E-09	6.73E-09	KAL1	chrX	-	8496915	8700227	6314
ENSG00000(	814.1324	664.7668	705.8864	758.0645	486.9085	578.6633	0.25896	0.1299	0.21711	AKAP8L	chr19	-	15490861	15529952	2749
ENSG00000(	389.4578	428.7264	419.5736	332.5895	381.9793	278.6461	0.31671	0.060834	0.11499	MBTD1	chr17	-	49254786	49337524	5382
ENSG00000(	654.6205	610.5739	616.1662	1050.204	1034.566	1059.513	-0.73885	2.38E-09	1.26E-08	UTP18	chr17	+	49337889	49375297	1894
ENSG00000(	1359.995	1164.546	1271.915	1029.23	1069.542	994.5776	0.29548	0.01531	0.034111	RNF216	chr7	-	5659678	5821370	5639
ENSG00000(	666.0142	687.6483	742.83	1111.628	1032.725	1022.524	-0.59492	2.34E-06	9.32E-06	TTC19	chr17	+	15902694	15948329	3075
ENSG00000(	6660.142	6309.263	6044.235	13310.32	14089.97	13900.25	-1.1175	1.45E-29	2.16E-28	PTBP1	chr19	+	797075	812327	4661
ENSG00000(	83.89914	72.25726	80.48424	29.21395	35.89685	50.96182	1.0139	0.002533	0.006627	DPF1	chr19	-	38701646	38720354	2341
ENSG00000(	15.53688	24.08575	21.11062	716.1162	1086.11	927.1764	-5.4496	2.59E-94	1.79E-92	SYT7	chr11	-	61282785	61348620	4854
ENSG00000(	394.6367	402.2321	366.797	675.6661	721.6187	662.5037	-0.82055	5.07E-09	2.62E-08	LARS2	chr3	+	45429998	45590913	4744
ENSG00000(	831.7409	829.7542	1175.598	1655.457	1803.126	1497.62	-0.80354	1.34E-07	6.09E-07	PIK3C2A	chr11	-	17099277	17229530	8227
ENSG00000(	1247.093	1335.555	1159.765	549.0724	347.9233	413.4484	1.5064	3.77E-20	3.84E-19	PLAUR	chr19	-	44150247	44174699	1610
ENSG00000(	785.1303	597.3267	861.5772	3374.585	3149.718	2614.67	-2.0201	3.05E-41	6.50E-40	ANLN	chr7	+	36429415	36493400	4787
ENSG00000(	2757.278	2455.543	2471.262	1925.124	1817.853	1731.88	0.48843	1.44E-05	5.26E-05	WIZ	chr19	-	15530792	15560762	6738
ENSG00000(	1663.482	1729.357	1833.985	847.2044	1156.063	969.9186	0.81255	2.51E-09	1.33E-08	RABGAP1	chr9	+	1.26E+08	1.26E+08	4997
ENSG00000(	9773.732	10320.75	8324.182	3436.01	2622.311	2875.233	1.6655	9.54E-38	1.85E-36	DCN	chr12	-	91539025	91576900	2924
ENSG00000(	504.4307	517.8437	414.2959	435.962	402.2288	353.4449	0.26962	0.094775	0.16769	QPCTL	chr19	+	46195741	46207247	2310
ENSG00000(	1803.314	1763.077	1768.014	1824.748	1611.676	1719.551	0.048757	0.66232	0.76658	PPP5C	chr19	+	46850251	46896238	4675
ENSG00000(	483.7148	454.0165	455.1978	226.2208	235.6306	211.245	1.0467	3.99E-11	2.43E-10	CEP68	chr2	+	65283500	65314138	5847
ENSG00000(	374.9567	398.6192	494.7802	842.71	816.4232	734.8366	-0.91612	1.63E-09	8.74E-09	MAP4K3	chr2	-	39476407	39664453	4362
ENSG00000(	5.17896	9.634302	11.87472	5.243529	0	5.753754	1.0873	0.23554	0.34992	ZBTB32	chr19	+	36195429	36207940	2068
ENSG00000(	421.5673	422.705	353.6029	391.7665	404.9901	383.8576	0.022601	0.88423	0.92775	TMEM159	chr16	+	21169698	21191937	2014
ENSG00000(	0	2.408575	0	226.9699	183.166	156.9953	-7.0844	4.01E-21	4.25E-20	GABRA3	chrX	-	1.51E+08	1.52E+08	3712
ENSG00000(	118.0803	116.8159	157.0102	749.0755	767.6403	679.765	-2.482	5.01E-47	1.26E-45	BRCA1	chr17	-	41196312	41322290	7114
ENSG00000(	1501.898	1415.038	1209.902	761.0608	687.5627	812.1013	0.86646	1.09E-10	6.47E-10	ERCC1	chr19	-	45910591	45982086	3828
ENSG00000(	161.5835	142.106	114.789	173.7855	174.8821	207.9571	-0.4046	0.066656	0.12444	SEMA3B	chr3	+	50304990	50314977	3283
ENSG00000(	437.1042	438.3607	630.6798	282.4015	367.2524	333.7178	0.6115	0.000936	0.002634	MBTPS2	chrX	+	21857754	21903542	4457
ENSG00000(	194.7289	195.0946	167.5656	293.6376	280.7318	232.6161	-0.52961	0.005833	0.014255	PRICKLE3	chrX	-	49031151	49042845	2814
ENSG00000(	3269.995	2907.151	3307.77	1632.236	1800.365	1563.377	0.92348	1.16E-15	9.48E-15	EXTL3	chr8	+	28457986	28613116	8257
ENSG00000(	3662.56	3638.153	4476.771	1725.87	1664.141	1531.321	1.256	8.70E-25	1.07E-23	ELOVL5	chr6	-	53132196	53213947	3070
ENSG00000(	0	0	0	2.247227	1.840864	3.28786	-2.048	0.1277	0.21422	ALOX5	chr10	+	45869661	45941561	2504
ENSG00000(	747.8418	598.531	773.1765	510.1204	496.1128	544.9627	0.44883	0.00239	0.006284	KDM5D	chrY	-	21865751	21906825	5579
ENSG00000(	808.9535	882.7429	777.1347	216.4828	239.3123	252.3432	1.7975	2.57E-34	4.51E-33	CALCOCO1	chr12	-	54104903	54121529	3888
ENSG00000(	242.3753	270.9647	312.7011	764.8061	628.6551	533.4552	-1.2199	5.43E-12	3.53E-11	UBR7	chr14	+	93673401	93695561	3694
ENSG00000(	934.2843	1073.02	1278.512	801.5108	783.2876	691.2725	0.52688	0.000298	0.000908	MAP4K5	chr14	-	50885219	51027844	4812
ENSG00000(	574.8645	491.3494	593.7362	499.6334	561.4635	568.7997	0.026726	0.85532	0.90803	EHD3	chr2	+	31456880	31492313	4636
ENSG00000(	1249.165	1258.481	1225.735	2587.307	1784.718	2105.052	-0.79314	1.92E-08	9.45E-08	PSMC4	chr19	+	40476912	40487348	1623

ENSG0000(	1761.882	1645.057	1787.806	719.1125	741.8682	698.6702	1.2641	2.24E-27	3.06E-26	MAN2B2	chr4	+	6576902	6625089	7719
ENSG0000(	131.5456	119.2245	234.8557	5.243529	0.920432	2.465895	5.5378	8.95E-28	1.24E-26	SLC7A14	chr3	-	1.7E+08	1.7E+08	5122
ENSG0000(	6510.988	6092.492	5169.463	89.13999	69.0324	55.89361	6.3468	0	0	CLDN11	chr3	+	1.7E+08	1.71E+08	2169
ENSG0000(	2804.924	2860.183	2278.628	2898.922	2312.125	2761.802	-0.00517	0.96872	0.98169	SLC25A39	chr17	-	42396993	42402238	2217
ENSG0000(	6811.368	6617.561	5823.892	309.3682	292.6974	316.4565	4.3807	3.07E-297	2.19E-294	MVP	chr16	+	29831715	29859355	2865
ENSG0000(	512.717	488.9408	542.2791	525.102	589.9969	562.224	-0.11904	0.397	0.52808	NUB1	chr7	+	1.51E+08	1.51E+08	3210
ENSG0000(	1082.403	1156.116	1209.902	629.9725	640.6207	567.9778	0.90492	1.33E-12	9.06E-12	PGM3	chr6	-	83870869	83903655	6107
ENSG0000(	88.04231	85.50443	67.2901	70.4131	67.19154	61.64737	0.27317	0.34583	0.47527	RWDD2A	chr6	+	83903098	83906382	2192
ENSG0000(	720.9112	786.3999	713.8029	602.2567	476.7838	475.0957	0.51247	0.000528	0.001547	CLK1	chr2	-	2.02E+08	2.02E+08	3208
ENSG0000(	186.4425	163.7831	248.0498	265.9218	301.9017	244.1236	-0.4402	0.031441	0.064773	POLR3B	chr12	+	1.07E+08	1.07E+08	4273
ENSG0000(	332.4892	321.5448	291.5904	200.0032	269.6866	229.3282	0.43726	0.01671	0.036925	ANGEL1	chr14	-	77253588	77292589	4109
ENSG0000(	643.2268	631.0468	724.3582	675.6661	613.9281	507.9743	0.15147	0.31583	0.44253	RNF14	chr5	+	1.41E+08	1.41E+08	4235
ENSG0000(	268.2701	260.1261	314.0205	49.43899	48.7829	60.8254	2.3868	2.53E-26	3.30E-25	DNASE1L1	chrX	-	1.54E+08	1.54E+08	3008
ENSG0000(	232.0174	250.4918	191.315	1062.189	990.3848	1162.258	-2.2449	9.49E-49	2.54E-47	DDX11	chr12	+	31226779	31257725	4182
ENSG0000(	804.8103	814.0985	738.8717	1015.746	823.7866	1157.327	-0.34516	0.019311	0.04204	HEBP1	chr12	-	13127798	13153207	2056
ENSG0000(	111.8655	111.9988	121.3861	460.6815	390.2632	332.0738	-1.7692	5.69E-19	5.50E-18	GPRC5A	chr12	+	13043716	13070871	7362
ENSG0000(	16.57267	15.65574	29.0271	48.68991	40.49901	43.56414	-1.0982	0.012182	0.027773	MAMLD1	chrX	+	1.5E+08	1.5E+08	4854
ENSG0000(	0	0	0	0.749076	1.840864	3.28786	-1.711	0.20694	NA	CD6	chr11	+	60739115	60787849	3252
ENSG0000(	563.4708	467.2636	472.3501	2409.776	2496.212	2426.44	-2.2793	5.63E-75	2.71E-73	TACC3	chr4	+	1723227	1746898	2781
ENSG0000(	567.614	611.7782	697.9699	544.5779	589.0765	411.8044	0.27898	0.091842	0.16346	UFL1	chr6	+	96969471	97003152	4224
ENSG0000(	242.3753	171.0089	234.8557	1078.669	956.3288	905.8053	-2.1727	6.44E-40	1.33E-38	POLA2	chr11	+	65029233	65073060	3744
ENSG0000(	650.4773	604.5524	522.4879	853.9461	802.6167	789.0863	-0.45768	0.000949	0.002669	ZC3H3	chr8	-	1.45E+08	1.45E+08	3280
ENSG0000(	3850.039	3633.336	3266.869	5133.415	4843.313	5489.082	-0.52355	2.79E-06	1.10E-05	CAPN1	chr11	+	64948037	64979477	3086
ENSG0000(	1.035792	0	3.958241	40.45008	52.46462	34.52253	-4.3189	6.43E-09	3.29E-08	ACPP	chr3	+	1.32E+08	1.32E+08	3125
ENSG0000(	1892.392	1686.003	1620.24	3060.723	2720.797	2692.757	-0.70318	2.19E-09	1.16E-08	MDH1	chr2	+	63815743	63834331	1650
ENSG0000(	893.8884	958.613	1105.669	1227.735	1170.789	1006.085	-0.20341	0.13735	0.22723	SLC30A9	chr4	+	41992489	42089551	3295
ENSG0000(	328.346	301.0719	316.6593	179.0291	188.6886	202.2034	0.72899	3.24E-05	0.000113	MTMR11	chr1	-	1.5E+08	1.5E+08	3332
ENSG0000(	659.7994	662.3582	576.5838	750.5737	728.0617	719.2193	-0.20968	0.11509	0.19697	COX15	chr10	-	1.01E+08	1.01E+08	2788
ENSG0000(	17.60846	14.45145	27.70769	450.1944	650.7454	537.5651	-4.7427	4.94E-66	1.98E-64	CCDC88C	chr14	-	91737667	91884188	7474
ENSG0000(	105.6508	110.7945	138.5384	147.5679	123.3379	125.7606	-0.16383	0.49061	0.61965	YAF2	chr12	-	42550906	42632151	5095
ENSG0000(	727.1259	762.3141	936.7838	945.3333	860.6039	751.2759	-0.07718	0.60247	0.71756	ZMYND11	chr10	+	180405	300577	4393
ENSG0000(	7.250543	9.634302	18.47179	2.996302	17.48821	14.79537	0.001226	0.99865	0.99905	WAS	chrX	+	48534985	48549818	1849
ENSG0000(	0	0	0	1.498151	11.04518	5.753754	-3.3468	0.007777	0.018541	DPEP1	chr16	+	89679716	89704839	1772
ENSG0000(	482.679	369.7163	395.8241	698.8875	556.8614	540.031	-0.52173	0.001721	0.004636	BID	chr22	-	18216906	18257536	2493
ENSG0000(	4797.788	4801.495	5491.4	6585.123	6007.66	5204.682	-0.23776	0.048272	0.094116	MATR3	chr5	+	1.39E+08	1.39E+08	7306
ENSG0000(	1.035792	2.408575	2.638828	0	0.920432	3.28786	0.3588	0.77621	0.85302	NPC1L1	chr7	-	44552134	44580914	5048
ENSG0000(	1109.333	1133.235	1093.794	442.7036	476.7838	513.7281	1.2167	4.34E-21	4.59E-20	XYLT2	chr17	+	48423453	48440499	3507
ENSG0000(	4.143168	8.430014	7.916483	12.73428	8.283888	5.753754	-0.36433	0.64022	0.7481	RGPD5	chr2	+	1.11E+08	1.11E+08	7253
ENSG0000(	0	2.408575	2.638828	0.749076	0	0	1.296	0.33942	NA	STMN4	chr8	-	27092840	27115937	2288
ENSG0000(	1619.979	1561.961	1618.921	1289.908	1299.65	1234.591	0.32767	0.003165	0.008147	NUDCD3	chr7	-	44421969	44530479	5007
ENSG0000(	46.61064	38.53721	31.66593	369.2942	335.0372	348.5131	-3.1362	1.20E-40	2.54E-39	ISL1	chr5	+	50678921	50690564	2755
ENSG0000(	11.39371	1.204288	11.87472	40.45008	26.69253	70.68898	-2.368	5.52E-05	0.000186	CHDH	chr3	-	53850387	53880417	3640
ENSG0000(	0	0	0	1.498151	0.920432	2.465895	-1.4807	0.27499	NA	IL20RA	chr6	-	1.37E+08	1.37E+08	3503
ENSG0000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	CLCA1	chr1	+	86934051	86965972	3310

ENSG00000(	1009.897	1095.902	1013.31	742.3339	551.3388	623.8714	0.69859	1.00E-06	4.16E-06	GLT8D1	chr3	-	52728505	52740048	2320
ENSG00000(	2075.727	2015.978	2518.761	1692.162	1794.842	1548.582	0.39139	0.002066	0.005493	ATP2C1	chr3	+	1.31E+08	1.31E+08	5067
ENSG00000(	0	0	1.319414	56.92974	72.71413	68.22309	-6.1166	1.15E-11	7.28E-11	SRCIN1	chr17	-	36686251	36762183	7058
ENSG00000(	3.107376	9.634302	6.597069	23.22134	13.80648	21.37109	-1.5068	0.024956	0.052884	IGF1	chr12	-	1.03E+08	1.03E+08	7370
ENSG00000(	88.04231	104.773	88.40072	85.39461	56.14635	60.00344	0.47059	0.10661	0.18487	SLC38A5	chrX	-	48316920	48328644	2662
ENSG00000(	26.93059	13.24716	26.38828	15.73059	5.522592	19.72716	0.65774	0.26853	0.38882	MAGIX	chrX	+	49019061	49024822	2991
ENSG00000(	1811.6	1661.917	1706.002	1486.915	1357.637	1437.617	0.274	0.015391	0.034269	RALBP1	chr18	+	9475007	9538114	4368
ENSG00000(	1004.718	1027.257	1158.445	494.3899	571.5883	543.3188	0.98505	1.70E-13	1.23E-12	RUFY3	chr4	+	71569921	71673032	4233
ENSG00000(	36.25272	37.33292	36.94359	35.95563	48.7829	60.00344	-0.37971	0.316	0.44274	CNTN1	chr12	+	41086244	41466220	5557
ENSG00000(	1.035792	0	1.319414	0	7.363456	0	-0.94591	0.47828	0.60737	SLC11A1	chr2	+	2.19E+08	2.19E+08	5772
ENSG00000(	2782.137	2804.786	3330.2	1429.236	1613.517	1288.019	1.0396	5.73E-16	4.79E-15	WWTR1	chr3	-	1.49E+08	1.49E+08	5030
ENSG00000(	307.6302	417.8878	428.8095	1118.37	1400.897	1153.217	-1.6664	2.01E-25	2.53E-24	AGPS	chr2	+	1.78E+08	1.78E+08	7764
ENSG00000(	0	3.612863	0	1.498151	0.920432	2.465895	-0.27842	0.8321	0.89251	ZNF806	chr2	+	1.33E+08	1.33E+08	1774
ENSG00000(	316.9523	251.6961	267.841	449.4453	351.605	379.7478	-0.4944	0.004975	0.012329	CXorf56	chrX	-	1.19E+08	1.19E+08	2372
ENSG00000(	151.2256	131.2674	142.4967	17.97781	48.7829	25.48091	2.1852	5.84E-11	3.51E-10	ATP1A2	chr1	+	1.6E+08	1.6E+08	5421
ENSG00000(	418.4599	378.1463	345.6864	585.028	482.3064	527.7015	-0.47907	0.002145	0.005685	TTC27	chr2	+	32853099	33046118	2876
ENSG00000(	24.85901	61.41867	31.66593	66.66772	58.90765	53.42772	-0.59414	0.12642	0.21252	ZNF582	chr19	-	56887413	56904914	2824
ENSG00000(	0	0	0	2.996302	1.840864	0	-1.3549	0.31496	NA	VSIG2	chr11	-	1.25E+08	1.25E+08	1191
ENSG00000(	4268.498	4528.122	4199.694	575.29	956.3288	916.4909	2.4011	1.45E-50	4.07E-49	PHLDB1	chr11	+	1.18E+08	1.19E+08	5945
ENSG00000(	0	0	0	0	2.761296	3.28786	-1.6293	0.2296	0.34285	MARCO	chr2	+	1.2E+08	1.2E+08	1843
ENSG00000(	20.71584	36.12863	17.15238	67.4168	65.35067	49.3179	-1.2689	0.001673	0.004516	CYP24A1	chr20	-	52769988	52790512	3262
ENSG00000(	89.0781	67.44011	100.2754	30.7121	57.98722	37.81039	1.0113	0.002967	0.007671	PRDM11	chr11	+	45115564	45247734	3111
ENSG00000(	7.250543	1.204288	0	14.98151	4.60216	4.109825	-1.2054	0.23103	0.34437	SYT13	chr11	-	45261852	45307870	5144
ENSG00000(	6999.882	7099.276	7143.306	1084.661	1125.688	988.0018	2.7276	8.30E-147	1.22E-144	SNAI2	chr8	-	49830249	49834299	2204
ENSG00000(	2.071584	4.817151	0	157.3059	149.11	161.9271	-5.7505	1.07E-23	1.25E-22	CD74	chr5	-	1.5E+08	1.5E+08	1727
ENSG00000(	392.5651	378.1463	431.4483	0	0	0	9.5558	3.60E-25	4.48E-24	HGF	chr7	-	81328322	81399754	5989
ENSG00000(	547.9339	586.4881	628.041	528.8473	456.5343	417.5582	0.32642	0.030715	0.063447	ZRANB1	chr10	+	1.27E+08	1.27E+08	5695
ENSG00000(	1121.763	1205.492	1151.848	580.5336	623.1325	655.106	0.90261	5.60E-13	3.90E-12	NCDN	chr1	+	36023074	36032875	3683
ENSG00000(	3884.22	3627.315	3356.589	112.3613	162.9165	167.6808	4.6075	3.83E-206	1.20E-203	GPR124	chr8	+	37641709	37702414	6270
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CCT8L1P	chr7	+	1.52E+08	1.52E+08	1674
ENSG00000(	341.8113	340.8134	303.4652	524.3529	466.659	455.3686	-0.55019	0.000396	0.001182	ZFP64	chr20	-	50668202	50820847	3264
ENSG00000(	166.7625	164.9874	182.0791	276.4089	279.8113	257.275	-0.66084	0.000345	0.001041	MNAT1	chr14	+	61201460	61436671	2635
ENSG00000(	506.5022	460.0379	509.2937	1570.811	2334.216	1994.087	-1.992	1.09E-38	2.17E-37	SAMD4A	chr14	+	55033815	55260033	6565
ENSG00000(	63.18331	68.6444	46.17948	244.1986	236.551	212.0669	-1.9395	6.95E-16	5.78E-15	RUNX3	chr1	-	25226002	25291612	4340
ENSG00000(	167.7983	193.8903	163.6073	346.822	386.5814	289.3317	-0.95577	5.38E-07	2.30E-06	MRE11A	chr11	-	94152895	94227074	2746
ENSG00000(	6.214751	3.612863	6.597069	9.737982	6.443024	16.4393	-0.9017	0.24894	0.36609	PLEKHB1	chr11	+	73357223	73373864	2380
ENSG00000(	162.6193	125.2459	130.622	158.804	156.4734	125.7606	-0.07209	0.75304	0.83667	SERPINB1	chr6	-	2832566	2842240	2619
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CYP3A43	chr7	+	99425636	99463718	1848
ENSG00000(	15.53688	2.408575	11.87472	14.23244	4.60216	10.68554	0.011989	0.98752	0.99251	SLC7A9	chr19	-	33321415	33360672	1998
ENSG00000(	340.7755	299.8676	348.3252	339.3312	327.6738	277.8241	0.065439	0.69924	0.79551	SPAST	chr2	+	32288680	32382706	5117
ENSG00000(	128.4382	105.9773	120.0667	220.2282	329.5147	261.3848	-1.183	7.63E-08	3.54E-07	NRXN3	chr14	+	78708734	80330762	6446
ENSG00000(	998.5034	1034.483	938.1032	375.2868	370.9341	420.0241	1.3459	1.50E-23	1.75E-22	OSBPL5	chr11	-	3108346	3187969	3889
ENSG00000(	418.4599	517.8437	618.8051	1071.927	1073.224	847.4458	-0.94331	1.06E-08	5.31E-08	AQR	chr15	-	35147732	35262040	5945
ENSG00000(	163.6551	158.966	164.9267	163.2985	175.8025	140.556	0.024136	0.90837	0.94364	CPS1	chr2	+	2.11E+08	2.12E+08	5821

ENSG00000(	5354.008	5215.77	5435.985	465.925	378.2976	349.3351	3.7354	3.24E-190	8.36E-188	FHL1	chrX	+	1.35E+08	1.35E+08	2888
ENSG00000(	1278.167	1293.405	1215.18	988.0306	1046.531	1080.062	0.28182	0.016328	0.036159	RTFDC1	chr20	+	55043647	55093943	2193
ENSG00000(	0	0	1.319414	1.498151	0	0	-0.08979	0.94423	NA	GABRA1	chr5	+	1.61E+08	1.61E+08	4273
ENSG00000(	32.10955	30.10719	26.38828	1219.495	1038.247	1008.551	-5.1624	2.59E-123	2.81E-121	NLRP2	chr19	+	55464498	55512510	3744
ENSG00000(	94.25706	80.68728	75.20659	132.5864	158.3143	179.1884	-0.89769	0.000296	0.000901	SLC45A4	chr8	-	1.42E+08	1.42E+08	7483
ENSG00000(	2915.754	2696.4	2559.663	2670.454	2335.136	2465.073	0.12931	0.25244	0.37018	RNF10	chr12	+	1.21E+08	1.21E+08	3825
ENSG00000(	145.0109	227.6104	137.219	251.6894	242.994	217.8207	-0.47994	0.031818	0.065429	ZNF839	chr14	+	1.03E+08	1.03E+08	3325
ENSG00000(	484.7506	444.3822	452.5589	642.7068	485.9881	482.4934	-0.22147	0.16917	0.26908	ZDHHC6	chr10	-	1.14E+08	1.14E+08	2170
ENSG00000(	54.89697	49.3758	91.03955	20.97412	18.40864	22.19305	1.6217	4.72E-05	0.000161	GRAMD1B	chr11	+	1.23E+08	1.23E+08	7723
ENSG00000(	4168.027	4025.934	3522.835	3476.46	2486.087	3019.077	0.38244	0.004717	0.011745	RNH1	chr11	-	494512	507300	3281
ENSG00000(	1084.474	980.2902	1267.957	1302.642	1429.431	1278.977	-0.26707	0.043822	0.086655	NDUFS1	chr2	-	2.07E+08	2.07E+08	5211
ENSG00000(	407.0662	466.0593	584.5003	368.5452	458.3751	324.6761	0.33751	0.065999	0.12337	RB1CC1	chr8	-	53535016	53658403	6635
ENSG00000(	809.9893	788.8085	858.9384	1446.465	1253.628	1285.553	-0.69679	2.20E-08	1.08E-07	ERP44	chr9	-	1.03E+08	1.03E+08	4854
ENSG00000(	734.3765	697.2826	738.8717	1010.503	850.4792	867.995	-0.33014	0.012604	0.028634	ALAS1	chr3	+	52232102	52248343	2430
ENSG00000(	8.286335	7.225726	7.916483	45.69361	47.86246	46.03004	-2.4789	9.23E-07	3.84E-06	BIRC3	chr11	+	1.02E+08	1.02E+08	5197
ENSG00000(	1216.02	1106.74	1818.152	662.1828	856.0018	585.239	0.97249	1.81E-07	8.09E-07	AKAP11	chr13	+	42846289	42897396	9913
ENSG00000(	167.7983	175.826	207.148	258.4311	218.1424	318.1004	-0.52913	0.010191	0.023653	GLRX2	chr1	-	1.93E+08	1.93E+08	1131
ENSG00000(	200.9436	228.8147	221.6615	232.9625	171.2004	188.23	0.13295	0.50716	0.63468	SNAPC1	chr14	+	62229075	62263146	2656
ENSG00000(	304.5228	267.3519	320.6175	841.2118	694.0057	736.4806	-1.3446	1.85E-18	1.74E-17	DERA	chr12	+	16064106	16190220	1709
ENSG00000(	3152.951	3328.651	3514.918	4529.66	4217.419	4247.915	-0.37825	0.000306	0.000929	STRAP	chr12	+	16035325	16056412	1866
ENSG00000(	65.25489	55.39724	58.05421	121.3502	142.667	132.3364	-1.1344	1.73E-05	6.25E-05	ABCC2	chr10	+	1.02E+08	1.02E+08	5312
ENSG00000(	31.07376	31.31148	13.19414	56.92974	43.2603	46.03004	-0.91863	0.031139	0.064242	DEF6	chr6	+	35265595	35289548	2262
ENSG00000(	1340.315	1212.718	1101.711	1047.957	982.1009	874.5707	0.3313	0.012458	0.028351	PLEKHO1	chr1	+	1.5E+08	1.5E+08	3743
ENSG00000(	522.0391	534.7037	625.4021	1022.488	912.1481	842.514	-0.72304	3.72E-07	1.62E-06	GCLM	chr1	-	94350761	94374966	4857
ENSG00000(	506.5022	480.5108	556.7926	432.9657	539.3732	480.0275	0.088295	0.56084	0.68124	UBR2	chr6	+	42531800	42661242	7857
ENSG00000(	10884.1	10414.68	9606.652	654.692	577.1109	539.209	4.1169	6.82E-274	4.11E-271	EHD2	chr19	+	48216600	48246391	3585
ENSG00000(	203.0152	189.0732	224.3003	1016.496	995.9074	941.9718	-2.2559	1.80E-53	5.36E-52	DEPDC1	chr1	-	68939835	68962904	5331
ENSG00000(	64.2191	55.39724	75.20659	169.2911	133.4626	141.378	-1.1817	6.06E-06	2.31E-05	CCDC28A	chr6	+	1.39E+08	1.39E+08	1496
ENSG00000(	8.286335	16.86003	2.638828	79.40201	65.35067	52.60575	-2.72	3.58E-08	1.72E-07	RRAGD	chr6	-	90074355	90121989	4900
ENSG00000(	244.4469	254.1047	292.9099	301.8774	219.9832	225.2184	0.079282	0.68312	0.7832	HSF2	chr6	+	1.23E+08	1.23E+08	2643
ENSG00000(	739.5554	746.6584	829.9113	680.9097	680.1992	565.5119	0.26432	0.058418	0.11117	PHF20	chr20	+	34359896	34538303	5922
ENSG00000(	10.35792	9.634302	5.277655	14.98151	13.80648	13.15144	-0.6737	0.31331	0.43976	HSD17B6	chr12	+	57145945	57181574	1751
ENSG00000(	71.46964	73.46155	47.4989	221.7264	163.8369	175.9005	-1.5257	4.81E-09	2.49E-08	NR1H3	chr11	+	47269851	47290396	2731
ENSG00000(	42.46747	40.94578	31.66593	6.74168	15.64734	13.15144	1.6503	0.000908	0.002562	TYMP	chr22	-	50964181	50968485	2049
ENSG00000(	570.7213	649.1111	498.7384	1416.502	1263.753	1402.272	-1.2445	1.39E-19	1.38E-18	NCAPH2	chr22	+	50946645	50961901	2077
ENSG00000(	1701.806	1596.886	1740.307	1235.975	914.9094	992.1117	0.67837	6.51E-07	2.75E-06	TOMM34	chr20	-	43570771	43589127	2062
ENSG00000(	2715.846	2865	2992.43	1593.284	1670.584	1640.642	0.80434	6.57E-14	4.85E-13	SEC63	chr6	-	1.08E+08	1.08E+08	6411
ENSG00000(	1291.633	1185.019	1370.871	1546.841	1905.294	1591.324	-0.38935	0.002483	0.006507	KPNA6	chr1	+	32573639	32642169	7378
ENSG00000(	27709.51	30344.44	24638.73	17857.21	10897.91	12388.66	1.0036	1.80E-10	1.04E-09	VIM	chr10	+	17270258	17279592	2666
ENSG00000(	33.14534	27.69862	29.0271	5.243529	29.45382	32.8786	0.40189	0.47036	0.59945	RTEL1-TNFF	chr20	+	62290653	62330037	5751
ENSG00000(	932.2127	988.7202	1017.268	857.6915	677.4379	600.0344	0.45798	0.002367	0.006229	FAS	chr10	+	90750414	90775542	2563
ENSG00000(	243.4111	268.5562	178.1209	143.0734	164.7573	254.8091	0.29419	0.22682	0.3398	RNASET2	chr6	-	1.67E+08	1.67E+08	2445
ENSG00000(	10903.78	11215.53	11401.05	1785.047	1551.848	1370.216	2.8264	6.53E-127	7.49E-125	CD44	chr11	+	35160417	35253949	4589
ENSG00000(	59.04014	71.05298	75.20659	223.9736	378.2976	417.5582	-2.2948	3.30E-19	3.22E-18	KCNG1	chr20	-	49620193	49639666	2211

ENSG00000(	444.3547	466.0593	478.9472	427.7221	406.8309	390.4333	0.18012	0.21823	0.32961	AGPAT4	chr6	-	1.62E+08	1.62E+08	7865
ENSG00000(	0	0	0	9.737982	3.681728	2.465895	-3.1695	0.012502	0.028434	SLAMF7	chr1	+	1.61E+08	1.61E+08	3542
ENSG00000(	316.9523	299.8676	265.2022	20.22504	13.80648	11.50751	4.2167	8.39E-50	2.30E-48	BTN3A1	chr6	+	26402465	26415444	3442
ENSG00000(	334.5608	355.2649	333.8117	487.6482	390.2632	432.3535	-0.35616	0.025554	0.054004	MIPEP	chr13	-	24304328	24463558	2400
ENSG00000(	76.6486	63.82725	58.05421	403.7517	484.1472	375.638	-2.6455	1.74E-35	3.16E-34	PRKCH	chr14	+	61654277	62017694	3582
ENSG00000(	8.286335	14.45145	6.597069	0.749076	0	1.64393	2.9434	0.003784	0.009607	INSRR	chr1	-	1.57E+08	1.57E+08	5101
ENSG00000(	431.9252	447.995	519.849	892.149	758.436	766.8933	-0.78823	6.09E-08	2.85E-07	IFNGR1	chr6	-	1.38E+08	1.38E+08	2139
ENSG00000(	699.1595	644.2939	569.9868	437.4601	364.4911	457.8345	0.60122	0.000101	0.000329	B4GALT7	chr5	+	1.77E+08	1.77E+08	2653
ENSG00000(	1.035792	4.817151	0	2.247227	5.522592	6.575719	-1.0123	0.35939	0.48893	SH2D2A	chr1	-	1.57E+08	1.57E+08	1673
ENSG00000(	141.9035	114.4073	143.8161	191.0143	251.2779	205.4912	-0.68867	0.001453	0.003961	VRK2	chr2	+	58134786	58387055	2446
ENSG00000(	139.8319	177.0303	134.5802	52.43529	32.21512	28.76877	1.961	5.77E-11	3.48E-10	TNFRSF1B	chr1	+	12227060	12269285	3683
ENSG00000(	1618.943	1728.153	1687.53	991.027	948.9654	784.9765	0.8834	5.63E-12	3.65E-11	VEZT	chr12	+	95611522	95696566	4562
ENSG00000(	110.8297	121.6331	88.40072	337.8331	223.665	262.2068	-1.3495	3.66E-09	1.91E-08	POU2F2	chr19	-	42590262	42700737	6901
ENSG00000(	1165.266	1095.902	1101.711	1414.255	1127.529	963.3429	-0.05985	0.6862	0.78531	BRD9	chr5	-	850406	892939	4865
ENSG00000(	2249.74	2255.631	2392.097	1350.583	1290.446	1365.284	0.78216	6.42E-13	4.45E-12	SNX1	chr15	+	64386322	64438289	8119
ENSG00000(	378.064	358.8777	393.1853	642.7068	428.0009	512.0841	-0.48572	0.005098	0.012611	TBPL1	chr6	+	1.34E+08	1.34E+08	1295
ENSG00000(	215.4447	227.6104	287.6322	568.5483	598.2808	512.9061	-1.1996	1.06E-12	7.23E-12	ARNTL2	chr12	+	27485787	27576241	4804
ENSG00000(	2151.34	2236.362	2583.412	2755.1	2964.711	2293.282	-0.2008	0.12334	0.20852	BCLAF1	chr6	-	1.37E+08	1.37E+08	7263
ENSG00000(	1299.919	1445.145	1496.215	1105.636	1145.938	980.6041	0.39072	0.001765	0.004749	SLC39A9	chr14	+	69864732	69929105	5192
ENSG00000(	29.00217	31.31148	22.43003	307.121	532.9301	372.3501	-3.8237	6.72E-43	1.52E-41	ANK1	chr8	-	41510739	41754280	8366
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	IBSP	chr4	+	88720733	88733074	1033
ENSG00000(	146.0467	130.0631	109.5113	269.6672	214.4607	265.4947	-0.95022	6.98E-06	2.64E-05	TFB1M	chr6	-	1.56E+08	1.56E+08	1424
ENSG00000(	792.3808	916.463	986.9215	962.5621	972.8966	766.0713	-0.00405	0.97781	0.98705	RABEP1	chr17	+	5185558	5289129	5387
ENSG00000(	846.242	783.9913	885.3266	1962.578	2255.058	2123.957	-1.3313	2.20E-28	3.14E-27	HMGB3	chrX	+	1.5E+08	1.5E+08	3560
ENSG00000(	767.5218	859.8614	927.5479	1282.417	1669.664	1462.276	-0.78734	1.57E-08	7.76E-08	NUP160	chr11	-	47799639	47870107	5376
ENSG00000(	521.0033	419.0921	451.2395	880.1638	1021.68	1343.091	-1.2156	6.43E-13	4.46E-12	BAK1	chr6	-	33540329	33548019	2136
ENSG00000(	22.78742	4.817151	21.11062	0	0.920432	2.465895	3.3185	0.000331	0.001001	MUSK	chr9	+	1.13E+08	1.14E+08	3303
ENSG00000(	75.61281	77.07441	137.219	166.2948	185.0068	166.8589	-0.8371	0.001394	0.003818	IKZF2	chr2	-	2.14E+08	2.14E+08	9405
ENSG00000(	6090.456	6034.686	5195.851	3327.394	2533.949	2553.023	1.039	3.33E-15	2.66E-14	GRN	chr17	+	42422614	42430470	2148
ENSG00000(	487.858	594.9181	664.9845	483.9028	566.0657	457.0125	0.21197	0.18948	0.29462	FAM13B	chr5	-	1.37E+08	1.37E+08	5465
ENSG00000(	569.6855	502.188	571.3062	152.0623	216.3015	155.3514	1.646	7.43E-20	7.47E-19	ARHGAP31	chr3	+	1.19E+08	1.19E+08	9317
ENSG00000(	0	6.021439	1.319414	3.745378	3.681728	7.397684	-0.82508	0.44524	0.5748	NR2E3	chr15	+	72084977	72110600	2102
ENSG00000(	65.25489	85.50443	64.65128	221.7264	149.11	192.3398	-1.3767	7.22E-08	3.36E-07	CENPQ	chr6	+	49431091	49460820	1733
ENSG00000(	3884.22	3712.819	3772.204	3457.733	2673.855	2811.942	0.34525	0.004686	0.011677	SARS	chr1	+	1.1E+08	1.1E+08	1882
ENSG00000(	1362.066	1404.199	1205.944	1985.799	1702.799	1926.686	-0.49823	4.76E-05	0.000163	RANBP3	chr19	-	5916150	5978153	3233
ENSG00000(	371.8493	323.9534	480.2666	152.0623	200.6542	178.3664	1.1414	9.12E-09	4.59E-08	ARID4A	chr14	+	58765103	58840605	5891
ENSG00000(	456.7842	408.2535	439.3648	674.168	481.3859	562.224	-0.39661	0.014488	0.032471	TSSC1	chr2	-	3192696	3381653	2932
ENSG00000(	1827.137	1732.97	1422.328	1623.996	1493.861	1620.915	0.072795	0.56881	0.68797	PNPLA6	chr19	+	7598890	7626650	4617
ENSG00000(	319.0239	314.3191	257.2857	163.2985	179.4842	179.1884	0.76984	3.51E-05	0.000122	IFT88	chr13	+	21140585	21265503	3931
ENSG00000(	680.5153	663.5625	575.2644	435.962	411.4331	340.2935	0.69089	8.60E-06	3.22E-05	ALG1	chr16	+	5083703	5137380	2671
ENSG00000(	269.3059	340.8134	224.3003	552.8178	455.6138	500.5766	-0.85054	2.43E-06	9.66E-06	ZCCHC8	chr12	-	1.23E+08	1.23E+08	4393
ENSG00000(	1552.652	1464.414	1460.591	2328.876	1908.976	1934.905	-0.46232	0.000162	0.000513	ABCF2	chr7	-	1.51E+08	1.51E+08	3546
ENSG00000(	4810.218	4625.669	4536.145	1063.687	1434.953	1310.212	1.8719	1.94E-49	5.28E-48	CHPF2	chr7	+	1.51E+08	1.51E+08	3973
ENSG00000(	6.214751	10.83859	10.55531	35.95563	17.48821	26.30288	-1.4708	0.011992	0.027381	LRRC7	chr1	+	70034081	70617628	6507

ENSG00000(	438.14	337.2006	393.1853	1308.635	1365.001	1225.55	-1.7321	7.11E-35	1.27E-33	FUT8	chr14	+	65877310	66210839	5166
ENSG00000(	684.6584	679.2183	861.5772	990.2779	1018.918	813.7453	-0.34316	0.021315	0.045935	UBA6	chr4	-	68481479	68566897	6455
ENSG00000(	246.5185	239.6533	255.9663	1400.771	2158.413	1854.353	-2.856	4.11E-67	1.68E-65	GAB2	chr11	-	77926343	78129394	6092
ENSG00000(	986.0739	823.7328	959.2138	878.6656	816.4232	859.7753	0.11587	0.37293	0.50346	ATP6V0A1	chr17	+	40610862	40674629	4652
ENSG00000(	324.2029	278.1905	397.1435	447.9472	353.4459	337.0056	-0.18928	0.30911	0.43524	PIAS1	chr15	+	68346517	68483096	2932
ENSG00000(	1022.327	1112.762	1457.952	665.1791	727.1413	561.402	0.87523	4.06E-08	1.93E-07	SLC4A7	chr3	-	27414214	27525911	7757
ENSG00000(	696.0522	638.2725	560.7509	420.9805	384.7406	333.7178	0.73229	2.98E-06	1.18E-05	APBA2	chr15	+	29129629	29410518	4031
ENSG00000(	798.5956	759.9056	758.6629	1810.516	2003.78	1980.935	-1.3193	2.39E-29	3.55E-28	UHRF1	chr19	+	4903092	4962165	4308
ENSG00000(	609.0456	679.2183	630.6798	761.0608	572.5087	632.913	-0.03661	0.80615	0.87429	MAP2K3	chr17	+	21187984	21218552	2401
ENSG00000(	77.68439	69.84869	89.72014	11.23613	10.12475	15.61733	2.6195	3.37E-11	2.06E-10	EFCAB1	chr8	-	49623348	49647870	2286
ENSG00000(	38737.58	38532.39	30314.85	14953.05	15874.69	22389.5	1.0124	2.45E-11	1.52E-10	TMSB10	chr2	+	85132749	85133795	492
ENSG00000(	71.46964	72.25726	101.5949	74.90755	90.20234	80.55256	-0.00495	0.98612	0.99155	ASTE1	chr3	-	1.31E+08	1.31E+08	2669
ENSG00000(	230.9816	207.1375	261.2439	254.6857	242.0736	201.3814	0.001144	0.99525	0.99695	RNF19A	chr8	-	1.01E+08	1.01E+08	4330
ENSG00000(	127.4024	125.2459	141.1773	176.7818	177.6434	159.4612	-0.3828	0.072249	0.13331	PEX3	chr6	+	1.44E+08	1.44E+08	1969
ENSG00000(	943.6064	948.9787	868.1743	1034.473	811.821	946.9036	-0.01721	0.89886	0.93728	GABARAPL2	chr16	+	75600249	75611779	2274
ENSG00000(	679.4795	681.6268	723.0388	289.1432	358.9685	312.3467	1.1157	5.51E-14	4.10E-13	SH3YL1	chr2	-	217730	266398	3540
ENSG00000(	484.7506	555.1766	519.849	1163.314	1094.394	1127.736	-1.1165	4.07E-18	3.77E-17	FAM136A	chr2	-	70523107	70529222	2398
ENSG00000(	5418.227	5159.169	6558.806	7505.737	7407.637	6082.54	-0.29258	0.022677	0.048505	VCL	chr10	+	75757872	75879918	5482
ENSG00000(	82.86335	96.34302	93.67838	619.4855	580.7926	523.5917	-2.6506	2.25E-47	5.71E-46	DEPDC1B	chr5	-	59892739	59996017	2499
ENSG00000(	1.035792	2.408575	13.19414	8.239831	1.840864	4.93179	0.09376	0.9238	0.95385	DAPK2	chr15	-	64199235	64364232	4835
ENSG00000(	428.8178	457.6293	455.1978	620.2346	527.4075	515.372	-0.31022	0.036292	0.073465	NSMAF	chr8	-	59496063	59572403	3569
ENSG00000(	500.2875	520.2523	626.7215	880.9128	972.8966	745.5222	-0.65717	1.71E-05	6.16E-05	ADSS	chr1	-	2.45E+08	2.45E+08	2780
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	STAP1	chr4	+	68424446	68473055	1511
ENSG00000(	13612.38	13645.78	13509.48	3116.903	2734.603	2594.943	2.2672	7.35E-99	5.50E-97	TIMP2	chr17	-	76849059	76921469	3652
ENSG00000(	812.0609	821.3242	860.2578	1133.351	1125.688	844.158	-0.31485	0.029173	0.060687	RFC1	chr4	-	39289076	39367995	4886
ENSG00000(	1018.183	1077.838	1132.057	449.4453	452.8525	356.7328	1.3543	2.11E-21	2.26E-20	TBC1D23	chr3	+	99979844	1E+08	4054
ENSG00000(	1340.315	1206.696	1278.512	1845.722	1801.285	1449.124	-0.41255	0.001559	0.004229	CUL3	chr2	-	2.25E+08	2.25E+08	6741
ENSG00000(	34.18113	27.69862	40.90183	47.94084	39.57858	42.74218	-0.33899	0.37952	0.51027	MYOM2	chr8	+	1993155	2113475	5014
ENSG00000(	42.46747	37.33292	29.0271	2.996302	4.60216	9.863579	2.5219	1.13E-05	4.17E-05	CYP46A1	chr14	+	1E+08	1E+08	6609
ENSG00000(	692.9448	657.5411	753.3853	726.6033	760.2768	589.3488	0.018841	0.89725	0.93627	ZZZ3	chr1	-	78028101	78149104	4737
ENSG00000(	0	0	0	8.239831	5.522592	4.109825	-3.3794	0.006637	0.016039	SLC18A1	chr8	-	20002366	20040717	2956
ENSG00000(	8.286335	6.021439	9.235896	25.46857	24.85166	10.68554	-1.2918	0.045171	0.088874	USP2	chr11	-	1.19E+08	1.19E+08	3732
ENSG00000(	415.3526	428.7264	295.5487	113.1104	110.4518	123.2947	1.7081	2.53E-17	2.26E-16	TUBG2	chr17	+	40811323	40819024	1776
ENSG00000(	476.4643	503.3923	412.9765	825.4813	624.0529	828.5406	-0.70729	8.55E-06	3.20E-05	RPL26L1	chr5	+	1.72E+08	1.72E+08	742
ENSG00000(	2.071584	6.021439	17.15238	55.43159	77.31629	79.7306	-3.0083	3.96E-09	2.06E-08	FLT4	chr5	-	1.8E+08	1.8E+08	5857
ENSG00000(	1223.27	1073.02	1300.942	2559.591	2451.11	2418.221	-1.0446	9.55E-19	9.13E-18	NSUN2	chr5	-	6599352	6633404	3558
ENSG00000(	575.9003	610.5739	601.6527	553.5668	507.158	446.327	0.24524	0.090813	0.16194	FBXO42	chr1	-	16573334	16678949	6202
ENSG00000(	642.191	671.9925	971.0885	850.9498	811.821	764.4274	-0.08857	0.5886	0.70573	MFAP3	chr5	+	1.53E+08	1.54E+08	5049
ENSG00000(	182.2994	132.4716	150.4132	137.0808	134.3831	141.378	0.17364	0.43547	0.5651	MRI1	chr19	+	13875346	13885096	3027
ENSG00000(	137.7603	175.826	102.9143	207.4939	158.3143	198.9155	-0.4351	0.068433	0.12727	METTL1	chr12	-	58162254	58166576	2066
ENSG00000(	223.7311	104.773	158.3297	65.91865	28.53339	32.8786	1.8969	4.09E-08	1.95E-07	HOXC8	chr12	+	54402832	54407570	3371
ENSG00000(	157.4404	164.9874	143.8161	194.7596	159.2347	191.5178	-0.22571	0.2788	0.4009	AGA	chr4	-	1.78E+08	1.78E+08	2107
ENSG00000(	375.9925	402.2321	432.7677	603.7549	731.7434	596.7465	-0.67247	9.70E-06	3.61E-05	PI4K2B	chr4	+	25162263	25280714	3540
ENSG00000(	668.0858	523.8652	832.5501	496.6371	630.4959	482.4934	0.32939	0.066595	0.12435	BOD1L1	chr4	-	13570362	13629347	10565

ENSG00000(	660.8352	668.3797	696.6505	1050.204	1020.759	1006.907	-0.60271	9.20E-07	3.83E-06	MAT2B	chr5	+	1.63E+08	1.63E+08	3409
ENSG00000(	31.07376	48.17151	62.01245	17.97781	10.12475	12.32947	1.7337	0.000227	0.000704	TLL1	chr4	+	1.67E+08	1.67E+08	6708
ENSG00000(	1107.262	1045.322	955.2556	845.7063	1195.641	927.1764	0.067486	0.65156	0.75752	EDC4	chr16	+	67906926	67918406	5267
ENSG00000(	5292.897	4748.506	6243.466	2116.138	2995.086	2253.006	1.1418	8.52E-15	6.64E-14	TRIO	chr5	+	14143811	14532235	11100
ENSG00000(	2969.615	2678.336	4032.129	1009.754	1193.8	829.3626	1.6682	4.54E-24	5.41E-23	VCAN	chr5	+	82767284	82878122	12625
ENSG00000(	590.4014	582.8753	580.5421	615.7401	844.0361	667.4355	-0.2763	0.06923	0.12856	CLEC16A	chr16	+	11038345	11276046	6891
ENSG00000(	24.85901	32.51577	18.47179	0	0	0	5.9175	4.76E-08	2.26E-07	MSR1	chr8	-	15965387	16424999	3572
ENSG00000(	1.035792	0	1.319414	4541.645	5196.759	4543.822	-11.461	5.23E-67	2.14E-65	CDH1	chr16	+	68771128	68869445	4875
ENSG00000(	912.5327	1026.053	1067.406	1199.27	1058.497	835.9383	-0.04229	0.77836	0.85409	SKIV2L2	chr5	+	54603588	54721409	4192
ENSG00000(	9.322127	1.204288	7.916483	40.45008	42.33987	49.3179	-2.6964	1.90E-06	7.64E-06	DNAH5	chr5	-	13690440	13944652	15633
ENSG00000(	540.6834	555.1766	700.6087	708.6255	942.5224	745.5222	-0.41506	0.009641	0.022504	ZFYVE16	chr5	+	79703832	79775169	6773
ENSG00000(	763.3786	733.4112	699.2893	830.7248	827.4684	867.173	-0.20047	0.11066	0.19045	FAM65A	chr16	+	67552321	67580691	4260
ENSG00000(	11.39371	14.45145	18.47179	2.247227	0	0	3.5512	0.000198	0.00062	C6	chr5	-	41142336	41261540	3661
ENSG00000(	1286.454	1217.535	1671.697	1520.623	1571.177	1283.087	-0.06774	0.64233	0.74983	RAI14	chr5	+	34656342	34832732	5092
ENSG00000(	2.071584	9.634302	0	4.494453	2.761296	2.465895	0.21259	0.84496	0.90101	SOX30	chr5	-	1.57E+08	1.57E+08	3265
ENSG00000(	865.922	873.1086	774.4959	697.3893	767.6403	950.1914	0.0581	0.69387	0.79124	PNKP	chr19	-	50364461	50371166	2102
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	BEST2	chr19	+	12862516	12869272	2183
ENSG00000(	254.8048	225.2018	310.0622	325.8479	486.9085	359.1987	-0.56576	0.004294	0.010781	PHLPP2	chr16	-	71671738	71758604	8467
ENSG00000(	317.9881	380.5549	381.3106	1240.469	1168.028	1135.956	-1.7128	1.88E-35	3.41E-34	SPDL1	chr5	+	1.69E+08	1.69E+08	2668
ENSG00000(	256.8764	242.0618	344.367	531.8436	466.659	403.5848	-0.73315	6.90E-05	0.00023	STAU2	chr8	-	74332604	74659943	4061
ENSG00000(	377.0283	284.2119	203.1897	604.504	439.9665	509.6182	-0.83774	5.72E-05	0.000193	PQLC2	chr1	+	19638820	19655794	2153
ENSG00000(	384.2788	397.4149	327.2146	397.7591	348.8437	327.142	0.046836	0.77735	0.85334	CTNS	chr17	+	3539762	3564836	2866
ENSG00000(	15.53688	10.83859	14.51355	128.841	104.0088	90.41614	-2.9192	2.07E-14	1.58E-13	RTN4R	chr22	-	20228938	20270769	2157
ENSG00000(	1160.087	1136.848	1134.696	1210.506	1118.325	1237.057	-0.05542	0.63576	0.74472	PHF23	chr17	-	7138347	7143041	2037
ENSG00000(	35.21692	38.53721	32.98534	406.748	396.7062	336.1837	-3.3887	2.09E-46	5.18E-45	CDH10	chr5	-	24487209	24645087	3438
ENSG00000(	458.8558	413.0707	530.4043	388.0211	520.0441	399.475	0.10111	0.55396	0.67484	INPP4A	chr2	+	99061317	99207496	6752
ENSG00000(	1413.856	1400.587	2237.726	44.19546	50.62376	57.53754	5.0233	3.73E-130	4.45E-128	RAB27B	chr18	+	52385091	52562747	7281
ENSG00000(	1630.336	1487.295	1432.883	3182.073	3036.505	3105.383	-1.0326	5.70E-21	6.00E-20	PSMA4	chr15	+	78832747	78841604	2741
ENSG00000(	0	0	2.638828	24.71949	14.72691	13.15144	-3.703	0.000117	0.000378	MYO16	chr13	+	1.09E+08	1.1E+08	6874
ENSG00000(	433.9968	440.7693	486.8637	817.2414	685.7218	748.81	-0.72548	3.51E-07	1.53E-06	LSG1	chr3	-	1.94E+08	1.94E+08	3572
ENSG00000(	98.40023	102.3645	83.12307	12.73428	10.12475	16.4393	2.7937	6.85E-14	5.05E-13	PARP3	chr3	+	51976361	51982883	2472
ENSG00000(	4513.981	4200.556	5193.213	10472.83	14208.71	11473.81	-1.3751	5.56E-25	6.85E-24	TNC	chr9	-	1.18E+08	1.18E+08	7641
ENSG00000(	307.6302	297.4591	266.5216	255.4348	230.108	284.3999	0.17874	0.31241	0.43884	THAP3	chr1	+	6684926	6695646	2053
ENSG00000(	267.2343	350.4477	273.1187	10.48706	14.72691	13.15144	4.4917	2.47E-51	7.07E-50	FAM65C	chr20	-	49202645	49308065	4377
ENSG00000(	299.3439	286.6205	296.8681	698.1384	642.4615	671.5453	-1.1853	2.42E-16	2.06E-15	TDP1	chr14	+	90421283	90511106	3696
ENSG00000(	109.7939	86.70872	105.5531	181.2763	161.996	185.7641	-0.80244	0.000414	0.001233	AIFM2	chr10	-	71857979	71892690	3240
ENSG00000(	1.035792	6.021439	0	0	0	0	2.0906	0.12335	0.20852	C2orf83	chr2	-	2.28E+08	2.28E+08	2086
ENSG00000(	240.3037	292.6419	261.2439	118.3539	115.9744	79.7306	1.3289	1.46E-09	7.88E-09	SPATA7	chr14	+	88851268	88936694	3610
ENSG00000(	515.8244	638.2725	544.9179	791.7729	596.4399	545.7847	-0.18749	0.26513	0.38502	MED17	chr11	+	93517393	93547861	4874
ENSG00000(	1203.59	1042.913	1166.362	471.9176	561.4635	687.1627	0.98564	1.45E-10	8.49E-10	RETSAT	chr2	-	85569211	85581743	3100
ENSG00000(	3449.187	3031.192	2729.867	889.1527	786.9694	1059.513	1.7467	6.01E-36	1.11E-34	CAPG	chr2	-	85621871	85645555	1442
ENSG00000(	4657.956	4617.239	4033.448	4806.069	3486.596	4444.364	0.063101	0.63448	0.74381	AP2S1	chr19	-	47341393	47354249	935
ENSG00000(	3.107376	0	2.638828	0	0	0	1.8293	0.17689	NA	USH2A	chr1	-	2.16E+08	2.17E+08	18955
ENSG00000(	22.78742	39.74149	47.4989	1.498151	6.443024	4.93179	2.9456	1.63E-06	6.59E-06	TG	chr8	+	1.34E+08	1.34E+08	8450

ENSG00000(	0	1.204288	0	0	1.840864	0	-0.18234	0.88799	NA	ADAM28	chr8	+	24151553	24216531	7052
ENSG00000(	2.071584	0	0	249.4422	210.7789	216.1768	-7.3367	4.78E-23	5.47E-22	BARX2	chr11	+	1.29E+08	1.29E+08	2148
ENSG00000(	396.7083	392.5978	453.8783	511.6186	620.3712	539.209	-0.42577	0.005258	0.012973	DCUN1D1	chr3	-	1.83E+08	1.83E+08	7954
ENSG00000(	340.7755	357.6735	352.2835	242.7005	358.048	288.5097	0.24163	0.18352	0.28747	PHF15	chr5	+	1.34E+08	1.34E+08	6463
ENSG00000(	275.5206	240.8575	258.6051	32.95932	39.57858	38.63235	2.784	1.41E-31	2.26E-30	ZIC2	chr13	+	1.01E+08	1.01E+08	2974
ENSG00000(	0	2.408575	0	10.48706	3.681728	8.219649	-2.4863	0.025767	0.05439	LCP2	chr5	-	1.7E+08	1.7E+08	4678
ENSG00000(	296.2365	298.6634	312.7011	369.2942	361.7298	346.0472	-0.24686	0.11869	0.20199	TRIT1	chr1	-	40306723	40349183	2112
ENSG00000(	17.60846	7.225726	6.597069	22.47227	15.64734	22.19305	-0.87192	0.15668	0.2527	ADRB1	chr10	+	1.16E+08	1.16E+08	2862
ENSG00000(	2147.197	2012.365	2021.342	682.4078	841.2748	828.5406	1.3919	1.70E-28	2.45E-27	CUL7	chr6	-	43005355	43021683	5504
ENSG00000(	5299.111	4830.398	5455.776	6669.769	6226.722	5600.047	-0.24672	0.027112	0.056933	CTNNA1	chr5	+	1.38E+08	1.38E+08	3756
ENSG00000(	217.5163	222.7932	226.9392	185.0217	231.9489	230.9721	0.043207	0.82043	0.88415	PHKA2	chrX	-	18910418	19002716	5559
ENSG00000(	239.2679	266.1476	336.4505	160.3022	136.2239	125.7606	0.98542	2.20E-06	8.77E-06	CNTLN	chr9	+	17134980	17503921	5576
ENSG00000(	403.9588	419.0921	486.8637	2.247227	17.48821	5.753754	5.3551	9.95E-17	8.59E-16	EPHA3	chr3	+	89156674	89531284	5809
ENSG00000(	15547.24	15617.2	15046.59	17507.39	16079.95	14842.22	-0.06756	0.51422	0.64102	HSPA5	chr9	-	1.28E+08	1.28E+08	3908
ENSG00000(	1833.352	1714.906	2111.062	4180.591	4546.014	3730.077	-1.1361	7.02E-20	7.07E-19	DSG2	chr18	+	29078006	29128971	5831
ENSG00000(	437.1042	426.3179	343.0476	196.2578	155.553	159.4612	1.2322	3.18E-11	1.95E-10	GEMIN8	chrX	-	14026398	14048012	1682
ENSG00000(	264.1269	291.4376	294.2293	386.523	413.274	387.1455	-0.48136	0.00253	0.006621	OFD1	chrX	+	13752832	13787480	4259
ENSG00000(	44.53905	63.82725	62.01245	176.0328	202.495	130.6924	-1.5683	1.37E-08	6.79E-08	GPM6B	chrX	-	13789150	13956757	3957
ENSG00000(	6.214751	10.83859	13.19414	36.7047	66.2711	23.83698	-1.9915	0.000276	0.000846	PREX2	chr8	+	68864353	69149265	10750
ENSG00000(	529.2897	491.3494	577.9032	453.1907	486.9085	434.8194	0.21664	0.13789	0.22795	WDR37	chr10	+	1095478	1178237	4582
ENSG00000(	414.3168	332.3834	486.8637	429.2203	441.8074	391.2553	-0.03393	0.84281	0.89968	YTHDC2	chr5	+	1.13E+08	1.13E+08	6708
ENSG00000(	277.5922	291.4376	310.0622	448.6963	497.9537	455.3686	-0.67198	1.57E-05	5.69E-05	CTPS2	chrX	-	16606126	16731059	4319
ENSG00000(	602.8309	621.4125	631.9992	1150.58	985.7827	997.0434	-0.75449	8.27E-09	4.18E-08	ATP6V1H	chr8	-	54628117	54756118	2365
ENSG00000(	2191.736	2131.589	2291.822	2340.112	2371.953	1787.774	0.025276	0.84692	0.90246	POLR2B	chr4	+	57843888	57897334	4108
ENSG00000(	279.6638	249.2876	370.7553	86.89276	100.3271	68.22309	1.8038	3.85E-15	3.06E-14	FAM214A	chr15	-	52873514	53002014	4590
ENSG00000(	14.50109	13.24716	9.235896	109.365	140.8261	112.6092	-3.2129	1.79E-17	1.61E-16	ARAP2	chr4	-	36067620	36246131	7514
ENSG00000(	1684.198	1574.004	1960.649	2259.961	2774.182	2319.585	-0.49373	0.00016	0.000506	TPR	chr1	-	1.86E+08	1.86E+08	7538
ENSG00000(	1.035792	7.225726	3.958241	3.745378	0.920432	4.109825	0.36872	0.72772	0.81762	CP	chr3	-	1.49E+08	1.49E+08	4676
ENSG00000(	625.6183	612.9824	580.5421	397.01	425.2396	504.6865	0.45452	0.002406	0.006323	KIAA0556	chr16	+	27561454	27791690	6616
ENSG00000(	136.7245	166.1917	124.0249	280.9033	266.9253	254.8091	-0.90524	5.54E-06	2.12E-05	DTNBP1	chr6	-	15523032	15663289	1880
ENSG00000(	6.214751	4.817151	7.916483	59.92604	54.30549	36.98842	-2.8812	6.66E-08	3.11E-07	XK	chrX	+	37545012	37591383	5206
ENSG00000(	0	2.408575	1.319414	22.47227	21.16994	12.32947	-3.4294	0.000125	0.000402	ANO2	chr12	-	5641035	6055398	3717
ENSG00000(	355.2766	415.4793	451.2395	468.1722	439.9665	383.0357	-0.08145	0.6171	0.72969	C12orf4	chr12	-	4596894	4647674	3826
ENSG00000(	190.5857	232.4275	257.2857	202.2504	223.665	179.1884	0.16589	0.40739	0.53818	SCML1	chrX	+	17755588	17773105	4615
ENSG00000(	819.3114	787.6042	854.9801	942.337	1249.947	985.5359	-0.36664	0.009852	0.022949	WWC3	chrX	+	9983602	10112518	6647
ENSG00000(	172.9772	127.6545	167.5656	46.44268	42.33987	62.46933	1.6126	3.49E-09	1.83E-08	ARHGAP6	chrX	-	11136239	11683821	6299
ENSG00000(	270.3417	316.7277	266.5216	188.767	183.166	222.7525	0.51849	0.005353	0.01318	FAM184B	chr4	-	17630929	17783135	6622
ENSG00000(	10405.57	10466.46	10399.62	6615.835	8892.294	8524.598	0.3792	0.002085	0.005539	MAP4	chr3	-	47892182	48130769	8920
ENSG00000(	935.3201	991.1288	1178.237	943.8352	997.7483	798.1279	0.17916	0.2083	0.3178	GOPC	chr6	-	1.18E+08	1.18E+08	4604
ENSG00000(	0	3.612863	2.638828	0	0	0	1.93	0.15472	0.25026	ROS1	chr6	-	1.18E+08	1.18E+08	7435
ENSG00000(	333.525	360.082	432.7677	526.6001	480.4655	482.4934	-0.4047	0.010605	0.024504	USP28	chr11	-	1.14E+08	1.14E+08	4669
ENSG00000(	171.9415	242.0618	284.9934	137.8299	156.4734	140.556	0.67708	0.002465	0.006463	HDAC9	chr7	+	18126572	19036993	4659
ENSG00000(	1136.264	1187.428	1245.527	524.3529	624.0529	745.5222	0.91173	6.06E-10	3.38E-09	TSPAN17	chr5	+	1.76E+08	1.76E+08	4445
ENSG00000(	416.3883	334.792	255.9663	681.6587	474.9429	548.2506	-0.75305	0.000112	0.000361	NOP16	chr5	-	1.76E+08	1.76E+08	1256

ENSG00000(	568.6498	582.8753	591.0974	348.3201	326.7534	326.3201	0.7962	2.77E-08	1.34E-07	CC2D2A	chr4	+	15471489	15603180	5249
ENSG00000(	1585.797	1502.951	2107.104	1079.418	1231.538	1031.566	0.6342	1.63E-05	5.89E-05	RRM2B	chr8	-	1.03E+08	1.03E+08	4931
ENSG00000(	182.2994	213.1589	270.4798	271.9144	274.2887	223.5745	-0.21161	0.29515	0.41956	ZNF800	chr7	-	1.27E+08	1.27E+08	4358
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	TNFRSF17	chr16	+	12058964	12061925	994
ENSG00000(	281.7354	307.0934	432.7677	138.579	200.6542	150.4196	1.0544	1.30E-06	5.34E-06	SNX29	chr16	+	12070594	12668146	8171
ENSG00000(	7.250543	10.83859	13.19414	8.239831	10.12475	14.79537	-0.08602	0.89941	0.93765	LMO3	chr12	-	16701307	16763528	3759
ENSG00000(	511.6812	528.6823	497.419	893.6471	814.5823	735.6586	-0.66669	1.57E-06	6.37E-06	MRPS10	chr6	-	42174539	42185603	2110
ENSG00000(	2.071584	1.204288	1.319414	21.72319	29.45382	31.23467	-3.7248	2.39E-06	9.49E-06	GUCA1A	chr6	+	42123144	42147794	2233
ENSG00000(	871.101	912.8501	1101.711	451.6926	731.7434	555.6483	0.72836	2.99E-05	0.000104	RSF1	chr11	-	77371041	77532063	11550
ENSG00000(	832.7767	759.9056	981.6439	382.7776	482.3064	367.4183	1.0596	2.71E-11	1.67E-10	VPS13D	chr1	+	12290124	12572099	16318
ENSG00000(	474.3927	451.6079	543.5985	835.9683	985.7827	747.9881	-0.80408	1.23E-07	5.60E-07	CELF2	chr10	+	11047259	11378666	9233
ENSG00000(	2133.731	2232.749	2696.882	1670.438	1688.993	1370.216	0.57675	1.75E-05	6.30E-05	FAM120A	chr9	+	96214004	96328397	5118
ENSG00000(	776.8439	752.6798	841.786	966.3075	965.5332	880.3244	-0.24595	0.052467	0.10127	R3HDM1	chr2	+	1.36E+08	1.36E+08	4648
ENSG00000(	73.54123	78.2787	84.44248	202.9995	291.7769	292.6195	-1.7248	1.62E-13	1.17E-12	COL9A2	chr1	-	40766159	40783488	2887
ENSG00000(	1456.323	1492.112	2153.283	630.7216	822.8662	600.8564	1.3071	1.77E-14	1.35E-13	KITLG	chr12	-	88886570	88974628	5191
ENSG00000(	147.0825	128.8588	114.789	184.2726	152.7917	143.8439	-0.2955	0.19275	0.2986	ERCC8	chr5	-	60169658	60240900	3424
ENSG00000(	8.286335	22.88147	18.47179	52.43529	61.66894	23.83698	-1.4321	0.004668	0.011635	ADAMTS6	chr5	-	64444563	64777747	7311
ENSG00000(	2455.863	2412.188	2219.254	658.4374	636.0185	699.4921	1.8263	2.20E-55	6.87E-54	H6PD	chr1	+	9294834	9331396	9146
ENSG00000(	2523.189	2300.19	2468.623	3086.191	2324.091	2229.991	-0.06741	0.62209	0.73416	VAMP3	chr1	+	7831329	7841492	2205
ENSG00000(	30.03797	33.72006	62.01245	23.22134	16.56778	25.48091	0.90789	0.044605	0.087952	PER3	chr1	+	7844380	7905237	6279
ENSG00000(	0	1.204288	1.319414	2.247227	8.283888	2.465895	-1.7352	0.14665	0.23955	TNFRSF9	chr1	-	7979907	8000926	1923
ENSG00000(	5.17896	3.612863	2.638828	426.224	470.3408	405.2287	-6.5886	5.53E-48	1.43E-46	EPN3	chr17	+	48609904	48621111	4071
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	SRD5A2	chr2	-	31747550	31806136	4647
ENSG00000(	14747.61	13400.11	17003.29	1083.912	1240.742	983.07	3.763	3.46E-192	9.14E-190	LTBP1	chr2	+	33172039	33624576	6333
ENSG00000(	7435.95	7802.58	7698.779	4850.264	4973.094	4256.956	0.70294	3.62E-11	2.21E-10	RCN1	chr11	+	31833939	32127301	2653
ENSG00000(	2.071584	13.24716	6.597069	14.23244	7.363456	21.37109	-0.90581	0.22791	0.34113	ELN	chr7	+	73442119	73484237	3781
ENSG00000(	403.9588	376.9421	298.1875	1279.421	959.0901	1034.854	-1.5932	1.07E-22	1.21E-21	RFC2	chr7	-	73645829	73668774	1695
ENSG00000(	1232.592	1169.363	1384.065	850.9498	1237.061	951.8354	0.3163	0.037195	0.075132	ARID1B	chr6	+	1.57E+08	1.58E+08	8246
ENSG00000(	1731.844	1521.015	1607.046	2912.406	2342.499	2506.993	-0.67406	5.00E-08	2.36E-07	CLPTM1L	chr5	-	1317859	1345214	3540
ENSG00000(	286.9144	362.4906	372.0747	925.1083	806.2984	722.5072	-1.263	3.82E-15	3.04E-14	NEDD4L	chr18	+	55711599	56068772	8436
ENSG00000(	4.143168	21.67718	7.916483	6.74168	7.363456	2.465895	0.91931	0.25942	0.3782	FOXP3	chrX	-	49106897	49121288	2382
ENSG00000(	209.23	192.686	160.9685	74.15848	65.35067	91.23811	1.2769	1.16E-07	5.29E-07	PPP1R3F	chrX	+	49126306	49157929	3421
ENSG00000(	1955.575	1784.754	1947.455	2137.113	1840.864	1801.747	-0.02334	0.84442	0.9007	HEXB	chr5	+	73935848	74018472	2021
ENSG00000(	107.7224	75.87013	104.2337	158.804	80.07758	108.4994	-0.27107	0.35736	0.48682	PTCD2	chr5	+	71616194	71656052	2648
ENSG00000(	0	0	0	9.737982	16.56778	11.50751	-4.5124	8.25E-05	0.000272	KIAA2022	chrX	-	73952684	74145320	11759
ENSG00000(	648.4057	588.8967	667.6234	558.0613	482.3064	403.5848	0.39763	0.011379	0.02611	JKAMP	chr14	+	59951161	59972128	2302
ENSG00000(	3756.817	3468.349	3832.897	2150.596	1860.193	1879.012	0.90689	1.02E-15	8.38E-15	DKK3	chr11	-	11984653	12031316	2650
ENSG00000(	44.53905	42.15007	68.60952	93.63444	173.0412	165.2149	-1.4598	3.62E-06	1.41E-05	ARHGEF5	chr7	+	1.44E+08	1.44E+08	5544
ENSG00000(	67.32647	51.78437	35.62417	966.3075	714.2552	600.0344	-3.8373	5.11E-60	1.79E-58	NFE2L3	chr7	+	26191860	26226745	3686
ENSG00000(	254.8048	254.1047	242.7721	623.9799	541.214	528.5234	-1.168	1.09E-13	7.99E-13	MCUR1	chr6	-	13791020	13814800	1826
ENSG00000(	3109.447	3084.181	3528.112	5116.935	5024.638	4183.801	-0.55844	3.12E-06	1.22E-05	LIMA1	chr12	-	50569571	50677329	3920
ENSG00000(	743.6986	810.4856	692.6922	644.954	598.2808	628.8032	0.26264	0.049692	0.096579	LETMD1	chr12	+	51441745	51454207	2948
ENSG00000(	8.286335	7.225726	10.55531	86.14369	133.4626	102.7456	-3.5406	1.16E-16	9.96E-16	SLC4A8	chr12	+	51785101	51902980	4395
ENSG00000(	0	8.430014	0	5.992604	12.88605	6.575719	-1.3206	0.19644	0.30317	LAMC3	chr9	+	1.34E+08	1.34E+08	6133

ENSG00000(	0	0	5.277655	139.3281	185.0068	139.734	-6.1603	1.41E-21	1.53E-20	PTGER3	chr1	-	71318036	71513491	6982
ENSG00000(	2.071584	4.817151	1.319414	4.494453	1.840864	4.93179	-0.37497	0.72396	0.81464	TNIP3	chr4	-	1.22E+08	1.22E+08	2429
ENSG00000(	535.5044	508.2094	490.8219	838.9646	734.5047	683.8748	-0.55501	9.27E-05	0.000304	MAPK9	chr5	-	1.8E+08	1.8E+08	4815
ENSG00000(	24.85901	36.12863	36.94359	117.6049	156.4734	147.1317	-2.0861	7.36E-12	4.73E-11	COL23A1	chr5	-	1.78E+08	1.78E+08	3061
ENSG00000(	4328.574	3989.805	3864.563	5876.498	5263.951	5731.561	-0.46891	1.05E-05	3.89E-05	BCAR1	chr16	-	75262928	75301951	4659
ENSG00000(	586.2582	552.7681	581.8615	429.9694	472.1816	427.4218	0.37196	0.008222	0.019475	FAM160A2	chr11	-	6232565	6255941	3481
ENSG00000(	1216.02	1224.761	1293.026	807.5034	656.268	639.4887	0.82483	9.18E-10	5.04E-09	HERPUD1	chr16	+	56965960	56977798	2199
ENSG00000(	743.6986	621.4125	560.7509	194.7596	265.0844	262.2068	1.4128	1.23E-15	1.01E-14	HOMER3	chr19	-	19040010	19052070	1979
ENSG00000(	64.2191	71.05298	56.73479	708.6255	532.9301	573.7315	-3.221	2.00E-56	6.40E-55	RAD51	chr15	+	40986972	41024354	2266
ENSG00000(	108.7581	78.2787	121.3861	379.7813	468.4999	397.0091	-2.0023	2.29E-22	2.55E-21	POLQ	chr3	-	1.21E+08	1.21E+08	8775
ENSG00000(	148.1182	214.3632	201.8703	270.4163	337.7985	292.6195	-0.6735	0.000794	0.002264	PIK3CB	chr3	-	1.38E+08	1.39E+08	4747
ENSG00000(	84.93494	95.13873	63.33186	1742.35	1925.544	2547.269	-4.646	8.54E-135	1.08E-132	CYBA	chr16	-	88709691	88717560	1415
ENSG00000(	485.7864	401.0278	443.323	573.0428	670.0745	739.7684	-0.57268	0.000224	0.000693	THOC3	chr5	-	1.75E+08	1.75E+08	1796
ENSG00000(	993.3244	843.0014	821.9948	922.8611	890.0577	1208.288	-0.18326	0.22632	0.33918	HEBP2	chr6	+	1.39E+08	1.39E+08	990
ENSG00000(	251.6974	301.0719	362.8388	418.7332	408.6718	364.1305	-0.38186	0.031169	0.064286	MPHOSPH9	chr12	-	1.24E+08	1.24E+08	5799
ENSG00000(	385.3146	340.8134	449.9201	466.6741	564.2248	452.9027	-0.33435	0.044264	0.087376	PLEKHA5	chr12	+	19282648	19529334	6487
ENSG00000(	6.214751	0	0	965.5584	905.7051	984.714	-8.2971	4.70E-57	1.53E-55	PRSS8	chr16	-	31142756	31147083	1870
ENSG00000(	584.1866	675.6054	774.4959	927.3555	906.6255	829.3626	-0.38953	0.00645	0.015632	SIKE1	chr1	-	1.15E+08	1.15E+08	5506
ENSG00000(	813.0966	731.0026	637.2769	1307.886	1258.231	1314.322	-0.8274	3.15E-10	1.80E-09	RRP12	chr10	-	99116115	99161127	4399
ENSG00000(	234.089	195.0946	273.1187	433.7147	529.2484	413.4484	-0.96693	1.20E-07	5.46E-07	FNIP2	chr4	+	1.6E+08	1.6E+08	6925
ENSG00000(	2917.826	2915.581	3229.925	2244.23	1816.933	1869.148	0.61009	5.35E-07	2.29E-06	MSMO1	chr4	+	1.66E+08	1.66E+08	2269
ENSG00000(	1220.163	1053.752	1277.193	757.3154	775.0037	655.928	0.69681	2.47E-07	1.09E-06	TTC17	chr11	+	43380482	43516483	4469
ENSG00000(	49.71801	24.08575	31.66593	19.47596	84.67974	62.46933	-0.62786	0.18685	0.29148	ALX4	chr11	-	44281994	44331716	5750
ENSG00000(	13.46529	12.04288	19.79121	0	0	1.64393	3.934	6.46E-05	0.000216	FSTL4	chr5	-	1.33E+08	1.33E+08	5419
ENSG00000(	832.7767	839.3885	1015.949	537.0872	684.8014	518.6599	0.62529	4.74E-05	0.000162	FOXN3	chr14	-	89591215	90085493	7832
ENSG00000(	0	0	1.319414	3.745378	10.12475	3.28786	-2.6172	0.030302	0.062715	METTL24	chr6	-	1.11E+08	1.11E+08	1119
ENSG00000(	1658.303	1664.326	1249.485	1041.964	1087.03	1087.46	0.50703	0.000211	0.000657	AKR7A2	chr1	-	19630459	19638640	1362
ENSG00000(	1466.681	1323.512	1042.337	4239.768	2798.113	3275.53	-1.4224	1.48E-18	1.41E-17	MRTO4	chr1	+	19578033	19586622	2315
ENSG00000(	40.39588	24.08575	51.45714	2.996302	21.16994	16.4393	1.4559	0.010636	0.024564	NNAT	chr20	+	36149617	36152092	1294
ENSG00000(	348.0261	331.1791	258.6051	159.5531	97.56579	148.7757	1.198	6.25E-08	2.92E-07	USE1	chr19	+	17326155	17330638	1776
ENSG00000(	26.93059	25.29004	19.79121	8.239831	6.443024	13.9734	1.2661	0.028023	0.058543	MCF2L2	chr3	-	1.83E+08	1.83E+08	7813
ENSG00000(	97.36444	103.5687	75.20659	45.69361	50.62376	62.46933	0.79155	0.00855	0.020188	NRIP2	chr12	-	2934514	2944710	2746
ENSG00000(	78.72018	45.76293	80.48424	68.16587	74.55499	75.62077	-0.08871	0.77694	0.85319	LAMA3	chr18	+	21269407	21535030	10661
ENSG00000(	312.8092	325.1577	370.7553	670.4226	641.5411	451.2587	-0.80363	6.60E-06	2.50E-05	AP5M1	chr14	+	57735627	57756797	3074
ENSG00000(	371.8493	372.1249	336.4505	483.1537	402.2288	448.7928	-0.30339	0.052152	0.10075	ANAPC4	chr4	+	25378835	25420120	3807
ENSG00000(	0	0	1.319414	5.992604	0	0.821965	-1.3152	0.32844	0.45614	KCNQ1	chr11	+	2465914	2870339	3245
ENSG00000(	943.6064	851.4314	845.7442	1284.665	1132.131	1320.898	-0.49971	8.22E-05	0.000271	TRAPPC3	chr1	-	36602173	36615098	2428
ENSG00000(	2926.112	3123.922	3195.62	2414.27	3728.67	3248.405	-0.02227	0.87866	0.92418	THRAP3	chr1	+	36690017	36770958	4432
ENSG00000(	2352.283	2332.705	1836.624	1190.281	1336.467	1655.437	0.63964	1.56E-05	5.66E-05	PHPT1	chr9	+	1.4E+08	1.4E+08	1316
ENSG00000(	7.250543	4.817151	6.597069	5.243529	8.283888	15.61733	-0.57891	0.46154	0.59077	ENTPD2	chr9	-	1.4E+08	1.4E+08	2095
ENSG00000(	0	2.408575	0	0	0.920432	0.821965	0.212	0.87508	NA	LY75	chr2	-	1.61E+08	1.61E+08	6886
ENSG00000(	785.1303	709.3255	976.3662	461.4305	506.2376	400.2969	0.84961	1.12E-07	5.09E-07	ARID4B	chr1	-	2.35E+08	2.35E+08	6067
ENSG00000(	237.1963	175.826	278.3963	87.64184	71.7937	69.86702	1.5763	6.59E-11	3.96E-10	OPN3	chr1	-	2.42E+08	2.42E+08	2620
ENSG00000(	391.5293	427.5221	395.8241	216.4828	200.6542	206.3132	0.958	5.17E-09	2.67E-08	SDCCAG8	chr1	+	2.43E+08	2.44E+08	2567

ENSG0000(	200.9436	250.4918	113.4696	13.48336	27.61296	13.9734	3.3173	8.29E-21	8.67E-20	PTPRN	chr2	-	2.2E+08	2.2E+08	5099
ENSG0000(	110.8297	79.48299	126.6637	116.1067	166.5982	166.8589	-0.49879	0.055254	0.10602	HHAT	chr1	+	2.11E+08	2.11E+08	3626
ENSG0000(	1449.073	1369.275	1914.469	1313.129	1648.494	1224.728	0.1762	0.25849	0.37722	KIF1B	chr1	+	10270863	10441661	10669
ENSG0000(	619.4036	529.8866	633.3186	173.7855	122.4175	125.7606	2.0654	1.50E-29	2.25E-28	FOXC1	chr6	+	1610681	1614127	3447
ENSG0000(	776.8439	868.2914	683.4563	554.3159	450.0912	528.5234	0.60082	6.11E-05	0.000205	TBC1D22A	chr22	+	47158518	47571336	3787
ENSG0000(	386.3504	358.8777	494.7802	650.9467	915.8298	813.7453	-0.93803	4.98E-08	2.35E-07	SYNE2	chr14	+	64319683	64693165	21878
ENSG0000(	13.46529	10.83859	17.15238	217.981	352.5255	251.5213	-4.2484	8.05E-37	1.52E-35	PLEKHH1	chr14	+	68000018	68056329	6604
ENSG0000(	579.0077	535.908	621.4439	117.6049	158.3143	134.8022	2.0747	6.98E-33	1.17E-31	ATP9A	chr20	-	50213053	50385173	8106
ENSG0000(	2.071584	0	2.638828	4.494453	4.60216	0	-0.67109	0.58635	0.70371	CHRDL2	chr11	-	74407474	74442430	1971
ENSG0000(	1329.957	1383.727	1690.169	499.6334	645.2228	521.9477	1.398	3.23E-21	3.43E-20	FAM168A	chr11	-	73111532	73309234	7296
ENSG0000(	105.6508	48.17151	46.17948	202.9995	191.4499	232.6161	-1.616	2.94E-08	1.42E-07	RELT	chr11	+	73087309	73108519	4346
ENSG0000(	220.6237	177.0303	199.2315	226.9699	259.5618	196.4496	-0.19081	0.33888	0.46747	GALC	chr14	-	88304164	88460009	3883
ENSG0000(	969.5012	944.1616	880.049	2587.307	1981.69	2210.264	-1.2758	2.33E-22	2.59E-21	NOP58	chr2	+	2.03E+08	2.03E+08	2046
ENSG0000(	4329.61	4031.955	4219.485	2146.851	2537.631	2917.975	0.72536	1.05E-08	5.24E-08	SZRD1	chr1	+	16679070	16724640	3636
ENSG0000(	2.071584	2.408575	0	3.745378	11.04518	17.26126	-2.3478	0.016708	0.036925	KCNH2	chr7	-	1.51E+08	1.51E+08	4717
ENSG0000(	855.5641	952.5916	940.742	2390.3	1994.576	1891.341	-1.1892	6.57E-20	6.62E-19	CUL1	chr7	+	1.48E+08	1.48E+08	3064
ENSG0000(	337.6682	317.932	325.8952	208.9921	197.8929	173.4346	0.75491	1.83E-05	6.56E-05	FAM114A2	chr5	-	1.53E+08	1.53E+08	4443
ENSG0000(	889.7452	846.6143	924.9091	1612.76	1368.682	1304.458	-0.68648	1.21E-07	5.51E-07	CYFIP2	chr5	+	1.57E+08	1.57E+08	6791
ENSG0000(	1921.394	1954.559	2148.006	1128.857	1179.073	1017.593	0.85532	6.96E-13	4.82E-12	TAB2	chr6	+	1.5E+08	1.5E+08	4553
ENSG0000(	632.8689	566.0152	572.6256	372.2905	287.1748	339.4715	0.82272	1.50E-07	6.76E-07	GINM1	chr6	+	1.5E+08	1.5E+08	2024
ENSG0000(	1287.489	1325.921	1513.368	997.0196	1140.415	950.1914	0.41741	0.001294	0.003568	EIF2AK2	chr2	-	37326353	37384208	10042
ENSG0000(	1267.809	1119.988	1153.168	1157.322	1084.269	1113.762	0.077884	0.51541	0.64203	USP36	chr17	-	76783463	76837523	5885
ENSG0000(	923.9264	986.3116	1302.261	552.8178	823.7866	572.9095	0.71773	5.26E-05	0.000178	MLL3	chr7	-	1.52E+08	1.52E+08	17029
ENSG0000(	5.17896	0	11.87472	181.2763	179.4842	212.0669	-4.9676	4.21E-29	6.17E-28	MCOLN3	chr1	-	85483765	85514182	2953
ENSG0000(	63.18331	83.09585	69.92893	74.15848	57.98722	60.8254	0.15792	0.60168	0.71684	CCDC85A	chr2	+	56411258	56613308	3982
ENSG0000(	1385.89	1382.522	1621.56	1588.04	1522.395	1176.232	0.033742	0.81127	0.87761	PUM2	chr2	-	20448452	20551995	6117
ENSG0000(	630.7973	737.0241	544.9179	716.1162	487.829	558.9361	0.11649	0.49988	0.62814	MRPL43	chr10	-	1.03E+08	1.03E+08	2134
ENSG0000(	0	3.612863	0	0	1.840864	0	0.45719	0.73538	NA	ITIH4	chr3	-	52846991	52865495	3336
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	ITIH1	chr3	+	52811603	52826078	2911
ENSG0000(	413.281	419.0921	402.4212	414.9879	403.1492	415.0923	0.001859	0.98988	0.99415	C4orf27	chr4	-	1.71E+08	1.71E+08	1230
ENSG0000(	1653.124	1543.897	1906.553	1501.147	1640.21	1263.36	0.21177	0.12023	0.20411	ZFR	chr5	-	32354456	32444867	4738
ENSG0000(	217.5163	174.6217	252.008	254.6857	203.4155	191.5178	-0.01464	0.94435	0.9667	ZNF280C	chrX	-	1.29E+08	1.29E+08	4634
ENSG0000(	0	0	0	1.498151	3.681728	1.64393	-1.9249	0.15383	0.24921	NPFFR2	chr4	+	72897521	73013784	1922
ENSG0000(	10.35792	6.021439	17.15238	59.17697	80.99802	69.86702	-2.5848	8.45E-09	4.26E-08	PHF21B	chr22	-	45277042	45405880	3671
ENSG0000(	33.14534	49.3758	38.263	20.22504	25.7721	19.72716	0.85659	0.045912	0.090158	TRAF1	chr9	-	1.24E+08	1.24E+08	6324
ENSG0000(	1019.219	1074.225	1388.023	1089.905	1288.605	1037.32	0.026702	0.85756	0.90947	RC3H2	chr9	-	1.26E+08	1.26E+08	9248
ENSG0000(	870.0652	959.8173	808.8006	1198.521	1003.271	1060.335	-0.30549	0.021443	0.046168	PCGF2	chr17	-	36890150	36906070	3062
ENSG0000(	71.46964	43.35436	81.80365	62.17327	55.22592	67.40112	0.086049	0.79406	0.86534	IL17RB	chr3	+	53880607	53899827	2822
ENSG0000(	624.5825	573.241	604.2915	427.7221	395.7858	331.2519	0.63994	2.88E-05	0.000101	TRAF3IP2	chr6	-	1.12E+08	1.12E+08	5128
ENSG0000(	101.5076	60.21439	102.9143	288.3941	267.8457	287.6877	-1.6604	4.35E-13	3.06E-12	GYG2	chrX	+	2746829	2800859	3393
ENSG0000(	4819.54	4743.689	6195.967	1833.737	1715.685	1379.257	1.672	4.31E-32	6.99E-31	DCBLD2	chr3	-	98514785	98620533	6122
ENSG0000(	0	2.408575	2.638828	0	0	0	1.6365	0.22501	NA	SERPINB3	chr18	-	61322431	61329197	1777
ENSG0000(	910.4611	930.9144	1074.003	768.5515	771.322	698.6702	0.37939	0.003899	0.009876	SOAT1	chr1	+	1.79E+08	1.79E+08	6835
ENSG0000(	67.32647	74.66584	73.88717	2195.54	1918.18	1518.991	-4.6869	1.34E-143	1.91E-141	PKP2	chr12	-	32943679	33049774	4302

ENSG00000(	13.46529	6.021439	9.235896	5.243529	3.681728	9.863579	0.55906	0.47543	0.60463	MSH4	chr1	+	76262567	76378923	3266
ENSG00000(	0	0	0	0	2.761296	3.28786	-1.6293	0.2296	0.34285	F7	chr13	+	1.14E+08	1.14E+08	3109
ENSG00000(	7443.201	7358.198	7347.815	7781.397	7999.474	7123.148	-0.04823	0.63085	0.74092	GDI2	chr10	-	5807186	5884095	2499
ENSG00000(	61.11172	63.82725	56.73479	98.1289	91.12277	59.18147	-0.44495	0.15275	0.24777	PRDM1	chr6	+	1.07E+08	1.07E+08	5164
ENSG00000(	344.9187	321.5448	325.8952	772.2969	567.9065	583.5951	-0.9519	8.24E-09	4.16E-08	ATG5	chr6	-	1.07E+08	1.07E+08	3216
ENSG00000(	16.57267	24.08575	14.51355	103.3724	149.11	126.5826	-2.73	7.48E-15	5.85E-14	TMCC3	chr12	-	94960900	95044338	5877
ENSG00000(	1883.07	1740.196	1760.098	1071.178	960.931	1071.02	0.79315	1.07E-11	6.80E-11	PITHD1	chr1	+	24104895	24114722	1603
ENSG00000(	870.0652	951.3873	808.8006	624.729	664.5519	664.1477	0.42881	0.001085	0.003026	MTA3	chr2	+	42721709	42984087	5832
ENSG00000(	592.473	454.0165	655.7486	435.962	429.8417	399.475	0.42593	0.009541	0.022296	USP13	chr3	+	1.79E+08	1.8E+08	8323
ENSG00000(	569.6855	507.0051	705.8864	424.7258	500.715	400.2969	0.42528	0.010432	0.024151	ATP11B	chr3	+	1.83E+08	1.83E+08	7325
ENSG00000(	129.474	125.2459	171.5238	1343.842	1417.465	1166.368	-3.1977	2.36E-85	1.38E-83	LAMC2	chr1	+	1.83E+08	1.83E+08	5147
ENSG00000(	445.3905	427.5221	460.4754	211.2393	241.1532	138.0901	1.1699	5.46E-09	2.81E-08	CDK14	chr7	+	90095738	90839905	5163
ENSG00000(	14821.15	13760.19	13864.4	7263.037	7378.183	7697.701	0.92492	2.76E-21	2.95E-20	SEC61A1	chr3	+	1.28E+08	1.28E+08	3635
ENSG00000(	1074.116	983.9031	1281.151	1076.422	1122.007	946.9036	0.085506	0.53842	0.66223	PPP1R12A	chr12	-	80167343	80329240	5721
ENSG00000(	0	0	0	12.73428	12.88605	12.32947	-4.5296	7.38E-05	0.000245	RASGRF1	chr15	-	79252289	79383115	6294
ENSG00000(	14.50109	12.04288	15.83297	2.247227	2.761296	0.821965	2.5606	0.002063	0.005487	CAMK2B	chr7	-	44256749	44374176	4447
ENSG00000(	379.0998	388.9849	327.2146	224.7227	256.8005	305.7709	0.47595	0.007953	0.018905	CROCC	chr1	+	17066768	17299474	6656
ENSG00000(	451.6053	413.0707	442.0036	786.5293	761.1973	770.1811	-0.82465	8.81E-10	4.85E-09	POLR3E	chr16	+	22308730	22346424	4800
ENSG00000(	3869.719	4043.998	4986.065	963.3112	1503.986	1006.907	1.8864	9.37E-31	1.46E-29	ATP2B4	chr1	+	2.04E+08	2.04E+08	8968
ENSG00000(	2848.428	2819.238	3174.51	1632.985	1807.728	1503.374	0.83715	1.55E-12	1.05E-11	ZC3H11A	chr1	+	2.04E+08	2.04E+08	8404
ENSG00000(	319.0239	455.2208	377.3523	462.1796	346.0824	387.1455	-0.05626	0.75659	0.83898	RIOK2	chr5	-	96496571	96518964	3922
ENSG00000(	334.5608	254.1047	275.7575	388.7702	273.3683	349.3351	-0.2252	0.23653	0.35104	YIPF1	chr1	-	54317392	54356407	1803
ENSG00000(	427.7821	401.0278	514.5714	1710.889	1476.373	1438.439	-1.7809	4.20E-36	7.77E-35	TMEM48	chr1	-	54231133	54304533	5134
ENSG00000(	5.17896	6.021439	1.319414	4.494453	6.443024	4.109825	-0.21186	0.82317	0.88592	DGKG	chr3	-	1.86E+08	1.86E+08	6054
ENSG00000(	1239.843	1020.032	1011.99	683.1569	668.2336	699.4921	0.67319	4.68E-07	2.01E-06	FLYWCH1	chr16	+	2961938	3001209	5141
ENSG00000(	339.7397	280.599	310.0622	572.2937	724.38	720.8632	-1.1107	5.57E-12	3.62E-11	UNKL	chr16	-	1413206	1464752	5078
ENSG00000(	103.5792	96.34302	129.3026	3.745378	9.20432	4.109825	4.1835	1.64E-21	1.77E-20	TBXAS1	chr7	+	1.39E+08	1.4E+08	2367
ENSG00000(	21.75163	34.92434	30.34652	55.43159	26.69253	23.01502	-0.27444	0.55702	0.67755	PARP12	chr7	-	1.4E+08	1.4E+08	3796
ENSG00000(	2143.053	2024.408	2220.573	1634.483	1584.984	1472.961	0.44412	7.37E-05	0.000245	ALDH18A1	chr10	-	97365696	97416463	3349
ENSG00000(	234.089	252.9004	282.3545	422.4786	365.4115	321.3883	-0.52836	0.003015	0.007787	TARBP1	chr1	-	2.35E+08	2.35E+08	5130
ENSG00000(	392.5651	382.9635	325.8952	519.1094	409.5922	437.2853	-0.30898	0.05989	0.11353	PET112	chr4	-	1.53E+08	1.53E+08	6552
ENSG00000(	183.3352	146.9231	232.2168	112.3613	119.6562	120.0069	0.66967	0.003776	0.009589	MXD1	chr2	+	70124820	70170077	5587
ENSG00000(	1500.862	1527.037	1684.891	410.4934	445.4891	268.7825	2.0594	1.58E-34	2.79E-33	CDK17	chr12	-	96672039	96794338	4157
ENSG00000(	177.1204	232.4275	254.6469	229.9662	173.0412	161.1051	0.22919	0.29638	0.42085	DNAJC25	chr9	+	1.14E+08	1.14E+08	2572
ENSG00000(	1753.596	1836.539	1742.946	29854.41	32629.31	28537.8	-4.0872	0	0	SLC2A3	chr12	-	8071826	8088871	4414
ENSG00000(	74.57702	72.25726	67.2901	8.239831	12.88605	8.219649	2.8087	2.54E-11	1.57E-10	PSD	chr10	-	1.04E+08	1.04E+08	4183
ENSG00000(	533.4328	578.0581	587.1391	844.9572	895.5803	1003.619	-0.69097	3.46E-07	1.51E-06	CTDP1	chr18	+	77439801	77514510	3753
ENSG00000(	4857.864	4542.573	4034.767	9355.954	7874.296	7193.015	-0.86021	8.81E-12	5.63E-11	YBX3	chr12	-	10851683	10875911	6393
ENSG00000(	0	0	0	41.94823	36.81728	53.42772	-6.2756	1.87E-09	9.99E-09	STYK1	chr12	-	10771538	10826917	2995
ENSG00000(	2416.503	2423.027	3252.355	1698.154	2081.097	1692.426	0.56274	9.27E-05	0.000304	WNK1	chr12	+	861759	1020618	11232
ENSG00000(	1228.449	1181.406	1285.109	2391.049	2114.232	2186.427	-0.85574	8.23E-14	6.04E-13	CCAR1	chr10	+	70480769	70552134	4683
ENSG00000(	1235.7	1200.675	1018.587	964.0602	1015.236	1144.175	0.1461	0.27143	0.39219	OGFR	chr20	+	61436187	61445352	4506
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	GNA15	chr19	+	3136191	3163767	2133
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CREB3L3	chr19	+	4153598	4173051	2618

ENSG0000(	162.6193	157.7617	197.9121	154.3096	162.9165	127.4046	0.21827	0.31634	0.44316	PIGV	chr1	+	27113963	27124889	2713
ENSG0000(	348.0261	355.2649	288.9516	832.2229	937.9202	958.4111	-1.4528	6.20E-23	7.05E-22	PTPRU	chr1	+	29563028	29653325	5579
ENSG0000(	479.5717	402.2321	409.0183	1436.727	1215.891	1286.375	-1.6039	5.35E-31	8.40E-30	SNRNP40	chr1	-	31732417	31769662	1928
ENSG0000(	1.035792	0	0	7.490755	2.761296	10.68554	-2.9623	0.012462	0.028357	RIMBP2	chr12	-	1.31E+08	1.31E+08	6321
ENSG0000(	20956.14	20787.21	24554.29	8167.92	12222.42	10867.2	1.0819	2.15E-14	1.63E-13	COL11A1	chr1	-	1.03E+08	1.04E+08	7327
ENSG0000(	788.2376	873.1086	1204.625	1188.034	1438.635	1044.717	-0.35694	0.035409	0.071874	QSER1	chr11	+	32914724	33014862	9335
ENSG0000(	336.6324	258.9219	343.0476	262.9255	215.3811	214.5328	0.43464	0.021261	0.04584	MPC1	chr6	-	1.67E+08	1.67E+08	962
ENSG0000(	689.8374	718.9598	661.0263	683.1569	611.1668	681.4089	0.066644	0.61592	0.72889	ACAA1	chr3	-	38164201	38178733	4720
ENSG0000(	2767.636	2765.045	3158.677	3625.526	4100.525	3345.397	-0.34864	0.003511	0.008963	BCAT1	chr12	-	24964295	25102393	8335
ENSG0000(	3108.412	3129.944	2712.715	1613.509	1774.593	1856.819	0.77019	4.19E-11	2.55E-10	HDAC7	chr12	-	48176505	48226915	6414
ENSG0000(	1067.901	981.4945	1106.988	757.3154	795.2532	723.3291	0.47096	0.000173	0.000546	LZTS1	chr8	-	20103676	20161474	5706
ENSG0000(	14.50109	22.88147	14.51355	2.996302	3.681728	4.109825	2.0943	0.003636	0.00926	PRDM6	chr5	+	1.22E+08	1.23E+08	3052
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	WNT8A	chr5	+	1.37E+08	1.37E+08	1597
ENSG0000(	135.6887	174.6217	127.9831	10.48706	20.2495	14.79537	3.231	1.26E-21	1.37E-20	SPAG4	chr20	+	34203814	34208971	1453
ENSG0000(	1713.2	1777.529	2324.807	3097.427	2894.759	2339.312	-0.51785	0.000426	0.001266	NCKAP1	chr2	-	1.84E+08	1.84E+08	4989
ENSG0000(	943.6064	1000.763	971.0885	1317.624	859.6835	892.6539	-0.07526	0.64389	0.75113	MRPS35	chr12	+	27863706	27909228	1888
ENSG0000(	8.286335	24.08575	25.06886	173.7855	206.1768	186.586	-3.2809	6.12E-23	6.97E-22	GUCY1B3	chr4	+	1.57E+08	1.57E+08	3124
ENSG0000(	1111.405	1166.955	1124.141	986.5325	1051.133	1027.456	0.15052	0.19844	0.30572	SFSWAP	chr12	+	1.32E+08	1.32E+08	5593
ENSG0000(	619.4036	572.0367	456.5172	934.0972	925.0342	1168.834	-0.87288	2.50E-08	1.21E-07	TNK2	chr3	-	1.96E+08	1.96E+08	5940
ENSG0000(	971.5728	1053.752	1249.485	511.6186	601.9625	432.3535	1.0793	5.83E-12	3.77E-11	MON2	chr12	+	62860597	62991363	10382
ENSG0000(	51.7896	54.19295	39.58241	4915.434	4486.186	4579.167	-6.5501	0	0	CDH3	chr16	+	68670092	68756519	3702
ENSG0000(	873.1726	998.3545	1087.197	1267.436	1076.905	943.6157	-0.15312	0.29448	0.41889	GPBP1	chr5	+	56469775	56560506	4683
ENSG0000(	1.035792	3.612863	6.597069	0	0.920432	3.28786	1.0428	0.37912	0.50984	DGAT2	chr11	+	75470557	75512579	5926
ENSG0000(	138.7961	107.1816	127.9831	64.4205	102.168	76.44274	0.62113	0.021408	0.046106	ZNF112	chr19	-	44830708	44871377	3654
ENSG0000(	3739.209	3506.886	3687.762	4346.136	3771.01	3507.324	-0.08831	0.44365	0.57332	CS	chr12	-	56665483	56694176	3057
ENSG0000(	21.75163	8.430014	39.58241	17.22874	11.04518	4.109825	1.0279	0.11788	0.20093	LTK	chr15	-	41795836	41806085	3444
ENSG0000(	2.071584	10.83859	1.319414	15.73059	5.522592	3.28786	-0.68832	0.4579	0.58749	MRPS24	chr7	-	43906157	43909492	1727
ENSG0000(	700.1953	700.8955	827.2724	721.3598	642.4615	572.9095	0.20039	0.1693	0.26923	ELMO2	chr20	-	44994688	45061704	4121
ENSG0000(	767.5218	816.5071	911.7149	1030.728	1188.278	950.1914	-0.34427	0.012428	0.028288	WAPAL	chr10	-	88195013	88281572	6333
ENSG0000(	2540.798	2569.95	2662.577	1769.316	1359.478	1506.662	0.74352	2.44E-09	1.30E-08	VMP1	chr17	+	57784553	57919616	4325
ENSG0000(	1134.192	1166.955	1308.858	760.3117	730.823	612.3639	0.77655	1.09E-08	5.46E-08	APPBP2	chr17	-	58520520	58603580	6468
ENSG0000(	390.4935	458.8336	329.8534	1783.549	1865.716	2149.438	-2.29	4.12E-55	1.28E-53	POLD1	chr19	+	50887461	50921273	3474
ENSG0000(	11.39371	19.2686	6.597069	0.749076	9.20432	1.64393	1.5184	0.079561	0.14469	SEZ6	chr17	-	27281919	27333458	4471
ENSG0000(	16549.88	17345.36	17050.78	6184.368	6625.27	6076.787	1.4298	1.47E-48	3.90E-47	EIF4B	chr12	+	53399942	53435993	4148
ENSG0000(	166.7625	197.5032	199.2315	20.22504	34.97642	23.01502	2.8274	6.78E-23	7.71E-22	SLC6A16	chr19	-	49792895	49828482	2983
ENSG0000(	556.2203	651.5197	506.6549	670.4226	809.0597	747.9881	-0.37549	0.011612	0.026586	GLTSCR1	chr19	+	48111453	48206533	5684
ENSG0000(	487.858	498.5751	320.6175	506.3751	485.9881	646.0644	-0.32251	0.085718	0.15447	SPHK2	chr19	+	49122548	49133974	3092
ENSG0000(	22014.72	21354.43	14974.03	15150.8	11502.64	14028.48	0.51862	0.000522	0.00153	RPL18	chr19	-	49118585	49122793	3844
ENSG0000(	71.46964	86.70872	72.56776	2.996302	4.60216	4.109825	4.1585	9.37E-17	8.10E-16	CA11	chr19	-	49141199	49149569	1844
ENSG0000(	1209.805	1216.331	973.7274	553.5668	381.9793	464.4102	1.2746	1.85E-15	1.50E-14	ISOC2	chr19	-	55964352	55973710	2283
ENSG0000(	4355.505	4133.115	3926.575	6137.176	6489.046	7843.189	-0.71977	2.07E-09	1.10E-08	U2AF2	chr19	+	56165512	56186081	3022
ENSG0000(	6042.81	5697.485	4530.867	5116.186	4312.224	4910.418	0.18213	0.15928	0.25624	EPN1	chr19	+	56186592	56221224	2621
ENSG0000(	992.2886	979.0859	1113.585	822.485	864.2856	828.5406	0.29348	0.018304	0.040071	MED29	chr19	+	39881943	39891277	3653
ENSG0000(	2143.053	2101.482	2120.298	29.96302	48.7829	26.30288	5.9113	9.06E-225	3.49E-222	AHRR	chr5	+	304291	438406	5661

ENSG00000(	560.3634	538.3166	678.1787	211.2393	231.9489	152.0635	1.5705	2.51E-17	2.24E-16	ZNF275	chrX	+	1.53E+08	1.53E+08	6418
ENSG00000(	323.1671	323.9534	394.5047	577.5372	645.2228	633.735	-0.83275	4.98E-08	2.36E-07	MTMR1	chrX	+	1.5E+08	1.5E+08	4516
ENSG00000(	5425.478	5112.201	4499.201	2309.4	2140.004	2319.585	1.1496	3.35E-24	4.02E-23	GPC1	chr2	+	2.41E+08	2.41E+08	3711
ENSG00000(	71.46964	72.25726	67.2901	188.767	127.94	139.734	-1.104	2.50E-05	8.84E-05	ADCK1	chr14	+	78266426	78401355	3560
ENSG00000(	150.1898	109.5902	117.4278	267.42	293.6178	310.7027	-1.1966	4.70E-09	2.43E-08	HAGH	chr16	-	1845621	1877195	1744
ENSG00000(	1261.595	1188.632	1195.389	1659.202	1515.031	1551.87	-0.37373	0.001091	0.003041	RNF4	chr4	+	2463947	2627047	4123
ENSG00000(	384.2788	344.4263	310.0622	295.8848	275.2092	263.8507	0.31543	0.061996	0.11686	CASP8	chr2	+	2.02E+08	2.02E+08	2930
ENSG00000(	71.46964	68.6444	71.24834	233.7116	211.6994	173.4346	-1.5381	1.11E-10	6.53E-10	LIMCH1	chr4	+	41361624	41702061	6165
ENSG00000(	711.589	714.1426	694.0116	685.4041	629.5755	568.7997	0.16962	0.21287	0.32307	ASUN	chr12	-	27058114	27091259	2974
ENSG00000(	543.7907	440.7693	612.208	1494.406	1612.597	1417.889	-1.4991	1.62E-25	2.04E-24	TM7SF3	chr12	-	27126128	27167367	2709
ENSG00000(	0	0	0	168.542	221.8241	162.7491	-8.1264	9.41E-17	8.13E-16	DLX3	chr17	-	48067369	48072588	2602
ENSG00000(	13.46529	14.45145	26.38828	44.94453	26.69253	47.67397	-1.1146	0.019837	0.043077	SPA17	chr11	+	1.25E+08	1.25E+08	4949
ENSG00000(	16.57267	22.88147	32.98534	0	2.761296	4.93179	2.9736	7.71E-05	0.000255	TSPAN32	chr11	+	2323227	2339430	3325
ENSG00000(	10.35792	8.430014	11.87472	0	0	0	4.582	9.58E-05	0.000314	WISP2	chr20	+	43343485	43357150	2759
ENSG00000(	0	0	0	3.745378	4.60216	0.821965	-2.3295	0.080339	0.14587	DMRT3	chr9	+	976964	991731	2183
ENSG00000(	59.04014	51.78437	50.13772	64.4205	78.23672	59.18147	-0.3173	0.31707	0.44399	ST3GAL6	chr3	+	98451080	98540045	3148
ENSG00000(	8.286335	16.86003	3.958241	20.22504	24.85166	31.23467	-1.3118	0.029431	0.061139	ATP2C2	chr16	+	84402133	84497793	3600
ENSG00000(	9.322127	4.817151	3.958241	26.96672	28.53339	54.24968	-2.4404	4.45E-05	0.000152	NGFR	chr17	+	47572655	47592379	3417
ENSG00000(	240.3037	356.4692	312.7011	310.8664	490.5903	387.1455	-0.38433	0.059719	0.11325	CDON	chr11	-	1.26E+08	1.26E+08	9138
ENSG00000(	544.8265	587.6924	705.8864	636.7142	632.3368	590.9928	-0.01863	0.89864	0.93722	TAF2	chr8	-	1.21E+08	1.21E+08	5048
ENSG00000(	7285.76	6719.925	8929.792	513.1168	822.8662	588.5269	3.5638	1.97E-107	1.69E-105	HIPK2	chr7	-	1.39E+08	1.39E+08	15049
ENSG00000(	1212.912	1129.622	1290.387	1258.447	1464.407	1166.368	-0.0979	0.45336	0.5831	TNPO3	chr7	-	1.29E+08	1.29E+08	3771
ENSG00000(	0	2.408575	0	0	0.920432	0.821965	0.212	0.87508	NA	MEF2BNB-M	chr19	-	19256376	19303400	1804
ENSG00000(	603.8667	558.7895	501.3772	543.0798	508.9989	572.9095	0.035254	0.80707	0.87475	RFXANK	chr19	+	19303008	19312678	1391
ENSG00000(	911.4969	857.4529	664.9845	454.6889	401.3084	446.327	0.89999	6.52E-09	3.33E-08	TMEM161A	chr19	-	19229978	19249322	1930
ENSG00000(	43.50326	109.5902	64.65128	283.8996	241.1532	258.9189	-1.8358	1.90E-11	1.19E-10	LPAR2	chr19	-	19734477	19739739	2546
ENSG00000(	5135.456	5083.298	4643.017	1193.277	953.5675	1020.88	2.225	1.66E-76	8.37E-75	CTSA	chr20	+	44519591	44527459	2187
ENSG00000(	1298.883	1201.879	1307.539	864.4332	1203.005	1052.115	0.28794	0.041119	0.082008	SUGP2	chr19	-	19101697	19144832	5565
ENSG00000(	591.4372	485.328	604.2915	290.6413	414.1944	318.9224	0.71456	4.08E-05	0.00014	SLC12A2	chr5	+	1.27E+08	1.28E+08	6885
ENSG00000(	142.9393	130.0631	153.052	496.6371	416.9557	397.0091	-1.6153	1.60E-18	1.52E-17	SNX24	chr5	+	1.22E+08	1.22E+08	2158
ENSG00000(	7.250543	9.634302	9.235896	66.66772	80.07758	85.48435	-3.0716	5.79E-12	3.76E-11	EYA2	chr20	+	45523263	45817492	2702
ENSG00000(	10319.59	10011.24	9090.761	13848.91	12331.95	13414.47	-0.42775	4.62E-05	0.000158	CNN2	chr19	+	1026212	1039068	2548
ENSG00000(	74.57702	74.66584	65.97069	213.4865	246.6758	295.9074	-1.7966	9.11E-15	7.08E-14	ABCA7	chr19	+	1040102	1065571	6816
ENSG00000(	295.2007	289.0291	298.1875	8.988907	4.60216	3.28786	5.5701	3.82E-52	1.11E-50	SNCAIP	chr5	+	1.22E+08	1.22E+08	4986
ENSG00000(	256.8764	240.8575	282.3545	657.6883	591.8378	495.6448	-1.1586	4.33E-12	2.83E-11	DDX20	chr1	+	1.12E+08	1.12E+08	4332
ENSG00000(	1480.147	1470.435	1698.086	1249.458	1214.05	1030.744	0.41039	0.001415	0.003866	BTBD1	chr15	-	83685174	83736106	3297
ENSG00000(	160.5477	128.8588	157.0102	310.8664	307.4243	225.2184	-0.91175	1.30E-05	4.76E-05	FAR2	chr12	+	29302036	29493913	2095
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	BCAS1	chr20	-	52553316	52687304	6112
ENSG00000(	15.53688	13.24716	22.43003	19.47596	9.20432	23.83698	-0.04499	0.93796	0.96238	CHI3L2	chr1	+	1.12E+08	1.12E+08	2169
ENSG00000(	2501.437	2283.33	2021.342	1200.019	1357.637	1487.757	0.74958	8.35E-09	4.21E-08	SBNO2	chr19	-	1107636	1174282	4922
ENSG00000(	290.0217	273.3733	250.6886	448.6963	400.3879	356.7328	-0.56345	0.000879	0.002487	PMS1	chr2	+	1.91E+08	1.91E+08	3225
ENSG00000(	1968.005	1811.249	1431.564	1106.385	992.2257	1069.376	0.71662	2.23E-07	9.91E-07	HMG20B	chr19	+	3572775	3579086	2434
ENSG00000(	170.9057	219.1804	215.0644	21.72319	39.57858	24.65895	2.7949	1.32E-22	1.48E-21	CALCRL	chr2	-	1.88E+08	1.88E+08	5223
ENSG00000(	378.064	416.6836	320.6175	698.8875	590.9173	619.7615	-0.77251	7.92E-07	3.32E-06	TAF11	chr6	-	34845555	34855866	1580

ENSG00000(	814.1324	751.4755	833.8695	6028.56	8065.746	7229.181	-3.1444	8.00E-131	9.74E-129	ANKS1A	chr6	+	34857042	35059179	6336
ENSG00000(	6764.757	6333.349	6069.303	4753.633	4903.141	5442.23	0.34382	0.001351	0.003712	AP3D1	chr19	-	2100988	2164464	5034
ENSG00000(	386.3504	351.652	348.3252	321.3534	260.4823	284.3999	0.32493	0.051673	0.099942	ZNF76	chr6	+	35226686	35263762	4651
ENSG00000(	759.2355	799.647	575.2644	107.1178	111.3723	106.0335	2.7071	9.55E-52	2.75E-50	SLC9A3R2	chr16	+	2075357	2089027	2194
ENSG00000(	133.6172	174.6217	112.1502	321.3534	200.6542	258.9189	-0.88748	0.000161	0.000511	NTHL1	chr16	-	2089816	2097867	1067
ENSG00000(	156.4046	97.54731	166.2461	402.2536	485.0677	442.2171	-1.6516	1.06E-15	8.70E-15	UHRF1BP1	chr6	+	34759857	34850915	9570
ENSG00000(	1941.074	1959.376	2059.605	2599.292	2392.203	2121.491	-0.25497	0.030242	0.062628	GNAI3	chr1	+	1.1E+08	1.1E+08	3206
ENSG00000(	4670.386	4378.79	4860.72	6246.541	5807.005	5240.026	-0.3137	0.004595	0.011471	IPO5	chr13	+	98605912	98676551	6003
ENSG00000(	1943.146	1899.162	2122.937	1541.597	1629.165	1556.802	0.33477	0.002716	0.007069	OAT	chr10	-	1.26E+08	1.26E+08	2048
ENSG00000(	579.0077	640.6811	668.9428	841.9609	809.9802	675.6552	-0.30178	0.035132	0.071382	WDR3	chr1	+	1.18E+08	1.19E+08	3858
ENSG00000(	776.8439	756.2927	982.9633	901.887	1134.893	849.0898	-0.19756	0.20405	0.3123	PKN2	chr1	+	89149905	89301938	6121
ENSG00000(	670.1574	614.1867	500.0578	1674.184	1505.827	1611.873	-1.4195	7.29E-25	8.96E-24	WDR18	chr19	+	983174	994569	1548
ENSG00000(	6545.169	6129.824	7229.068	1416.502	2030.473	1654.615	1.9596	2.44E-46	6.04E-45	TRAM2	chr6	-	52362200	52441713	6908
ENSG00000(	988.1455	988.7202	880.049	162.5494	234.7102	201.3814	2.2508	3.50E-44	8.17E-43	NTN1	chr17	+	8924859	9147317	5954
ENSG00000(	0	1.204288	2.638828	0	0	0	1.2853	0.33195	NA	GLP2R	chr17	+	9725523	9795419	4572
ENSG00000(	76.6486	66.23582	97.63662	944.5843	1042.849	891.01	-3.5711	9.79E-88	5.93E-86	MCM10	chr10	+	13203554	13253104	4587
ENSG00000(	852.4567	840.5928	726.997	681.6587	629.5755	684.6968	0.27785	0.037857	0.076299	DGKA	chr12	+	56321103	56347811	5436
ENSG00000(	22.78742	7.225726	19.79121	414.9879	600.1217	546.6067	-4.8963	9.93E-62	3.62E-60	ERBB3	chr12	+	56473641	56497289	5919
ENSG00000(	3.107376	0	0	1.498151	6.443024	0	-0.80867	0.53667	0.66063	ROPN1	chr3	-	1.24E+08	1.24E+08	2056
ENSG00000(	78.72018	45.76293	105.5531	3.745378	13.80648	14.79537	2.7542	6.80E-09	3.47E-08	ANKRD44	chr2	-	1.98E+08	1.98E+08	3686
ENSG00000(	2952.007	2875.839	2659.938	4937.157	3832.679	3477.734	-0.52771	0.000107	0.000347	KARS	chr16	-	75661622	75682541	2171
ENSG00000(	191.6215	215.5675	236.1751	432.2166	370.9341	351.801	-0.84391	2.08E-06	8.34E-06	ADAT1	chr16	-	75630879	75657198	2768
ENSG00000(	1948.325	1735.379	1661.142	859.9387	857.8426	908.2712	1.0238	1.94E-17	1.74E-16	PDIA5	chr3	+	1.23E+08	1.23E+08	2232
ENSG00000(	207.1584	178.2346	209.7868	217.981	233.7897	246.5895	-0.22899	0.22439	0.33686	TBC1D22B	chr6	+	37225548	37300746	3462
ENSG00000(	1411.784	1435.511	1232.332	1418.749	1133.052	1527.211	0.00015	0.99914	0.99935	NDUFB4	chr3	+	1.2E+08	1.2E+08	1426
ENSG00000(	927.0338	897.1944	1308.858	991.776	1406.42	1001.975	-0.11789	0.49973	0.62806	SPEN	chr1	+	16174359	16266955	12232
ENSG00000(	1776.383	1801.614	2221.893	597.7623	805.378	567.9778	1.5527	9.03E-24	1.07E-22	MYLK	chr3	-	1.23E+08	1.24E+08	10027
ENSG00000(	973.6444	918.8715	919.6314	1623.996	1292.287	1396.518	-0.61574	1.97E-06	7.91E-06	ZC3H15	chr2	+	1.87E+08	1.87E+08	2138
ENSG00000(	513.7528	602.1439	592.4168	692.1458	659.0293	590.9928	-0.18593	0.19336	0.29924	MAP2K4	chr17	+	11924141	12047147	3856
ENSG00000(	126.3666	101.1602	106.8725	279.4052	185.9273	215.3548	-1.0172	1.03E-05	3.81E-05	TMEM206	chr1	-	2.13E+08	2.13E+08	2475
ENSG00000(	1.035792	0	0	5.243529	0.920432	0.821965	-1.5004	0.26073	0.37985	SNAP91	chr6	-	84262599	84419410	4726
ENSG00000(	713.6606	794.8299	1074.003	964.0602	1150.54	951.0134	-0.24778	0.12497	0.21058	SLK	chr10	+	1.06E+08	1.06E+08	7766
ENSG00000(	194.7289	230.019	219.0227	262.9255	227.3467	241.6577	-0.18688	0.3128	0.43921	CYB5R4	chr6	+	84569362	84670146	2255
ENSG00000(	14.50109	15.65574	25.06886	780.5367	1009.714	861.4192	-5.5555	1.66E-99	1.26E-97	COL17A1	chr10	-	1.06E+08	1.06E+08	5734
ENSG00000(	20.71584	16.86003	23.74945	35.95563	48.7829	27.12484	-0.84075	0.066699	0.1245	GSTO2	chr10	+	1.06E+08	1.06E+08	2694
ENSG00000(	181.2636	143.3102	186.0373	184.2726	157.3939	199.7375	-0.08506	0.68929	0.78777	SEC61A2	chr10	+	12171636	12211960	2462
ENSG00000(	7.250543	0	2.638828	80.90016	89.2819	69.86702	-4.3117	3.42E-14	2.57E-13	PRKCQ	chr10	-	6469105	6622263	3285
ENSG00000(	8.286335	6.021439	5.277655	19.47596	22.09037	16.4393	-1.4583	0.024599	0.052216	TLE2	chr19	-	2997636	3047633	2705
ENSG00000(	1153.872	1150.095	1209.902	547.5742	816.4232	729.0829	0.74622	1.00E-06	4.16E-06	ASB1	chr2	+	2.39E+08	2.39E+08	6994
ENSG00000(	255.8406	199.9118	290.271	1319.122	1445.999	1127.736	-2.3759	3.58E-48	9.37E-47	FAM107B	chr10	-	14560556	14816896	3785
ENSG00000(	464.0348	532.2952	563.3897	813.496	742.7886	603.3223	-0.46956	0.002714	0.007067	ME1	chr6	-	83920108	84140797	3371
ENSG00000(	937.3917	934.5273	1085.878	2067.449	2026.791	1748.319	-0.98075	1.03E-14	7.96E-14	TBC1D1	chr4	+	37892708	38140796	5700
ENSG00000(	821.383	800.8513	1021.226	747.5774	739.1069	669.9014	0.29176	0.039311	0.078803	CDK13	chr7	+	39989636	40136733	7298
ENSG00000(	934.2843	1005.58	1009.352	1582.048	1515.951	1395.696	-0.60701	3.91E-07	1.69E-06	MTHFD2	chr2	+	74425689	74444692	4456

ENSG00000(	7.250543	18.06432	14.51355	82.39831	101.2475	83.01846	-2.6974	3.82E-11	2.33E-10	SLC9A7	chrX	-	46464753	46618490	3838
ENSG00000(	523.0749	584.0795	647.8322	570.7956	705.0509	608.254	-0.1027	0.49311	0.62203	FOXJ2	chr12	+	8185299	8208099	5523
ENSG00000(	28512.24	26831.53	23889.31	22875.27	24110.72	24396.74	0.15037	0.15397	0.24939	YBX1	chr1	+	43148098	43168020	1524
ENSG00000(	444.3547	440.7693	398.463	29.96302	46.0216	45.20807	3.3919	5.08E-54	1.53E-52	PDE4A	chr19	+	10527449	10580305	4603
ENSG00000(	221.6595	221.5889	241.4527	188.767	231.9489	193.1618	0.15755	0.40703	0.53794	PPP2R5A	chr1	+	2.12E+08	2.13E+08	3123
ENSG00000(	2.071584	0	3.958241	57.67882	48.7829	57.53754	-4.452	5.37E-11	3.25E-10	CTNNA2	chr2	+	79412357	80875905	4349
ENSG00000(	1749.453	1625.788	1666.42	3289.191	2956.428	2925.373	-0.86165	7.09E-15	5.55E-14	ELAVL1	chr19	-	8023463	8070543	6015
ENSG00000(	0	4.817151	0	17.97781	14.72691	23.01502	-3.101	0.000431	0.00128	TIE1	chr1	+	43766664	43788779	3882
ENSG00000(	736.448	670.7883	932.8255	913.8722	1041.009	867.173	-0.27012	0.074418	0.1367	DIP2B	chr12	+	50898768	51142450	8593
ENSG00000(	1160.087	1088.676	1150.529	2404.533	2151.05	2159.302	-0.98049	1.13E-17	1.02E-16	SMARCD1	chr12	+	50478755	50494495	3658
ENSG00000(	1068.937	1077.838	1232.332	518.3603	592.7582	495.6448	1.07	3.59E-15	2.87E-14	KDM4A	chr1	+	44115829	44171186	4474
ENSG00000(	791.345	828.55	737.5523	1021.739	866.1265	892.6539	-0.23776	0.071589	0.13235	NFYC	chr1	+	41157320	41237275	2363
ENSG00000(	0	3.612863	0	5.243529	3.681728	8.219649	-1.7309	0.12723	0.21361	ZMYND12	chr1	-	42896000	42921938	1775
ENSG00000(	829.6693	952.5916	592.4168	68.16587	113.2131	170.9687	2.6929	1.47E-11	9.22E-11	SLC9A3	chr5	-	473425	524447	2584
ENSG00000(	82.86335	93.93444	79.16483	14.23244	10.12475	19.72716	2.4802	7.02E-11	4.20E-10	NGEF	chr2	-	2.34E+08	2.34E+08	3215
ENSG00000(	410.1736	398.6192	628.041	942.337	1002.35	727.439	-0.893	1.58E-06	6.42E-06	ASPM	chr1	-	1.97E+08	1.97E+08	10887
ENSG00000(	2227.988	2137.611	2060.924	2366.33	1881.363	2350.82	-0.03819	0.75838	0.84022	ELOVL1	chr1	-	43829068	43833696	1477
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	SPI1	chr11	-	47376411	47400127	1403
ENSG00000(	67.32647	67.44011	59.37362	53.18436	52.46462	60.8254	0.22019	0.47945	0.60847	ZNRD1	chr6	+	30026676	30032686	3672
ENSG00000(	1.035792	2.408575	1.319414	12.73428	2.761296	4.93179	-1.7264	0.097655	0.17197	MPPED2	chr11	-	30406040	30608419	5591
ENSG00000(	20.71584	27.69862	34.30476	4.494453	10.12475	6.575719	1.8762	0.001406	0.003844	CLDN18	chr3	+	1.38E+08	1.38E+08	3520
ENSG00000(	357.3482	310.7062	354.9223	284.6487	312.9469	230.1502	0.30521	0.087729	0.15744	ZBTB11	chr3	-	1.01E+08	1.01E+08	6020
ENSG00000(	249.6258	244.4704	271.7992	272.6635	274.2887	298.3733	-0.14274	0.40568	0.53658	ATXN3	chr14	-	92524896	92572965	6950
ENSG00000(	724.0185	685.2397	717.7611	594.766	538.4527	493.179	0.38575	0.005373	0.013224	GOLGA5	chr14	+	93260576	93306308	2969
ENSG00000(	1063.758	1021.236	1081.919	493.6408	617.6099	470.9859	0.99962	2.04E-12	1.37E-11	FGFR2	chr10	-	1.23E+08	1.23E+08	4255
ENSG00000(	259.9838	345.6306	299.5069	799.2636	600.1217	618.1176	-1.1541	2.21E-11	1.37E-10	LRRC40	chr1	-	70610488	70671303	2884
ENSG00000(	121.1877	116.8159	93.67838	847.9535	673.7562	627.1592	-2.6787	2.06E-46	5.12E-45	ISOC1	chr5	+	1.28E+08	1.28E+08	1940
ENSG00000(	663.9426	627.4339	804.8424	187.2689	160.1552	149.5976	2.0657	3.65E-34	6.38E-33	EML1	chr14	+	1E+08	1E+08	4535
ENSG00000(	169.8699	163.7831	167.5656	402.2536	294.5382	328.786	-1.029	7.27E-08	3.38E-07	TRMT11	chr6	+	1.26E+08	1.26E+08	2409
ENSG00000(	507.538	505.8008	601.6527	717.6144	770.4016	559.7581	-0.34208	0.03203	0.065832	THUMPD1	chr16	-	20744986	20753406	4122
ENSG00000(	333.525	283.0076	288.9516	509.3714	411.4331	364.9524	-0.50308	0.004526	0.011309	MSANTD3	chr9	+	1.03E+08	1.03E+08	1991
ENSG00000(	126.3666	51.78437	98.95603	322.8516	410.5127	484.1373	-2.1102	3.18E-16	2.69E-15	KIF26A	chr14	+	1.05E+08	1.05E+08	6714
ENSG00000(	352.1692	396.2107	538.3208	217.2319	222.7445	147.9537	1.1214	1.08E-07	4.93E-07	ATG2B	chr14	-	96747595	96830207	11628
ENSG00000(	693.9806	638.2725	927.5479	626.2272	814.5823	653.4621	0.10891	0.51624	0.64282	ARFGEF1	chr8	-	68085747	68255912	7225
ENSG00000(	0	3.612863	0	0	0	1.64393	0.50971	0.70603	NA	ACSM2B	chr16	-	20547548	20587749	2935
ENSG00000(	163.6551	116.8159	205.8285	115.3576	127.0196	120.0069	0.41965	0.087903	0.15767	ZFAT	chr8	-	1.35E+08	1.36E+08	5472
ENSG00000(	327.3102	356.4692	315.3399	358.8072	420.6374	327.964	-0.14665	0.38096	0.51166	MTFR1	chr8	+	66556969	66683496	2640
ENSG00000(	34.18113	56.60152	75.20659	20.97412	25.7721	27.94681	1.1195	0.006561	0.015874	STAG3	chr7	+	99775186	99819111	4450
ENSG00000(	261.0196	278.1905	304.7846	542.3307	511.7602	497.2888	-0.87762	1.48E-08	7.31E-08	FECH	chr18	-	55215515	55254004	3853
ENSG00000(	453.6769	485.328	728.3164	250.1912	416.9557	217.8207	0.90768	9.70E-05	0.000317	MYO9A	chr15	-	72114632	72410918	12409
ENSG00000(	1293.704	1203.083	1527.881	1121.366	1162.506	992.9336	0.2954	0.027486	0.057611	DDX3Y	chrY	+	15016019	15032390	4445
ENSG00000(	2755.206	2893.903	2228.49	5179.108	4158.512	4511.765	-0.81186	6.74E-10	3.75E-09	PFKP	chr10	+	3109712	3179904	2769
ENSG00000(	1170.445	1094.698	1246.846	1626.243	1202.084	1194.315	-0.1961	0.17672	0.27875	IDI1	chr10	-	1085848	1095110	2301
ENSG00000(	711.589	608.1653	697.9699	44.94453	62.58938	77.2647	3.435	1.70E-66	6.89E-65	SP100	chr2	+	2.31E+08	2.31E+08	3882

ENSG00000(	3676.025	3742.926	4412.12	2291.422	2440.986	2072.996	0.7961	3.58E-11	2.19E-10	KLF6	chr10	-	3818188	3827473	4656
ENSG00000(	606.9741	728.5941	575.2644	219.4791	219.9832	264.6727	1.435	2.85E-18	2.66E-17	PPAP2A	chr5	-	54720682	54830878	1597
ENSG00000(	947.7496	922.4844	1038.379	230.7153	335.0372	263.0288	1.8076	1.19E-29	1.79E-28	NEO1	chr15	+	73344051	73597547	7342
ENSG00000(	2418.574	2259.244	2950.209	1037.47	1241.663	983.07	1.2224	1.76E-18	1.66E-17	TRAM1	chr8	-	71485677	71520622	3394
ENSG00000(	117.0445	119.2245	130.622	128.841	102.168	82.19649	0.22311	0.38268	0.51334	PHKA1	chrX	-	71798664	71934167	6173
ENSG00000(	6086.313	5721.571	5465.012	1835.235	1600.631	1494.332	1.8053	2.49E-54	7.58E-53	TNFRSF1A	chr12	-	6437923	6451280	2223
ENSG00000(	328.346	301.0719	283.674	29.21395	34.05598	55.07165	2.9249	1.43E-31	2.29E-30	CACNB1	chr17	-	37329709	37353956	5308
ENSG00000(	582.1151	587.6924	696.6505	269.6672	342.4007	341.9374	0.96523	2.26E-09	1.20E-08	EVI5	chr1	-	92974253	93257961	7403
ENSG00000(	288.9859	250.4918	236.1751	119.103	78.23672	154.5294	1.1295	2.93E-06	1.15E-05	STOML1	chr15	-	74275547	74286963	3060
ENSG00000(	57782.69	53817.21	50577.09	38347.42	31094.95	31805.11	0.67845	3.66E-09	1.91E-08	PKM	chr15	-	72491370	72524164	3016
ENSG00000(	525.1465	510.618	694.0116	740.8357	726.2208	539.209	-0.21451	0.21121	0.32113	DHX29	chr5	-	54552073	54603550	4557
ENSG00000(	594.5446	703.304	577.9032	1473.432	1113.723	1253.497	-1.0314	1.95E-12	1.31E-11	DNTTIP2	chr1	-	94333373	94345474	4363
ENSG00000(	433.9968	470.8765	427.4901	281.6524	288.0952	260.5629	0.68027	1.35E-05	4.93E-05	METTL22	chr16	+	8715540	8740081	1672
ENSG00000(	1737.023	1689.616	2060.924	1046.459	1217.732	933.7521	0.77706	1.69E-08	8.34E-08	TP53BP1	chr15	-	43699407	43802926	6346
ENSG00000(	1733.916	1719.723	1748.223	747.5774	721.6187	834.2944	1.1727	6.97E-23	7.91E-22	TRO	chrX	+	54946895	54957864	4647
ENSG00000(	343.8829	327.5663	350.9641	901.1379	818.264	728.2609	-1.2562	1.24E-17	1.12E-16	RRP15	chr1	+	2.18E+08	2.19E+08	7771
ENSG00000(	10431.46	10773.56	10009.07	13103.58	10717.51	10826.92	-0.15037	0.18271	0.28633	RHOA	chr3	-	49396578	49450431	2031
ENSG00000(	680.5153	635.8639	806.1618	708.6255	821.9458	725.795	-0.08838	0.53764	0.66147	DHX8	chr17	+	41561233	41621831	6215
ENSG00000(	42.46747	54.19295	34.30476	15.73059	34.97642	19.72716	0.88085	0.04745	0.092728	PMS2P4	chr7	-	66752528	66767894	1052
ENSG00000(	13.46529	6.021439	10.55531	325.8479	439.9665	521.9477	-5.3122	3.05E-53	9.08E-52	PRKCZ	chr1	+	1981909	2116834	2326
ENSG00000(	226.8384	293.8462	266.5216	191.7633	211.6994	154.5294	0.49317	0.014258	0.032042	ZFY	chrY	+	2803112	2850547	5239
ENSG00000(	1501.898	1434.307	1614.962	2212.02	2068.211	1774.622	-0.41133	0.000967	0.002716	IARS2	chr1	+	2.2E+08	2.2E+08	3557
ENSG00000(	430.8894	419.0921	530.4043	349.0692	377.3771	340.2935	0.36953	0.021126	0.045581	SYT1	chr12	+	79257773	79845788	4808
ENSG00000(	131.5456	132.4716	197.9121	459.9324	589.9969	434.8194	-1.6794	1.87E-16	1.59E-15	NAV3	chr12	+	78224685	78606790	9821
ENSG00000(	1127.977	1110.353	869.4937	854.6952	527.4075	558.9361	0.67538	0.000204	0.000636	IDH3G	chrX	-	1.53E+08	1.53E+08	1712
ENSG00000(	274.4849	237.2447	263.8828	267.42	244.8349	327.964	-0.11493	0.5347	0.65907	ROGDI	chr16	-	4846969	4852951	2684
ENSG00000(	151.2256	118.0202	125.3443	72.66033	112.2927	112.6092	0.4087	0.11843	0.20169	PDZD4	chrX	-	1.53E+08	1.53E+08	3689
ENSG00000(	9.322127	7.225726	1.319414	2.996302	2.761296	0	1.3267	0.21534	0.32604	ATP2B3	chrX	+	1.53E+08	1.53E+08	6742
ENSG00000(	972.6086	970.6559	1191.431	737.0903	1050.213	805.5256	0.27317	0.0815	0.1477	ROCK1	chr18	-	18529701	18691812	6650
ENSG00000(	784.0945	798.4428	862.8966	1107.134	1162.506	1052.115	-0.44142	0.000352	0.00106	CBFB	chr16	+	67063019	67134961	3136
ENSG00000(	55.93276	68.6444	59.37362	58.42789	55.22592	41.09825	0.24418	0.45833	0.58781	PDK3	chrX	+	24483338	24557954	1921
ENSG00000(	591.4372	579.2624	558.112	1053.949	744.6295	874.5707	-0.62737	3.76E-05	0.00013	HYAL2	chr3	-	50355221	50360337	4054
ENSG00000(	370.8135	346.8349	473.6695	210.4902	301.9017	304.949	0.54099	0.005655	0.013866	HDAC4	chr2	-	2.4E+08	2.4E+08	8976
ENSG00000(	447.4621	396.2107	352.2835	698.1384	563.3044	706.8898	-0.71497	7.10E-06	2.68E-05	RASSF1	chr3	-	50367219	50378411	2060
ENSG00000(	71.46964	65.03154	55.41538	239.7042	281.6522	283.5779	-2.0473	1.83E-19	1.81E-18	FGFR3	chr4	+	1795034	1810599	4293
ENSG00000(	187.4783	171.0089	147.7743	12.73428	16.56778	9.863579	3.6478	9.65E-29	1.40E-27	IFI35	chr17	+	41158742	41166473	1241
ENSG00000(	268.2701	272.169	314.0205	256.1838	236.551	187.408	0.32575	0.086085	0.15495	HEATR6	chr17	-	58120555	58156292	3932
ENSG00000(	1067.901	1105.536	876.0908	1788.792	1573.018	1832.982	-0.76602	7.00E-09	3.57E-08	COASY	chr17	+	40713485	40718295	2458
ENSG00000(	1007.826	883.9472	639.9157	321.3534	321.2308	410.1605	1.2617	2.46E-12	1.64E-11	PLEKHH3	chr17	-	40819932	40829048	4339
ENSG00000(	675.3363	629.8425	820.6754	281.6524	348.8437	258.097	1.2543	9.35E-14	6.84E-13	MEF2A	chr15	+	1E+08	1E+08	5824
ENSG00000(	1490.505	1495.725	1401.217	1361.819	1271.117	1413.78	0.11645	0.31134	0.4376	OTUD5	chrX	-	48779305	48815648	2740
ENSG00000(	2021.866	1985.87	2136.131	1171.554	1245.344	1206.645	0.76052	6.39E-12	4.13E-11	TFE3	chrX	-	48886242	48901012	3415
ENSG00000(	431.9252	403.4364	376.0329	272.6635	258.6414	263.8507	0.60608	0.00015	0.000479	TBC1D25	chrX	+	48397845	48420997	4042
ENSG00000(	1035.792	1045.322	1384.065	892.149	929.6363	742.2343	0.43234	0.00432	0.010838	ACSL4	chrX	-	1.09E+08	1.09E+08	5333

ENSG00000(	539.6476	503.3923	568.6673	814.9942	726.2208	655.928	-0.44653	0.001879	0.005032	INPP5A	chr10	+	1.34E+08	1.35E+08	2962
ENSG00000(	384.2788	404.6407	339.0893	361.8035	377.3771	431.5316	-0.0523	0.7454	0.83053	GPKOW	chrX	-	48970334	48980151	1735
ENSG00000(	761.307	738.2284	672.901	582.7808	658.1089	739.7684	0.13412	0.34758	0.47722	GRIPAP1	chrX	-	48830134	48858675	3278
ENSG00000(	876.28	870.7	749.427	824.7322	809.0597	742.2343	0.071999	0.58608	0.70346	FTSJ1	chrX	+	48334541	48344752	1986
ENSG00000(	475.4285	445.5865	505.3355	1395.528	1358.558	1332.405	-1.5159	2.42E-33	4.11E-32	PRR11	chr17	+	57232860	57282066	2334
ENSG00000(	7.250543	28.90291	23.74945	111.6123	101.2475	78.08667	-2.2487	3.12E-08	1.50E-07	REEP1	chr2	-	86441116	86565206	3857
ENSG00000(	185.4068	189.0732	195.2732	459.1833	778.6855	528.5234	-1.6225	8.61E-16	7.11E-15	ATP11A	chr13	+	1.13E+08	1.14E+08	8858
ENSG00000(	2200.022	2119.546	2154.603	2406.78	3086.208	2665.632	-0.33253	0.006184	0.015041	POLR1A	chr2	-	86247339	86333278	12749
ENSG00000(	7250.543	7285.941	7161.778	3560.356	3143.275	3542.669	1.0807	1.72E-25	2.17E-24	LAPTM4A	chr2	-	20232411	20251789	1765
ENSG00000(	299.3439	249.2876	263.8828	630.7216	802.6167	768.5372	-1.4306	5.03E-19	4.88E-18	TTC7A	chr2	+	47143296	47303276	5157
ENSG00000(	1913.108	1958.172	1735.029	1398.524	1321.74	1373.503	0.45298	6.72E-05	0.000224	IP6K2	chr3	-	48725436	48777786	2490
ENSG00000(	0	0	0	17.97781	16.56778	19.72716	-5.0501	4.94E-06	1.90E-05	STON1-GTF	chr2	+	48757064	49003654	3824
ENSG00000(	222.6953	168.6003	222.9809	367.047	358.048	291.7975	-0.7232	0.000151	0.00048	SRBD1	chr2	-	45615819	45839304	3681
ENSG00000(	2346.069	2323.071	2504.247	2906.413	2912.247	2917.153	-0.28409	0.006184	0.015041	CYFIP1	chr15	+	22892005	23006016	6863
ENSG00000(	497.1801	475.6936	585.8197	970.8019	922.2729	715.9314	-0.74182	2.40E-06	9.56E-06	KIF2A	chr5	+	61601989	61833076	3360
ENSG00000(	1.035792	0	0	2.996302	4.60216	5.753754	-2.3605	0.058299	0.11101	RASGRP2	chr11	-	64494383	64512928	2983
ENSG00000(	999.5392	955.0002	1113.585	1722.125	1970.645	1577.351	-0.77889	2.30E-09	1.22E-08	PSME4	chr2	-	54091204	54197977	7099
ENSG00000(	287.9501	276.9862	302.1458	231.4643	185.0068	208.7791	0.46739	0.009795	0.022826	IFT80	chr3	-	1.6E+08	1.6E+08	4306
ENSG00000(	1674.876	1610.133	1364.274	452.4416	357.1276	432.3535	1.8982	1.90E-40	3.99E-39	SIRT2	chr19	-	39369197	39390502	4734
ENSG00000(	819.3114	779.1742	799.5648	594.766	526.4871	537.5651	0.52994	6.05E-05	0.000203	ERLEC1	chr2	+	54014181	54045956	2433
ENSG00000(	532.397	585.2838	411.6571	117.6049	90.20234	110.1433	2.252	1.15E-30	1.78E-29	PPP2R5B	chr11	+	64685025	64701945	2745
ENSG00000(	10.35792	24.08575	7.916483	10.48706	0	9.041614	0.9887	0.22898	0.34235	PYGM	chr11	-	64513861	64527769	3198
ENSG00000(	850.3852	796.0342	647.8322	167.7929	103.0884	98.63579	2.6153	5.15E-38	1.01E-36	PITX1	chr5	-	1.34E+08	1.34E+08	3216
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	TRPC7	chr5	-	1.36E+08	1.36E+08	2987
ENSG00000(	195.7647	228.8147	261.2439	127.3428	127.94	108.4994	0.90665	1.91E-05	6.83E-05	MAST4	chr5	+	65892176	66465423	10733
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	GPR116	chr6	-	46820249	46922680	5810
ENSG00000(	183.3352	122.8373	219.0227	353.5637	490.5903	380.5698	-1.214	2.39E-08	1.16E-07	SDK2	chr17	-	71330523	71640228	10723
ENSG00000(	690.8732	621.4125	701.9281	1165.562	1226.015	978.1383	-0.74031	7.33E-08	3.41E-07	NUP133	chr1	-	2.3E+08	2.3E+08	4169
ENSG00000(	4357.577	3893.462	5372.653	3573.839	5217.929	4018.586	0.088574	0.56316	0.68291	NUCKS1	chr1	-	2.06E+08	2.06E+08	6496
ENSG00000(	2080.906	2007.548	2483.137	3019.524	2786.148	2566.996	-0.34927	0.004948	0.012268	VPS35	chr16	-	46690054	46723430	6780
ENSG00000(	1006.79	914.0544	1038.379	1577.553	1492.02	1482.825	-0.62048	1.71E-07	7.68E-07	DNAJA2	chr16	-	46989299	47007699	3097
ENSG00000(	660.8352	585.2838	567.3479	75.65663	61.66894	56.71558	3.2056	3.03E-65	1.19E-63	BCL3	chr19	+	45250962	45263301	2038
ENSG00000(	274.4849	276.9862	290.271	8.239831	9.20432	13.9734	4.6825	9.36E-52	2.70E-50	KCNAB2	chr1	+	6051526	6161253	4273
ENSG00000(	0	0	1.319414	27.7158	38.65814	29.59074	-5.1134	1.11E-07	5.07E-07	ABCC9	chr12	-	21950335	22094336	8293
ENSG00000(	26.93059	13.24716	14.51355	298.1321	160.1552	208.7791	-3.5288	7.46E-25	9.15E-24	GAL	chr11	+	68451247	68458643	818
ENSG00000(	55.93276	57.80581	68.60952	47.19176	66.2711	54.24968	0.11953	0.71206	0.80537	CLEC2D	chr12	+	9809270	9848413	1855
ENSG00000(	241.3395	221.5889	186.0373	339.3312	277.05	375.638	-0.6074	0.001489	0.004051	FUNDC1	chrX	-	44382885	44402247	1196
ENSG00000(	14.50109	7.225726	17.15238	1.498151	0.920432	0	3.3491	0.000521	0.001527	MAOB	chrX	-	43625858	43741693	2566
ENSG00000(	239.2679	245.6747	358.8805	47.19176	59.82808	36.16646	2.538	5.53E-23	6.32E-22	RORA	chr15	-	60780483	61521518	10844
ENSG00000(	18.64425	44.55865	29.0271	10.48706	14.72691	14.79537	1.1571	0.027751	0.058063	DRD4	chr11	+	637293	640706	1375
ENSG00000(	1133.156	1060.977	1355.038	190.2652	256.8005	217.8207	2.4103	5.81E-52	1.69E-50	TGFBR3	chr1	-	92145902	92371892	6416
ENSG00000(	27.96638	30.10719	18.47179	2.996302	15.64734	10.68554	1.3284	0.029874	0.061942	KIAA1107	chr1	+	92632542	92650280	4622
ENSG00000(	1.035792	3.612863	0	5.243529	3.681728	2.465895	-0.97872	0.39648	0.5275	PLA2G10	chr16	-	14766405	14788526	997
ENSG00000(	31.07376	13.24716	22.43003	108.616	196.052	172.6126	-2.775	2.92E-15	2.34E-14	HES2	chr1	-	6472478	6484730	4262

ENSG00000(	3048.336	2834.893	3051.804	4225.535	3369.702	3748.16	-0.34389	0.003424	0.008764	ATP1B3	chr3	+	1.42E+08	1.42E+08	1951
ENSG00000(	321.0955	358.8777	377.3523	827.7285	848.6383	683.8748	-1.1565	2.86E-14	2.16E-13	NEDD4	chr15	-	56119120	56285944	7235
ENSG00000(	94.25706	107.1816	114.789	91.38722	114.1336	91.23811	0.090393	0.72284	0.81374	PIGB	chr15	+	55611158	55647846	2172
ENSG00000(	1218.091	1212.718	1600.449	1975.312	1834.421	1503.374	-0.39806	0.007159	0.017209	MAPK6	chr15	+	52244303	52358462	4238
ENSG00000(	271.3775	333.5877	296.8681	230.7153	198.8133	167.6808	0.58966	0.002201	0.005823	GNB5	chr15	-	52413117	52483566	3091
ENSG00000(	222.6953	244.4704	265.2022	215.7338	221.8241	192.3398	0.21484	0.24714	0.36391	RAB27A	chr15	-	55495164	55611311	3459
ENSG00000(	891.8168	865.8829	628.041	711.6218	719.7778	807.1696	0.093077	0.54865	0.67019	CECR5	chr22	-	17618401	17646177	3614
ENSG00000(	952.9286	926.0973	835.1889	1642.723	1192.88	1468.851	-0.66346	3.20E-06	1.25E-05	UFD1L	chr22	-	19437464	19466738	5038
ENSG00000(	381.1714	446.7907	519.849	332.5895	468.4999	380.5698	0.18857	0.29323	0.41753	LRP6	chr12	-	12268959	12419946	10020
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	GUCY2C	chr12	-	14765576	14849519	3834
ENSG00000(	8.286335	6.021439	14.51355	3.745378	2.761296	11.50751	0.60081	0.46099	0.59045	SCT	chr11	-	626431	627143	366
ENSG00000(	2300.494	2235.158	1855.096	2104.153	2845.055	3154.701	-0.34095	0.024164	0.051428	PHRF1	chr11	+	576486	612222	5523
ENSG00000(	755.0923	673.1968	884.0072	951.3259	892.819	811.2794	-0.20006	0.16236	0.26025	IKBKAP	chr9	-	1.12E+08	1.12E+08	5905
ENSG00000(	1218.091	1268.115	1205.944	511.6186	441.8074	471.8079	1.3692	8.64E-27	1.15E-25	NUCB2	chr11	+	17229700	17371521	3402
ENSG00000(	4622.739	4959.257	4693.155	9035.349	7851.285	7494.676	-0.7711	3.09E-12	2.04E-11	PFN2	chr3	-	1.5E+08	1.5E+08	2261
ENSG00000(	69.39806	54.19295	62.01245	138.579	165.6778	126.5826	-1.1992	5.81E-06	2.22E-05	PTPN3	chr9	-	1.12E+08	1.12E+08	8765
ENSG00000(	62.14751	46.96722	29.0271	318.3571	397.6266	407.6946	-2.9796	4.62E-33	7.77E-32	SPTB	chr14	-	65213002	65346601	10063
ENSG00000(	7.250543	1.204288	2.638828	36.7047	28.53339	13.9734	-2.581	0.000315	0.000956	DAPP1	chr4	+	1.01E+08	1.01E+08	2955
ENSG00000(	4.143168	4.817151	3.958241	0	0	0	3.2125	0.01292	0.029275	FGF10	chr5	-	44303646	44389808	2193
ENSG00000(	641.1552	643.0896	758.6629	2632.251	2921.451	2409.179	-1.9593	5.38E-52	1.56E-50	SLC44A1	chr9	+	1.08E+08	1.08E+08	10511
ENSG00000(	295.2007	346.8349	427.4901	176.0328	238.3919	207.1352	0.77842	7.95E-05	0.000263	TMEM260	chr14	+	56955072	57117324	4264
ENSG00000(	1381.746	1481.274	1372.19	1204.513	1389.852	1156.505	0.17531	0.15525	0.25101	SMG6	chr17	-	1963133	2207065	6331
ENSG00000(	956.0359	1082.655	1368.232	1231.48	1393.534	1198.425	-0.16696	0.25695	0.37542	EXOC5	chr14	-	57670518	57735726	7296
ENSG00000(	195.7647	225.2018	265.2022	107.1178	104.9292	98.63579	1.1329	1.41E-07	6.35E-07	CLTCL1	chr22	-	19166986	19279239	5513
ENSG00000(	5.17896	4.817151	3.958241	7.490755	8.283888	2.465895	-0.33213	0.71196	0.80531	FGF22	chr19	+	639588	643703	1712
ENSG00000(	483.7148	498.5751	511.9325	134.8336	99.40666	129.0485	2.027	8.92E-30	1.35E-28	FSTL3	chr19	+	676392	683385	2501
ENSG00000(	2521.117	2412.188	2281.266	1768.567	2119.755	1976.004	0.29906	0.010412	0.024112	DGCR2	chr22	-	19023795	19109967	4814
ENSG00000(	904.2463	734.6155	692.6922	1885.423	1295.968	1480.359	-0.99536	4.22E-10	2.38E-09	RNF126	chr19	-	647526	663209	2092
ENSG00000(	676.3721	623.821	606.9303	270.4163	312.0264	355.9108	1.0213	7.34E-11	4.39E-10	MNT	chr17	-	2287354	2304412	4996
ENSG00000(	317.9881	375.7378	325.8952	361.8035	361.7298	458.6564	-0.21312	0.21083	0.32071	ZXDC	chr3	-	1.26E+08	1.26E+08	4639
ENSG00000(	605.9383	572.0367	507.9743	613.4929	558.7022	589.3488	-0.06218	0.65988	0.76435	JMJD6	chr17	-	74708919	74722866	5298
ENSG00000(	251.6974	275.7819	269.1604	431.4675	328.5942	388.7894	-0.52828	0.002238	0.005912	POLB	chr8	+	42195972	42229326	1341
ENSG00000(	766.486	741.8412	715.1223	367.047	410.5127	357.5547	0.96875	4.27E-12	2.80E-11	WIPI1	chr17	-	66417089	66453654	1886
ENSG00000(	0	0	1.319414	10.48706	11.96562	9.041614	-3.5237	0.001402	0.003836	FRMPD1	chr9	+	37650997	37746901	5465
ENSG00000(	796.524	844.2057	773.1765	1349.085	1262.833	1283.909	-0.68927	8.96E-09	4.50E-08	GBA2	chr9	-	35736863	35749983	3757
ENSG00000(	3057.658	3037.214	3225.967	3960.362	7362.536	6914.369	-0.96419	3.73E-08	1.78E-07	NDST1	chr5	+	1.5E+08	1.5E+08	8030
ENSG00000(	852.4567	926.0973	723.0388	1715.383	1156.063	1093.213	-0.66176	0.00012	0.000388	ASNS	chr7	-	97481430	97501854	2356
ENSG00000(	330.4176	281.8033	376.0329	405.9989	357.1276	373.994	-0.20338	0.22837	0.34168	AP3M2	chr8	+	42010464	42029191	3669
ENSG00000(	1.035792	0	0	1.498151	0.920432	0	-0.39626	0.76684	NA	CNGB1	chr16	-	57917503	58005020	4364
ENSG00000(	25.8948	24.08575	15.83297	54.68252	45.10117	45.20807	-1.1047	0.007925	0.018855	ST6GALNAC	chr17	-	74559792	74583038	5654
ENSG00000(	0	0	0	2.247227	0	2.465895	-1.3312	0.32317	NA	CHAT	chr10	+	50817141	50901925	2528
ENSG00000(	30534.11	30531.1	27313.18	27751.75	22017.65	20024.71	0.33981	0.008183	0.019388	PABPC1	chr8	-	1.02E+08	1.02E+08	3485
ENSG00000(	49.71801	62.62296	43.54065	71.16218	82.83888	64.11326	-0.47525	0.13616	0.22555	TESK2	chr1	-	45809555	45956872	3074
ENSG00000(	328.346	337.2006	265.2022	636.7142	551.3388	652.6401	-0.97888	9.28E-10	5.10E-09	C16orf80	chr16	-	58147496	58163354	1605

ENSG0000(	1670.732	1623.38	1493.576	1895.161	2035.996	1847.777	-0.27033	0.017478	0.038473	CSNK2A2	chr16	-	58191811	58231824	4978
ENSG0000(	484.7506	423.9093	498.7384	392.5156	489.6698	355.0888	0.18635	0.26511	0.38502	PTPN21	chr14	-	88932122	89021077	6166
ENSG0000(	390.4935	327.5663	373.3941	531.8436	452.8525	418.3801	-0.36113	0.026717	0.056187	EIF2B3	chr1	-	45316450	45452282	1659
ENSG0000(	3.107376	4.817151	10.55531	6.74168	8.283888	2.465895	0.057351	0.94819	0.96872	CAMK2A	chr5	-	1.5E+08	1.5E+08	5322
ENSG0000(	1226.378	1174.181	1139.974	4916.932	5152.578	5304.14	-2.1146	1.50E-88	9.14E-87	TCOF1	chr5	+	1.5E+08	1.5E+08	5240
ENSG0000(	5311.541	5538.519	5950.556	6537.931	6913.365	6808.335	-0.26985	0.007983	0.018973	CDC42	chr1	+	22379120	22419437	2254
ENSG0000(	795.4882	671.9925	853.6607	877.1675	796.1737	633.735	0.008256	0.95797	0.97513	OSBPL3	chr7	-	24836158	25021253	6760
ENSG0000(	221.6595	230.019	252.008	578.2863	554.1001	600.0344	-1.2977	4.97E-17	4.35E-16	RAD18	chr3	-	8817088	9005457	5886
ENSG0000(	1336.172	1386.135	1934.261	2441.237	2832.169	2201.222	-0.68129	9.26E-06	3.46E-05	ATP2B1	chr12	-	89981828	90103077	7032
ENSG0000(	3.107376	0	0	0	1.840864	0	0.36193	0.78835	NA	TRPM5	chr11	-	2425745	2444275	3932
ENSG0000(	2250.776	2266.469	1934.261	1274.927	1088.871	1030.744	0.92423	7.47E-13	5.16E-12	NCK2	chr2	+	1.06E+08	1.07E+08	2683
ENSG0000(	7145.928	6915.02	7783.222	3647.998	4664.749	3693.088	0.86191	2.66E-12	1.77E-11	MAP4K4	chr2	+	1.02E+08	1.03E+08	6958
ENSG0000(	5.17896	8.430014	21.11062	31.46117	34.05598	32.05663	-1.451	0.009086	0.021334	MGAT4A	chr2	-	99235569	99347589	8382
ENSG0000(	16513.63	16548.12	14079.46	9048.084	7715.981	11046.39	0.75945	1.98E-08	9.72E-08	RPL31	chr2	+	1.02E+08	1.02E+08	2328
ENSG0000(	13903.43	12879.86	13520.03	15598	14224.36	13764.62	-0.11285	0.26726	0.38738	WDR1	chr4	-	10075963	10118573	4482
ENSG0000(	451.6053	356.4692	659.7069	340.0803	375.5363	332.8958	0.48129	0.016847	0.037211	SNX13	chr7	-	17832466	17980124	6816
ENSG0000(	0	0	0	4.494453	2.761296	6.575719	-2.9819	0.019879	0.043149	MS4A12	chr11	+	60260251	60274903	1167
ENSG0000(	802.7387	793.6256	825.953	1111.628	1017.077	1011.017	-0.37399	0.002292	0.006046	ARHGAP10	chr4	+	1.49E+08	1.49E+08	8188
ENSG0000(	2175.163	2065.353	2376.264	297.383	417.8761	323.8542	2.6656	9.04E-76	4.44E-74	RPS6KA2	chr6	-	1.67E+08	1.67E+08	5992
ENSG0000(	149.154	192.686	175.482	283.1506	208.9381	208.7791	-0.43914	0.038093	0.076729	ING3	chr7	+	1.21E+08	1.21E+08	3777
ENSG0000(	285.8786	309.5019	314.0205	73.4094	161.996	129.8705	1.3098	1.01E-07	4.64E-07	VASH1	chr14	+	77228532	77249354	5724
ENSG0000(	53.86118	62.62296	55.41538	244.1986	177.6434	192.3398	-1.8239	4.01E-13	2.82E-12	LMCD1	chr3	+	8543393	8609805	1851
ENSG0000(	1272.988	1176.589	1038.379	1722.125	1334.626	1696.536	-0.44503	0.001413	0.003862	WBSCR22	chr7	+	73097355	73119491	3886
ENSG0000(	1866.497	1810.044	2401.333	799.2636	1081.508	784.9765	1.1855	3.55E-14	2.67E-13	SEL1L	chr14	-	81937893	82000205	7925
ENSG0000(	272.4133	231.2232	245.411	1713.136	1307.013	1242.811	-2.4988	6.82E-55	2.10E-53	TRIP13	chr5	+	892758	919472	2672
ENSG0000(	3771.318	3686.325	3549.223	2301.909	2143.686	2187.249	0.72961	1.99E-12	1.33E-11	ATP6AP1	chrX	+	1.54E+08	1.54E+08	4515
ENSG0000(	3962.94	3954.881	3423.879	4315.424	4261.6	4204.351	-0.17186	0.11025	0.18996	TCF3	chr19	-	1609291	1652604	4723
ENSG0000(	1864.425	1623.38	1922.386	857.6915	926.875	840.0481	1.0417	2.50E-17	2.23E-16	TRIB2	chr2	+	12857015	12882860	4391
ENSG0000(	2768.672	2797.56	2557.024	4791.087	4811.098	5697.039	-0.91152	1.69E-15	1.37E-14	DAZAP1	chr19	+	1407584	1435719	3940
ENSG0000(	1524.686	1371.684	1192.75	1988.796	1739.616	1866.682	-0.45061	0.000438	0.001297	MBD3	chr19	-	1576639	1592882	2782
ENSG0000(	692.9448	739.4327	828.5919	282.4015	325.8329	296.7293	1.3172	6.39E-19	6.17E-18	HLTF	chr3	-	1.49E+08	1.49E+08	5317
ENSG0000(	1651.052	1613.746	1401.217	1014.248	824.7071	1043.073	0.69322	2.84E-07	1.25E-06	FAM50A	chrX	+	1.54E+08	1.54E+08	1470
ENSG0000(	747.8418	710.5298	680.8175	494.3899	381.0588	516.194	0.61748	5.85E-05	0.000197	FAM3A	chrX	-	1.54E+08	1.54E+08	3997
ENSG0000(	1992.864	1784.754	1754.82	2286.179	2443.747	2318.763	-0.34817	0.001855	0.004974	CPSF1	chr8	-	1.46E+08	1.46E+08	4510
ENSG0000(	19.68005	13.24716	3.958241	0	1.840864	1.64393	2.9162	0.002496	0.006538	MYO3B	chr2	+	1.71E+08	1.72E+08	6084
ENSG0000(	1259.523	1284.975	1596.491	32.95932	47.86246	33.70056	5.1604	1.68E-156	2.79E-154	CYBRD1	chr2	+	1.72E+08	1.72E+08	4365
ENSG0000(	1001.611	994.7417	886.6461	1680.176	1307.013	1395.696	-0.60277	8.06E-06	3.03E-05	PDCD2	chr6	-	1.71E+08	1.71E+08	3378
ENSG0000(	67.32647	80.68728	84.44248	286.1469	287.1748	242.4797	-1.8042	1.84E-16	1.57E-15	SLC6A15	chr12	-	85253492	85307394	4229
ENSG0000(	1371.388	1377.705	1518.645	1439.723	1411.022	1385.011	0.01029	0.92822	0.95685	RDH11	chr14	-	68143518	68162531	4035
ENSG0000(	1711.128	1641.444	1708.641	1150.58	1197.482	1416.246	0.42629	0.00056	0.001632	PRKACA	chr19	-	14202500	14228896	3105
ENSG0000(	424.6747	416.6836	353.6029	130.3391	270.607	230.9721	0.91664	6.00E-05	0.000201	LPHN1	chr19	-	14260750	14316999	5658
ENSG0000(	10779.49	10220.79	10829.75	27681.34	26929.08	25034.59	-1.3215	4.56E-41	9.66E-40	ACTN1	chr14	-	69340860	69446157	4674
ENSG0000(	589.3656	632.2511	684.7758	409.7443	581.713	480.8495	0.37219	0.020534	0.044386	ZFYVE26	chr14	-	68194091	68283307	9675
ENSG0000(	34.18113	22.88147	23.74945	33.7084	32.21512	15.61733	-0.00694	0.98845	0.99306	RPS6KA6	chrX	-	83318984	83442933	2547

ENSG00000(	1148.693	1060.977	994.838	420.9805	558.7022	549.8945	1.0657	5.59E-13	3.89E-12	EPN2	chr17	+	19118928	19240028	4871
ENSG00000(	474.3927	503.3923	362.8388	509.3714	407.7514	503.8645	-0.08301	0.62664	0.73784	PTPN18	chr2	+	1.31E+08	1.31E+08	3669
ENSG00000(	39.36009	26.49433	11.87472	385.0248	318.4695	276.1802	-3.5816	3.74E-34	6.53E-33	LIMS2	chr2	-	1.28E+08	1.28E+08	4807
ENSG00000(	8.286335	6.021439	2.638828	5.243529	0	0.821965	1.1693	0.27952	0.40175	ASIC4	chr2	+	2.2E+08	2.2E+08	3340
ENSG00000(	3059.729	3158.847	2636.189	62.17327	95.72493	127.4046	4.938	4.36E-160	7.82E-158	SPEG	chr2	+	2.2E+08	2.2E+08	10782
ENSG00000(	37.28851	45.76293	47.4989	98.1289	66.2711	80.55256	-0.90179	0.005565	0.013665	LNX1	chr4	-	54325468	54567572	3757
ENSG00000(	351.1335	308.2977	398.463	390.2684	424.3192	354.2669	-0.14382	0.3889	0.5195	ALDH3A2	chr17	+	19551449	19580911	3928
ENSG00000(	4016.801	3991.01	5004.536	2465.208	2427.179	1827.228	0.95061	1.92E-11	1.20E-10	TFRC	chr3	-	1.96E+08	1.96E+08	5111
ENSG00000(	1069.973	952.5916	828.5919	1468.937	1514.111	1454.056	-0.63508	9.16E-07	3.81E-06	SREBF1	chr17	-	17713713	17740325	4653
ENSG00000(	1.035792	0	3.958241	0	0	0	1.6134	0.2311	NA	TRPC5	chrX	-	1.11E+08	1.11E+08	5839
ENSG00000(	2494.187	2314.641	3320.964	1459.199	1809.569	1286.375	0.83286	1.44E-07	6.49E-07	AFF4	chr5	-	1.32E+08	1.32E+08	9552
ENSG00000(	316.9523	370.9206	386.5882	641.2087	567.9065	522.7697	-0.6889	1.24E-05	4.56E-05	UBE2D1	chr10	+	60094735	60129403	1549
ENSG00000(	533.4328	505.8008	591.0974	768.5515	849.5587	717.5754	-0.51762	0.000229	0.00071	MPP5	chr14	+	67707826	67802536	5552
ENSG00000(	616.2962	638.2725	756.0241	341.5785	372.775	324.6761	0.94886	3.55E-10	2.01E-09	RHOBTB1	chr10	-	62629196	62761198	4473
ENSG00000(	0	2.408575	0	0.749076	0	0.821965	0.26015	0.84677	NA	ASAH2C	chr10	-	48001603	48055018	2050
ENSG00000(	981.9307	980.2902	1236.291	2086.924	2543.154	1931.618	-1.0344	5.55E-13	3.86E-12	SMC1A	chrX	-	53401070	53449677	9784
ENSG00000(	974.6802	940.5487	754.7047	1239.72	1131.211	1453.234	-0.51592	0.000397	0.001184	HSD17B10	chrX	-	53458206	53461320	960
ENSG00000(	831.7409	787.6042	734.9135	1262.192	1499.384	1646.396	-0.90147	4.27E-11	2.59E-10	MARK2	chr11	+	63606400	63678491	4728
ENSG00000(	172.9772	161.3746	182.0791	1161.816	971.9762	801.4158	-2.4976	1.76E-47	4.51E-46	HMMR	chr5	+	1.63E+08	1.63E+08	3101
ENSG00000(	494.0727	523.8652	484.2249	595.5151	590.9173	736.4806	-0.35522	0.016743	0.036995	CHFR	chr12	-	1.33E+08	1.33E+08	3258
ENSG00000(	35.21692	71.05298	52.77655	368.5452	335.0372	345.2253	-2.7102	1.44E-29	2.16E-28	TRHDE	chr12	+	72481046	73059422	5618
ENSG00000(	2767.636	2825.259	2396.055	219.4791	229.1876	198.9155	3.6173	4.26E-165	8.49E-163	P4HA2	chr5	-	1.32E+08	1.32E+08	3349
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	FCGR2B	chr1	+	1.62E+08	1.62E+08	4680
ENSG00000(	167.7983	167.396	248.0498	214.9847	269.6866	195.6277	-0.22287	0.3133	0.43976	NFATC3	chr16	+	68118654	68263162	6328
ENSG00000(	335.5966	338.4048	345.6864	492.8917	515.4419	469.342	-0.53365	0.000326	0.000986	TRNT1	chr3	+	3168600	3192563	2276
ENSG00000(	3431.579	3522.542	2748.339	3671.968	3395.474	4659.719	-0.27247	0.055436	0.10628	ACADVL	chr17	+	7120444	7128592	2352
ENSG00000(	1721.486	1608.928	1609.685	931.85	1119.245	1147.463	0.62658	6.40E-07	2.71E-06	STK10	chr5	-	1.71E+08	1.72E+08	6060
ENSG00000(	1181.839	1073.02	1315.456	829.2266	948.9654	819.499	0.45785	0.000568	0.001654	FBXW11	chr5	-	1.71E+08	1.71E+08	4539
ENSG00000(	67.32647	83.09585	67.2901	24.71949	25.7721	35.34449	1.3196	0.000175	0.000552	ACAP1	chr17	+	7239848	7254797	4898
ENSG00000(	2415.467	2311.028	2458.068	1850.217	1749.741	1542.828	0.48133	3.35E-05	0.000116	CRMP1	chr4	-	5749811	5894785	3146
ENSG00000(	1465.646	1590.864	1691.488	228.468	372.775	281.112	2.4219	1.02E-48	2.74E-47	EVC	chr4	+	5712924	5830772	7063
ENSG00000(	833.8125	838.1843	761.3018	893.6471	784.2081	753.7418	0.001036	0.99377	0.99606	DERL2	chr17	-	5374571	5390131	4209
ENSG00000(	3.107376	1.204288	1.319414	2.247227	0	0	0.78889	0.5513	0.67247	SIDT1	chr3	+	1.13E+08	1.13E+08	5080
ENSG00000(	417.4241	349.2434	461.7948	547.5742	453.773	441.3952	-0.23253	0.1613	0.25885	NDE1	chr16	+	15737124	15820210	3936
ENSG00000(	344.9187	321.5448	340.4088	51.68621	69.95283	46.03004	2.5757	4.65E-32	7.53E-31	MRVI1	chr11	-	10594638	10715535	6208
ENSG00000(	38.3243	20.47289	26.38828	15.73059	26.69253	32.8786	0.18167	0.70741	0.80217	TMEM38A	chr19	+	16771938	16800840	2649
ENSG00000(	1745.309	1522.22	1459.272	1914.637	1566.575	1597.078	-0.10298	0.42826	0.55846	AP1M1	chr19	+	16308389	16346160	2635
ENSG00000(	801.7029	702.0997	790.3289	877.1675	821.9458	771.8251	-0.10688	0.41715	0.54774	PVR	chr19	+	45147098	45166850	3325
ENSG00000(	179.192	143.3102	126.6637	93.63444	115.054	120.8288	0.44868	0.063513	0.11935	IKBKG	chrX	+	1.54E+08	1.54E+08	5465
ENSG00000(	504.4307	456.425	395.8241	591.7697	552.2592	625.5153	-0.38035	0.011618	0.026597	XRCC1	chr19	-	44047192	44084625	2802
ENSG00000(	1616.871	1553.531	1486.979	1145.337	856.0018	890.188	0.68528	6.99E-07	2.94E-06	SCARB1	chr12	-	1.25E+08	1.25E+08	5527
ENSG00000(	13.46529	2.408575	13.19414	5.992604	11.04518	12.32947	-0.00715	0.99244	0.99523	CYP2W1	chr7	+	1022835	1029276	2361
ENSG00000(	590.4014	510.618	509.2937	3012.033	2638.879	2742.075	-2.3753	1.67E-81	9.27E-80	MCM2	chr3	+	1.27E+08	1.27E+08	3619
ENSG00000(	14.50109	12.04288	3.958241	0	0.920432	0	3.8242	0.000623	0.001804	MOV10L1	chr22	+	50528308	50600119	3960

ENSG00000(	46.61064	33.72006	36.94359	9.737982	15.64734	3.28786	1.9608	0.000289	0.00088	PANX2	chr22	+	50609160	50618723	3051
ENSG00000(	608.0098	541.9295	477.6278	510.8695	410.5127	433.9975	0.26366	0.096499	0.17033	SELO	chr22	+	50639408	50656045	2315
ENSG00000(	2.071584	0	1.319414	0	1.840864	0.821965	0.21443	0.87358	0.92056	TP63	chr3	+	1.89E+08	1.9E+08	4909
ENSG00000(	205.0868	185.4603	146.4549	3.745378	3.681728	1.64393	5.6946	4.94E-33	8.31E-32	ALPK1	chr4	+	1.13E+08	1.13E+08	5633
ENSG00000(	6.214751	1.204288	9.235896	743.0829	694.0057	697.0263	-6.863	6.92E-69	2.96E-67	LLGL2	chr17	+	73521161	73571289	3527
ENSG00000(	516.8602	572.0367	635.9574	329.5932	334.1168	286.0438	0.85677	4.30E-08	2.04E-07	PDE8A	chr15	+	85523671	85682376	4664
ENSG00000(	118.0803	138.4931	124.0249	44.94453	49.70333	41.09825	1.473	8.30E-08	3.84E-07	CLCN4	chrX	+	10125024	10205700	6750
ENSG00000(	684.6584	702.0997	554.1538	703.3819	589.9969	569.6217	0.059373	0.69732	0.79394	NLE1	chr17	-	33455772	33469334	5286
ENSG00000(	2826.676	2659.067	2509.525	2018.759	1884.124	1986.689	0.44045	5.56E-05	0.000188	SDHA	chr5	+	218356	256815	3001
ENSG00000(	873.1726	916.463	1046.295	984.2853	751.0725	703.602	0.21533	0.16173	0.25938	SMARCE1	chr17	-	38781214	38804760	5840
ENSG00000(	3.107376	6.021439	1.319414	2.996302	11.04518	6.575719	-0.8281	0.37984	0.5105	FNDC8	chr17	+	33448598	33457751	1388
ENSG00000(	264.1269	329.9748	238.8139	132.5864	177.6434	172.6126	0.78455	0.00016	0.000506	GSDMB	chr17	-	38060848	38076107	4655
ENSG00000(	705.3743	692.4654	949.9779	480.1574	662.711	516.194	0.49896	0.003483	0.008902	KDM5A	chr12	-	389295	498620	10763
ENSG00000(	33.14534	15.65574	26.38828	17.22874	38.65814	27.12484	-0.12705	0.79792	0.86834	ADAM11	chr17	+	42836399	42859214	4571
ENSG00000(	387.3862	452.8122	525.1267	357.309	399.4675	253.9872	0.43066	0.025106	0.053169	PPP2R3A	chr3	+	1.36E+08	1.36E+08	6795
ENSG00000(	1747.381	1831.722	2041.133	2339.363	2223.764	1814.077	-0.18237	0.1614	0.25897	FERMT2	chr14	-	53323986	53419153	6001
ENSG00000(	1.035792	1.204288	2.638828	0	0	0	1.7123	0.20641	NA	ABCB11	chr2	-	1.7E+08	1.7E+08	4775
ENSG00000(	1.035792	7.225726	3.958241	0	0	0	3.0594	0.019495	0.04241	DHRS9	chr2	+	1.7E+08	1.7E+08	2864
ENSG00000(	80.79177	110.7945	164.9267	47.19176	60.74851	37.81039	1.2695	9.28E-05	0.000304	PTGS2	chr1	-	1.87E+08	1.87E+08	4514
ENSG00000(	1796.063	1694.433	1771.973	2828.509	2934.337	2684.537	-0.68152	2.20E-10	1.27E-09	IGF2BP2	chr3	-	1.85E+08	1.86E+08	3688
ENSG00000(	169.8699	174.6217	191.315	166.2948	202.495	211.245	-0.11391	0.57451	0.69315	MAP3K13	chr3	+	1.85E+08	1.85E+08	9876
ENSG00000(	178.1562	156.5574	238.8139	228.468	308.3447	267.9606	-0.48716	0.021536	0.046338	ST6GAL1	chr3	+	1.87E+08	1.87E+08	4893
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	TBX21	chr17	+	45810610	45823485	2572
ENSG00000(	2.071584	0	1.319414	2.996302	0	0.821965	-0.10598	0.93667	0.96172	VDAC1P1	chrX	+	80184999	80185846	848
ENSG00000(	98.40023	96.34302	130.622	21.72319	22.09037	8.219649	2.5926	4.36E-12	2.85E-11	FRY	chr13	+	32605437	32870794	10735
ENSG00000(	2606.052	2765.045	3051.804	3442.002	3356.815	3122.645	-0.23627	0.034467	0.070196	PICALM	chr11	-	85668727	85780924	3613
ENSG00000(	859.7073	845.41	936.7838	495.1389	419.717	397.831	1.0048	1.82E-12	1.22E-11	NSF	chr17	+	44668035	44834830	3983
ENSG00000(	458.8558	437.1564	440.6842	209.7412	294.5382	239.1918	0.84576	1.08E-06	4.45E-06	GLI2	chr2	+	1.21E+08	1.22E+08	6799
ENSG00000(	1088.617	1192.245	1155.806	906.3814	1127.529	729.9048	0.31377	0.043936	0.086852	CLASP1	chr2	-	1.22E+08	1.22E+08	8090
ENSG00000(	1366.21	1175.385	1035.74	1886.921	1567.496	2045.049	-0.61791	1.59E-05	5.75E-05	MRPS34	chr16	-	1821891	1823156	1040
ENSG00000(	5214.176	5135.083	4533.506	1876.434	2719.877	2392.74	1.0882	3.77E-15	3.00E-14	NOTCH3	chr19	-	15270444	15311792	8071
ENSG00000(	1036.828	1091.085	922.2702	1826.995	1457.964	1355.42	-0.60365	2.14E-05	7.62E-05	CLNS1A	chr11	-	77225981	77348850	2993
ENSG00000(	5.17896	0	0	5.243529	11.96562	12.32947	-2.0178	0.044951	0.0885	PPP2R2C	chr4	-	6322305	6565327	4538
ENSG00000(	1217.055	1177.793	1165.042	811.9979	857.8426	822.7869	0.51372	1.37E-05	5.01E-05	TEAD2	chr19	-	49843852	49865714	2440
ENSG00000(	332.4892	454.0165	344.367	596.2641	536.6119	632.913	-0.64155	0.0001	0.000328	EED	chr11	+	85955586	85989855	2767
ENSG00000(	23.82321	38.53721	30.34652	2.247227	3.681728	4.109825	3.024	2.02E-06	8.09E-06	CDHR2	chr5	+	1.76E+08	1.76E+08	4509
ENSG00000(	9.322127	13.24716	7.916483	0	2.761296	1.64393	2.4094	0.011741	0.026852	SNCB	chr5	-	1.76E+08	1.76E+08	1383
ENSG00000(	660.8352	682.8311	748.1076	823.234	705.0509	741.4124	-0.119	0.37839	0.50911	TSG101	chr11	-	18489883	18548779	2101
ENSG00000(	622.5109	635.8639	717.7611	641.2087	801.6963	812.9233	-0.19059	0.19262	0.29847	C17orf85	chr17	-	3714460	3749545	4096
ENSG00000(	33.14534	31.31148	21.11062	13.48336	16.56778	11.50751	1.0117	0.047342	0.092579	ATP2A3	chr17	-	3827169	3867736	4799
ENSG00000(	4610.31	4537.756	5007.175	0.749076	2.761296	4.93179	10.456	6.20E-137	8.04E-135	CA12	chr15	-	63613577	63674360	6413
ENSG00000(	377.0283	338.4048	521.1684	1007.507	1066.781	1172.122	-1.3897	3.09E-17	2.74E-16	MGLL	chr3	-	1.27E+08	1.28E+08	4941
ENSG00000(	599.7235	507.0051	785.0512	197.0069	200.6542	220.2866	1.6057	1.25E-18	1.19E-17	NTN4	chr12	-	96051583	96184930	3615
ENSG00000(	523.0749	498.5751	412.9765	744.5811	567.9065	671.5453	-0.46543	0.003377	0.008656	BCS1L	chr2	+	2.2E+08	2.2E+08	2015

ENSG00000(	816.204	797.2385	940.742	1391.782	2022.189	1605.297	-0.97163	1.22E-10	7.18E-10	NUAK1	chr12	-	1.06E+08	1.07E+08	6828
ENSG00000(	567.614	528.6823	645.1933	479.4084	523.7258	458.6564	0.25152	0.087433	0.15698	DPP8	chr15	-	65734801	65810042	8699
ENSG00000(	166.7625	208.3418	217.7033	196.2578	247.5962	232.6161	-0.19101	0.34189	0.47081	SLC24A1	chr15	+	65903704	65953333	5768
ENSG00000(	1641.73	1669.143	2054.327	1223.989	1354.876	1089.104	0.54696	5.74E-05	0.000193	ZNF532	chr18	+	56529832	56653712	6696
ENSG00000(	9.322127	9.634302	11.87472	2.247227	3.681728	13.15144	0.62348	0.43748	0.56711	SCARF1	chr17	-	1537152	1549041	3443
ENSG00000(	4000.228	3939.225	4930.649	1778.305	1807.728	1594.612	1.3098	5.10E-26	6.57E-25	LMAN1	chr18	-	56995055	57027194	5521
ENSG00000(	2385.429	2485.65	2634.869	2975.328	2868.987	2563.709	-0.16378	0.14529	0.2378	PTPLAD1	chr15	+	65822756	65870687	3225
ENSG00000(	1.035792	0	2.638828	2.247227	0.920432	1.64393	-0.27281	0.83249	0.89276	IPCEF1	chr6	-	1.54E+08	1.55E+08	6689
ENSG00000(	958.1075	1000.763	1219.138	692.8949	966.4536	822.7869	0.35547	0.021136	0.0456	ZZEF1	chr17	-	3907739	4046314	11456
ENSG00000(	0	0	0	7.490755	0	6.575719	-2.8359	0.030975	0.063925	NOX3	chr6	-	1.56E+08	1.56E+08	2042
ENSG00000(	58868.2	57306.03	47715.28	49354.34	42644.53	43138.36	0.2778	0.017072	0.037672	ENO1	chr1	-	8921061	8939308	2266
ENSG00000(	1.035792	0	0	0.749076	0	0.821965	-0.11768	0.9281	NA	SLC12A1	chr15	+	48483861	48596275	8632
ENSG00000(	6326.617	6336.962	5796.185	1714.634	1698.197	2414.933	1.6589	2.94E-32	4.79E-31	C19orf10	chr19	-	4641386	4670382	1018
ENSG00000(	497.1801	502.188	360.2	256.1838	309.2652	411.8044	0.47573	0.017342	0.038208	ANO8	chr19	-	17434032	17445638	4618
ENSG00000(	156.4046	198.7075	183.3985	207.4939	115.054	146.3098	0.1932	0.42872	0.55885	TUBE1	chr6	-	1.12E+08	1.12E+08	3610
ENSG00000(	157.4404	192.686	159.6491	101.8743	131.6218	124.1167	0.50971	0.023917	0.050939	ARHGEF10l	chr1	+	17866330	18024369	4585
ENSG00000(	12.4295	4.817151	5.277655	2.996302	2.761296	4.93179	0.9525	0.28617	0.40952	TXK	chr4	-	48068410	48136273	2914
ENSG00000(	0	0	0	5.992604	0	0.821965	-1.772	0.19153	0.29714	WSCD2	chr12	+	1.09E+08	1.09E+08	4710
ENSG00000(	7.250543	3.612863	9.235896	38.20285	61.66894	57.53754	-2.8537	6.69E-08	3.12E-07	KCNQ2	chr20	-	62037542	62103993	3275
ENSG00000(	6.214751	3.612863	7.916483	9.737982	9.20432	22.19305	-1.1176	0.13345	0.22215	TACR2	chr10	-	71163659	71176623	2083
ENSG00000(	253.769	234.8361	267.841	293.6376	276.1296	244.1236	-0.10596	0.5509	0.67209	ACTR6	chr12	+	1.01E+08	1.01E+08	2464
ENSG00000(	70.43385	80.68728	110.8308	479.4084	411.4331	467.698	-2.3711	6.96E-31	1.09E-29	TIPIN	chr15	-	66628544	66679084	1744
ENSG00000(	866.9578	820.1199	736.2329	865.9313	634.1776	780.8667	0.086839	0.56109	0.68128	SRI	chr7	-	87834433	87856308	2010
ENSG00000(	2060.19	1966.602	2758.894	1241.218	1592.347	1185.273	0.75321	1.33E-06	5.45E-06	EIF4G3	chr1	-	21132963	21503377	6196
ENSG00000(	185.4068	203.5246	176.8014	695.1421	628.6551	517.8379	-1.6957	1.11E-22	1.25E-21	NUP37	chr12	-	1.02E+08	1.03E+08	1286
ENSG00000(	175.0488	171.0089	252.008	725.8542	740.0273	600.8564	-1.7854	8.63E-23	9.77E-22	SEMA3A	chr7	-	83587659	84122040	5659
ENSG00000(	442.2831	351.652	369.4359	1229.982	1239.822	1204.179	-1.6523	3.57E-33	6.05E-32	GTSE1	chr22	+	46692638	46726707	3112
ENSG00000(	854.5283	882.7429	1223.097	939.3407	1159.744	870.4608	-0.00517	0.97488	0.98535	SEMA3C	chr7	-	80371854	80551675	5174
ENSG00000(	692.9448	656.3368	646.5128	476.412	418.7966	354.2669	0.67324	1.10E-05	4.05E-05	TTC38	chr22	+	46663858	46689905	2610
ENSG00000(	893.8884	994.7417	877.4102	745.3302	626.8142	654.2841	0.44699	0.000903	0.00255	ACAT1	chr11	+	1.08E+08	1.08E+08	2258
ENSG00000(	442.2831	484.1237	373.3941	115.3576	200.6542	192.3398	1.35	2.62E-10	1.50E-09	GRAMD4	chr22	+	46971909	47075688	4484
ENSG00000(	181.2636	211.9546	205.8285	401.5045	586.3152	432.3535	-1.2394	6.79E-11	4.07E-10	CELSR1	chr22	-	46756731	46933067	11389
ENSG00000(	3.107376	6.021439	0	1.498151	0	0	1.5856	0.2256	0.33832	WNT8B	chr10	+	1.02E+08	1.02E+08	2112
ENSG00000(	1150.765	1230.782	1303.581	1278.672	1276.639	988.8238	0.05569	0.6846	0.78423	ZNF638	chr2	+	71503691	71662199	6821
ENSG00000(	96.32865	128.8588	125.3443	211.2393	198.8133	213.7109	-0.83079	0.000122	0.000393	SLC25A40	chr7	-	87462883	87505672	4045
ENSG00000(	542.755	450.4036	498.7384	902.636	736.3456	842.514	-0.73172	4.86E-07	2.09E-06	TIMM21	chr18	+	71815746	71826197	2524
ENSG00000(	0	0	0	44.19546	34.05598	27.12484	-5.9672	1.77E-08	8.71E-08	ADD2	chr2	-	70834750	70995357	5856
ENSG00000(	334.5608	311.9105	542.2791	546.8252	712.4144	501.3986	-0.56522	0.006349	0.015412	RASAL2	chr1	+	1.78E+08	1.78E+08	10898
ENSG00000(	358.384	254.1047	271.7992	109.365	89.2819	157.8173	1.3009	3.93E-08	1.88E-07	VPS9D1	chr16	-	89773542	89787394	2791
ENSG00000(	543.7907	559.9938	676.8593	304.8737	316.6286	253.1652	1.021	4.21E-10	2.38E-09	ZNF37A	chr10	+	38383264	38412276	7027
ENSG00000(	1298.883	1309.061	1341.844	1224.739	1105.439	1008.551	0.24151	0.050446	0.097868	MARK3	chr14	+	1.04E+08	1.04E+08	3584
ENSG00000(	11968.58	11393.77	10829.75	10708.03	9684.785	10300.86	0.15553	0.12456	0.21003	SLC25A3	chr12	+	98987369	98995946	3236
ENSG00000(	1760.846	1743.809	2223.212	1146.086	1348.433	1101.433	0.66974	1.23E-06	5.07E-06	FNDC3B	chr3	+	1.72E+08	1.72E+08	7904
ENSG00000(	15527.56	16363.86	16967.66	2499.665	3435.973	2921.263	2.4589	4.69E-86	2.80E-84	FOSL2	chr2	+	28615315	28640179	6708

ENSG00000(	36.25272	14.45145	31.66593	987.2816	1008.793	827.7187	-5.0487	9.41E-102	7.32E-100	CACNG4	chr17	+	64961026	65029514	3380
ENSG00000(	550.0055	596.1224	802.2036	444.2018	416.0353	430.7096	0.58931	0.000355	0.001069	FRYL	chr4	-	48499378	48782339	11706
ENSG00000(	1688.341	1641.444	2137.45	1256.949	1240.742	989.6458	0.6463	7.50E-06	2.82E-05	TMEM131	chr2	-	98372799	98612388	7473
ENSG00000(	20552.18	18678.5	16470.24	19567.35	18892.79	19697.57	-0.06208	0.5726	0.69135	FSCN1	chr7	+	5632439	5646286	2777
ENSG00000(	99905.24	91864.27	85537.6	219640.2	167154.1	169896.9	-1.0032	1.53E-15	1.24E-14	ACTB	chr7	-	5566782	5603415	2245
ENSG00000(	15.53688	2.408575	5.277655	62.92235	79.15715	57.53754	-2.9436	8.04E-09	4.06E-08	MOCOS	chr18	+	33767482	33852120	6160
ENSG00000(	58.00435	89.11729	104.2337	172.2874	159.2347	108.4994	-0.80633	0.004563	0.011397	PLD1	chr3	-	1.71E+08	1.72E+08	5855
ENSG00000(	95.29286	83.09585	65.97069	913.8722	820.1049	850.7337	-3.3786	6.09E-80	3.29E-78	WDR62	chr19	+	36545783	36596008	5971
ENSG00000(	1057.544	1152.503	1422.328	1690.664	1660.459	1416.246	-0.39236	0.005234	0.012922	DLG1	chr3	-	1.97E+08	1.97E+08	5034
ENSG00000(	4424.903	4311.35	4562.533	4915.434	4230.305	4371.209	-0.02365	0.82553	0.88756	RAB7A	chr3	+	1.28E+08	1.29E+08	2244
ENSG00000(	603.8667	608.1653	584.5003	647.9503	556.8614	614.0078	-0.01828	0.89384	0.93429	BCAP29	chr7	+	1.07E+08	1.07E+08	5773
ENSG00000(	207.1584	275.7819	237.4945	47.19176	77.31629	66.57916	1.904	8.10E-15	6.32E-14	SEC31B	chr10	-	1.02E+08	1.02E+08	5087
ENSG00000(	768.5576	733.4112	872.1325	1124.362	1006.032	1135.956	-0.46037	0.000432	0.001281	SART3	chr12	-	1.09E+08	1.09E+08	4004
ENSG00000(	0	0	1.319414	0	0.920432	0.821965	-0.17431	0.89516	NA	ARHGAP15	chr2	+	1.44E+08	1.45E+08	2968
ENSG00000(	39.36009	37.33292	11.87472	11.98521	23.0108	22.19305	0.61932	0.24693	0.36372	TUBA3D	chr2	+	1.32E+08	1.32E+08	1546
ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	PAX2	chr10	+	1.02E+08	1.03E+08	4209
ENSG00000(	302.4512	307.0934	283.674	358.0581	337.7985	464.4102	-0.37561	0.033216	0.067911	EXOSC7	chr3	+	45016733	45077558	1647
ENSG00000(	592.473	598.531	664.9845	1597.029	1569.337	1601.188	-1.3595	2.55E-29	3.77E-28	KIFAP3	chr1	-	1.7E+08	1.7E+08	4111
ENSG00000(	994.3602	942.9573	1017.268	558.0613	526.4871	455.3686	0.93739	5.22E-12	3.40E-11	MKRN2	chr3	+	12598513	12625212	2848
ENSG00000(	449.5337	431.135	418.2542	1692.162	1658.618	1463.92	-1.885	2.04E-48	5.41E-47	MCM6	chr2	-	1.37E+08	1.37E+08	3736
ENSG00000(	575.9003	610.5739	600.3333	1027.732	704.1305	872.1048	-0.54286	0.000484	0.001426	REXO2	chr11	+	1.14E+08	1.14E+08	1161
ENSG00000(	388.422	472.0808	426.1707	501.8806	502.5559	490.7131	-0.21702	0.14375	0.23565	RBM7	chr11	+	1.14E+08	1.14E+08	6725
ENSG00000(	529.2897	492.5537	641.2351	410.4934	485.9881	341.1154	0.42452	0.013931	0.031381	RBMS2	chr12	+	56915713	56984745	3147
ENSG00000(	1840.602	1884.71	2034.536	1536.354	2966.552	2257.938	-0.22981	0.19938	0.30698	BAZ2A	chr12	-	56989380	57030600	8844
ENSG00000(	1902.75	1860.625	1581.977	1961.829	1825.217	1844.489	-0.07462	0.53082	0.6556	PTPN23	chr3	+	47422501	47454931	5244
ENSG00000(	624.5825	609.3696	563.3897	985.0343	943.4428	914.847	-0.65948	2.76E-07	1.21E-06	MLH1	chr3	+	37034823	37107380	2752
ENSG00000(	494.0727	527.478	505.3355	1441.97	1390.773	1546.938	-1.5175	4.71E-34	8.20E-33	UNG	chr12	+	1.1E+08	1.1E+08	2234
ENSG00000(	14.50109	13.24716	31.66593	16.47966	14.72691	21.37109	0.1568	0.77879	0.8544	FMO4	chr1	+	1.71E+08	1.71E+08	2252
ENSG00000(	355.2766	299.8676	484.2249	271.9144	266.9253	259.7409	0.50807	0.008176	0.019375	KLHL20	chr1	+	1.74E+08	1.74E+08	3421
ENSG00000(	3.107376	4.817151	3.958241	0	2.761296	1.64393	1.1159	0.32974	0.45754	RGS11	chr16	-	318300	325980	4294
ENSG00000(	36.25272	33.72006	35.62417	114.6086	112.2927	120.0069	-1.6945	1.31E-08	6.53E-08	SLC46A1	chr17	-	26721661	26734215	6487
ENSG00000(	604.9025	621.4125	708.5252	1796.283	2568.926	2204.51	-1.7589	9.10E-33	1.51E-31	PLXNA2	chr1	-	2.08E+08	2.08E+08	11444
ENSG00000(	73.54123	71.05298	112.1502	160.3022	308.3447	175.9005	-1.3156	4.32E-06	1.67E-05	SPAG5	chr17	-	26904592	26926297	4040
ENSG00000(	1008.861	1142.869	1158.445	403.7517	425.2396	275.3582	1.5778	2.39E-21	2.57E-20	ANKRD13A	chr12	+	1.1E+08	1.1E+08	4148
ENSG00000(	3.107376	3.612863	2.638828	1405.266	1170.789	1202.535	-8.3591	9.95E-71	4.38E-69	TPD52	chr8	-	80870571	81143467	3918
ENSG00000(	65.25489	87.913	65.97069	22.47227	51.54419	30.4127	1.0573	0.004677	0.011657	ACACB	chr12	+	1.1E+08	1.1E+08	9360
ENSG00000(	1178.731	1174.181	969.7691	2441.986	1969.724	2545.625	-1.063	9.46E-15	7.35E-14	TRAF4	chr17	+	27071002	27077974	2921
ENSG00000(	38.3243	24.08575	31.66593	71.91125	88.36147	87.95025	-1.3701	6.53E-05	0.000218	PAG1	chr8	-	81882526	82024303	4387
ENSG00000(	154.333	132.4716	117.4278	191.0143	179.4842	195.6277	-0.47944	0.0244	0.05186	GPATCH1	chr19	+	33571786	33621448	3492
ENSG00000(	270.3417	331.1791	254.6469	200.0032	246.6758	245.7675	0.30623	0.10532	0.18297	ICAM3	chr19	-	10444452	10450499	2491
ENSG00000(	989.1813	911.6458	1041.017	1754.335	1505.827	1619.271	-0.72908	3.29E-09	1.73E-08	NT5C2	chr10	-	1.05E+08	1.05E+08	5263
ENSG00000(	85.97073	133.6759	88.40072	831.4739	622.212	702.78	-2.7947	8.59E-45	2.04E-43	MCAM	chr11	-	1.19E+08	1.19E+08	4865
ENSG00000(	1719.415	1775.12	1789.125	1131.853	1223.254	1057.869	0.62952	6.09E-08	2.85E-07	GPC4	chrX	-	1.32E+08	1.33E+08	4960
ENSG00000(	47.64643	38.53721	60.69303	404.5008	538.4527	348.5131	-3.1154	1.14E-37	2.21E-36	MBNL3	chrX	-	1.32E+08	1.32E+08	11294

ENSG00000(	4.143168	3.612863	2.638828	471.1685	535.6914	511.2622	-6.9349	2.73E-50	7.58E-49	CAMSAP3	chr19	+	7660788	7683190	4179
ENSG00000(	11.39371	10.83859	15.83297	8.988907	7.363456	10.68554	0.45487	0.495	0.62379	RAP1GAP	chr1	-	21922708	21995801	4294
ENSG00000(	1056.508	1245.234	823.3142	1409.011	1237.981	1356.242	-0.3557	0.018733	0.04091	XAB2	chr19	-	7684411	7694451	4555
ENSG00000(	1487.397	1543.897	1339.205	2162.581	1702.799	2109.162	-0.45006	0.000549	0.001601	ARHGEF1	chr19	+	42387228	42434302	3439
ENSG00000(	4.143168	2.408575	5.277655	403.0026	303.7426	342.7594	-6.2771	4.21E-42	9.23E-41	STXBP2	chr19	+	7701767	7712759	1974
ENSG00000(	1046.15	1065.795	866.8549	682.4078	823.7866	1062.801	0.21362	0.19656	0.30331	MAP2K7	chr19	+	7968728	7979363	3497
ENSG00000(	0	0	0	37.45378	39.57858	36.16646	-6.0731	7.83E-09	3.96E-08	NMRK2	chr19	+	3933101	3942414	1126
ENSG00000(	716.768	715.3469	771.8571	1454.705	1895.169	1941.481	-1.2602	2.22E-19	2.19E-18	DGKD	chr2	+	2.34E+08	2.34E+08	6297
ENSG00000(	55.93276	54.19295	64.65128	211.2393	242.0736	184.9421	-1.8554	3.32E-14	2.49E-13	CTTNBP2	chr7	-	1.17E+08	1.18E+08	5970
ENSG00000(	384.2788	415.4793	455.1978	104.8706	126.0992	101.1017	1.9105	9.55E-25	1.17E-23	RARB	chr3	+	25215823	25639423	3084
ENSG00000(	2154.447	2062.945	2363.07	1898.157	2145.527	1692.426	0.19774	0.11442	0.19601	TOP2B	chr3	-	25639475	25706398	5389
ENSG00000(	3940.152	3823.614	4672.044	3572.341	3995.595	3458.828	0.17303	0.14737	0.24042	TM9SF3	chr10	-	98277866	98347209	6141
ENSG00000(	879.3873	847.8186	696.6505	546.0761	528.328	674.8332	0.46993	0.002141	0.005677	NFKB2	chr10	+	1.04E+08	1.04E+08	3101
ENSG00000(	98.40023	104.773	109.5113	1047.208	649.825	719.2193	-2.9363	1.97E-47	5.02E-46	UBE2T	chr1	-	2.02E+08	2.02E+08	922
ENSG00000(	406.0304	466.0593	459.156	158.804	332.276	282.7559	0.77965	0.000478	0.001408	PPP1R12B	chr1	+	2.02E+08	2.03E+08	11111
ENSG00000(	1662.446	1619.767	1988.357	2393.296	2188.787	1851.887	-0.28765	0.032609	0.066858	DNAJC10	chr2	+	1.84E+08	1.84E+08	5272
ENSG00000(	3247.208	2920.398	3419.921	2457.717	2763.137	2378.766	0.33475	0.004006	0.010123	GTF3C1	chr16	-	27470876	27561234	7018
ENSG00000(	695.0164	573.241	741.5105	662.9319	639.7002	674.0112	0.023473	0.86958	0.91816	IL4R	chr16	+	27324989	27376099	3685
ENSG00000(	783.0587	829.7542	964.4915	795.5182	687.5627	681.4089	0.24946	0.075115	0.13781	USP33	chr1	-	78161672	78225537	4502
ENSG00000(	43.50326	32.51577	44.86007	13.48336	10.12475	21.37109	1.3778	0.003508	0.008957	PAK3	chrX	+	1.1E+08	1.1E+08	2638
ENSG00000(	6.214751	10.83859	7.916483	557.3122	530.1688	446.327	-5.8528	3.40E-63	1.28E-61	CAPN6	chrX	-	1.1E+08	1.11E+08	3568
ENSG00000(	0	0	3.958241	5.243529	3.681728	2.465895	-1.1497	0.33939	0.46804	DCX	chrX	-	1.11E+08	1.11E+08	9405
ENSG00000(	922.8906	916.463	733.5941	1945.349	1469.009	1788.596	-1.0124	2.89E-12	1.91E-11	SNRPA	chr19	+	41256542	41271294	1621
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	SPAG6	chr10	+	22634399	22743153	2808
ENSG00000(	179.192	181.8474	118.7472	470.4194	433.5235	474.2738	-1.5101	2.12E-15	1.71E-14	EXOSC5	chr19	-	41892279	41903384	1118
ENSG00000(	2004.257	1870.259	2260.156	2495.92	2614.027	2234.923	-0.25947	0.032406	0.066481	DYNC1I2	chr2	+	1.73E+08	1.73E+08	2605
ENSG00000(	1.035792	0	3.958241	28.46487	24.85166	8.219649	-3.2229	0.000214	0.000665	APBB1IP	chr10	+	26727132	26856732	2771
ENSG00000(	862.8147	776.7656	614.8468	1047.957	992.2257	1148.285	-0.49697	0.000778	0.00222	LRCH4	chr7	-	1E+08	1E+08	4754
ENSG00000(	187.4783	169.8046	183.3985	275.6598	303.7426	214.5328	-0.55004	0.00603	0.0147	FAM76B	chr11	-	95502106	95523573	3952
ENSG00000(	526.1823	494.9623	447.2813	492.8917	415.1148	461.9443	0.1002	0.50702	0.63465	SIRT6	chr19	-	4174106	4182601	1641
ENSG00000(	156.4046	181.8474	184.7179	559.5594	578.0313	551.5385	-1.6883	3.94E-25	4.89E-24	POLD3	chr11	+	74204896	74380162	3821
ENSG00000(	15.53688	12.04288	5.277655	3.745378	4.60216	4.93179	1.1959	0.13185	0.21981	ACTN2	chr1	+	2.37E+08	2.37E+08	4863
ENSG00000(	7889.627	7230.543	6623.457	7331.202	6139.281	6371.872	0.13182	0.25612	0.37445	CAPZB	chr1	-	19665267	19812066	2068
ENSG00000(	410.1736	374.5335	455.1978	144.5716	168.4391	104.3895	1.5634	8.20E-15	6.40E-14	GPR137B	chr1	+	2.36E+08	2.36E+08	2039
ENSG00000(	31.07376	25.29004	31.66593	29.21395	53.38506	27.94681	-0.31416	0.47202	0.60107	NAALAD2	chr11	+	89864683	89926062	3600
ENSG00000(	136.7245	156.5574	112.1502	889.9018	737.266	653.4621	-2.4783	1.66E-41	3.59E-40	PHF17	chr4	+	1.3E+08	1.3E+08	5771
ENSG00000(	321.0955	292.6419	376.0329	211.2393	150.9508	167.6808	0.89293	5.75E-06	2.20E-05	SLC25A43	chrX	+	1.19E+08	1.19E+08	2783
ENSG00000(	847.2778	914.0544	915.6732	1205.263	1049.292	983.892	-0.27495	0.035316	0.071706	UBE2A	chrX	+	1.19E+08	1.19E+08	2643
ENSG00000(	2811.139	2786.722	2670.493	1763.324	1994.576	1906.959	0.54513	5.67E-07	2.42E-06	FGFR1	chr8	-	38268656	38326352	5900
ENSG00000(	0	4.817151	0	0.749076	0	0	1.1462	0.39668	NA	FKBP6	chr7	+	72742167	72772634	1933
ENSG00000(	1327.885	1235.599	1550.311	691.3967	882.6943	650.1743	0.88493	3.32E-09	1.74E-08	GTF2I	chr7	+	74071994	74175026	4548
ENSG00000(	3.107376	2.408575	1.319414	3.745378	10.12475	1.64393	-0.94219	0.36947	0.49987	SMC1B	chr22	-	45739944	45809500	4201
ENSG00000(	19328.91	18702.59	17112.8	5870.505	4495.39	4404.91	1.8961	4.13E-50	1.14E-48	FBLN1	chr22	+	45898118	45997015	2947
ENSG00000(	42.46747	55.39724	75.20659	115.3576	173.9616	127.4046	-1.2594	2.02E-05	7.22E-05	ITGA8	chr10	-	15555948	15762124	6755

ENSG00000(	0	0	2.638828	0.749076	0.920432	0.821965	0.020893	0.9877	NA	CST7	chr20	+	24929866	24940564	930
ENSG00000(	18.64425	32.51577	47.4989	762.5589	849.5587	839.2262	-4.6336	7.03E-90	4.41E-88	MAP2	chr2	+	2.1E+08	2.11E+08	9711
ENSG00000(	554.1487	462.4465	474.989	357.309	338.719	290.1536	0.5958	0.000219	0.000679	PIAS2	chr18	-	44388353	44500123	5909
ENSG00000(	556.2203	514.2309	539.6402	49.43899	79.15715	59.18147	3.0926	2.00E-54	6.11E-53	AMPH	chr7	-	38423305	38671167	3418
ENSG00000(	844.1704	781.5827	728.3164	1047.208	907.5459	811.2794	-0.23158	0.10062	0.17636	ARAF	chrX	+	47420516	47431307	2458
ENSG00000(	226.8384	258.9219	270.4798	223.9736	284.4135	212.8889	0.067928	0.72308	0.8139	MCCC1	chr3	-	1.83E+08	1.83E+08	2874
ENSG00000(	1.035792	0	1.319414	52.43529	23.93123	34.52253	-4.8085	3.16E-08	1.53E-07	LAMP3	chr3	-	1.83E+08	1.83E+08	3375
ENSG00000(	1316.492	1324.716	1357.677	31.46117	25.7721	10.68554	5.8338	2.26E-156	3.72E-154	FAP	chr2	-	1.63E+08	1.63E+08	2780
ENSG00000(	804.8103	808.0771	953.9362	862.186	921.3524	749.632	0.018381	0.89512	0.93512	NEBL	chr10	-	21068902	21463116	9216
ENSG00000(	297.2723	275.7819	312.7011	744.5811	682.9605	601.6783	-1.1928	1.11E-14	8.62E-14	ACER3	chr11	+	76571911	76737841	7378
ENSG00000(	1214.984	1278.954	1385.384	1933.364	2147.368	1918.466	-0.62821	9.33E-08	4.29E-07	UBE2K	chr4	+	39699664	39784412	5245
ENSG00000(	915.64	858.6571	934.145	641.2087	567.9065	503.8645	0.65858	2.39E-06	9.51E-06	PIK3C3	chr18	+	39535171	39667794	9443
ENSG00000(	182.2994	255.309	296.8681	346.822	518.2032	396.1871	-0.77794	0.000213	0.000663	N4BP2	chr4	+	40058446	40159872	9747
ENSG00000(	321.0955	289.0291	424.8512	844.2081	922.2729	872.9267	-1.3483	4.27E-17	3.76E-16	C12orf5	chr12	+	4430371	4462338	1361
ENSG00000(	1129.013	1174.181	1110.946	668.1754	551.3388	473.4518	1.0082	6.81E-12	4.39E-11	TULP3	chr12	+	2986389	3050306	3076
ENSG00000(	563.4708	553.9724	691.3728	378.2832	365.4115	352.623	0.71857	2.43E-06	9.64E-06	SYNJ2	chr6	+	1.58E+08	1.59E+08	7378
ENSG00000(	396.7083	487.7365	471.0307	5.992604	5.522592	4.109825	6.3132	1.52E-67	6.33E-66	ADCY2	chr5	+	7396321	7830194	9908
ENSG00000(	1680.054	1652.283	1859.054	1352.83	1309.775	1376.791	0.36083	0.001573	0.004266	PPP2R5C	chr14	+	1.02E+08	1.02E+08	4481
ENSG00000(	78.72018	90.32158	73.88717	73.4094	80.07758	79.7306	0.059528	0.82974	0.89079	PMS2P1	chr7	-	99918615	99939531	1044
ENSG00000(	8108.179	8077.158	7989.05	9858.583	9322.135	9651.512	-0.25391	0.007783	0.018553	GNB1	chr1	-	1716729	1822495	3128
ENSG00000(	256.8764	275.7819	317.9787	32.21025	11.96562	17.26126	3.7228	2.47E-37	4.72E-36	HOXA9	chr7	-	27202054	27210117	2060
ENSG00000(	11.39371	12.04288	26.38828	749.0755	523.7258	466.0541	-5.0932	3.87E-63	1.45E-61	EDN1	chr6	+	12290596	12297427	2033
ENSG00000(	527.2181	572.0367	647.8322	727.3524	733.5843	625.5153	-0.2568	0.076645	0.14016	MLLT10	chr10	+	21823094	22032559	5126
ENSG00000(	37.28851	31.31148	26.38828	44.19546	45.10117	35.34449	-0.37731	0.3415	0.47039	ZCWPW1	chr7	-	99998449	1E+08	2356
ENSG00000(	17.60846	12.04288	3.958241	0	1.840864	0.821965	3.0724	0.002239	0.005914	ADCYAP1R1	chr7	+	31092076	31151089	6487
ENSG00000(	0	1.204288	3.958241	8.988907	2.761296	9.863579	-1.7268	0.099966	0.17544	FGF20	chr8	-	16849678	16859690	1688
ENSG00000(	65.25489	50.58008	51.45714	190.2652	184.0864	153.7074	-1.6377	1.85E-10	1.07E-09	ITM2A	chrX	-	78615881	78623164	1698
ENSG00000(	1859.246	1889.527	2055.647	1743.099	1619.96	1551.048	0.23926	0.036042	0.073023	NRD1	chr1	-	52254863	52344477	3895
ENSG00000(	1330.993	1288.588	1266.637	2546.857	2326.852	2230.813	-0.86873	1.80E-14	1.37E-13	VDAC3	chr8	+	42249142	42263415	1429
ENSG00000(	1296.811	1317.491	1657.184	1458.45	1588.666	1185.273	0.012717	0.93081	0.95835	PCM1	chr8	+	17780349	17885478	6820
ENSG00000(	312.8092	301.0719	397.1435	113.8595	183.166	134.8022	1.2221	1.35E-08	6.71E-08	TNRC6C	chr17	+	76000249	76104916	9740
ENSG00000(	524.1107	575.6495	580.5421	376.785	420.6374	338.6495	0.56296	0.00021	0.000653	CBFA2T2	chr20	+	32077881	32237842	7803
ENSG00000(	0	1.204288	2.638828	19.47596	34.97642	18.08323	-3.7882	1.04E-05	3.85E-05	DBC1	chr9	-	1.22E+08	1.22E+08	3202
ENSG00000(	966.3938	1062.182	1285.109	829.2266	1010.634	805.5256	0.32354	0.029218	0.060754	ITCH	chr20	+	32951041	33099198	6401
ENSG00000(	7.250543	4.817151	3.958241	2.996302	8.283888	4.109825	0.070008	0.93813	0.96242	PKD2L2	chr5	+	1.37E+08	1.37E+08	2333
ENSG00000(	646.3341	708.1212	785.0512	146.0697	196.9724	189.0519	2.0017	1.84E-32	3.02E-31	TP53INP2	chr20	+	33292094	33301243	4184
ENSG00000(	8322.588	7814.623	6531.098	3952.123	3392.712	3965.981	1.0009	4.53E-16	3.81E-15	SDF4	chr1	-	1152288	1167411	3516
ENSG00000(	64.2191	55.39724	27.70769	5.992604	30.37426	21.37109	1.3174	0.010665	0.024627	MYH7B	chr20	+	33563206	33590240	6293
ENSG00000(	1.035792	3.612863	0	0	0.920432	2.465895	0.28605	0.8289	0.89014	BPIFB2	chr20	+	31595406	31611515	1898
ENSG00000(	0	3.612863	0	20.22504	14.72691	13.15144	-3.2032	0.000587	0.001706	TP73	chr1	+	3569084	3652765	5188
ENSG00000(	1500.862	1284.975	1237.61	892.8981	898.3416	891.01	0.58466	3.36E-06	1.31E-05	TOLLIP	chr11	-	1295601	1330884	3666
ENSG00000(	12.4295	21.67718	25.06886	21.72319	18.40864	26.30288	-0.17229	0.73957	0.82557	UBE2D4	chr7	+	43966037	43993166	1405
ENSG00000(	41.43168	45.76293	35.62417	9.737982	5.522592	4.109825	2.5446	1.81E-06	7.31E-06	CLUL1	chr18	+	596988	650334	2449
ENSG00000(	355.2766	417.8878	361.5194	200.7522	312.0264	205.4912	0.65872	0.000959	0.002694	RUNX1T1	chr8	-	92967203	93115514	7537

ENSG00000(	2.071584	9.634302	14.51355	0	0	1.64393	3.048	0.006131	0.014928	CDH17	chr8	-	95139399	95229531	3693
ENSG00000(	389.4578	399.8235	385.2688	798.5145	582.6335	550.7165	-0.71605	2.26E-05	8.04E-05	THOC1	chr18	-	214520	268050	2791
ENSG00000(	1569.225	1501.747	1369.552	166.2948	131.6218	124.9387	3.3788	7.55E-110	6.69E-108	FKBP7	chr2	-	1.79E+08	1.79E+08	2834
ENSG00000(	132.5814	119.2245	151.7326	381.2795	294.5382	318.1004	-1.2965	7.52E-11	4.49E-10	OSBPL6	chr2	+	1.79E+08	1.79E+08	7055
ENSG00000(	1274.024	1389.748	1378.787	1390.284	1492.02	1298.705	-0.04866	0.68189	0.78237	SLC1A3	chr5	+	36606457	36688436	4170
ENSG00000(	4776.036	4557.025	4889.747	10147.73	8477.179	7682.906	-0.88561	2.79E-13	1.99E-12	XRCC5	chr2	+	2.17E+08	2.17E+08	3761
ENSG00000(	179.192	149.3317	184.7179	100.3761	59.82808	52.60575	1.2515	5.86E-06	2.23E-05	LXN	chr3	-	1.58E+08	1.58E+08	1116
ENSG00000(	27.96638	16.86003	31.66593	33.7084	34.97642	41.09825	-0.50843	0.2438	0.35978	SP140	chr2	+	2.31E+08	2.31E+08	3246
ENSG00000(	277.5922	337.2006	316.6593	550.5705	594.5991	461.1223	-0.78435	2.04E-06	8.18E-06	MKNK1	chr1	-	47023090	47082515	3408
ENSG00000(	2418.574	2383.285	2407.93	61.42419	161.996	95.34793	4.4088	4.75E-30	7.22E-29	TNS1	chr2	-	2.19E+08	2.19E+08	10331
ENSG00000(	721.947	534.7037	474.989	1101.141	1172.63	1238.701	-1.014	1.61E-10	9.37E-10	REXO1	chr19	-	1815248	1848452	4578
ENSG00000(	2448.612	2303.802	2636.189	1997.035	2135.402	2144.506	0.23479	0.034347	0.069999	SAR1A	chr10	-	71909960	71930279	3227
ENSG00000(	61.11172	57.80581	75.20659	210.4902	243.9145	212.0669	-1.7694	5.50E-14	4.09E-13	CDC14A	chr1	+	1.01E+08	1.01E+08	4181
ENSG00000(	55.93276	44.55865	39.58241	40.45008	61.66894	40.27628	-0.01423	0.96906	0.98176	RAPGEF3	chr12	-	48128455	48164823	5751
ENSG00000(	7.250543	14.45145	5.277655	98.1289	86.52061	90.41614	-3.2589	6.49E-14	4.80E-13	CEACAM1	chr19	-	43011456	43065386	3519
ENSG00000(	175.0488	186.6646	201.8703	424.7258	361.7298	328.786	-0.98288	7.47E-08	3.47E-07	SENP1	chr12	-	48436681	48500091	4969
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	DUSP13	chr10	-	76854190	76868976	1768
ENSG00000(	4960.407	4519.692	3802.551	1539.35	2012.064	2156.014	1.2157	4.28E-17	3.77E-16	CIC	chr19	+	42772689	42799949	8218
ENSG00000(	85.97073	97.54731	116.1084	52.43529	70.87326	90.41614	0.48042	0.10375	0.18082	LIPE	chr19	-	42905659	42931578	3813
ENSG00000(	3480.261	3528.563	3683.803	4986.596	4029.651	4154.211	-0.30044	0.009841	0.022926	FDFT1	chr8	+	11653082	11696818	2176
ENSG00000(	424.6747	480.5108	357.5611	464.4268	278.8909	332.8958	0.22806	0.2526	0.37034	PAFAH1B3	chr19	-	42801185	42807698	1098
ENSG00000(	124.295	142.106	228.2586	78.65293	141.7465	81.37453	0.70465	0.016756	0.037019	OPHN1	chrX	-	67262186	67653755	7879
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	AFM	chr4	+	74347400	74369691	2032
ENSG00000(	536.5402	569.6281	522.4879	2437.492	2130.8	2467.539	-2.1067	2.45E-65	9.67E-64	KIF22	chr16	+	29802040	29816706	2505
ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	SCGN	chr6	+	25652464	25702011	1447
ENSG00000(	97.36444	95.13873	108.1919	578.2863	705.0509	566.3338	-2.6104	3.82E-46	9.39E-45	LRRC16A	chr6	+	25279306	25620758	5431
ENSG00000(	1587.869	1710.089	1588.574	645.7031	598.2808	617.2957	1.3893	1.81E-31	2.89E-30	PGM1	chr1	+	64058947	64125916	2657
ENSG00000(	2323.281	2168.922	2233.768	2860.72	2764.057	2739.609	-0.31394	0.002644	0.006899	DDX1	chr2	+	15731302	15771235	2817
ENSG00000(	2939.577	2964.956	2783.963	3085.442	2777.864	3305.121	-0.07748	0.48857	0.61766	DNM2	chr19	+	10828755	10944164	5651
ENSG00000(	800.6671	846.6143	905.1179	1238.222	1561.973	1360.352	-0.7034	1.18E-07	5.35E-07	EPB41L2	chr6	-	1.31E+08	1.31E+08	4457
ENSG00000(	9.322127	9.634302	29.0271	3.745378	2.761296	1.64393	2.2896	0.004359	0.010926	RIMS1	chr6	+	72596406	73112845	7055
ENSG00000(	1833.352	1966.602	2182.31	74.90755	75.47542	85.48435	4.6492	1.20E-202	3.65E-200	MOXD1	chr6	-	1.33E+08	1.33E+08	3059
ENSG00000(	985.0381	986.3116	1190.111	969.3038	952.6471	843.336	0.19177	0.15263	0.24765	STX7	chr6	-	1.33E+08	1.33E+08	3689
ENSG00000(	620.4394	593.7138	550.1955	867.4295	734.5047	829.3626	-0.46109	0.000763	0.002184	RABL2B	chr22	-	51205929	51222091	2498
ENSG00000(	1211.877	1101.923	1089.836	928.8537	959.0901	1093.213	0.19142	0.13173	0.21964	KEAP1	chr19	-	10596796	10614417	2955
ENSG00000(	0	0	0	0.749076	2.761296	0	-0.97685	0.45852	NA	DDX43	chr6	+	74104471	74127292	2513
ENSG00000(	6.214751	16.86003	6.597069	0	0	0	4.4956	0.000155	0.000493	PTPRH	chr19	-	55692616	55720874	3877
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	DCT	chr13	-	95089558	95131936	4568
ENSG00000(	796.524	743.0455	649.1516	729.5996	642.4615	845.8019	-0.01838	0.90214	0.93928	SLC35C2	chr20	-	44978167	44993043	2510
ENSG00000(	317.9881	372.1249	391.8659	173.0365	179.4842	97.81383	1.2554	2.25E-08	1.10E-07	CRYBG3	chr3	+	97595819	97663810	4782
ENSG00000(	6.214751	0	0	11.23613	7.363456	18.90519	-2.1458	0.024163	0.051428	EPHA6	chr3	+	96533425	97471304	3971
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	SCTR	chr2	-	1.2E+08	1.2E+08	2275
ENSG00000(	283.807	302.2762	432.7677	235.2097	292.6974	252.3432	0.38121	0.054112	0.10412	RFX3	chr9	-	3218297	3526004	9307
ENSG00000(	496.1443	490.1451	703.2475	776.0423	950.8063	704.4239	-0.52424	0.002414	0.00634	RIF1	chr2	+	1.52E+08	1.52E+08	10180

ENSG00000(	876.28	930.9144	989.5603	1305.639	1268.355	1188.561	-0.42797	0.000436	0.001294	RAB21	chr12	+	72148654	72184699	6180
ENSG00000(	17.60846	4.817151	19.79121	5.992604	18.40864	8.219649	0.35513	0.61293	0.72627	SLC4A4	chr4	+	72053003	72437804	7640
ENSG00000(	1062.722	1085.063	1229.694	656.1902	920.432	700.3141	0.56774	0.000169	0.000534	SMARCA2	chr9	+	2015342	2193624	5867
ENSG00000(	885.6021	885.1515	992.1992	749.0755	716.0961	648.5303	0.38473	0.003431	0.00878	SESN1	chr6	-	1.09E+08	1.09E+08	3509
ENSG00000(	13.46529	6.021439	26.38828	19.47596	25.7721	8.219649	-0.21358	0.73897	0.82521	MID2	chrX	+	1.07E+08	1.07E+08	2876
ENSG00000(	3104.268	3013.128	2563.621	53.93344	82.83888	72.33291	5.3659	1.57E-236	6.97E-234	COL5A3	chr19	-	10070237	10121147	6174
ENSG00000(	2901.253	2573.563	2662.577	2268.201	3540.902	2958.252	-0.10672	0.47214	0.6012	SRCAP	chr16	+	30709530	30755602	10804
ENSG00000(	706.4101	738.2284	707.2058	1895.161	1587.745	1568.309	-1.2287	8.30E-22	9.07E-21	KIAA0020	chr9	-	2720469	2844241	2321
ENSG00000(	0	3.612863	3.958241	0.749076	1.840864	4.93179	-0.00904	0.9939	0.99615	CPB2	chr13	-	46627321	46679211	1717
ENSG00000(	8.286335	22.88147	18.47179	2.247227	9.20432	10.68554	1.0813	0.1294	0.2164	CHRNA3	chr15	-	78885394	78913637	3202
ENSG00000(	0	0	0	20.22504	9.20432	10.68554	-4.5913	5.99E-05	0.000201	KCNN2	chr5	+	1.14E+08	1.14E+08	3216
ENSG00000(	430.8894	407.0492	477.6278	349.0692	371.8545	271.2484	0.40527	0.017907	0.039299	CNOT4	chr7	-	1.35E+08	1.35E+08	4642
ENSG00000(	852.4567	877.9257	898.5208	976.0454	935.1589	851.5557	-0.07199	0.56589	0.68521	PSEN1	chr14	+	73603126	73690399	6078
ENSG00000(	651.5131	551.5638	757.3435	807.5034	813.6619	687.9846	-0.23617	0.12117	0.20554	CPOX	chr3	-	98239976	98312567	2825
ENSG00000(	390.4935	421.5007	415.6153	1107.134	809.0597	868.8169	-1.1794	2.66E-14	2.01E-13	CLDND1	chr3	-	98216756	98241910	2818
ENSG00000(	246.5185	179.4389	145.1355	56.92974	73.63456	60.00344	1.5754	2.53E-09	1.34E-08	MOK	chr14	-	1.03E+08	1.03E+08	3809
ENSG00000(	10782.59	10331.58	11734.87	26004.91	23306.26	22030.3	-1.1172	8.87E-25	1.09E-23	HSP90AA1	chr14	-	1.03E+08	1.03E+08	3510
ENSG00000(	121.1877	105.9773	143.8161	253.9366	255.8801	203.8473	-0.94001	1.29E-05	4.73E-05	RBL1	chr20	-	35624752	35724398	5684
ENSG00000(	2861.893	2607.283	2609.8	2218.762	2577.21	2264.513	0.19462	0.08798	0.15777	DLGAP4	chr20	+	34894258	35157040	5056
ENSG00000(	6.214751	7.225726	1.319414	21.72319	63.50981	33.70056	-2.8032	1.00E-05	3.72E-05	IGSF9B	chr11	-	1.34E+08	1.34E+08	7309
ENSG00000(	279.6638	268.5562	234.8557	56.92974	109.5314	97.81383	1.561	1.98E-10	1.15E-09	CROCCP3	chr1	-	16793931	16825752	5368
ENSG00000(	248.5901	220.3847	215.0644	826.2303	723.4595	785.7985	-1.764	3.11E-31	4.92E-30	NDC80	chr18	+	2571510	2616634	2172
ENSG00000(	181.2636	171.0089	230.8974	245.6968	300.9813	254.8091	-0.4578	0.020403	0.044144	AP4E1	chr15	+	51200869	51298097	6758
ENSG00000(	207.1584	289.0291	335.1311	250.9403	252.1984	222.7525	0.19083	0.34681	0.47639	RSBN1	chr1	-	1.14E+08	1.14E+08	6621
ENSG00000(	194.7289	217.9761	275.7575	146.0697	168.4391	107.6774	0.69917	0.002305	0.006075	MAGI3	chr1	+	1.14E+08	1.14E+08	6508
ENSG00000(	19.68005	7.225726	23.74945	7.490755	6.443024	0.821965	1.6206	0.03446	0.070187	CXCL2	chr4	-	74962752	74965010	1218
ENSG00000(	80.79177	52.98866	0	10.48706	37.73771	59.18147	0.23328	0.84606	0.9018	AFP	chr4	+	74296855	74321891	2484
ENSG00000(	15.53688	6.021439	6.597069	5.992604	16.56778	7.397684	-0.05934	0.93659	0.96168	COL4A4	chr2	-	2.28E+08	2.28E+08	9895
ENSG00000(	1023.362	935.7316	876.0908	251.6894	305.5834	289.3317	1.7411	8.39E-33	1.40E-31	TCF7	chr5	+	1.33E+08	1.33E+08	5340
ENSG00000(	258.948	268.5562	341.7282	496.6371	499.7946	461.1223	-0.7459	6.68E-06	2.53E-05	OSTM1	chr6	-	1.08E+08	1.08E+08	4467
ENSG00000(	0	2.408575	0	47.19176	53.38506	29.59074	-5.0293	3.44E-09	1.80E-08	CDH7	chr18	+	63417488	63548638	3766
ENSG00000(	14.50109	7.225726	17.15238	2.247227	8.283888	4.109825	1.2988	0.092923	0.16505	IMPG2	chr3	-	1.01E+08	1.01E+08	4157
ENSG00000(	2282.885	2502.51	2616.398	2420.263	2188.787	2206.976	0.11813	0.29477	0.41908	PCNP	chr3	+	1.01E+08	1.01E+08	2342
ENSG00000(	383.243	398.6192	374.7135	328.8442	381.9793	351.801	0.12299	0.4298	0.55987	EXD2	chr14	+	69658228	69709075	3404
ENSG00000(	111.8655	99.95588	134.5802	205.9958	201.5746	165.2149	-0.723	0.00134	0.003684	ARG2	chr14	+	68086515	68118437	2045
ENSG00000(	254.8048	303.4805	291.5904	362.5526	359.8889	236.7259	-0.17464	0.37886	0.50963	MEF2C	chr5	-	88013975	88199922	6458
ENSG00000(	0	1.204288	0	0	0	2.465895	-0.37534	0.77612	NA	PTPRC	chr1	+	1.99E+08	1.99E+08	5321
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	PKP1	chr1	+	2.01E+08	2.01E+08	5447
ENSG00000(	574.8645	584.0795	588.4585	660.6846	686.6423	554.8263	-0.12201	0.3913	0.52203	UBA5	chr3	+	1.32E+08	1.32E+08	3902
ENSG00000(	605.9383	657.5411	571.3062	425.4749	400.3879	341.1154	0.65076	1.81E-05	6.52E-05	STK17B	chr2	-	1.97E+08	1.97E+08	5287
ENSG00000(	526.1823	487.7365	585.8197	537.8362	627.7346	520.3038	-0.07537	0.61401	0.72738	CDC14B	chr9	-	99252523	99382112	5589
ENSG00000(	180.2278	158.966	167.5656	101.1252	159.2347	97.81383	0.50126	0.041251	0.082209	ZNF510	chr9	-	99518147	99540411	5616
ENSG00000(	0	0	0	998.5177	1455.203	981.4261	-10.436	1.24E-31	1.98E-30	LRP2	chr2	-	1.7E+08	1.7E+08	15808
ENSG00000(	82.86335	105.9773	79.16483	47.94084	44.18074	63.2913	0.77492	0.011429	0.026209	ZNF506	chr19	-	19896648	19932560	4140

ENSG00000(	68.36227	54.19295	50.13772	64.4205	57.98722	94.52597	-0.3206	0.32707	0.45476	JMJD4	chr1	-	2.28E+08	2.28E+08	3749
ENSG00000(	276.5564	285.4162	241.4527	529.5964	451.0117	495.6448	-0.87389	6.08E-08	2.85E-07	DUSP12	chr1	+	1.62E+08	1.62E+08	1270
ENSG00000(	882.4947	776.7656	688.734	722.8579	625.8938	615.6517	0.25742	0.076492	0.13995	AACS	chr12	+	1.26E+08	1.26E+08	6640
ENSG00000(	1105.19	1223.556	1143.932	831.4739	739.1069	706.8898	0.60653	2.14E-06	8.55E-06	KIAA0141	chr5	+	1.41E+08	1.41E+08	4970
ENSG00000(	80.79177	63.82725	77.84541	74.90755	65.35067	23.01502	0.43703	0.25606	0.37441	CADPS2	chr7	-	1.22E+08	1.23E+08	6045
ENSG00000(	44.53905	38.53721	55.41538	20.22504	10.12475	6.575719	1.8289	0.000198	0.000617	PCDHB4	chr5	+	1.41E+08	1.41E+08	3621
ENSG00000(	9.322127	7.225726	15.83297	11.23613	6.443024	2.465895	0.61065	0.43111	0.56093	PCDHA6	chr5	+	1.4E+08	1.4E+08	5374
ENSG00000(	5.17896	8.430014	5.277655	0	1.840864	0	2.5787	0.024441	0.051918	PCDHGA2	chr5	+	1.41E+08	1.41E+08	4605
ENSG00000(	301.4154	303.4805	277.0769	408.9952	387.5019	480.8495	-0.53188	0.00121	0.003347	HSPB11	chr1	-	54387234	54411975	915
ENSG00000(	87.00652	81.89156	79.16483	376.0359	444.5687	323.8542	-2.1898	1.09E-25	1.39E-24	PHLPP1	chr18	+	60382672	60647666	6401
ENSG00000(	131.5456	133.6759	188.6762	185.0217	199.7337	165.2149	-0.27869	0.21125	0.32116	ATP8B1	chr18	-	55313658	55470333	5935
ENSG00000(	5.17896	2.408575	2.638828	14.23244	11.96562	21.37109	-1.9978	0.00968	0.022585	IL12RB2	chr1	+	67773047	67862583	4040
ENSG00000(	1183.91	1105.536	928.8673	92.13629	105.8497	81.37453	3.5162	1.96E-96	1.42E-94	SMARCD3	chr7	-	1.51E+08	1.51E+08	2415
ENSG00000(	446.4263	364.8992	444.6424	650.9467	551.3388	554.8263	-0.48323	0.001804	0.004848	WDR70	chr5	+	37379314	37753537	5716
ENSG00000(	1.035792	0	3.958241	13.48336	12.88605	10.68554	-2.525	0.006499	0.015734	FYB	chr5	-	39105338	39274630	4750
ENSG00000(	47.64643	45.76293	39.58241	16.47966	18.40864	13.9734	1.4108	0.001135	0.003154	MPP4	chr2	-	2.03E+08	2.03E+08	2462
ENSG00000(	497.1801	555.1766	595.0556	943.8352	676.5175	592.6367	-0.42581	0.015621	0.03472	STRADB	chr2	+	2.02E+08	2.02E+08	2293
ENSG00000(	2379.214	2120.751	2574.176	5212.817	4693.283	4427.103	-1.017	1.14E-17	1.03E-16	BZW1	chr2	+	2.02E+08	2.02E+08	3383
ENSG00000(	1877.891	1766.69	1624.198	27.7158	24.85166	35.34449	5.8723	5.93E-208	1.88E-205	C1QTNF3	chr5	-	33987279	34124633	3424
ENSG00000(	394.6367	433.5436	395.8241	878.6656	688.4831	640.3107	-0.84874	9.94E-08	4.56E-07	ME2	chr18	+	48405419	48474691	3164
ENSG00000(	219.5879	202.3203	273.1187	478.6593	391.1836	387.1455	-0.85417	2.69E-06	1.07E-05	C5orf22	chr5	+	31532373	31555165	3799
ENSG00000(	575.9003	686.444	782.4124	645.7031	601.9625	536.7431	0.19386	0.20889	0.31845	CCNT2	chr2	+	1.36E+08	1.36E+08	6917
ENSG00000(	128.4382	167.396	179.4403	198.505	192.3703	169.3248	-0.2399	0.26451	0.38438	FAM135A	chr6	+	71122644	71270877	6415
ENSG00000(	39.36009	34.92434	29.0271	31.46117	38.65814	38.63235	-0.06598	0.8686	0.9175	COL19A1	chr6	+	70576463	70919679	6232
ENSG00000(	1132.121	1162.138	1399.898	1598.527	1966.963	1606.119	-0.48457	0.000384	0.001149	EPB41L3	chr18	-	5392383	5630699	4908
ENSG00000(	269.3059	290.2333	347.0058	248.6931	317.549	211.245	0.22006	0.26655	0.38656	COBLL1	chr2	-	1.66E+08	1.66E+08	9367
ENSG00000(	432.961	367.3078	438.0454	575.29	594.5991	635.3789	-0.54201	0.000233	0.00072	DLG3	chrX	+	69664711	69725337	6109
ENSG00000(	101.5076	96.34302	135.8996	16.47966	7.363456	4.93179	3.4286	7.24E-17	6.30E-16	KCNK2	chr1	+	2.15E+08	2.15E+08	3379
ENSG00000(	79.75598	43.35436	98.95603	447.1981	431.6826	368.2403	-2.4733	3.40E-25	4.23E-24	SERTAD4	chr1	+	2.1E+08	2.1E+08	5219
ENSG00000(	150.1898	163.7831	130.622	384.2758	396.7062	320.5663	-1.3006	6.84E-12	4.41E-11	TRAF5	chr1	+	2.11E+08	2.12E+08	4958
ENSG00000(	394.6367	456.425	365.4776	577.5372	565.1452	615.6517	-0.52948	0.000407	0.001215	MRPL22	chr5	+	1.54E+08	1.54E+08	3176
ENSG00000(	762.3428	663.5625	795.6065	859.1897	820.1049	651.8182	-0.06949	0.64154	0.74914	GEMIN5	chr5	-	1.54E+08	1.54E+08	5397
ENSG00000(	0	0	0	43.44638	43.2603	35.34449	-6.1724	3.88E-09	2.02E-08	OPRK1	chr8	-	54138284	54164257	5014
ENSG00000(	6312.116	6235.802	6385.963	2346.854	3393.633	3414.442	1.0459	7.42E-14	5.46E-13	NFE2L1	chr17	+	46125691	46138849	4774
ENSG00000(	2.071584	4.817151	7.916483	9.737982	23.0108	27.94681	-1.9008	0.008573	0.020242	SEMA5B	chr3	-	1.23E+08	1.23E+08	4832
ENSG00000(	1638.623	1651.078	2324.807	1799.279	2168.538	1569.953	0.01938	0.90325	0.94023	GSK3B	chr3	-	1.2E+08	1.2E+08	7711
ENSG00000(	3014.154	2914.376	2984.514	3887.702	3903.552	3809.807	-0.3797	0.000143	0.000457	ITGB5	chr3	-	1.24E+08	1.25E+08	4372
ENSG00000(	1175.624	1134.439	1439.48	755.8172	1153.301	992.1117	0.36909	0.022634	0.048421	ERC1	chr12	+	1099675	1605090	9451
ENSG00000(	2125.445	2065.353	2559.663	3805.304	3863.974	3395.537	-0.71194	5.41E-09	2.78E-08	XPO1	chr2	-	61704984	61765761	6776
ENSG00000(	1.035792	0	3.958241	0	4.60216	0.821965	-0.07646	0.95296	0.97195	C4orf6	chr4	+	5526296	5529528	873
ENSG00000(	328.346	343.222	386.5882	370.7924	290.8565	263.0288	0.19103	0.29137	0.41549	RNF13	chr3	+	1.5E+08	1.5E+08	2866
ENSG00000(	7.250543	0	6.597069	54.68252	61.66894	48.49593	-3.3874	3.42E-09	1.79E-08	TRPM3	chr9	-	73149949	74061820	6269
ENSG00000(	125.3308	144.5145	176.8014	200.7522	222.7445	175.0785	-0.42311	0.052333	0.10105	PALB2	chr16	-	23614488	23652631	4003
ENSG00000(	214.4089	151.7403	283.674	135.5827	183.166	106.8554	0.60533	0.020271	0.04391	DOPEY1	chr6	+	83777385	83881069	8210

ENSG00000(	728.1617	794.8299	679.4981	818.7396	759.3564	779.2227	-0.09774	0.45592	0.58565	LYRM2	chr6	-	90277863	90348472	5353
ENSG00000(	416.3883	492.5537	485.5443	526.6001	566.0657	531.8113	-0.22071	0.13011	0.21738	BCKDHB	chr6	+	80816364	81055987	3767
ENSG00000(	960.1791	827.3457	1245.527	493.6408	1063.099	745.5222	0.39584	0.068013	0.12663	KAT6A	chr8	-	41786997	41909508	9285
ENSG00000(	760.2713	753.8841	1000.116	255.4348	342.4007	219.4646	1.6149	1.33E-18	1.26E-17	ZCCHC6	chr9	-	88902648	88969369	5724
ENSG00000(	283.807	233.6318	265.2022	258.4311	232.8693	212.0669	0.15363	0.40398	0.53496	ULK2	chr17	-	19674142	19771249	6010
ENSG00000(	4.143168	1.204288	0	956.5695	1198.402	1018.415	-8.6321	3.96E-55	1.23E-53	GRHL2	chr8	+	1.03E+08	1.03E+08	5239
ENSG00000(	4983.195	4801.495	6979.699	3627.773	3926.563	3234.432	0.63384	1.41E-05	5.16E-05	TNPO1	chr5	+	72112139	72212560	11183
ENSG00000(	11485.9	11372.09	10177.96	3046.49	2630.595	2618.78	1.99	2.74E-71	1.22E-69	PLOD1	chr1	+	11994262	12035595	2940
ENSG00000(	5.17896	2.408575	11.87472	8.988907	10.12475	1.64393	-0.09067	0.91849	0.9507	P2RX5	chr17	-	3575493	3599698	2309
ENSG00000(	185.4068	227.6104	175.482	344.5748	294.5382	371.5281	-0.77699	3.75E-05	0.000129	ITGAE	chr17	-	3617922	3704537	3858
ENSG00000(	827.5977	927.3015	1145.251	1093.65	971.0558	900.0516	-0.03338	0.82244	0.88538	DIS3	chr13	-	73329540	73356234	7371
ENSG00000(	240.3037	204.7289	270.4798	210.4902	154.6326	191.5178	0.35704	0.081285	0.1474	PIBF1	chr13	+	73356197	73590591	3146
ENSG00000(	150.1898	183.0517	195.2732	208.243	165.6778	184.9421	-0.08477	0.68568	0.78495	TDRD3	chr13	+	60970591	61148012	3019
ENSG00000(	218.5521	174.6217	221.6615	334.0877	277.05	274.5363	-0.52482	0.005685	0.013932	NUFIP1	chr13	-	45513384	45563618	3492
ENSG00000(	946.7138	812.8942	1087.197	731.0977	891.8986	727.439	0.27575	0.064688	0.12117	PDS5B	chr13	+	33160564	33352157	7497
ENSG00000(	1069.973	1107.945	1203.305	641.2087	723.4595	701.1361	0.70927	2.34E-08	1.14E-07	OXCT1	chr5	-	41730167	41870621	3388
ENSG00000(	392.5651	499.7794	474.989	147.5679	159.2347	124.1167	1.658	1.91E-19	1.89E-18	RRAGB	chrX	+	55744172	55785207	2061
ENSG00000(	304.5228	395.0064	399.7824	89.88907	97.56579	98.63579	1.9306	2.87E-22	3.18E-21	CYLD	chr16	+	50775961	50835846	8713
ENSG00000(	40.39588	39.74149	25.06886	33.7084	37.73771	70.68898	-0.41785	0.31833	0.44535	SLC27A5	chr19	-	58990879	59023780	5032
ENSG00000(	248.5901	322.7491	270.4798	217.981	277.9705	250.6993	0.1728	0.35695	0.48645	ZNF324	chr19	+	58978423	58984945	3795
ENSG00000(	143.9751	137.2888	139.8579	80.15108	112.2927	127.4046	0.3962	0.11101	0.19089	ZNF671	chr19	-	58231119	58238992	2903
ENSG00000(	105.6508	79.48299	56.73479	95.88167	49.70333	71.51095	0.15514	0.6417	0.74925	ZNF416	chr19	-	58082934	58090295	2561
ENSG00000(	121.1877	136.0845	187.3568	133.3354	126.0992	163.571	0.06632	0.78328	0.85729	ZNF586	chr19	+	58281023	58331307	2265
ENSG00000(	127.4024	178.2346	131.9414	59.92604	95.72493	85.48435	0.85459	0.001469	0.003999	ZNF446	chr19	+	58985384	58992597	3922
ENSG00000(	9.322127	33.72006	21.11062	12.73428	12.88605	21.37109	0.41924	0.47368	0.6028	ZNF8	chr19	+	58790317	58807254	2211
ENSG00000(	165.7267	171.0089	205.8285	71.16218	101.2475	77.2647	1.113	3.93E-06	1.53E-05	ZNF264	chr19	+	57702868	57724724	2673
ENSG00000(	18896.99	18007.71	13447.47	18102.16	12390.86	13769.56	0.18538	0.229	0.34235	RPS5	chr19	+	58897767	58906173	1747
ENSG00000(	6669.464	6084.062	9470.752	3567.847	3945.892	2923.729	1.0865	1.12E-11	7.10E-11	FAT1	chr4	-	1.88E+08	1.88E+08	14786
ENSG00000(	1061.687	1012.806	1068.725	1224.739	1218.652	1042.252	-0.14884	0.23265	0.34636	YTHDC1	chr4	-	69176105	69215807	6232
ENSG00000(	433.9968	354.0606	391.8659	695.8912	636.0185	580.3072	-0.69343	5.28E-06	2.02E-05	CHMP2B	chr3	+	87276421	87304698	2606
ENSG00000(	1633.444	1513.79	1621.56	447.9472	404.9901	433.9975	1.885	1.64E-52	4.80E-51	SMAP2	chr1	+	40810522	40888998	2939
ENSG00000(	711.589	697.2826	547.5567	846.4554	759.3564	743.0563	-0.26178	0.073795	0.13576	PPIE	chr1	+	40157854	40229586	4651
ENSG00000(	1280.239	1217.535	1546.353	1422.494	1377.887	1234.591	0.002505	0.98489	0.99109	ZMPSTE24	chr1	+	40723779	40759856	3108
ENSG00000(	1868.569	1695.637	2018.703	3355.858	3151.559	2910.578	-0.75328	1.48E-10	8.66E-10	STARD7	chr2	-	96850597	96874563	3368
ENSG00000(	1047.186	1169.363	985.6021	685.4041	638.7798	565.5119	0.75885	2.89E-08	1.40E-07	NOA1	chr4	-	57829536	57844989	3415
ENSG00000(	801.7029	745.4541	1043.656	686.9023	882.6943	668.2575	0.21029	0.19938	0.30698	REST	chr4	+	57774075	57802010	7300
ENSG00000(	2.071584	1.204288	3.958241	6.74168	6.443024	2.465895	-0.93153	0.36332	0.49313	HAL	chr12	-	96366440	96390143	3913
ENSG00000(	1527.793	1256.072	1798.361	1339.347	1791.161	1405.56	0.014681	0.92462	0.95436	SSH1	chr12	-	1.09E+08	1.09E+08	8538
ENSG00000(	9827.594	9478.949	7941.552	12505.07	10172.61	10895.15	-0.30046	0.013915	0.031354	GSTP1	chr11	+	67351066	67354131	1681
ENSG00000(	9533.429	9416.326	10338.93	14884.13	13518.38	11790.26	-0.45586	6.99E-05	0.000233	APLP2	chr11	+	1.3E+08	1.3E+08	3720
ENSG00000(	129.474	131.2674	89.72014	210.4902	205.2563	212.0669	-0.83095	0.000172	0.000542	KIAA1467	chr12	+	13197218	13295455	4808
ENSG00000(	0	1.204288	0	20.97412	17.48821	12.32947	-4.2198	4.97E-05	0.000169	SLCO1A2	chr12	-	21417534	21572528	7682
ENSG00000(	1122.798	1083.859	1074.003	2406.78	2146.447	1797.637	-0.95065	5.76E-13	4.00E-12	WBP11	chr12	-	14939410	14956474	2749
ENSG00000(	4207.387	4072.901	3496.447	4996.334	3800.464	4418.061	-0.16581	0.19741	0.30446	EIF3I	chr1	+	32687529	32697205	1458

ENSG0000(	68.36227	68.6444	51.45714	132.5864	110.4518	131.5144	-0.97775	0.000301	0.000916	NKAIN1	chr1	-	31652592	31712401	2589
ENSG0000(	5583.954	5634.862	4464.896	115.3576	218.1424	220.2866	4.8058	4.38E-149	6.69E-147	COL16A1	chr1	-	32117848	32169920	5736
ENSG0000(	2386.465	2351.974	2422.444	1890.667	2507.257	2014.636	0.15934	0.21246	0.32254	TXLNA	chr1	+	32645287	32663886	5012
ENSG0000(	27.96638	24.08575	1.319414	0	8.283888	17.26126	0.76253	0.53357	0.65808	APOB	chr2	-	21224301	21266945	14121
ENSG0000(	346.9903	381.7592	494.7802	133.3354	196.9724	128.2265	1.4087	3.73E-11	2.28E-10	NCOA1	chr2	+	24714783	24993571	7405
ENSG0000(	685.6942	690.0569	654.4292	845.7063	763.0381	797.306	-0.24462	0.056895	0.10868	AGBL5	chr2	+	27265232	27293490	3261
ENSG0000(	33.14534	25.29004	10.55531	30.7121	62.58938	39.45432	-0.89582	0.059992	0.11369	EFR3B	chr2	+	25264999	25378243	5162
ENSG0000(	1593.048	1496.93	1661.142	473.4157	667.3132	584.4171	1.4589	2.95E-24	3.55E-23	KIF3C	chr2	-	26149471	26205618	5462
ENSG0000(	2656.806	2574.767	2931.737	2430.75	2262.422	2256.294	0.23147	0.03593	0.072822	RAB10	chr2	+	26256976	26360323	3535
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	GCKR	chr2	+	27719709	27746554	2186
ENSG0000(	5463.802	5415.682	5367.375	3232.261	3101.856	2966.471	0.80363	1.22E-15	9.99E-15	HADHA	chr2	-	26413504	26467594	3037
ENSG0000(	963.2865	861.0657	860.2578	134.8336	165.6778	209.6011	2.3882	5.99E-44	1.39E-42	MAPRE3	chr2	+	27193480	27250064	1892
ENSG0000(	2551.155	2333.91	2495.011	2887.686	2847.817	2986.199	-0.24053	0.022124	0.047475	CAD	chr2	+	27440258	27466811	7265
ENSG0000(	5698.927	5218.179	5558.69	2682.44	2259.661	2184.783	1.2065	2.94E-25	3.66E-24	CD59	chr11	-	33719807	33757991	3716
ENSG0000(	525.1465	463.6508	463.1142	29.21395	47.86246	42.74218	3.5874	1.70E-61	6.17E-60	CD82	chr11	+	44585977	44641913	2289
ENSG0000(	398.7799	451.6079	485.5443	591.0206	968.2945	852.3776	-0.84862	2.53E-06	1.00E-05	BCORL1	chrX	+	1.29E+08	1.29E+08	7127
ENSG0000(	1544.366	1502.951	2281.266	707.1273	996.8279	687.9846	1.1507	1.46E-10	8.56E-10	ATRX	chrX	-	76760356	77041702	11268
ENSG0000(	874.2084	915.2587	771.8571	1588.04	1075.065	1189.383	-0.58718	0.000176	0.000554	TAF9	chr5	-	68646811	68665840	1648
ENSG0000(	237.1963	213.1589	220.3421	188.018	208.9381	193.1618	0.18569	0.32002	0.44719	MYNN	chr3	+	1.69E+08	1.7E+08	4999
ENSG0000(	132.5814	205.9332	224.3003	62.92235	65.35067	59.18147	1.5678	2.27E-09	1.21E-08	MECOM	chr3	-	1.69E+08	1.69E+08	5732
ENSG0000(	672.2289	749.067	814.0783	360.3053	387.5019	321.3883	1.0603	1.25E-12	8.50E-12	SCAMP1	chr5	+	77656339	77776562	6245
ENSG0000(	809.9893	779.1742	761.3018	1161.816	1137.654	993.7556	-0.48506	0.00014	0.000446	PREP	chr6	-	1.06E+08	1.06E+08	2905
ENSG0000(	274.4849	248.0833	325.8952	289.8922	314.7877	262.2068	-0.03179	0.86007	0.9111	HACE1	chr6	-	1.05E+08	1.05E+08	5318
ENSG0000(	391.5293	473.2851	568.6673	1134.849	1128.45	906.6273	-1.1435	1.55E-12	1.05E-11	SEH1L	chr18	+	12947132	12987535	5206
ENSG0000(	329.3818	367.3078	494.7802	296.6339	290.8565	293.4415	0.4307	0.01796	0.039389	WDR47	chr1	-	1.1E+08	1.1E+08	4264
ENSG0000(	1153.872	1242.825	1614.962	547.5742	730.823	548.2506	1.1311	4.33E-12	2.84E-11	WDFY1	chr2	-	2.25E+08	2.25E+08	4660
ENSG0000(	69.39806	59.0101	72.56776	30.7121	30.37426	31.23467	1.1034	0.001386	0.003797	OVGP1	chr1	-	1.12E+08	1.12E+08	2243
ENSG0000(	907.3537	902.0115	1071.364	1635.981	1704.64	1369.394	-0.70825	1.52E-07	6.85E-07	SLC25A24	chr1	-	1.09E+08	1.09E+08	4271
ENSG0000(	259.9838	226.4061	270.4798	382.7776	347.9233	344.4033	-0.50517	0.0028	0.00727	MAP3K4	chr6	+	1.61E+08	1.62E+08	5490
ENSG0000(	16.57267	16.86003	1.319414	17.22874	8.283888	8.219649	0.04711	0.94994	0.96992	PILRA	chr7	+	99965153	99997719	1313
ENSG0000(	24.85901	43.35436	42.22124	521.3566	563.3044	572.0876	-3.8975	3.90E-66	1.57E-64	IGSF9	chr1	-	1.6E+08	1.6E+08	4205
ENSG0000(	2.071584	1.204288	0	8.239831	1.840864	9.863579	-2.0087	0.067505	0.12584	ABCB1	chr7	-	87133175	87342611	4645
ENSG0000(	362.5272	332.3834	281.0351	388.0211	333.1964	266.3166	-0.01569	0.93353	0.96015	ZNF213	chr16	+	3179778	3192806	5889
ENSG0000(	1222.234	1207.901	1141.293	2109.397	1573.939	1712.975	-0.59425	9.77E-06	3.63E-05	AKR1B1	chr7	-	1.34E+08	1.34E+08	1930
ENSG0000(	1447.001	1451.167	1927.664	1100.392	1168.949	1002.797	0.55839	8.25E-05	0.000272	CPNE3	chr8	+	87497059	87573726	4864
ENSG0000(	673.2647	608.1653	778.4541	988.0306	937.9202	822.7869	-0.41601	0.003733	0.009486	RRN3	chr16	-	15153879	15188174	3762
ENSG0000(	6434.339	6489.907	6603.666	5094.463	6073.931	6196.794	0.16915	0.12811	0.21482	CTTN	chr11	+	70244510	70282690	3272
ENSG0000(	102.5434	131.2674	125.3443	22.47227	26.69253	42.74218	1.9378	1.94E-09	1.04E-08	WNT11	chr11	-	75897369	75921780	1930
ENSG0000(	490.9654	431.135	449.9201	607.5003	515.4419	499.7547	-0.24121	0.11015	0.1898	MTIF2	chr2	-	55463731	55496483	2947
ENSG0000(	776.8439	782.787	948.6585	766.3043	857.8426	803.0597	0.046574	0.73298	0.8214	DDHD2	chr8	+	38082736	38133076	4921
ENSG0000(	12.4295	6.021439	17.15238	18.72689	18.40864	11.50751	-0.42912	0.49389	0.62272	TTC39A	chr1	-	51752930	51810788	6287
ENSG0000(	858.6715	800.8513	1014.629	1069.68	1208.527	922.2446	-0.25881	0.07665	0.14016	EPS15	chr1	-	51819935	51985000	5225
ENSG0000(	100.4718	72.25726	87.08131	844.9572	667.3132	642.7766	-3.0327	2.68E-55	8.35E-54	ORC1	chr1	-	52838501	52870131	3157
ENSG0000(	96.32865	65.03154	54.09597	87.64184	80.07758	125.7606	-0.43315	0.16362	0.26178	MGST2	chr4	+	1.41E+08	1.41E+08	1780

ENSG00000(	758.1997	726.1855	662.3457	953.5732	1226.015	1108.831	-0.61209	1.09E-05	4.04E-05	CHERP	chr19	-	16628700	16653341	4173
ENSG00000(	397.7441	332.3834	407.6989	967.0565	812.7415	841.6921	-1.201	6.07E-16	5.06E-15	ATG16L1	chr2	+	2.34E+08	2.34E+08	4208
ENSG00000(	646.3341	587.6924	641.2351	623.9799	593.6786	519.4818	0.11004	0.43625	0.5659	USP40	chr2	-	2.34E+08	2.34E+08	5692
ENSG00000(	1062.722	916.463	989.5603	848.7026	806.2984	866.351	0.23544	0.061585	0.11614	POMGNT1	chr1	-	46654354	46685977	3480
ENSG00000(	116.0087	80.68728	89.72014	592.5188	520.9645	481.6714	-2.4584	2.57E-36	4.77E-35	RAD54L	chr1	+	46713360	46744145	3108
ENSG00000(	1431.464	1547.51	1453.994	1895.161	2174.06	1817.364	-0.40815	0.000639	0.001848	MAST2	chr1	+	46252659	46501796	5738
ENSG00000(	2661.985	2585.606	2678.41	5940.169	5036.604	5227.697	-1.0302	4.82E-21	5.09E-20	DNAJA1	chr9	+	33025209	33039905	2381
ENSG00000(	2072.62	1994.3	2219.254	2122.131	2094.903	1895.451	0.040133	0.72185	0.813	B4GALT1	chr9	-	33104080	33167354	4201
ENSG00000(	776.8439	777.9699	738.8717	987.2816	844.0361	919.7787	-0.26202	0.041573	0.082794	CHMP5	chr9	+	33264940	33281977	1707
ENSG00000(	788.2376	841.7971	774.4959	860.6878	750.1521	811.2794	-0.01103	0.93185	0.95908	NFX1	chr9	+	33290509	33371155	4604
ENSG00000(	1.035792	0	0	0	0.920432	1.64393	-0.43567	0.74499	NA	AQP6	chr12	+	50360977	50370922	5129
ENSG00000(	575.9003	704.5083	690.0534	1081.665	800.7758	858.9533	-0.47675	0.001954	0.005215	DIMT1	chr5	-	61683081	61699766	2859
ENSG00000(	237.1963	286.6205	320.6175	753.57	717.0165	600.0344	-1.2926	8.98E-15	6.99E-14	IPO11	chr5	+	61699799	61924409	4356
ENSG00000(	0	0	0	2.996302	2.761296	3.28786	-2.35	0.076628	0.14015	FOLH1	chr11	-	49168187	49230222	2697
ENSG00000(	1740.13	1760.669	1691.488	2653.975	2235.729	2011.348	-0.40971	0.001278	0.003526	EIF2AK1	chr7	-	6061881	6098861	4463
ENSG00000(	0	0	0	3.745378	1.840864	0.821965	-1.8318	0.17592	0.27779	NME8	chr7	+	37888199	37940003	2312
ENSG00000(	564.5066	566.0152	684.7758	496.6371	474.0225	468.52	0.33239	0.022489	0.048151	EPDR1	chr7	+	37723446	37991543	2599
ENSG00000(	0	0	1.319414	82.39831	82.83888	69.86702	-6.3537	8.85E-13	6.08E-12	SNX10	chr7	+	26331541	26413949	2546
ENSG00000(	826.5619	757.497	832.5501	2226.253	1848.227	1731.058	-1.2617	2.24E-21	2.40E-20	SEPHS1	chr10	-	13359424	13390297	3273
ENSG00000(	1103.118	1106.74	1055.531	1351.332	1241.663	1730.236	-0.40379	0.004339	0.010879	MRPL28	chr16	-	417384	420527	2229
ENSG00000(	4.143168	1.204288	2.638828	9.737982	5.522592	14.79537	-1.6575	0.064456	0.12082	HBQ1	chr16	+	230452	231180	536
ENSG00000(	418.4599	441.9736	343.0476	571.5446	524.6462	585.239	-0.47974	0.001897	0.005073	ITPKC	chr19	+	41223008	41246765	3385
ENSG00000(	30.03797	10.83859	35.62417	17.97781	19.32907	11.50751	0.62006	0.26289	0.38254	FAT2	chr5	-	1.51E+08	1.51E+08	14534
ENSG00000(	655.6563	728.5941	651.7904	1118.37	912.1481	912.3811	-0.53075	0.000136	0.000435	RBM22	chr5	-	1.5E+08	1.5E+08	2342
ENSG00000(	4701.459	4581.11	4846.207	3655.489	3316.316	3475.268	0.43472	2.20E-05	7.82E-05	TMED2	chr12	+	1.24E+08	1.24E+08	2552
ENSG00000(	79.75598	92.73015	98.95603	30.7121	14.72691	23.01502	1.939	5.85E-08	2.74E-07	ERO1LB	chr1	-	2.36E+08	2.36E+08	4567
ENSG00000(	779.9513	820.1199	898.5208	1139.344	960.931	1020.88	-0.32165	0.014259	0.032042	ZFAND6	chr15	+	80351910	80430735	2594
ENSG00000(	15.53688	20.47289	10.55531	3.745378	0	0	3.078	0.000784	0.002238	HSD17B2	chr16	+	82068609	82132139	4210
ENSG00000(	161.5835	186.6646	159.6491	399.2573	428.9213	325.4981	-1.1777	3.12E-10	1.78E-09	TXLNG	chrX	+	16804550	16862642	4401
ENSG00000(	4.143168	0	0	0	0	0.821965	0.9919	0.46158	NA	PPEF1	chrX	+	18694029	18846039	2890
ENSG00000(	25.8948	30.10719	23.74945	65.91865	35.89685	53.42772	-0.94204	0.020508	0.044338	LAT2	chr7	+	73613982	73644161	2527
ENSG00000(	6620.782	6414.036	6608.944	4219.543	8576.585	5809.648	0.078171	0.66592	0.76949	HUWE1	chrX	-	53559057	53713673	14796
ENSG00000(	348.0261	356.4692	386.5882	782.7839	721.6187	637.0228	-0.97126	6.62E-11	3.97E-10	ZW10	chr11	-	1.14E+08	1.14E+08	2992
ENSG00000(	180.2278	136.0845	141.1773	155.0586	174.8821	160.2832	-0.09467	0.66326	0.76729	ALG9	chr11	-	1.12E+08	1.12E+08	4485
ENSG00000(	1.035792	0	0	1.498151	0	0.821965	-0.37092	0.78098	NA	MYBPC2	chr19	+	50936160	50969578	3593
ENSG00000(	16.57267	27.69862	42.22124	44.19546	41.41944	36.98842	-0.50393	0.24547	0.36191	NOX4	chr11	-	89057524	89322779	4376
ENSG00000(	511.6812	438.3607	442.0036	275.6598	228.2671	205.4912	0.96819	2.44E-08	1.19E-07	ACOX3	chr4	-	8368009	8442450	2860
ENSG00000(	733.3407	776.7656	893.2431	1452.457	1351.194	1149.107	-0.71719	2.54E-07	1.12E-06	MTMR2	chr11	-	95566046	95658479	4787
ENSG00000(	1243.986	1343.985	1266.637	852.448	768.5607	871.2828	0.62721	2.85E-07	1.25E-06	PPP1R15A	chr19	+	49375649	49379314	2378
ENSG00000(	196.8005	161.3746	172.8432	86.89276	48.7829	106.0335	1.1203	4.84E-05	0.000165	HSD17B14	chr19	-	49316274	49339935	1238
ENSG00000(	4361.72	4504.036	3656.096	2643.488	2751.171	3335.534	0.51941	5.85E-05	0.000197	TRIP6	chr7	+	1E+08	1E+08	1942
ENSG00000(	124.295	179.4389	118.7472	246.4459	247.5962	178.3664	-0.66553	0.004229	0.010636	ACHE	chr7	-	1E+08	1E+08	2956
ENSG00000(	37044.06	35237.46	27739.36	26250.6	18036.79	18264.88	0.675	1.00E-05	3.73E-05	FTL	chr19	+	49468558	49470135	878
ENSG00000(	2101.622	1948.538	1893.359	3553.614	3264.772	3532.805	-0.79882	1.80E-13	1.29E-12	SRRT	chr7	+	1E+08	1E+08	2963

ENSG00000(	2816.318	2702.422	2357.792	3415.785	3101.856	4179.692	-0.44032	0.000957	0.002691	BAX	chr19	+	49458072	49465055	1358
ENSG00000(	296.2365	266.1476	275.7575	361.8035	508.9989	409.3385	-0.60602	0.000615	0.001783	NLK	chr17	+	26368763	26523407	4047
ENSG00000(	1447.001	1269.319	1302.261	1110.13	1075.985	1028.278	0.32199	0.007291	0.017484	PIGS	chr17	-	26880401	26898890	3088
ENSG00000(	159.512	79.48299	106.8725	56.92974	66.2711	63.2913	0.88576	0.003525	0.008995	ADAMTS2	chr5	-	1.79E+08	1.79E+08	6754
ENSG00000(	0	0	0	0.749076	3.681728	2.465895	-1.924	0.15425	0.24976	TMPRSS11E	chr4	+	69313167	69363322	2136
ENSG00000(	2129.588	2147.245	2187.588	1856.958	2089.381	2307.256	0.047851	0.68619	0.78531	ATXN7L3	chr17	-	42269173	42277481	3811
ENSG00000(	539.6476	519.048	618.8051	483.9028	481.3859	530.9893	0.16339	0.26027	0.37924	PGS1	chr17	+	76374721	76421195	3062
ENSG00000(	1502.934	1294.609	1122.821	2241.234	1806.808	1980.113	-0.61835	8.34E-06	3.12E-05	PSMC5	chr17	+	61904512	61909379	2586
ENSG00000(	480.6074	470.8765	438.0454	510.8695	456.5343	444.683	-0.02297	0.87592	0.92224	UIMC1	chr5	-	1.76E+08	1.76E+08	2604
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	CETP	chr16	+	56995762	57017757	1791
ENSG00000(	22131.77	21586.86	20592.09	5248.772	4802.814	4665.473	2.1245	7.58E-98	5.58E-96	MMP2	chr16	+	55423612	55540603	3741
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	MT3	chr16	+	56622986	56625000	1550
ENSG00000(	140.8677	108.3859	155.6908	878.6656	711.4939	868.8169	-2.5929	1.38E-48	3.68E-47	LPCAT2	chr16	+	55542910	55620582	5391
ENSG00000(	5.17896	27.69862	15.83297	89.88907	99.40666	138.0901	-2.7001	1.56E-10	9.11E-10	GNAO1	chr16	+	56225302	56391356	5574
ENSG00000(	697.088	705.7126	721.7193	1024.735	874.4104	943.6157	-0.42006	0.001117	0.003109	OGFOD1	chr16	+	56485402	56513012	4647
ENSG00000(	1947.289	2093.052	1874.887	443.4527	483.2268	482.4934	2.0662	5.55E-65	2.16E-63	SH3BP2	chr4	+	2794750	2842825	9211
ENSG00000(	589.3656	534.7037	605.6109	901.1379	777.765	887.7221	-0.5686	2.97E-05	0.000104	NOP14	chr4	-	2939660	2965112	3538
ENSG00000(	4592.701	4351.092	4306.567	3941.636	3805.066	3500.749	0.23617	0.024288	0.051655	ADD1	chr4	+	2845584	2931803	5179
ENSG00000(	65.25489	90.32158	125.3443	167.0438	248.5166	227.6843	-1.1906	6.20E-06	2.36E-05	L2HGDH	chr14	-	50704281	50779266	3446
ENSG00000(	83.89914	93.93444	109.5113	69.66403	88.36147	76.44274	0.28937	0.28931	0.41303	TXNDC16	chr14	-	52897308	53019240	4564
ENSG00000(	1982.506	2078.601	1843.221	2950.609	2105.948	2296.57	-0.31603	0.022122	0.047475	C14orf166	chr14	+	52456193	52471420	1080
ENSG00000(	4596.844	3913.935	5059.952	676.4152	686.6423	539.209	2.8275	1.84E-94	1.28E-92	NID2	chr14	-	52471521	52535712	4811
ENSG00000(	293.1291	323.9534	348.3252	352.8146	419.717	355.0888	-0.22395	0.1769	0.27901	GMCL1	chr2	+	70056774	70108528	4191
ENSG00000(	5525.95	5154.351	5313.279	4523.667	4980.458	4854.525	0.15554	0.1273	0.21371	SF3B2	chr11	+	65818200	65836779	3932
ENSG00000(	550.0055	537.1123	680.8175	826.2303	902.0234	733.1927	-0.47707	0.00139	0.003807	KLHL42	chr12	+	27932953	27955973	6703
ENSG00000(	24167.1	24092.98	20819.03	21678.25	13978.6	14233.97	0.46793	0.002323	0.006123	GNAS	chr20	+	57414773	57486247	4029
ENSG00000(	1138.335	1158.525	1203.305	1459.199	1382.489	1165.546	-0.19512	0.12633	0.21243	DNM1L	chr12	+	32832134	32898486	4439
ENSG00000(	89.0781	118.0202	113.4696	511.6186	447.33	453.7246	-2.1351	1.37E-29	2.04E-28	PTHLH	chr12	-	28111017	28125638	1891
ENSG00000(	19.68005	19.2686	38.263	5.243529	13.80648	16.4393	1.0677	0.068069	0.12669	PHACTR3	chr20	+	58152564	58422766	2728
ENSG00000(	678.4437	685.2397	774.4959	749.0755	567.9065	611.5419	0.14659	0.32625	0.45396	ERGIC2	chr12	-	29490285	29534122	5014
ENSG00000(	58.00435	49.3758	44.86007	426.9731	596.4399	478.3836	-3.2713	4.26E-49	1.15E-47	TFAP2C	chr20	+	55204358	55214339	2866
ENSG00000(	486.8222	378.1463	418.2542	2210.522	1907.135	1851.065	-2.2101	1.77E-56	5.67E-55	AURKA	chr20	-	54944445	54967393	2547
ENSG00000(	109.7939	85.50443	102.9143	12.73428	10.12475	9.863579	3.1191	1.90E-16	1.62E-15	CASS4	chr20	+	54987168	55034396	3155
ENSG00000(	16.57267	19.2686	27.70769	153.5605	150.9508	152.8855	-2.8238	6.85E-19	6.60E-18	PIR	chrX	-	15402921	15511687	1539
ENSG00000(	91.14969	97.54731	93.67838	29.96302	48.7829	49.3179	1.1301	0.000326	0.000988	AAMDC	chr11	+	77532155	77629478	726
ENSG00000(	121.1877	77.07441	94.99779	60.67512	37.73771	32.8786	1.1391	0.000634	0.001835	RFX2	chr19	-	5993175	6199583	3993
ENSG00000(	320.0597	360.082	300.8263	642.7068	489.6698	567.9778	-0.79135	1.28E-06	5.27E-06	METTL2A	chr17	+	60501228	60527454	2537
ENSG00000(	0	0	0	6.74168	1.840864	0.821965	-2.3512	0.077829	0.14197	SULT2B1	chr19	+	49055332	49102682	1447
ENSG00000(	131.5456	113.203	143.8161	232.9625	231.9489	256.4531	-0.88867	1.26E-05	4.62E-05	ALG6	chr1	+	63833261	63904233	3371
ENSG00000(	1117.619	1048.935	1051.573	1844.224	1606.154	1465.563	-0.60983	1.68E-06	6.78E-06	CNOT3	chr19	+	54641444	54659419	4517
ENSG00000(	1.035792	0	0	2.247227	0	5.753754	-1.5946	0.23277	0.34644	GP6	chr19	-	55525073	55549632	2268
ENSG00000(	147.0825	164.9874	207.148	258.4311	280.7318	203.8473	-0.51707	0.014992	0.033472	PTPN4	chr2	+	1.21E+08	1.21E+08	10300
ENSG00000(	908.3895	977.8816	1023.865	2486.182	2327.773	2238.21	-1.2756	5.33E-28	7.46E-27	DDX18	chr2	+	1.19E+08	1.19E+08	5674
ENSG00000(	7285.76	7040.266	5962.431	10159.71	11911.31	12769.23	-0.77827	2.69E-10	1.54E-09	KHSRP	chr19	-	6413359	6424805	2993

ENSG00000(	1395.212	1278.954	1178.237	1424.742	1424.829	1716.263	-0.24387	0.060327	0.11417	GNA11	chr19	+	3094408	3124002	4147
ENSG00000(	553.1129	563.6067	457.8366	259.9292	299.1404	332.0738	0.82004	7.38E-07	3.10E-06	ASAP3	chr1	-	23755056	23810685	4050
ENSG00000(	679.4795	638.2725	759.9823	453.9398	375.5363	396.1871	0.75737	3.47E-07	1.51E-06	EDEM2	chr20	-	33703160	33865928	2408
ENSG00000(	106.6866	102.3645	133.2608	790.2747	1124.768	787.4424	-2.969	6.14E-54	1.84E-52	DNMT3B	chr20	+	31350191	31397162	4336
ENSG00000(	1103.118	1026.053	1253.443	4640.523	4040.696	3657.744	-1.8634	5.05E-47	1.27E-45	TPX2	chr20	+	30327074	30389608	3605
ENSG00000(	310.7376	358.8777	219.0227	18.72689	12.88605	5.753754	4.4929	8.66E-43	1.95E-41	FER1L4	chr20	-	34146507	34195484	5995
ENSG00000(	234.089	244.4704	196.5927	453.1907	444.5687	566.3338	-1.1103	2.72E-10	1.56E-09	PDRG1	chr20	-	30532758	30539895	1385
ENSG00000(	856.5999	833.3671	928.8673	355.0618	380.1384	441.3952	1.151	1.01E-15	8.33E-15	EPB41L1	chr20	+	34679426	34820721	6266
ENSG00000(	5.17896	1.204288	1.319414	110.8632	97.56579	96.99186	-4.9685	6.43E-18	5.90E-17	SLC15A1	chr13	-	99336055	99404908	3106
ENSG00000(	105.6508	75.87013	143.8161	696.6403	1029.043	781.6886	-2.9319	4.28E-43	9.71E-42	DOCK9	chr13	-	99445741	99738879	7549
ENSG00000(	1370.353	1375.297	1410.453	1643.472	1537.121	1338.159	-0.12071	0.32363	0.451	ANKRD10	chr13	-	1.12E+08	1.12E+08	2588
ENSG00000(	149.154	119.2245	175.482	222.4754	211.6994	226.0404	-0.57151	0.006578	0.015909	TGDS	chr13	-	95226308	95248511	1902
ENSG00000(	10.35792	3.612863	14.51355	181.2763	257.721	231.7941	-4.4768	1.15E-32	1.91E-31	DOCK3	chr3	+	50712672	51421629	8755
ENSG00000(	181.2636	167.396	139.8579	15.73059	10.12475	9.863579	3.7029	5.52E-28	7.71E-27	C3orf18	chr3	-	50595462	50608458	2655
ENSG00000(	476.4643	444.3822	405.06	440.4564	320.3103	339.4715	0.26756	0.11831	0.2015	COQ9	chr16	+	57481337	57495187	1827
ENSG00000(	0	0	0	71.16218	45.10117	53.42772	-6.6041	1.53E-10	8.94E-10	TMEM40	chr3	-	12775024	12810956	2308
ENSG00000(	78.72018	98.75159	83.12307	60.67512	60.74851	92.88204	0.27743	0.3517	0.48148	KIF9	chr3	-	47269516	47324941	3357
ENSG00000(	604.9025	665.9711	725.6776	868.9276	1032.725	856.4874	-0.46559	0.000922	0.002597	ARHGAP28	chr18	+	6729717	6915715	5492
ENSG00000(	640.1194	673.1968	575.2644	1725.121	1555.53	1343.913	-1.2882	9.55E-21	9.97E-20	CRLS1	chr20	+	5986736	6020699	3958
ENSG00000(	73.54123	105.9773	89.72014	188.767	251.2779	240.0138	-1.329	1.46E-08	7.24E-08	PPP1R13B	chr14	-	1.04E+08	1.04E+08	4958
ENSG00000(	1405.57	1323.512	1678.294	684.6551	844.9566	666.6135	1.0024	3.31E-12	2.19E-11	ATRN	chr20	+	3451687	3631769	8633
ENSG00000(	946.7138	859.8614	864.216	429.2203	346.0824	332.0738	1.2654	1.57E-17	1.42E-16	SMOX	chr20	+	4101627	4168394	2233
ENSG00000(	4.143168	2.408575	0	0	0	0	2.023	0.13594	0.22523	SIGLEC1	chr20	-	3667617	3687775	6720
ENSG00000(	10518.47	10119.63	9892.965	9401.647	8138.46	8136.631	0.2494	0.018217	0.03989	FKBP1A	chr20	-	1349622	1373806	1622
ENSG00000(	502.3591	529.8866	504.0161	953.5732	736.3456	756.2077	-0.67	6.03E-06	2.29E-05	NSFL1C	chr20	-	1422807	1448417	3799
ENSG00000(	31.07376	27.69862	29.0271	131.0882	95.72493	111.7872	-1.9197	1.92E-09	1.03E-08	SLC4A11	chr20	-	3208063	3219887	3229
ENSG00000(	647.3699	693.6697	762.6212	222.4754	367.2524	291.7975	1.2514	4.79E-12	3.12E-11	C20orf194	chr20	-	3229951	3388272	6869
ENSG00000(	182.2994	216.7718	151.7326	105.6197	167.5186	141.378	0.4112	0.085382	0.15391	ZNF343	chr20	-	2462463	2505348	3632
ENSG00000(	72.50543	83.09585	55.41538	11.23613	0	4.109825	3.5727	4.38E-11	2.66E-10	EBF4	chr20	+	2673480	2740754	2910
ENSG00000(	7346.872	7111.319	6640.61	548.3233	548.5775	600.8564	3.6295	7.87E-239	3.62E-236	CPXM1	chr20	-	2774715	2781283	2391
ENSG00000(	2643.341	2574.767	2307.655	1432.232	1698.197	1788.596	0.61281	8.92E-07	3.72E-06	MAVS	chr20	+	3827487	3849280	4237
ENSG00000(	187.4783	132.4716	141.1773	250.9403	300.0608	298.3733	-0.87092	2.19E-05	7.80E-05	PROSAPIP1	chr20	-	3143263	3154192	5257
ENSG00000(	2.071584	0	6.597069	0	6.443024	0.821965	0.18643	0.87937	0.92459	F11	chr4	+	1.87E+08	1.87E+08	3122
ENSG00000(	2227.988	1982.258	2439.596	2018.01	2310.284	1966.14	0.079134	0.52399	0.64913	XRN2	chr20	+	21283942	21370463	3435
ENSG00000(	177.1204	204.7289	192.6344	38.95193	40.49901	40.27628	2.2429	3.58E-19	3.49E-18	PLK1S1	chr20	+	21106624	21227260	3855
ENSG00000(	2347.104	2395.328	2017.384	4654.006	3708.421	4376.963	-0.91214	2.92E-13	2.08E-12	DYNLL1	chr12	+	1.21E+08	1.21E+08	1376
ENSG00000(	0	0	0	11.23613	7.363456	4.93179	-3.7955	0.001689	0.004556	TESC	chr12	-	1.17E+08	1.18E+08	1057
ENSG00000(	2091.264	2029.225	1946.135	3098.176	2601.141	2576.86	-0.44725	0.000148	0.000471	SNX5	chr20	-	17922241	17949623	3087
ENSG00000(	36558.28	37187.2	29102.31	25034.85	21297.88	23273.11	0.56211	3.85E-06	1.50E-05	RPL6	chr12	-	1.13E+08	1.13E+08	2008
ENSG00000(	345.9545	327.5663	385.2688	668.1754	561.4635	484.9593	-0.69434	2.93E-05	0.000103	MAPKAPK5	chr12	+	1.12E+08	1.12E+08	2527
ENSG00000(	4.143168	3.612863	1.319414	0	0	0	2.6368	0.048148	0.09393	P2RX7	chr12	+	1.22E+08	1.22E+08	3003
ENSG00000(	352.1692	293.8462	399.7824	494.3899	478.6246	457.0125	-0.45095	0.005553	0.01364	ESF1	chr20	-	13694969	13765532	3216
ENSG00000(	498.2159	546.7466	538.3208	349.8183	301.9017	318.9224	0.70195	3.30E-06	1.29E-05	RBBP9	chr20	-	18467184	18477887	3861
ENSG00000(	2351.248	2161.696	2108.423	2471.2	1959.6	2038.473	0.033374	0.78947	0.86229	ANAPC5	chr12	-	1.22E+08	1.22E+08	6149

ENSG00000(	554.1487	574.4452	674.2204	215.7338	196.9724	198.9155	1.552	2.94E-22	3.26E-21	SLC23A2	chr20	-	4833002	4990939	6962
ENSG00000(	280.6996	287.8248	308.7428	134.0845	122.4175	138.9121	1.1421	1.31E-09	7.09E-09	SLC24A6	chr12	-	1.14E+08	1.14E+08	3289
ENSG00000(	2309.816	2247.201	2311.613	2127.375	1642.971	1718.729	0.32227	0.010606	0.024504	TMEM230	chr20	-	5080486	5093749	1735
ENSG00000(	85.97073	103.5687	85.7619	77.90386	55.22592	73.15488	0.40807	0.15296	0.24808	DZANK1	chr20	-	18364011	18447829	3739
ENSG00000(	493.0369	444.3822	489.5025	640.4596	786.9694	686.3407	-0.56425	0.000101	0.000329	KDM2B	chr12	-	1.22E+08	1.22E+08	6676
ENSG00000(	4.143168	0	5.277655	1.498151	0.920432	0	1.3146	0.29887	0.42382	C20orf26	chr20	+	20033158	20341346	4082
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	LHX5	chr12	-	1.14E+08	1.14E+08	2940
ENSG00000(	98.40023	107.1816	106.8725	157.3059	157.3939	197.2716	-0.70883	0.001956	0.005218	TASP1	chr20	-	13246709	13619587	2352
ENSG00000(	2873.287	2513.348	2963.403	3017.276	3501.323	3448.143	-0.25472	0.030085	0.062341	GCN1L1	chr12	-	1.21E+08	1.21E+08	8675
ENSG00000(	56475.52	56622	46456.56	47414.98	37348.37	42160.22	0.3294	0.007511	0.017967	RPLP0	chr12	-	1.21E+08	1.21E+08	2591
ENSG00000(	1637.587	1453.575	1851.138	2696.672	3357.736	3282.106	-0.91563	4.85E-12	3.16E-11	PXN	chr12	-	1.21E+08	1.21E+08	5457
ENSG00000(	29.00217	22.88147	25.06886	12.73428	26.69253	23.83698	0.28161	0.57092	0.68999	SIRT4	chr12	+	1.21E+08	1.21E+08	1217
ENSG00000(	2.071584	0	0	2.247227	0	0.821965	-0.26399	0.84571	NA	RPH3A	chr12	+	1.13E+08	1.13E+08	5188
ENSG00000(	171.9415	154.1488	159.6491	154.3096	224.5854	152.8855	-0.12611	0.57492	0.69339	KIF16B	chr20	-	16252749	16554078	5261
ENSG00000(	190.5857	207.1375	229.578	735.5922	676.5175	661.6818	-1.7226	2.88E-28	4.08E-27	TRMT6	chr20	-	5917881	5931182	3025
ENSG00000(	12.4295	9.634302	7.916483	28.46487	43.2603	44.38611	-1.8657	0.000301	0.000914	CHGB	chr20	+	5892076	5906007	2550
ENSG00000(	8838.412	9014.094	8119.672	6403.098	6194.507	6628.325	0.43336	1.80E-05	6.47E-05	PEBP1	chr12	+	1.19E+08	1.19E+08	1697
ENSG00000(	4.143168	1.204288	1.319414	0	0.920432	0	1.6534	0.21531	0.32601	TBX5	chr12	-	1.15E+08	1.15E+08	3825
ENSG00000(	357.3482	343.222	348.3252	500.3825	451.9321	401.9408	-0.36756	0.01964	0.042689	BRAP	chr12	-	1.12E+08	1.12E+08	4026
ENSG00000(	3077.338	3075.751	2374.945	3434.511	3627.422	4778.904	-0.47172	0.001399	0.00383	ERP29	chr12	+	1.12E+08	1.12E+08	1735
ENSG00000(	4.143168	0	0	2.247227	0.920432	0	0.23264	0.86288	0.91323	NOS1	chr12	-	1.18E+08	1.18E+08	12158
ENSG00000(	5021.519	5348.242	4673.364	5230.045	7236.436	9199.431	-0.52433	0.001205	0.003336	FUS	chr16	+	31191431	31203127	4920
ENSG00000(	1053.4	980.2902	761.3018	477.1611	387.5019	432.3535	1.1041	2.65E-12	1.76E-11	IGBP1	chrX	+	69353299	69386174	1862
ENSG00000(	922.8906	867.0872	748.1076	2609.03	1607.074	1879.012	-1.2588	4.61E-14	3.44E-13	FXYD5	chr19	+	35645633	35660786	1580
ENSG00000(	368.7419	395.0064	391.8659	364.7998	407.7514	363.3085	0.024909	0.87129	0.91912	ZNF302	chr19	+	35168544	35177302	3839
ENSG00000(	2801.817	2575.971	2289.183	1131.104	813.6619	917.3128	1.4171	1.91E-23	2.22E-22	GRAMD1A	chr19	+	35485688	35517375	2825
ENSG00000(	0	0	0	21.72319	10.12475	23.01502	-5.0431	5.83E-06	2.22E-05	FXYD3	chr19	+	35606732	35615228	1467
ENSG00000(	13.46529	3.612863	15.83297	508.6223	585.3947	482.4934	-5.5029	1.78E-66	7.16E-65	HEPH	chrX	+	65382391	65488709	6013
ENSG00000(	573.8287	580.4667	572.6256	307.121	300.9813	300.0172	0.92446	1.38E-10	8.10E-10	CDIP1	chr16	-	4560676	4588829	3009
ENSG00000(	25.8948	31.31148	42.22124	8.988907	16.56778	19.72716	1.0949	0.02936	0.06101	CMTM1	chr16	+	66600294	66613040	1064
ENSG00000(	1.035792	2.408575	1.319414	2.996302	2.761296	3.28786	-0.70934	0.53887	0.66258	KCNH4	chr17	-	40308913	40333296	3920
ENSG00000(	21380.82	21368.88	19318.86	9195.651	10503.97	10172.64	1.0536	8.81E-24	1.04E-22	GANAB	chr11	-	62392298	62414104	3906
ENSG00000(	337.6682	305.8891	306.104	200.7522	245.7553	260.5629	0.42598	0.017638	0.038775	GMIP	chr19	-	19740285	19754476	3538
ENSG00000(	169.8699	154.1488	200.5509	193.2615	219.9832	159.4612	-0.12647	0.55541	0.67608	RBM41	chrX	-	1.06E+08	1.06E+08	3315
ENSG00000(	222.6953	242.0618	278.3963	856.9424	691.2444	727.439	-1.6125	1.14E-23	1.34E-22	BIRC5	chr17	+	76210267	76221717	2711
ENSG00000(	21.75163	9.634302	5.277655	1.498151	7.363456	17.26126	0.4581	0.56801	0.68718	LAG3	chr12	+	6881678	6887621	2587
ENSG00000(	5506.27	5312.113	4734.057	4674.231	4094.082	4706.571	0.20658	0.067028	0.12503	MLF2	chr12	-	6857170	6876641	1958
ENSG00000(	77.68439	85.50443	75.20659	25.46857	15.64734	12.32947	2.1044	3.77E-08	1.80E-07	OTUB2	chr14	+	94492675	94515276	3922
ENSG00000(	1798.135	1791.98	1938.219	2138.611	1766.309	1655.437	-0.00889	0.94449	0.96675	DDX24	chr14	-	94517266	94547591	5573
ENSG00000(	50.7538	86.70872	58.05421	105.6197	82.83888	81.37453	-0.46299	0.13127	0.21896	ZBTB25	chr14	-	64915824	64971931	2094
ENSG00000(	548.9697	517.8437	610.8886	511.6186	432.603	543.3188	0.17146	0.25921	0.37797	NECAP1	chr12	+	8234807	8250367	3129
ENSG00000(	9.322127	20.47289	19.79121	18.72689	24.85166	24.65895	-0.45075	0.40249	0.53363	ARHGAP4	chrX	-	1.53E+08	1.53E+08	3372
ENSG00000(	38.3243	34.92434	27.70769	4.494453	7.363456	8.219649	2.2398	4.98E-05	0.000169	ANKRD24	chr19	+	4183351	4224811	4026
ENSG00000(	330.4176	382.9635	453.8783	545.327	490.5903	400.2969	-0.3006	0.088097	0.15791	DHX32	chr10	-	1.28E+08	1.28E+08	3070

ENSG00000(	618.3678	622.6168	791.6483	575.29	702.2896	501.3986	0.19121	0.24648	0.36319	RCOR1	chr14	+	1.03E+08	1.03E+08	5754
ENSG00000(	948.7854	934.5273	1393.301	622.4818	805.378	586.061	0.69896	7.22E-05	0.00024	GPATCH2L	chr14	+	76618259	76720685	14007
ENSG00000(	1382.782	1360.845	1027.823	14.98151	12.88605	30.4127	5.9636	1.04E-135	1.33E-133	LTBP4	chr19	+	41098789	41135725	5142
ENSG00000(	614.2246	717.7555	493.4608	304.8737	257.721	364.9524	0.97213	9.65E-08	4.43E-07	BLVRB	chr19	-	40953696	40971747	1392
ENSG00000(	673.2647	640.6811	696.6505	1251.705	1315.297	1465.563	-1.002	3.07E-15	2.46E-14	SLC9A1	chr1	-	27425306	27493472	4516
ENSG00000(	1174.588	1248.846	1332.608	1008.256	1014.316	820.321	0.40044	0.002552	0.006671	SPTLC1	chr9	-	94794281	94877666	1894
ENSG00000(	2499.366	2391.715	2811.671	3734.891	3511.448	3181.826	-0.43658	0.000189	0.000593	PAPOLA	chr14	+	96967770	97033448	4519
ENSG00000(	1216.02	1115.17	1142.612	1528.863	1316.218	1413.78	-0.2934	0.014892	0.033288	CCNK	chr14	+	99947506	1E+08	5627
ENSG00000(	1362.066	1419.855	1186.153	1229.982	1033.645	1181.986	0.20319	0.1167	0.19933	PCBP4	chr3	-	51991470	52008032	2599
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	RGS1	chr1	+	1.93E+08	1.93E+08	2653
ENSG00000(	493.0369	496.1665	397.1435	115.3576	124.2583	116.719	1.9536	3.11E-27	4.21E-26	YPEL3	chr16	-	30103635	30108236	1941
ENSG00000(	360.4556	344.4263	325.8952	628.4744	527.4075	650.9962	-0.80683	1.54E-07	6.94E-07	MRPS33	chr7	-	1.41E+08	1.41E+08	853
ENSG00000(	407.0662	346.8349	353.6029	403.7517	286.2544	370.7062	0.061504	0.72833	0.81801	NDUFB2	chr7	+	1.4E+08	1.4E+08	1666
ENSG00000(	2192.771	2025.612	1828.708	3277.206	3172.729	3830.357	-0.7635	5.10E-10	2.86E-09	NUDC	chr1	+	27226729	27273353	1800
ENSG00000(	1399.355	1276.545	1290.387	2056.961	1707.401	1759.827	-0.47696	0.000104	0.000337	MAEA	chr4	+	1283639	1333935	5371
ENSG00000(	217.5163	167.396	187.3568	34.45748	30.37426	21.37109	2.7004	5.96E-22	6.52E-21	ICAM1	chr19	+	10381511	10397291	3252
ENSG00000(	1901.714	1931.678	1618.921	2638.244	2247.695	2519.322	-0.44055	0.000311	0.000943	STRN4	chr19	-	47222764	47250251	3628
ENSG00000(	25.8948	38.53721	26.38828	5.992604	1.840864	8.219649	2.3487	0.00012	0.000386	IRAK3	chr12	+	66582659	66648402	8663
ENSG00000(	5.17896	6.021439	0	0	1.840864	4.93179	0.55689	0.63678	0.74546	LYZ	chr12	+	69742121	69748014	1530
ENSG00000(	612.153	568.4238	575.2644	671.1717	566.9861	549.8945	-0.0264	0.85417	0.90719	MUL1	chr1	-	20825943	20834654	2436
ENSG00000(	137.7603	140.9017	117.4278	376.0359	399.4675	422.49	-1.5866	3.73E-18	3.47E-17	TFAP4	chr16	-	4307187	4323076	6491
ENSG00000(	535.5044	533.4995	560.7509	531.8436	592.7582	594.2806	-0.07646	0.5801	0.69826	PDCD7	chr15	-	65409717	65426174	2851
ENSG00000(	1954.539	1914.817	1774.612	1324.366	1076.905	1016.771	0.72152	4.18E-08	1.99E-07	SPG21	chr15	-	65255362	65282648	2059
ENSG00000(	2.071584	2.408575	2.638828	0.749076	2.761296	3.28786	0.055129	0.96178	0.97793	FETUB	chr3	+	1.86E+08	1.86E+08	1640
ENSG00000(	1616.871	1828.109	1596.491	2142.356	2015.746	2111.628	-0.31416	0.005721	0.014011	DNAJB11	chr3	+	1.86E+08	1.86E+08	4079
ENSG00000(	1845.781	1752.239	1770.653	1462.195	1402.738	1389.121	0.33525	0.002239	0.005914	LEPREL1	chr3	-	1.9E+08	1.9E+08	3509
ENSG00000(	2.071584	1.204288	2.638828	0	0.920432	4.109825	0.16229	0.89692	0.93605	THPO	chr3	-	1.84E+08	1.84E+08	1855
ENSG00000(	100.4718	96.34302	105.5531	125.0956	141.7465	175.0785	-0.54308	0.024766	0.052529	CHRD	chr3	+	1.84E+08	1.84E+08	4719
ENSG00000(	3.107376	14.45145	5.277655	4.494453	3.681728	13.9734	0.031775	0.9702	0.98254	FLT3LG	chr19	+	49977464	49990894	1421
ENSG00000(	988.1455	1154.912	1022.546	619.4855	763.9586	692.0945	0.60811	8.73E-06	3.26E-05	RAB11FIP3	chr16	+	475619	573011	4831
ENSG00000(	1558.867	1443.941	1241.568	560.3085	487.829	577.8413	1.3807	1.44E-23	1.69E-22	GNPTG	chr16	+	1401924	1413352	2400
ENSG00000(	216.4805	187.8689	277.0769	248.6931	254.9597	241.6577	-0.13084	0.50317	0.63116	ZNF268	chr12	+	1.34E+08	1.34E+08	5756
ENSG00000(	4096.557	4104.213	3694.359	1624.745	2250.456	2031.897	1.0081	2.49E-14	1.89E-13	GOLGA3	chr12	-	1.33E+08	1.33E+08	9252
ENSG00000(	5604.67	5575.852	5325.154	6075.752	4903.141	5107.69	0.036929	0.74674	0.83155	PABPC4	chr1	-	40026488	40042462	3592
ENSG00000(	66.29068	75.87013	40.90183	277.907	267.8457	307.4149	-2.1953	6.36E-20	6.41E-19	CERS4	chr19	+	8271620	8327305	2401
ENSG00000(	579.0077	602.1439	626.7215	361.0544	298.22	306.5929	0.89961	2.58E-09	1.36E-08	MCOLN1	chr19	+	7587512	7598895	2253
ENSG00000(	1132.121	1216.331	1281.151	1101.141	1128.45	1098.145	0.12444	0.29223	0.41642	USP48	chr1	-	22004791	22110099	4595
ENSG00000(	1081.367	921.2801	869.4937	1461.446	1674.266	1828.05	-0.78592	8.69E-09	4.38E-08	EFNB1	chrX	+	68048840	68061990	3314
ENSG00000(	334.5608	352.8563	486.8637	197.7559	376.4567	226.0404	0.55022	0.017871	0.039228	PDPR	chr16	+	70147529	70195203	7999
ENSG00000(	3503.048	3490.026	3286.66	3218.778	3182.854	2988.664	0.13051	0.20753	0.31682	AARS	chr16	-	70286198	70323446	3477
ENSG00000(	5110.597	4734.055	5913.613	1603.771	2195.23	1856.819	1.4749	3.21E-27	4.34E-26	GLG1	chr16	-	74485856	74641012	4748
ENSG00000(	413.281	362.4906	409.0183	939.3407	1063.099	924.7105	-1.3007	1.15E-20	1.20E-19	KIF4A	chrX	+	69509879	69640682	4348
ENSG00000(	1299.919	1411.425	1531.839	805.2562	1247.185	907.4493	0.51841	0.001146	0.003186	TNRC6A	chr16	+	24741016	24838953	8438
ENSG00000(	45.57484	21.67718	26.38828	5.243529	8.283888	8.219649	2.021	0.000418	0.001244	FCGBP	chr19	-	40353963	40440533	16390

ENSG00000(	1297.847	1277.749	1386.704	1179.794	1269.276	1274.868	0.089262	0.4419	0.57162	PLEKHG2	chr19	+	39903225	39919054	7519
ENSG00000(	46.61064	45.76293	29.0271	20.97412	7.363456	19.72716	1.2846	0.008742	0.0206	DLL3	chr19	+	39989535	39999121	2332
ENSG00000(	818.2756	759.9056	662.3457	438.2092	469.4203	699.4921	0.47808	0.007933	0.018867	NAT14	chr19	+	55996371	55998935	1536
ENSG00000(	498.2159	568.4238	482.9054	268.169	367.2524	315.6345	0.70359	2.65E-05	9.33E-05	PITPNM2	chr12	-	1.23E+08	1.24E+08	6785
ENSG00000(	721.947	731.0026	829.9113	603.0058	421.5579	389.6114	0.68608	7.33E-05	0.000243	EXOC1	chr4	+	56719782	56771200	3551
ENSG00000(	457.82	472.0808	626.7215	593.2678	717.0165	580.3072	-0.28068	0.087987	0.15777	RBM27	chr5	+	1.46E+08	1.46E+08	6451
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	POU4F3	chr5	+	1.46E+08	1.46E+08	1182
ENSG00000(	1362.066	1463.21	2233.768	1112.377	1229.697	978.9602	0.60406	0.000457	0.00135	OSBPL8	chr12	-	76745577	76953589	7239
ENSG00000(	185.4068	195.0946	146.4549	518.3603	441.8074	462.7662	-1.4246	1.19E-15	9.79E-15	DTX2	chr7	+	76090993	76135312	2769
ENSG00000(	16.57267	12.04288	13.19414	11.98521	13.80648	22.19305	-0.1839	0.75663	0.83898	NLRC4	chr2	-	32449522	32490923	3581
ENSG00000(	425.7105	388.9849	505.3355	925.1083	748.3112	752.0979	-0.87675	1.96E-08	9.61E-08	PUS7	chr7	-	1.05E+08	1.05E+08	3480
ENSG00000(	36.25272	45.76293	29.0271	8.239831	4.60216	13.15144	2.003	0.000179	0.000564	LAMB4	chr7	-	1.08E+08	1.08E+08	5858
ENSG00000(	9.322127	18.06432	14.51355	476.412	601.0421	388.7894	-5.0783	6.64E-60	2.31E-58	NRCAM	chr7	-	1.08E+08	1.08E+08	6659
ENSG00000(	14519.73	14253.95	15675.96	6584.374	8168.834	6865.051	1.0382	1.02E-19	1.02E-18	LAMB1	chr7	-	1.08E+08	1.08E+08	5766
ENSG00000(	2.071584	3.612863	5.277655	2.247227	8.283888	4.109825	-0.35578	0.71675	0.8092	SLC26A4	chr7	+	1.07E+08	1.07E+08	4930
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	SLC26A3	chr7	-	1.07E+08	1.07E+08	2863
ENSG00000(	1268.845	1074.225	1318.094	1705.645	1513.19	1381.723	-0.32902	0.013532	0.030548	DLD	chr7	+	1.08E+08	1.08E+08	3755
ENSG00000(	162.6193	161.3746	197.9121	122.0993	194.2112	161.9271	0.12633	0.58398	0.70145	WDR7	chr18	+	54318574	54698828	9074
ENSG00000(	1547.473	1836.539	1607.046	1464.443	1350.274	1460.632	0.22241	0.064124	0.12028	TXNL1	chr18	-	54264439	54318831	6894
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	IL5RA	chr3	-	3111233	3168297	2514
ENSG00000(	19.68005	18.06432	19.79121	4.494453	9.20432	11.50751	1.131	0.070007	0.1298	ABCC6	chr16	-	16242785	16317379	5747
ENSG00000(	902.1747	758.7013	1109.627	1136.348	1177.233	1050.471	-0.27995	0.060194	0.11402	CMTM6	chr3	-	32522804	32544900	3863
ENSG00000(	51.7896	71.05298	81.80365	2621.015	3019.937	2413.289	-5.2907	2.36E-199	6.68E-197	ITGA6	chr2	+	1.73E+08	1.73E+08	5927
ENSG00000(	9.322127	12.04288	9.235896	6.74168	8.283888	8.219649	0.36855	0.6066	0.72109	RAPGEF4	chr2	+	1.74E+08	1.74E+08	4338
ENSG00000(	652.5489	579.2624	820.6754	1224.739	1257.31	1098.145	-0.80146	6.77E-08	3.16E-07	MLTK	chr2	+	1.74E+08	1.74E+08	7179
ENSG00000(	0	2.408575	1.319414	5.243529	2.761296	0.821965	-0.90418	0.46129	0.59062	SMPX	chrX	-	21724090	21776281	938
ENSG00000(	738.5196	661.154	720.3999	2220.26	1448.76	1615.983	-1.3137	1.11E-16	9.59E-16	FH	chr1	-	2.42E+08	2.42E+08	1797
ENSG00000(	1140.407	1106.74	1269.276	758.8135	905.7051	757.8517	0.53671	5.18E-05	0.000176	SEL1L3	chr4	-	25749055	25865382	4514
ENSG00000(	36.25272	30.10719	9.235896	2.996302	11.04518	14.79537	1.3203	0.043554	0.086198	TF	chr3	+	1.33E+08	1.33E+08	4602
ENSG00000(	4163.883	4192.126	4455.66	8594.893	9275.193	8084.847	-1.0171	2.42E-22	2.70E-21	CDV3	chr3	+	1.33E+08	1.33E+08	3621
ENSG00000(	7.250543	18.06432	10.55531	0.749076	0.920432	2.465895	2.6891	0.003373	0.008647	MYO15A	chr17	+	18012020	18083116	11863
ENSG00000(	2151.34	2043.676	1815.513	1768.567	1512.27	1547.76	0.31539	0.010126	0.023517	ALKBH5	chr17	+	18086392	18113268	2748
ENSG00000(	27.96638	10.83859	0	0	3.681728	6.575719	1.6303	0.10069	0.17645	APOH	chr17	-	64208151	64252643	1176
ENSG00000(	808.9535	812.8942	748.1076	139.3281	180.4047	169.3248	2.2725	8.02E-47	2.00E-45	NLRP1	chr17	-	5402747	5522744	5480
ENSG00000(	79.75598	60.21439	63.33186	4.494453	21.16994	25.48091	1.9426	3.46E-05	0.00012	PITPNM3	chr17	-	6354584	6459814	7086
ENSG00000(	1254.344	1309.061	1051.573	1039.717	903.8642	1064.445	0.26471	0.04921	0.095747	SPAG7	chr17	-	4862521	4871167	1668
ENSG00000(	149.154	178.2346	153.052	1523.62	1217.732	1382.545	-3.0929	3.13E-88	1.90E-86	ORC6	chr16	+	46723555	46732306	1833
ENSG00000(	1503.97	1451.167	2070.16	132.5864	258.6414	174.2566	3.1382	3.62E-54	1.10E-52	ZFHX4	chr8	+	77593454	77779521	14019
ENSG00000(	0	7.225726	1.319414	0	0	0	2.3536	0.08211	0.14869	CPA1	chr7	+	1.3E+08	1.3E+08	1931
ENSG00000(	274.4849	299.8676	298.1875	460.6815	399.4675	369.8842	-0.49527	0.002746	0.007142	ZC3HC1	chr7	-	1.3E+08	1.3E+08	1972
ENSG00000(	7.250543	12.04288	9.235896	0	0.920432	0	3.7493	0.000795	0.002266	ESR1	chr6	+	1.52E+08	1.52E+08	6466
ENSG00000(	94.25706	85.50443	110.8308	10.48706	21.16994	24.65895	2.3308	3.01E-10	1.72E-09	RGS17	chr6	-	1.53E+08	1.53E+08	1636
ENSG00000(	162.6193	160.1703	212.4256	282.4015	236.551	239.1918	-0.50378	0.012041	0.027485	ANGPT2	chr8	-	6357172	6420930	5416
ENSG00000(	832.7767	822.5285	653.1098	477.9102	437.2052	459.4784	0.74643	4.05E-07	1.75E-06	TMEM101	chr17	-	42088556	42101314	1830

ENSG00000(	0	1.204288	0	100.3761	74.55499	58.35951	-6.3347	1.42E-12	9.63E-12	CD200	chr3	+	1.12E+08	1.12E+08	2129
ENSG00000(	23574.62	24042.4	23110.85	535.589	574.3496	492.357	5.4563	0	0	CCDC80	chr3	-	1.12E+08	1.12E+08	4664
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CMA1	chr14	-	24974559	24977471	937
ENSG00000(	1156.98	1119.988	975.0468	676.4152	559.6227	659.2159	0.77678	1.66E-08	8.20E-08	PSME1	chr14	+	24605367	24608176	1136
ENSG00000(	235.1248	257.7176	248.0498	229.9662	109.5314	149.5976	0.58974	0.01603	0.035562	PPP2R3C	chr14	-	35554673	35591723	1846
ENSG00000(	55.93276	65.03154	46.17948	107.8669	80.07758	102.7456	-0.78843	0.008092	0.019202	HAUS4	chr14	-	23415437	23426370	1642
ENSG00000(	1.035792	2.408575	3.958241	0	0.920432	0	1.7734	0.18059	0.28356	JPH4	chr14	-	24037244	24048009	4386
ENSG00000(	1.035792	1.204288	0	0	0	0.821965	0.53698	0.68444	NA	CEBPE	chr14	-	23586513	23588825	1554
ENSG00000(	4250.89	4177.674	4360.663	1123.613	1404.579	1288.841	1.7418	4.46E-50	1.23E-48	SLC7A8	chr14	-	23594504	23652883	4216
ENSG00000(	417.4241	464.8551	319.2981	752.8209	629.5755	706.8898	-0.79394	1.45E-06	5.91E-06	OSGEP	chr14	-	20914570	20923264	3258
ENSG00000(	1592.012	1610.133	1187.472	195.5087	173.9616	193.9837	2.9512	4.44E-79	2.36E-77	SLC22A17	chr14	-	23815515	23822121	2409
ENSG00000(	363.563	327.5663	328.534	267.42	294.5382	288.5097	0.26264	0.10848	0.18746	RNF31	chr14	+	24615892	24629870	3627
ENSG00000(	955.0001	1063.386	1084.558	917.6175	809.9802	782.5106	0.304	0.019563	0.042538	SCFD1	chr14	+	31091318	31205018	2359
ENSG00000(	286.9144	373.3292	328.534	639.7105	635.0981	600.8564	-0.92244	2.21E-09	1.17E-08	G2E3	chr14	+	31028329	31089269	5804
ENSG00000(	1246.058	1178.998	1475.105	1327.362	1534.36	1131.024	-0.03393	0.81423	0.87941	HECTD1	chr14	-	31569318	31677010	9134
ENSG00000(	8804.231	8499.863	8308.349	12364.24	12992.82	12779.09	-0.5735	2.26E-09	1.20E-08	HNRNPC	chr14	-	21677295	21737653	4501
ENSG00000(	6.214751	0	3.958241	11.23613	17.48821	1.64393	-1.3286	0.16525	0.26384	RPGRIP1	chr14	+	21756098	21819460	3944
ENSG00000(	2159.626	2081.009	2378.903	4415.051	4451.209	4041.602	-0.96215	2.26E-18	2.11E-17	SUPT16H	chr14	-	21819631	21852425	4684
ENSG00000(	1311.313	1086.268	1084.558	1188.034	1051.133	1112.941	0.055393	0.67026	0.77303	TOX4	chr14	+	21944756	21967319	4697
ENSG00000(	132.5814	128.8588	98.95603	299.6302	254.9597	301.6611	-1.2378	1.85E-09	9.91E-09	GEMIN2	chr14	+	39583427	39606177	1476
ENSG00000(	17.60846	21.67718	30.34652	71.16218	73.63456	82.19649	-1.6847	5.58E-06	2.13E-05	TGM1	chr14	-	24718320	24733638	2777
ENSG00000(	501.3233	415.4793	412.9765	419.4823	320.3103	324.6761	0.31981	0.062627	0.11793	TINF2	chr14	-	24708849	24711880	2168
ENSG00000(	1.035792	6.021439	3.958241	0	0	0.821965	2.331	0.069379	0.12879	DAZL	chr3	-	16628299	16711813	3104
ENSG00000(	0	0	0	28.46487	31.29469	24.65895	-5.6698	1.18E-07	5.38E-07	TBL1Y	chrY	+	6778727	6959724	2407
ENSG00000(	163.6551	166.1917	212.4256	3498.183	4855.279	3795.834	-4.4745	5.38E-175	1.16E-172	SEMA6A	chr5	-	1.16E+08	1.16E+08	6878
ENSG00000(	621.4751	649.1111	844.4248	1031.477	1197.482	969.0966	-0.59593	9.13E-05	0.000299	TRPM7	chr15	-	50844670	50979012	7263
ENSG00000(	456.7842	404.6407	354.9223	1737.855	1976.167	1966.14	-2.2147	3.23E-59	1.10E-57	TYRO3	chr15	+	41849873	41871536	3949
ENSG00000(	67.32647	89.11729	92.35896	360.3053	313.8673	316.4565	-1.9886	4.76E-21	5.03E-20	WDR76	chr15	+	44119161	44160617	3978
ENSG00000(	4.143168	3.612863	0	3.745378	5.522592	4.109825	-0.61284	0.5632	0.68291	CAPN3	chr15	+	42640301	42704516	3228
ENSG00000(	435.0326	473.2851	525.1267	410.4934	527.4075	411.8044	0.086477	0.59497	0.71091	SNAP23	chr15	+	42783431	42837547	2687
ENSG00000(	1163.194	1198.266	1240.249	109.365	115.054	91.23811	3.5022	6.03E-117	6.05E-115	TBX15	chr1	-	1.19E+08	1.2E+08	3504
ENSG00000(	3582.804	3597.207	2843.337	4957.382	4391.381	4469.023	-0.46192	0.000178	0.000559	PHGDH	chr1	+	1.2E+08	1.2E+08	3180
ENSG00000(	111.8655	84.30014	116.1084	297.383	321.2308	428.2437	-1.7335	2.66E-15	2.15E-14	COL9A3	chr20	+	61447596	61472511	2485
ENSG00000(	424.6747	358.8777	513.252	14291.61	14290.63	13334.74	-5.0049	0	0	EZR	chr6	-	1.59E+08	1.59E+08	3096
ENSG00000(	7091.031	7072.782	6131.316	8096.009	6157.69	9341.631	-0.21677	0.12931	0.21628	MYL6	chr12	+	56551945	56557280	1564
ENSG00000(	1150.765	1203.083	1269.276	968.5547	1226.936	1026.634	0.16914	0.19975	0.30742	AGO1	chr1	+	36335409	36395211	12790
ENSG00000(	12.4295	9.634302	0	11.98521	4.60216	3.28786	0.13958	0.87906	0.92447	TEKT2	chr1	+	36549676	36553876	1738
ENSG00000(	62.14751	45.76293	81.80365	420.2314	606.5647	479.2055	-2.972	1.47E-38	2.92E-37	CLSPN	chr1	-	36185819	36235568	4769
ENSG00000(	140.8677	132.4716	126.6637	130.3391	134.3831	102.7456	0.1233	0.59681	0.71256	RFFL	chr17	-	33333009	33416338	7293
ENSG00000(	16.57267	4.817151	9.235896	7.490755	6.443024	18.08323	-0.0499	0.94581	0.96733	UNC13D	chr17	-	73823306	73840798	4393
ENSG00000(	276.5564	291.4376	290.271	406.748	258.6414	317.2785	-0.19688	0.30573	0.43121	MFSD11	chr17	+	74731947	74777531	3612
ENSG00000(	3913.222	3866.968	4032.129	1692.911	1949.475	1759.827	1.1272	3.16E-25	3.93E-24	DPYSL2	chr8	+	26371791	26515694	4603
ENSG00000(	18283.8	19278.24	20693.69	1835.235	1793.922	1484.469	3.5035	2.98E-200	8.74E-198	TGFB2	chr1	+	2.19E+08	2.19E+08	5053
ENSG00000(	177.1204	168.6003	236.1751	189.5161	191.4499	161.1051	0.098924	0.64053	0.74828	GPATCH2	chr1	-	2.18E+08	2.18E+08	5851

ENSG00000(	811.0251	721.3683	982.9633	1902.652	2069.131	1726.126	-1.1773	5.53E-17	4.84E-16	NUP50	chr22	+	45559722	45583892	5229
ENSG00000(	93.22127	93.93444	72.56776	787.2784	638.7798	699.4921	-3.0138	5.26E-60	1.84E-58	CDC45	chr22	+	19466982	19508135	2090
ENSG00000(	21.75163	12.04288	7.916483	516.1131	438.1256	473.4518	-4.9904	1.42E-63	5.40E-62	COMT	chr22	+	19929130	19957498	2437
ENSG00000(	1.035792	2.408575	0	65.16957	75.47542	53.42772	-5.2412	2.42E-12	1.62E-11	CECR1	chr22	-	17660194	17702879	3986
ENSG00000(	10.35792	1.204288	9.235896	3.745378	1.840864	1.64393	1.2771	0.19603	0.30268	XXbac-B46	chr22	-	18270418	18294263	4328
ENSG00000(	1033.72	1030.87	1134.696	1158.071	1045.611	1064.445	-0.03153	0.7957	0.86664	ECHDC1	chr6	-	1.28E+08	1.28E+08	2585
ENSG00000(	731.2691	773.1527	705.8864	1124.362	1108.2	1036.498	-0.56328	5.32E-06	2.04E-05	LRRFIP2	chr3	-	37094117	37225180	3814
ENSG00000(	653.5847	597.3267	687.4146	713.1199	672.8358	609.076	-0.04199	0.76182	0.84263	SEC22C	chr3	-	42589461	42642572	5955
ENSG00000(	124.295	101.1602	112.1502	101.1252	148.1896	129.0485	-0.15864	0.52442	0.64949	XYLB	chr3	+	38388251	38462839	3664
ENSG00000(	908.3895	1011.602	769.2182	844.2081	787.8898	923.8886	0.073506	0.60483	0.71968	HDAC6	chrX	+	48659784	48683392	4832
ENSG00000(	0	0	0	4086.956	3565.754	3564.862	-11.967	1.13E-45	2.76E-44	GABRP	chr5	+	1.7E+08	1.7E+08	3576
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	KRT31	chr17	-	39549976	39553844	1596
ENSG00000(	218.5521	216.7718	233.5362	1998.534	1878.602	1882.3	-3.1003	1.03E-123	1.13E-121	CDC6	chr17	+	38443885	38459171	3072
ENSG00000(	158.4762	127.6545	187.3568	170.0401	154.6326	111.7872	0.11463	0.63633	0.74502	UPRT	chrX	+	74493920	74524435	2234
ENSG00000(	540.6834	558.7895	543.5985	857.6915	893.7395	789.9083	-0.62759	1.85E-06	7.47E-06	CDC23	chr5	-	1.38E+08	1.38E+08	3153
ENSG00000(	836.9199	843.0014	740.1911	1259.196	1024.441	1358.708	-0.58807	3.15E-05	0.00011	AAAS	chr12	-	53701240	53718648	2016
ENSG00000(	4276.785	4258.361	3807.828	5995.601	7640.506	6141.722	-0.67849	3.38E-08	1.62E-07	CBX5	chr12	-	54624724	54673886	11528
ENSG00000(	1.035792	0	0	0	0	2.465895	-0.37334	0.77636	NA	FMO2	chr1	+	1.71E+08	1.71E+08	5181
ENSG00000(	782.0229	790.0127	1084.558	3972.348	4689.601	3955.295	-2.2429	3.27E-55	1.02E-53	SUCO	chr1	+	1.73E+08	1.73E+08	5917
ENSG00000(	402.9231	399.8235	493.4608	1483.17	1484.657	1143.353	-1.6617	9.61E-28	1.33E-26	MSH2	chr2	+	47630108	47789450	3628
ENSG00000(	208.1942	195.0946	267.841	489.1463	608.4055	533.4552	-1.2778	4.49E-13	3.15E-12	MAP3K1	chr5	+	56111401	56191979	7011
ENSG00000(	920.819	864.6786	762.6212	791.0238	747.3908	845.8019	0.096539	0.47063	0.59966	DHPS	chr19	-	12786531	12792716	1363
ENSG00000(	536.5402	528.6823	427.4901	575.29	485.0677	737.3025	-0.2664	0.12901	0.21592	HOOK2	chr19	-	12873817	12983554	2603
ENSG00000(	5.17896	4.817151	2.638828	0	1.840864	0.821965	1.7032	0.14722	0.24027	NXPE1	chr11	-	1.14E+08	1.14E+08	2289
ENSG00000(	4127.631	4015.095	4260.387	3785.828	3628.343	3069.217	0.24208	0.035069	0.071266	ARCN1	chr11	+	1.18E+08	1.18E+08	4038
ENSG00000(	14.50109	16.86003	30.34652	601.5077	617.6099	581.9512	-4.8534	1.47E-78	7.76E-77	EPB41L4B	chr9	-	1.12E+08	1.12E+08	5800
ENSG00000(	142.9393	138.4931	213.745	284.6487	227.3467	184.1201	-0.49248	0.036621	0.074061	TMEM38B	chr9	+	1.08E+08	1.09E+08	3956
ENSG00000(	930.1411	1000.763	1081.919	1223.989	1119.245	974.0284	-0.13953	0.29871	0.42368	PSMD5	chr9	-	1.24E+08	1.24E+08	3443
ENSG00000(	9.322127	2.408575	5.277655	0	0	2.465895	2.0892	0.071953	0.13287	PTGS1	chr9	+	1.25E+08	1.25E+08	4964
ENSG00000(	964.3223	939.3444	890.6043	2352.097	1944.873	1661.191	-1.0893	1.31E-14	1.00E-13	NUP188	chr9	+	1.32E+08	1.32E+08	5689
ENSG00000(	993.3244	1011.602	898.5208	170.0401	112.2927	133.1583	2.7891	1.43E-61	5.20E-60	CRAT	chr9	-	1.32E+08	1.32E+08	2763
ENSG00000(	30.03797	26.49433	25.06886	17.22874	7.363456	14.79537	1.0012	0.059582	0.11302	SH2D3C	chr9	-	1.31E+08	1.31E+08	3124
ENSG00000(	559.3276	610.5739	538.3208	447.9472	357.1276	383.8576	0.51995	0.000677	0.001949	NANS	chr9	+	1.01E+08	1.01E+08	3027
ENSG00000(	366.6703	332.3834	373.3941	268.169	292.6974	235.082	0.42923	0.011478	0.026315	TBC1D2	chr9	-	1.01E+08	1.01E+08	3198
ENSG00000(	79.75598	55.39724	81.80365	165.5457	232.8693	175.0785	-1.3874	6.65E-08	3.11E-07	DFNB31	chr9	-	1.17E+08	1.17E+08	3566
ENSG00000(	13.46529	1.204288	9.235896	1.498151	1.840864	4.93179	1.3088	0.17527	0.27701	PDE6C	chr10	+	95372345	95425767	3307
ENSG00000(	281.7354	313.1148	271.7992	549.0724	566.0657	590.9928	-0.97383	1.22E-10	7.16E-10	CWF19L1	chr10	-	1.02E+08	1.02E+08	2694
ENSG00000(	240.3037	185.4603	179.4403	41.19916	51.54419	56.71558	2.0052	3.30E-15	2.64E-14	SEMA4G	chr10	+	1.03E+08	1.03E+08	4656
ENSG00000(	619.4036	559.9938	971.0885	507.8732	663.6315	489.8911	0.36957	0.061239	0.1156	BTAF1	chr10	+	93683526	93790082	7250
ENSG00000(	143.9751	191.4817	179.4403	178.28	133.4626	125.7606	0.22885	0.32036	0.44757	IKZF5	chr10	-	1.25E+08	1.25E+08	4555
ENSG00000(	1.035792	0	0	2.247227	0	1.64393	-0.82311	0.54382	NA	BLNK	chr10	-	97951458	98031344	1784
ENSG00000(	70.43385	67.44011	68.60952	19.47596	5.522592	14.79537	2.2948	1.10E-07	5.04E-07	TLL2	chr10	-	98124363	98273675	6756
ENSG00000(	2.071584	4.817151	1.319414	60.67512	88.36147	64.93523	-4.4382	2.45E-13	1.75E-12	CYP26A1	chr10	+	94833232	94837647	2245
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	TDRD1	chr10	+	1.16E+08	1.16E+08	4510

ENSG00000(	35.21692	46.96722	42.22124	513.8658	644.3024	574.5535	-3.7812	3.18E-67	1.31E-65	SORBS1	chr10	-	97071528	97321171	7354
ENSG00000(	2.071584	0	2.638828	5.992604	9.20432	9.863579	-2.0093	0.044166	0.087197	CRTAC1	chr10	-	99624757	99790585	2890
ENSG00000(	93.22127	89.11729	71.24834	2794.801	2685.821	2740.431	-4.9946	2.82E-235	1.21E-232	BAMBI	chr10	+	28966271	28971868	1884
ENSG00000(	132.5814	77.07441	80.48424	23.22134	17.48821	27.12484	2.0589	1.29E-08	6.41E-08	IL11	chr19	-	55875757	55881831	2281
ENSG00000(	0	0	0	46.44268	29.45382	34.52253	-6.0323	1.13E-08	5.63E-08	MYO3A	chr10	+	26223196	26501456	5581
ENSG00000(	1700.77	1659.508	2046.411	1904.899	1840.864	1510.772	0.04	0.7667	0.84615	WAC	chr10	+	28821422	28909928	4526
ENSG00000(	298.3081	291.4376	327.2146	544.5779	445.4891	548.2506	-0.74567	3.46E-06	1.35E-05	CREM	chr10	+	35415719	35501886	2658
ENSG00000(	1151.801	1017.623	891.9237	1381.295	1129.37	1341.447	-0.32989	0.018149	0.039751	NUBP2	chr16	+	1832902	1839192	2235
ENSG00000(	1.035792	1.204288	1.319414	0	4.60216	1.64393	-0.52888	0.67912	0.78003	C19orf77	chr19	-	3474405	3480540	908
ENSG00000(	164.6909	144.5145	205.8285	282.4015	261.4027	176.7225	-0.4832	0.034601	0.070419	HIVEP1	chr6	+	12008995	12165232	9027
ENSG00000(	0	2.408575	0	0.749076	0	1.64393	-0.00317	0.99813	NA	TREM2	chr6	-	41126244	41130924	1044
ENSG00000(	0	0	0	5.992604	4.60216	6.575719	-3.3252	0.007727	0.018442	CRISP3	chr6	-	49695097	49712150	2205
ENSG00000(	6216.823	6316.489	6911.089	309.3682	322.1512	287.6877	4.3953	0	0	FKBP5	chr6	-	35541362	35696360	7384
ENSG00000(	728.1617	622.6168	858.9384	1535.605	1912.658	1459.81	-1.148	5.02E-14	3.75E-13	SRPK1	chr6	-	35800743	35889119	4762
ENSG00000(	1116.584	1174.181	1129.418	1047.957	1341.069	1001.153	0.013332	0.92352	0.9537	BRPF3	chr6	+	36164521	36200567	6052
ENSG00000(	200.9436	237.2447	147.7743	254.6857	245.7553	304.949	-0.45403	0.030723	0.063456	MRPS18A	chr6	-	43639040	43655528	1062
ENSG00000(	1.035792	0	0	0.749076	0	1.64393	-0.39004	0.77029	NA	PGC	chr6	-	41704449	41721847	1371
ENSG00000(	309.7018	363.6949	315.3399	435.2129	378.2976	418.3801	-0.3173	0.047855	0.09342	TMEM14A	chr6	+	52535907	52551386	992
ENSG00000(	409.1378	432.3393	434.0871	349.8183	289.9361	276.1802	0.4743	0.003714	0.009443	EFHC1	chr6	+	52285106	52387892	5445
ENSG00000(	0	0	0	3.745378	0	0.821965	-1.2809	0.34031	NA	NCR2	chr6	+	41303393	41318625	1154
ENSG00000(	22853.71	22378.07	21460.27	49716.14	44376.79	40629.73	-1.0128	6.36E-21	6.68E-20	HSP90AB1	chr6	+	44214824	44221620	2674
ENSG00000(	1.035792	2.408575	1.319414	0	1.840864	2.465895	0.10233	0.93635	0.96165	MLN	chr6	-	33762450	33771788	566
ENSG00000(	946.7138	956.2044	953.9362	1173.052	1179.073	1015.949	-0.23699	0.055969	0.10714	CDC5L	chr6	+	44355262	44418163	6423
ENSG00000(	88.04231	79.48299	110.8308	1089.905	1437.715	1173.766	-3.7214	1.31E-95	9.24E-94	ITPR3	chr6	+	33588522	33664351	9668
ENSG00000(	151.2256	166.1917	176.8014	94.38352	91.12277	100.2797	0.78246	0.000535	0.001565	ZNF184	chr6	-	27418522	27440897	3101
ENSG00000(	285.8786	262.5347	370.7553	11098.3	15720.06	11133.51	-5.3514	3.34E-243	1.63E-240	DSP	chr6	+	7541808	7586950	9796
ENSG00000(	332.4892	331.1791	378.6718	346.0729	449.1708	358.3767	-0.14543	0.3912	0.52198	SIRT1	chr10	+	69644427	69678147	4094
ENSG00000(	1514.328	1555.94	1525.242	1955.836	2326.852	2656.591	-0.59301	5.81E-06	2.22E-05	HNRNPH3	chr10	+	70090931	70102948	3356
ENSG00000(	195.7647	207.1375	197.9121	298.1321	235.6306	212.0669	-0.31185	0.11574	0.19798	IFT74	chr9	+	26947037	27062928	2163
ENSG00000(	226.8384	196.2989	277.0769	107.1178	108.611	97.81383	1.1503	1.24E-07	5.64E-07	JAK2	chr9	+	4985033	5128183	5285
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	IL12RB1	chr19	-	18169805	18209759	2906
ENSG00000(	5252.501	4803.904	4846.207	1486.166	2074.654	1708.043	1.4972	4.48E-30	6.82E-29	ABL1	chr9	+	1.34E+08	1.34E+08	5766
ENSG00000(	652.5489	561.1981	552.8344	3064.468	2216.4	2384.52	-2.1103	3.32E-47	8.41E-46	ACOT7	chr1	-	6324333	6454451	2429
ENSG00000(	1333.064	1284.975	1438.161	925.1083	783.2876	744.7002	0.7229	3.85E-08	1.84E-07	SH3GLB1	chr1	+	87170259	87213867	6371
ENSG00000(	137.7603	103.5687	139.8579	400.7554	428.9213	365.7744	-1.6399	1.38E-17	1.24E-16	CDC7	chr1	+	91966408	91991321	3313
ENSG00000(	3.107376	3.612863	7.916483	131.0882	144.5078	128.2265	-4.6716	6.48E-23	7.37E-22	SYDE2	chr1	-	85622556	85666729	5512
ENSG00000(	2799.746	2766.249	3100.622	719.1125	818.264	576.1974	2.0309	1.87E-48	4.95E-47	PCSK5	chr9	+	78505560	78977255	9538
ENSG00000(	7735.294	7612.303	10299.34	5051.016	6618.826	4914.528	0.6271	2.07E-05	7.40E-05	SCD	chr10	+	1.02E+08	1.02E+08	5362
ENSG00000(	186.4425	234.8361	200.5509	123.5975	127.0196	132.3364	0.69442	0.00085	0.00241	TMED1	chr19	-	10943114	10946994	1340
ENSG00000(	325.2387	303.4805	407.6989	1104.137	1312.536	1012.661	-1.7221	1.88E-27	2.58E-26	ABLIM1	chr10	-	1.16E+08	1.16E+08	7606
ENSG00000(	314.8807	303.4805	418.2542	518.3603	520.9645	517.0159	-0.58671	0.000367	0.001102	ERMP1	chr9	-	5765076	5833117	5376
ENSG00000(	1160.087	1294.609	1475.105	1406.015	1179.994	1234.591	0.039181	0.77002	0.84883	RAB18	chr10	+	27793197	27831143	4886
ENSG00000(	3561.053	3589.982	4249.832	502.6297	576.1904	407.6946	2.9318	1.91E-95	1.34E-93	NRP1	chr10	-	33466420	33625190	5882
ENSG00000(	0	0	0	0.749076	1.840864	0.821965	-1.0455	0.43461	NA	HSD17B7P2	chr10	+	38645305	38667433	1401

ENSG00000(	171.9415	236.0404	197.9121	184.2726	197.8929	195.6277	0.066813	0.73983	0.82574	PRTFDC1	chr10	-	25137536	25241533	1944
ENSG00000(	78.72018	90.32158	62.01245	2.996302	0	2.465895	5.0451	6.09E-17	5.31E-16	PALMD	chr1	+	1E+08	1E+08	5294
ENSG00000(	0	1.204288	0	801.5108	698.6079	745.5222	-9.3653	1.08E-32	1.80E-31	TSPAN15	chr10	+	71211229	71267425	1698
ENSG00000(	264.1269	240.8575	230.8974	1176.798	1155.142	1214.864	-2.2607	2.79E-60	9.79E-59	H2AFY2	chr10	+	71812552	71872036	1980
ENSG00000(	481.6432	468.4679	527.7655	357.309	362.6502	280.29	0.56077	0.000571	0.001661	FAM21A	chr10	+	51827648	51893269	4642
ENSG00000(	277.5922	252.9004	250.6886	33.7084	39.57858	63.2913	2.4956	1.07E-22	1.21E-21	MAST3	chr19	+	18208603	18262494	5888
ENSG00000(	488.8938	516.6394	369.4359	417.9842	324.9125	343.5813	0.33856	0.05602	0.10722	MZF1	chr19	-	59073298	59084942	3261
ENSG00000(	196.8005	126.4502	126.6637	68.16587	85.60018	80.55256	0.93859	0.000426	0.001265	OCEL1	chr19	+	17337013	17340028	1485
ENSG00000(	2130.624	2266.469	2056.966	1363.317	1811.41	1761.471	0.38646	0.003488	0.008914	MYO9B	chr19	+	17186591	17325346	7623
ENSG00000(	53.86118	74.66584	59.37362	83.14739	96.64536	88.77221	-0.51024	0.078612	0.14317	KCNK6	chr19	+	38810484	38819660	2666
ENSG00000(	4.143168	12.04288	10.55531	5.992604	18.40864	24.65895	-0.81962	0.24476	0.36105	CATSPERG	chr19	+	38826415	38861589	3785
ENSG00000(	3432.614	3452.693	2861.808	4009.052	2875.43	3411.976	-0.07894	0.56638	0.68563	PSMD8	chr19	+	38865176	38874464	1581
ENSG00000(	1608.585	1453.575	1489.618	1959.582	2250.456	2636.863	-0.58717	8.59E-06	3.21E-05	FBXL19	chr16	+	30934376	30960104	3965
ENSG00000(	132.5814	107.1816	101.5949	13.48336	5.522592	10.68554	3.431	5.46E-19	5.28E-18	STX1B	chr16	-	31000577	31021949	4664
ENSG00000(	103.5792	136.0845	77.84541	54.68252	34.05598	32.8786	1.3594	4.25E-05	0.000146	HSD3B7	chr16	+	30996519	31000473	2200
ENSG00000(	896.9958	916.463	911.7149	1060.691	1191.959	1256.784	-0.36391	0.003524	0.008994	SETD1A	chr16	+	30968615	30996437	6903
ENSG00000(	793.4166	791.217	637.2769	429.2203	404.0696	655.106	0.57574	0.001891	0.005059	BCL7C	chr16	-	30844947	30906281	2409
ENSG00000(	0	0	0	0	3.681728	1.64393	-1.4596	0.2805	NA	MAGEB2	chrX	+	30233677	30238206	1610
ENSG00000(	35.21692	37.33292	22.43003	50.18806	34.97642	35.34449	-0.33275	0.41989	0.55063	EFNA2	chr19	+	1286153	1301430	2143
ENSG00000(	5370.581	5907.031	5032.244	2256.216	2697.786	4195.309	0.83057	2.35E-06	9.34E-06	CIRBP	chr19	+	1259384	1274879	3528
ENSG00000(	2124.409	2043.676	1422.328	1906.397	1492.941	1710.509	0.12965	0.40646	0.53734	ATP5D	chr19	+	1241749	1244824	1587
ENSG00000(	454.7126	396.2107	287.6322	224.7227	220.9037	168.5028	0.88806	1.50E-05	5.44E-05	C19orf26	chr19	-	1228286	1238026	4261
ENSG00000(	0	0	1.319414	5.992604	16.56778	7.397684	-3.4176	0.002298	0.006059	PCDH11Y	chrY	+	4868267	5610265	8240
ENSG00000(	859.7073	936.9358	847.0636	411.9916	327.6738	422.49	1.1808	1.14E-15	9.39E-15	PRKY	chrY	+	7142013	7249589	7218
ENSG00000(	0	3.612863	0	0	2.761296	4.93179	-0.69256	0.59517	0.71099	IGFALS	chr16	-	1840414	1844972	2136
ENSG00000(	4417.652	4260.77	4076.989	10621.14	9890.962	10484.98	-1.2792	1.39E-37	2.67E-36	HNRNPM	chr19	+	8509651	8553998	2568
ENSG00000(	151.2256	93.93444	91.03955	265.1727	206.1768	226.8623	-1.0396	1.54E-05	5.60E-05	2-Mar	chr19	+	8478154	8503901	1667
ENSG00000(	1322.706	1288.588	988.2409	1412.007	1066.781	1486.935	-0.13897	0.37547	0.50601	NDUFB7	chr19	-	14676890	14682874	531
ENSG00000(	2180.342	2001.526	1555.589	3239.752	2134.482	2109.162	-0.38156	0.025524	0.053956	TECR	chr19	+	14627897	14676792	2899
ENSG00000(	1598.227	1463.21	1088.516	2234.492	1846.387	2622.068	-0.68854	1.81E-05	6.52E-05	TIMM13	chr19	-	2425622	2427892	1973
ENSG00000(	1362.066	1248.846	1142.612	2346.105	2213.639	2537.406	-0.9164	3.16E-14	2.38E-13	CDC34	chr19	+	531714	542087	1464
ENSG00000(	587.294	543.1338	614.8468	980.5399	1051.133	1032.388	-0.81024	2.78E-10	1.59E-09	MTAP	chr9	+	21802542	21932738	6122
ENSG00000(	2.071584	1.204288	0	1.498151	2.761296	4.93179	-1.0335	0.396	0.52698	C19orf21	chr19	+	751126	764318	2871
ENSG00000(	1382.782	1306.652	1238.93	1938.608	2544.994	3060.997	-0.93797	9.10E-10	5.01E-09	CEP170B	chr14	+	1.05E+08	1.05E+08	6784
ENSG00000(	3736.101	3392.479	2929.099	4876.482	4271.725	4813.427	-0.47188	0.000104	0.000339	POLR2E	chr19	-	1086594	1095598	2441
ENSG00000(	1377.603	1282.566	1213.861	1505.642	1335.547	1356.242	-0.11514	0.33855	0.46715	POLRMT	chr19	-	617223	633568	3800
ENSG00000(	1129.013	1032.075	919.6314	45.69361	37.73771	62.46933	4.3744	3.81E-116	3.77E-114	HCN2	chr19	+	589893	617159	3408
ENSG00000(	53.86118	86.70872	46.17948	6.74168	25.7721	54.24968	1.0688	0.036838	0.074462	CDHR5	chr11	-	616565	626078	3635
ENSG00000(	18.64425	28.90291	22.43003	12.73428	10.12475	22.19305	0.60327	0.26908	0.38945	IZUMO4	chr19	+	2096380	2099592	2144
ENSG00000(	59.04014	56.60152	44.86007	459.9324	425.2396	595.1026	-3.177	2.13E-46	5.27E-45	RASSF7	chr11	+	560404	564021	1928
ENSG00000(	715.7322	720.1641	567.3479	388.0211	319.3899	383.0357	0.87438	3.65E-08	1.75E-07	GADD45B	chr19	+	2476120	2478257	2007
ENSG00000(	1999.078	1942.516	1542.395	108.616	144.5078	171.7907	3.6786	3.50E-103	2.82E-101	PALM	chr19	+	708953	748329	2740
ENSG00000(	32.10955	24.08575	19.79121	10.48706	9.20432	21.37109	0.85326	0.12172	0.20631	MADCAM1	chr19	+	489176	505347	1723
ENSG00000(	6.214751	3.612863	11.87472	0	0	2.465895	2.4283	0.028737	0.059869	IGF2-AS	chr11	+	2161731	2169894	2061

ENSG00000(	2538.726	2296.577	2278.628	2758.096	2754.853	2634.398	-0.19498	0.07036	0.1303	MKNK2	chr19	-	2037470	2051243	4093
ENSG00000(	146.0467	143.3102	149.0938	602.2567	687.5627	684.6968	-2.1629	5.95E-40	1.23E-38	ARVCF	chr22	-	19957419	20004331	4041
ENSG00000(	396.7083	395.0064	336.4505	576.7882	509.9193	603.3223	-0.58027	0.000153	0.000487	TRMT2A	chr22	-	20099389	20104915	2964
ENSG00000(	1567.153	1419.855	1352.399	5648.779	4927.072	5763.618	-1.9087	2.26E-60	7.96E-59	RANBP1	chr22	+	20103461	20114878	2177
ENSG00000(	1500.862	1469.231	1153.168	775.2932	728.0617	756.2077	0.86618	2.19E-10	1.27E-09	ZDHHC8	chr22	+	20116979	20135530	5046
ENSG00000(	551.0413	557.5852	509.2937	312.3645	339.6394	313.9906	0.7431	5.04E-07	2.16E-06	KLHL22	chr22	-	20783528	20850170	2616
ENSG00000(	2755.206	2469.994	2054.327	2776.074	2555.119	2801.256	-0.15893	0.21355	0.32385	MED15	chr22	+	20850200	20941919	4701
ENSG00000(	5.17896	3.612863	2.638828	0.749076	5.522592	1.64393	0.45255	0.67373	0.7758	SERPIND1	chr22	+	21128167	21142008	2437
ENSG00000(	470.2495	475.6936	448.6007	477.1611	416.0353	387.1455	0.12247	0.4214	0.55206	SNAP29	chr22	+	21213271	21245502	4283
ENSG00000(	1351.708	1186.223	1480.382	1859.206	2018.507	1701.467	-0.47252	0.000233	0.00072	CRKL	chr22	+	21271714	21308037	5325
ENSG00000(	1708.021	1434.307	1526.562	702.6329	792.4919	955.1232	0.92827	7.05E-11	4.22E-10	LZTR1	chr22	+	21333751	21353327	4572
ENSG00000(	1428.357	1422.264	1271.915	71.91125	68.11197	57.53754	4.3667	3.49E-159	6.12E-157	MMP11	chr22	+	24110413	24126503	3823
ENSG00000(	0	0	0	61.42419	138.0648	113.4312	-7.372	2.91E-13	2.07E-12	CECR2	chr22	+	17840837	18033845	5637
ENSG00000(	2553.227	2578.38	2338.001	2783.565	2123.437	2389.452	0.033555	0.79006	0.86254	SMARCB1	chr22	+	24129150	24176703	1728
ENSG00000(	24.85901	12.04288	11.87472	0	2.761296	17.26126	1.149	0.17694	0.27905	P2RX6	chr22	+	21364097	21383119	3687
ENSG00000(	21.75163	36.12863	26.38828	29.96302	23.93123	24.65895	0.092866	0.83816	0.89651	DERL3	chr22	-	24176690	24181315	3525
ENSG00000(	0	0	0	14.23244	15.64734	16.4393	-4.8208	1.71E-05	6.17E-05	SLC7A4	chr22	-	21383007	21387129	2313
ENSG00000(	849.3494	802.0556	949.9779	889.1527	930.5567	866.351	-0.04656	0.71695	0.80939	BCL2L13	chr22	+	18111621	18213388	4458
ENSG00000(	17.60846	12.04288	6.597069	27.7158	22.09037	23.01502	-0.94566	0.093187	0.16544	DDTL	chr22	+	24309089	24314721	1545
ENSG00000(	9.322127	8.430014	10.55531	6.74168	3.681728	10.68554	0.3802	0.61719	0.7297	DDT	chr22	-	24313554	24322660	1048
ENSG00000(	0	0	0	1.498151	0	3.28786	-1.3443	0.31856	NA	GSTT2	chr22	+	24322339	24326106	1094
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	OSM	chr22	-	30658818	30662829	1854
ENSG00000(	3024.512	3073.342	2981.875	1702.649	2047.041	1920.932	0.6784	2.27E-09	1.21E-08	CABIN1	chr22	+	24407642	24574596	7480
ENSG00000(	459.8916	521.4566	406.3794	93.63444	122.4175	116.719	2.0538	2.51E-27	3.42E-26	TBC1D10A	chr22	-	30687979	30723035	5562
ENSG00000(	236.1606	222.7932	167.5656	63.67142	73.63456	36.16646	1.8378	2.65E-11	1.64E-10	SUSD2	chr22	+	24577227	24585078	4938
ENSG00000(	2161.698	1958.172	2120.298	2805.288	2803.636	2513.569	-0.37957	0.000652	0.001882	SF3A1	chr22	-	30727979	30752936	4923
ENSG00000(	408.102	467.2636	365.4776	5.992604	3.681728	2.465895	6.5003	5.73E-60	2.00E-58	GGT5	chr22	-	24615622	24641110	2494
ENSG00000(	299.3439	319.1362	217.7033	139.3281	100.3271	121.6508	1.2015	4.80E-08	2.27E-07	RNF215	chr22	-	30773835	30817760	1992
ENSG00000(	354.2408	339.6091	278.3963	59.92604	84.67974	91.23811	2.0353	2.68E-20	2.75E-19	SEC14L2	chr22	+	30792846	30821305	4381
ENSG00000(	1.035792	2.408575	0	0	1.840864	1.64393	0.005027	0.997	0.99811	SEC14L3	chr22	-	30843946	30868036	2474
ENSG00000(	750.9491	680.4226	691.3728	915.3703	852.32	922.2446	-0.34045	0.007536	0.018023	SPECC1L	chr22	+	24666786	24813708	6756
ENSG00000(	835.8841	830.9585	771.8571	691.3967	660.8702	627.9812	0.30006	0.01997	0.043314	PPIL2	chr22	+	22006559	22052565	4213
ENSG00000(	4.143168	0	0	0	0.920432	0.821965	0.66373	0.62457	NA	UPB1	chr22	+	24863206	24924358	3418
ENSG00000(	26.93059	27.69862	38.263	26.21764	30.37426	32.8786	0.048885	0.9091	0.94406	YPEL1	chr22	-	22051833	22090123	4329
ENSG00000(	1739.095	1732.97	1659.823	3559.607	2997.847	3798.3	-1.0109	5.86E-17	5.12E-16	SNRPD3	chr22	+	24951471	25005947	1763
ENSG00000(	3433.65	3559.874	2703.479	3169.339	3340.248	3824.603	-0.09122	0.48919	0.61831	PES1	chr22	-	30972615	31003070	2760
ENSG00000(	1669.697	1617.358	1964.607	2322.134	2393.123	1837.092	-0.31879	0.019185	0.041796	MAPK1	chr22	-	22108789	22221970	11022
ENSG00000(	11.39371	4.817151	14.51355	14.98151	20.2495	25.48091	-0.93061	0.13099	0.21855	GGT1	chr22	+	24979718	25024972	2632
ENSG00000(	4.143168	6.021439	2.638828	50.93714	92.0432	83.84042	-3.9541	4.47E-13	3.14E-12	PRODH	chr22	-	18900294	18924066	4676
ENSG00000(	1236.736	1038.096	1044.976	901.1379	1001.43	1066.088	0.16208	0.22217	0.33404	PPM1F	chr22	-	22273793	22307209	5587
ENSG00000(	360.4556	367.3078	292.9099	49.43899	44.18074	45.20807	2.8581	1.20E-38	2.40E-37	SLC35E4	chr22	+	31031639	31065003	2714
ENSG00000(	457.82	479.3065	434.0871	740.0866	597.3604	610.7199	-0.50563	0.000688	0.001979	TOP3B	chr22	-	22311397	22337213	4163
ENSG00000(	0	0	0	0.749076	4.60216	4.93179	-2.4861	0.060244	0.11408	CRYBB3	chr22	+	25595817	25603330	867
ENSG00000(	2.071584	0	5.277655	0	0	0	2.1617	0.11093	0.19077	CYTH4	chr22	+	37678068	37711382	3667

ENSG00000(	485.7864	473.2851	430.1289	374.5378	389.3427	454.5466	0.1897	0.22029	0.332	DGCR14	chr22	-	19117792	19132197	5392
ENSG00000(	406.0304	385.3721	331.1729	386.523	353.4459	435.6414	-0.06515	0.69191	0.78978	CRYBB2P1	chr22	+	25844072	25916821	1560
ENSG00000(	1.035792	7.225726	1.319414	2.996302	0.920432	0	0.90679	0.45819	0.58774	MFNG	chr22	-	37865101	37882439	2088
ENSG00000(	149.154	154.1488	175.482	208.9921	255.8801	286.0438	-0.64666	0.001577	0.004274	CARD10	chr22	-	37886400	37915549	4113
ENSG00000(	99.43602	96.34302	92.35896	71.91125	68.11197	81.37453	0.37665	0.16017	0.25746	LRP5L	chr22	-	25747385	25801344	3605
ENSG00000(	4243.639	4034.364	3332.839	2490.676	2155.652	2386.164	0.72198	6.19E-09	3.17E-08	SLC25A1	chr22	-	19163095	19166343	1641
ENSG00000(	233.0532	234.8361	222.9809	301.1284	300.9813	232.6161	-0.27102	0.14376	0.23565	ADRBK2	chr22	+	25960816	26125259	9101
ENSG00000(	4.143168	3.612863	2.638828	0.749076	4.60216	4.93179	0.027612	0.97898	0.98777	PLA2G3	chr22	-	31530795	31536593	2697
ENSG00000(	18.64425	16.86003	22.43003	2.996302	8.283888	6.575719	1.6028	0.015065	0.033622	LGALS2	chr22	-	37966255	37978623	589
ENSG00000(	992.2886	1016.419	864.216	1062.938	957.2493	1188.561	-0.15879	0.2397	0.35481	GGA1	chr22	+	38004481	38029571	3205
ENSG00000(	175.0488	220.3847	172.8432	448.6963	310.1856	364.1305	-0.97923	7.57E-07	3.18E-06	HIRA	chr22	-	19318221	19435224	4053
ENSG00000(	69.39806	96.34302	62.01245	283.8996	279.8113	341.9374	-1.9768	3.36E-18	3.13E-17	SH3BP1	chr22	+	38030661	38062939	3123
ENSG00000(	2.071584	0	0	32.21025	44.18074	34.52253	-4.8343	2.30E-08	1.12E-07	SEZ6L	chr22	+	26565440	26779562	6532
ENSG00000(	42863.14	43084.6	32735.98	420.9805	371.8545	549.0726	6.4462	0	0	LGALS1	chr22	+	38071615	38075813	637
ENSG00000(	548.9697	507.0051	485.5443	525.102	576.1904	524.4136	-0.07486	0.59725	0.71297	HPS4	chr22	-	26839389	26879803	6136
ENSG00000(	154.333	154.1488	166.2461	16.47966	24.85166	14.79537	3.0504	6.15E-23	7.00E-22	PIK3IP1	chr22	-	31677579	31688520	3030
ENSG00000(	87.00652	85.50443	91.03955	154.3096	151.8713	126.5826	-0.71048	0.003201	0.008236	SRRD	chr22	+	26879843	26887899	1295
ENSG00000(	448.4979	397.4149	415.6153	1151.329	1337.388	1145.819	-1.5213	6.72E-29	9.80E-28	PATZ1	chr22	-	31721790	31742218	3781
ENSG00000(	530.3255	468.4679	497.419	254.6857	206.1768	238.3698	1.0922	1.92E-11	1.20E-10	TRIOBP	chr22	+	38093011	38172563	10129
ENSG00000(	742.6628	705.7126	672.901	833.7211	763.0381	776.7568	-0.16134	0.21114	0.32108	TFIP11	chr22	-	26887191	26908471	3586
ENSG00000(	674.3005	714.1426	534.3626	407.4971	275.2092	327.964	0.92277	2.36E-07	1.05E-06	GCAT	chr22	+	38203912	38213183	1656
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	GGTLC2	chr22	+	22988780	22990368	952
ENSG00000(	23.82321	14.45145	17.15238	0	0	0	5.4702	8.27E-07	3.46E-06	CRYBB1	chr22	-	26995242	27014052	1102
ENSG00000(	516.8602	533.4995	471.0307	496.6371	414.1944	393.7212	0.22075	0.15473	0.25026	ANKRD54	chr22	-	38226862	38240438	2403
ENSG00000(	123.2592	93.93444	79.16483	80.15108	88.36147	116.719	0.06024	0.83025	0.89105	EIF3L	chr22	+	38244875	38285414	3220
ENSG00000(	2275.635	2308.62	1872.248	2946.114	2309.364	2634.398	-0.28844	0.028624	0.059658	NHP2L1	chr22	-	42069934	42086508	1670
ENSG00000(	1811.6	1622.176	1613.643	4840.526	4845.154	4296.411	-1.4669	6.98E-39	1.40E-37	MICALL1	chr22	+	38301664	38338829	4710
ENSG00000(	1134.192	1039.3	909.0761	1125.861	1090.712	1380.901	-0.22139	0.11701	0.19979	POLR2F	chr22	+	38348614	38437113	2106
ENSG00000(	5.17896	3.612863	7.916483	0	3.681728	18.08323	-0.32391	0.74302	0.8287	SOX10	chr22	-	38366693	38383429	2879
ENSG00000(	45.57484	52.98866	46.17948	63.67142	65.35067	82.19649	-0.53806	0.093779	0.16634	CCDC134	chr22	+	42196683	42222303	1270
ENSG00000(	257.9122	230.019	237.4945	283.1506	262.3231	253.9872	-0.13898	0.42853	0.55866	DEPDC5	chr22	+	32149944	32303001	5410
ENSG00000(	185.4068	154.1488	166.2461	674.168	512.6806	642.7766	-1.8459	1.01E-25	1.29E-24	PICK1	chr22	+	38452318	38471708	2531
ENSG00000(	785.1303	917.6672	1038.379	537.8362	675.5971	525.2356	0.65447	2.55E-05	8.99E-05	TTC28	chr22	-	28374004	29075853	11793
ENSG00000(	6.214751	7.225726	0	11.98521	26.69253	24.65895	-2.0218	0.00632	0.015346	SLC16A8	chr22	-	38474141	38480100	1878
ENSG00000(	111.8655	95.13873	96.31721	324.3497	205.2563	259.7409	-1.3692	2.84E-09	1.49E-08	CENPM	chr22	-	42334725	42343168	1002
ENSG00000(	25.8948	27.69862	26.38828	3.745378	5.522592	4.93179	2.3662	0.00011	0.000358	3-Sep	chr22	+	42372276	42394225	4649
ENSG00000(	0	1.204288	0	2.996302	0	0	-0.51443	0.69981	NA	TPTEP1	chr22	+	17082777	17179521	5725
ENSG00000(	5.17896	3.612863	2.638828	0	0	0	3.0137	0.021287	0.045877	SLC5A4	chr22	-	32614465	32651328	2028
ENSG00000(	1663.482	1720.927	1671.697	68.16587	77.31629	102.7456	4.3349	1.73E-161	3.23E-159	KDELR3	chr22	+	38864067	38879452	1728
ENSG00000(	4.143168	20.47289	1.319414	3.745378	1.840864	3.28786	1.312	0.17173	0.27268	CYP2D6	chr22	-	42522501	42526908	2257
ENSG00000(	9257.908	9422.347	11486.82	5400.835	6778.061	5707.724	0.75246	3.10E-09	1.63E-08	DDX17	chr22	-	38879445	38903665	6441
ENSG00000(	0	1.204288	1.319414	56.92974	46.0216	38.63235	-5.1577	6.85E-10	3.81E-09	DMC1	chr22	-	38914954	38966291	2371
ENSG00000(	593.5088	722.5726	740.1911	638.9614	1293.207	964.1648	-0.49121	0.014667	0.032824	TCF20	chr22	-	42556019	42739622	7410
ENSG00000(	123.2592	127.6545	120.0667	98.1289	69.95283	89.59418	0.51804	0.041027	0.081876	HSCB	chr22	+	29138019	29153503	1114

ENSG0000(	220.6237	214.3632	216.3839	275.6598	248.5166	247.4114	-0.24373	0.17228	0.27333	CBY1	chr22	+	39052641	39069859	1269
ENSG0000(	1773.276	1657.1	1789.125	2147.6	2174.981	2532.474	-0.39253	0.000826	0.002347	TOMM22	chr22	+	39077953	39080818	1432
ENSG0000(	1.035792	0	1.319414	0.749076	0.920432	0	0.23638	0.8615	NA	RTDR1	chr22	-	23401593	23487208	1291
ENSG0000(	2091.264	2034.042	1754.82	2158.087	1718.447	1884.766	0.029453	0.81871	0.88294	XBP1	chr22	-	29190543	29196585	2173
ENSG0000(	1466.681	1475.252	1409.134	2327.378	2184.185	2405.069	-0.66755	1.24E-09	6.76E-09	C22orf28	chr22	-	32783569	32808242	2027
ENSG0000(	1029.577	1095.902	1099.072	1248.709	1221.413	1157.327	-0.17002	0.14742	0.24047	JOSD1	chr22	-	39081548	39097561	3648
ENSG0000(	1796.063	1670.347	1583.297	2042.729	1879.522	1666.123	-0.14561	0.2358	0.35017	FBXO7	chr22	+	32870663	32894818	6884
ENSG0000(	516.8602	490.1451	551.515	490.6445	650.7454	658.3939	-0.20635	0.19066	0.29611	GTPBP1	chr22	+	39101728	39134304	5126
ENSG0000(	1923.466	1910	1911.831	2254.717	2324.091	2347.532	-0.26922	0.010119	0.023505	POLDIP3	chr22	-	42979727	43010968	3441
ENSG0000(	165.7267	240.8575	178.1209	189.5161	168.4391	182.4762	0.11089	0.60152	0.71668	RAB36	chr22	+	23487513	23506537	3828
ENSG0000(	1466.681	1513.79	1725.793	8994.15	8805.773	8396.372	-2.4734	4.25E-113	3.93E-111	TIMP3	chr22	+	33197687	33259030	4603
ENSG0000(	1540.223	1483.682	1203.305	1365.565	1308.854	1423.643	0.045445	0.72549	0.81586	PPP6R2	chr22	+	50781733	50883514	4030
ENSG0000(	4184.599	3695.959	3722.066	2579.816	3073.322	3238.542	0.38356	0.001584	0.004289	SBF1	chr22	-	50885184	50913454	6253
ENSG0000(	403.9588	438.3607	407.6989	564.0539	658.1089	741.4124	-0.64914	2.35E-05	8.33E-05	SUN2	chr22	-	39130730	39190148	4055
ENSG0000(	10043.04	9686.086	8168.491	4303.439	3374.304	3624.865	1.3005	9.37E-25	1.15E-23	CYB5R3	chr22	-	43013846	43045574	3938
ENSG0000(	330.4176	379.3506	333.8117	314.6117	292.6974	350.1571	0.12297	0.4575	0.58718	DNAL4	chr22	-	39174513	39190203	1504
ENSG0000(	3.107376	1.204288	0	0	0	0	1.4526	0.27741	NA	C22orf31	chr22	-	29454660	29457832	995
ENSG0000(	9.322127	8.430014	0	1.498151	2.761296	3.28786	1.0286	0.32404	0.45151	MIOX	chr22	+	50925213	50929077	1658
ENSG0000(	4943.835	4399.263	3987.268	2505.658	2008.383	2225.059	0.9819	6.81E-15	5.33E-14	LMF2	chr22	-	50941376	50946135	2658
ENSG0000(	426.7463	407.0492	353.6029	757.3154	680.1992	789.0863	-0.90295	7.41E-10	4.10E-09	RHBDD3	chr22	-	29655841	29664198	1794
ENSG0000(	1059.615	1191.041	1299.623	2015.013	2275.308	2345.066	-0.90113	7.26E-13	5.01E-12	PACSIN2	chr22	-	43231418	43411151	3249
ENSG0000(	158.4762	162.5788	145.1355	95.13259	68.11197	88.77221	0.87745	0.000299	0.000909	TTLL1	chr22	-	43435522	43485434	1686
ENSG0000(	4.143168	2.408575	2.638828	1.498151	1.840864	13.9734	-0.74706	0.46769	0.59699	RASL10A	chr22	-	29708922	29711745	1720
ENSG0000(	2160.662	2207.459	1952.732	3015.778	2770.5	2589.189	-0.40514	0.000428	0.001269	AP1B1	chr22	-	29723669	29819168	4176
ENSG0000(	450.5695	393.8021	514.5714	570.7956	606.5647	457.8345	-0.26648	0.10793	0.18669	HMGXB4	chr22	+	35653445	35691800	4216
ENSG0000(	927.0338	955.0002	757.3435	362.5526	321.2308	349.3351	1.3492	7.91E-20	7.95E-19	TOM1	chr22	+	35695268	35743985	2622
ENSG0000(	100.4718	83.09585	87.08131	57.67882	71.7937	57.53754	0.53191	0.063085	0.1187	NEFH	chr22	+	29876219	29887379	3783
ENSG0000(	0	0	3.958241	4.494453	0	2.465895	-0.54885	0.67441	0.77644	CHKB	chr22	-	51017378	51039884	2114
ENSG0000(	3.107376	1.204288	1.319414	236.7079	257.721	299.1952	-6.6984	1.80E-30	2.77E-29	BIK	chr22	+	43506754	43525718	953
ENSG0000(	2548.048	2376.06	2254.878	283.1506	204.3359	297.5513	3.1808	1.69E-103	1.38E-101	HMOX1	chr22	+	35776354	35790207	1822
ENSG0000(	309.7018	255.309	193.9538	447.1981	328.5942	418.3801	-0.64746	0.001222	0.003379	MCAT	chr22	-	43528886	43539400	1379
ENSG0000(	1034.756	1091.085	913.0343	1016.496	918.5911	886.0782	0.10722	0.41154	0.54226	THOC5	chr22	-	29901868	29951205	4753
ENSG0000(	314.8807	295.0505	288.9516	2540.864	2235.729	2365.615	-2.9823	3.06E-121	3.25E-119	MCM5	chr22	+	35796056	35821423	4599
ENSG0000(	0	0	0	4.494453	4.60216	2.465895	-2.7115	0.037259	0.075248	APOBEC3H	chr22	+	39493229	39500072	1047
ENSG0000(	662.9068	690.0569	522.4879	363.3016	382.8997	397.0091	0.71333	4.73E-06	1.82E-05	ARSA	chr22	-	51063446	51066607	2053
ENSG0000(	5107.49	4675.045	3883.035	403.7517	277.05	356.7328	3.7056	1.42E-133	1.77E-131	TSPO	chr22	+	43547520	43559248	955
ENSG0000(	0	1.204288	0	2.247227	5.522592	2.465895	-1.9532	0.1276	0.21411	RASD2	chr22	+	35936915	35950048	3412
ENSG0000(	1527.793	1523.424	1410.453	2018.759	1730.412	1865.038	-0.33089	0.004648	0.011592	TTLL12	chr22	-	43562628	43583139	3385
ENSG0000(	15.53688	6.021439	25.06886	17.22874	32.21512	45.20807	-0.98073	0.080206	0.14568	CBX7	chr22	-	39516172	39548679	4081
ENSG0000(	0	0	0	1399.273	1179.073	1335.693	-10.616	3.23E-33	5.48E-32	PDGFB	chr22	-	39619364	39640756	3497
ENSG0000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	ACR	chr22	+	51176624	51183762	1433
ENSG0000(	2.071584	6.021439	3.958241	8.239831	7.363456	4.109825	-0.62936	0.48753	0.61669	CABP7	chr22	+	30116073	30127828	3259
ENSG0000(	71338.1	70560.42	56466.95	42121.27	36031.23	38516.45	0.76425	1.84E-10	1.07E-09	RPL3	chr22	-	39708887	39716394	2108
ENSG0000(	229.9458	261.3304	232.2168	97.37982	96.64536	124.1167	1.1775	2.50E-08	1.21E-07	ZMAT5	chr22	-	30126945	30163000	2468

ENSG00000(	6851.763	7507.53	7900.65	2653.975	3614.536	3117.713	1.2433	2.96E-22	3.28E-21	RBFOX2	chr22	-	36134783	36424473	6932
ENSG00000(	650.4773	682.8311	544.9179	229.9662	199.7337	204.6693	1.56	5.75E-22	6.30E-21	SYNGR1	chr22	+	39745930	39781593	4391
ENSG00000(	703.3027	652.7239	625.4021	510.8695	541.214	522.7697	0.33176	0.014412	0.032337	TAB1	chr22	+	39795746	39833065	3237
ENSG00000(	1188.053	1186.223	1077.961	1462.945	1296.889	1344.735	-0.24906	0.037861	0.076301	ASCC2	chr22	-	30184597	30234271	2823
ENSG00000(	679.4795	652.7239	738.8717	371.5415	513.6011	453.7246	0.62849	5.78E-05	0.000194	MTMR3	chr22	+	30279144	30426855	8906
ENSG00000(	971.5728	826.1414	1038.379	1218.746	1365.001	1256.784	-0.43632	0.000882	0.002495	SMCR7L	chr22	+	39895437	39914137	5625
ENSG00000(	15.53688	28.90291	7.916483	1.498151	0.920432	3.28786	2.851	0.000565	0.001647	APOL4	chr22	-	36585172	36600886	3414
ENSG00000(	27.96638	36.12863	27.70769	8.988907	0.920432	3.28786	2.5918	6.24E-05	0.000209	APOL1	chr22	+	36649056	36663576	3000
ENSG00000(	557.256	599.7353	526.4461	114.6086	148.1896	152.8855	2.0125	1.13E-30	1.75E-29	PNPLA3	chr22	+	44319619	44360368	2805
ENSG00000(	32642.98	31263.31	33296.73	32752.58	52769.29	46856.93	-0.44426	0.002497	0.006539	MYH9	chr22	-	36677327	36784063	7501
ENSG00000(	5.17896	15.65574	6.597069	0	0	0	4.3715	0.000267	0.000817	CACNA1I	chr22	+	39966758	40085742	10015
ENSG00000(	970.537	824.9371	781.093	1362.568	1087.03	1162.258	-0.48529	0.000572	0.001666	SAMM50	chr22	+	44351301	44406411	3248
ENSG00000(	2119.23	2190.599	1890.72	1447.214	1303.332	1351.31	0.59502	3.80E-07	1.65E-06	TXN2	chr22	-	36863083	36878077	1736
ENSG00000(	556.2203	509.4137	526.4461	328.8442	237.4715	237.5479	0.98002	1.41E-08	7.00E-08	FOXRED2	chr22	-	36883237	36903148	4967
ENSG00000(	3.107376	0	0	0	1.840864	0	0.36193	0.78835	NA	GRAP2	chr22	+	40297086	40369725	3893
ENSG00000(	5970.305	6072.019	5111.409	5205.326	4264.361	3978.31	0.35034	0.006256	0.015199	EIF3D	chr22	-	36906897	36925483	2155
ENSG00000(	933.2485	885.1515	1021.226	796.2673	1277.56	893.4759	-0.06246	0.70983	0.80394	TNRC6B	chr22	+	40440821	40731811	18279
ENSG00000(	1164.23	1081.45	1009.352	1014.997	817.3436	1171.3	0.1156	0.43517	0.56493	SGSM3	chr22	+	40766595	40806122	4218
ENSG00000(	395.6725	323.9534	431.4483	288.3941	295.4587	253.1652	0.45751	0.008512	0.020105	IFT27	chr22	-	37154246	37172300	6475
ENSG00000(	1051.329	967.043	1056.85	1163.314	1226.936	1196.781	-0.22145	0.060894	0.11506	KIAA0930	chr22	-	45588114	45636650	6224
ENSG00000(	0	0	0	0.749076	2.761296	4.109825	-2.0633	0.12515	0.21082	NCF4	chr22	+	37257030	37274057	1641
ENSG00000(	0	0	0	0.749076	14.72691	9.863579	-3.7741	0.00222	0.005869	CSF2RB	chr22	+	37309670	37336491	4866
ENSG00000(	340.7755	398.6192	347.0058	922.8611	820.1049	894.2978	-1.2768	2.50E-19	2.46E-18	SLC25A17	chr22	-	41165634	41215403	2530
ENSG00000(	426.7463	413.0707	381.3106	290.6413	285.3339	317.2785	0.45034	0.00434	0.01088	FAM118A	chr22	+	45704849	45737836	3458
ENSG00000(	693.9806	579.2624	537.0014	234.4606	170.2799	266.3166	1.4239	2.35E-14	1.78E-13	KCTD17	chr22	+	37447779	37459430	1763
ENSG00000(	7606.856	8098.835	7709.335	7009.1	6206.473	6303.649	0.26204	0.011052	0.025445	ST13	chr22	-	41220539	41253026	3595
ENSG00000(	10.35792	0	3.958241	61.42419	56.14635	70.68898	-3.4918	5.69E-10	3.17E-09	IL2RB	chr22	-	37521878	37571094	4113
ENSG00000(	42.46747	78.2787	42.22124	62.17327	31.29469	52.60575	0.14886	0.70131	0.79702	RBX1	chr22	+	41347351	41369313	1871
ENSG00000(	1481.182	1325.921	1679.614	1145.337	1883.204	1375.969	0.027038	0.87171	0.91938	EP300	chr22	+	41487790	41576081	9585
ENSG00000(	330.4176	355.2649	344.367	458.4342	483.2268	401.9408	-0.38225	0.014422	0.032354	L3MBTL2	chr22	+	41601209	41627275	5875
ENSG00000(	1.035792	6.021439	1.319414	14.98151	10.12475	10.68554	-1.8593	0.032165	0.066062	CHADL	chr22	-	41625517	41636938	2533
ENSG00000(	1917.251	1725.744	1822.11	5983.615	5747.177	6978.482	-1.772	1.67E-52	4.88E-51	RANGAP1	chr22	-	41641615	41682255	4222
ENSG00000(	2816.318	2934.849	2695.562	2532.624	3917.359	4149.279	-0.3261	0.039021	0.078316	ZC3H7B	chr22	+	41697526	41756151	5909
ENSG00000(	447.4621	435.9522	395.8241	1362.568	1356.717	1578.995	-1.7429	9.67E-39	1.93E-37	PHF5A	chr22	-	41855721	41864729	1086
ENSG00000(	1196.34	1192.245	1118.863	985.7834	975.6579	855.6655	0.31588	0.010682	0.024664	ACO2	chr22	+	41865129	41924993	2811
ENSG00000(	1110.369	1309.061	1096.433	1096.647	1035.486	1134.312	0.10567	0.40389	0.53493	POLR3H	chr22	-	41921808	41940610	4416
ENSG00000(	535.5044	638.2725	443.323	1465.941	1116.484	1250.209	-1.2402	6.66E-15	5.22E-14	TRMU	chr22	+	46726772	46753237	2933
ENSG00000(	787.2018	709.3255	521.1684	343.8257	262.3231	311.5247	1.1318	3.14E-10	1.79E-09	PMM1	chr22	-	41972898	41985894	2538
ENSG00000(	1136.264	1027.257	1087.197	1318.373	1273.878	1458.166	-0.31648	0.009104	0.021374	DESI1	chr22	-	41994032	42017100	3833
ENSG00000(	1865.461	1869.055	1870.929	792.5219	1133.052	987.1799	0.94297	1.43E-11	8.97E-11	CERK	chr22	-	47080308	47134158	4450
ENSG00000(	788.2376	765.927	932.8255	847.2044	1081.508	941.1498	-0.20614	0.15013	0.24423	BRD1	chr22	-	50166931	50221160	4614
ENSG00000(	705.3743	673.1968	736.2329	802.2599	1118.325	775.9349	-0.34861	0.027499	0.057634	ZBED4	chr22	+	50247490	50282090	5257
ENSG00000(	8.286335	7.225726	6.597069	6.74168	0.920432	5.753754	0.62209	0.48228	0.61145	HDAC10	chr22	-	50683612	50689834	2687
ENSG00000(	0	2.408575	0	0.749076	2.761296	0	-0.27499	0.8393	NA	KCNK10	chr14	-	88649113	88793251	4835

ENSG00000(	466.1064	456.425	464.4337	942.337	765.7994	774.291	-0.83813	5.11E-09	2.64E-08	ABHD4	chr14	+	23067146	23081265	2510
ENSG00000(	821.383	880.3343	862.8966	303.3756	549.4979	507.9743	0.91147	1.29E-06	5.30E-06	KHNYN	chr14	+	24898492	24910540	6225
ENSG00000(	722.9827	773.1527	688.734	1020.99	1008.793	1071.842	-0.50419	5.33E-05	0.00018	FKBP3	chr14	-	45584803	45604522	1684
ENSG00000(	119.1161	101.1602	117.4278	96.63075	77.31629	91.23811	0.34395	0.17603	0.27793	SDR39U1	chr14	-	24908972	24912111	2336
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	GZMB	chr14	-	25100160	25103473	968
ENSG00000(	1047.186	918.8715	938.1032	1486.915	1152.381	1203.357	-0.40292	0.003463	0.008854	RBM23	chr14	-	23369854	23388393	4240
ENSG00000(	313.8449	233.6318	362.8388	385.7739	413.274	452.0807	-0.45745	0.012817	0.029054	PRMT5	chr14	-	23389720	23398794	2531
ENSG00000(	22.78742	28.90291	32.98534	17.97781	17.48821	27.94681	0.39822	0.40454	0.53542	COCH	chr14	+	31343720	31364271	2688
ENSG00000(	66.29068	89.11729	88.40072	164.7966	124.2583	161.9271	-0.8858	0.000529	0.001548	AP4S1	chr14	+	31494312	31562818	2256
ENSG00000(	56.96855	65.03154	44.86007	280.9033	251.2779	258.9189	-2.2246	1.69E-21	1.83E-20	POLE2	chr14	-	50110273	50155140	1792
ENSG00000(	142.9393	151.7403	151.7326	133.3354	157.3939	123.2947	0.10876	0.6219	0.734	METTL21D	chr14	-	50575350	50583318	1849
ENSG00000(	319.0239	348.0392	414.2959	358.0581	428.9213	355.0888	-0.07972	0.63958	0.74766	SOS2	chr14	-	50583847	50698276	5489
ENSG00000(	91.14969	84.30014	76.526	57.67882	51.54419	57.53754	0.58942	0.043866	0.086728	CDKL1	chr14	-	50796310	50883179	2982
ENSG00000(	903.2105	783.9913	1304.9	762.5589	928.7159	818.6771	0.25179	0.14885	0.24241	NIN	chr14	-	51186481	51297839	10293
ENSG00000(	1460.467	1447.554	1141.293	1463.694	1452.442	1229.66	-0.03306	0.80993	0.87669	PYGL	chr14	-	51324609	51411454	3048
ENSG00000(	40.39588	16.86003	35.62417	188.767	263.2436	152.0635	-2.6554	1.45E-16	1.24E-15	TRIM9	chr14	-	51441980	51562779	5284
ENSG00000(	979.8591	963.4302	990.8798	1628.49	1431.272	1497.62	-0.63445	7.96E-08	3.68E-07	PSMC6	chr14	+	53173890	53195305	2939
ENSG00000(	364.5988	428.7264	456.5172	432.2166	494.272	387.9674	-0.07353	0.65409	0.75974	GNPNAT1	chr14	-	53241912	53258386	3860
ENSG00000(	197.8363	151.7403	265.2022	216.4828	238.3919	186.586	-0.06264	0.78054	0.85532	DDHD1	chr14	-	53510686	53620000	5603
ENSG00000(	123.2592	133.6759	112.1502	465.925	364.4911	371.5281	-1.6944	2.25E-18	2.11E-17	CDKN3	chr14	+	54863567	54886936	1070
ENSG00000(	1868.569	1729.357	1770.653	1299.646	1209.448	1177.876	0.54116	2.04E-06	8.20E-06	CNIH	chr14	-	54893654	54908149	1417
ENSG00000(	85.97073	134.8802	127.9831	117.6049	80.07758	106.0335	0.1908	0.48343	0.61265	CGRRF1	chr14	+	54976530	55005567	2309
ENSG00000(	914.6043	909.2372	957.8944	1517.627	1156.983	1173.766	-0.46788	0.000767	0.002193	ATP6V1D	chr14	-	67761088	67826982	1845
ENSG00000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	C14orf105	chr14	-	57936019	57960585	3082
ENSG00000(	1.035792	8.430014	7.916483	24.71949	27.61296	30.4127	-2.1458	0.000914	0.002576	PLEK2	chr14	-	67853700	67878917	1549
ENSG00000(	315.9165	267.3519	200.5509	208.243	155.553	143.0219	0.62589	0.00538	0.01324	PIGH	chr14	-	68048672	68067004	1420
ENSG00000(	1097.939	1093.493	948.6585	2390.3	1850.068	2034.363	-0.99608	7.49E-14	5.51E-13	PSMA3	chr14	+	58711549	58738730	1279
ENSG00000(	360.4556	325.1577	358.8805	319.8553	308.3447	274.5363	0.20965	0.20092	0.30843	VTI1B	chr14	-	68113792	68141548	5351
ENSG00000(	234.089	251.6961	182.0791	349.8183	215.3811	295.0854	-0.36322	0.09132	0.16276	TIMM9	chr14	-	58875212	58894332	1336
ENSG00000(	245.4827	297.4591	195.2732	341.5785	310.1856	341.9374	-0.42555	0.024203	0.051492	GSTZ1	chr14	+	77787227	77797940	5356
ENSG00000(	269.3059	233.6318	327.2146	397.01	393.0245	263.0288	-0.3425	0.092549	0.16448	KIAA0586	chr14	+	58894103	59015216	5339
ENSG00000(	398.7799	388.9849	580.5421	321.3534	455.6138	309.0588	0.33114	0.10015	0.17571	TMED8	chr14	-	77801364	77843452	7784
ENSG00000(	52.82539	57.80581	63.33186	53.18436	49.70333	47.67397	0.20211	0.53497	0.65921	SAMD15	chr14	+	77843032	77857840	2564
ENSG00000(	1825.065	1893.14	1777.25	2746.86	2692.264	3127.577	-0.63936	1.58E-08	7.80E-08	AHSA1	chr14	+	77924213	77935817	1402
ENSG00000(	99.43602	136.0845	159.6491	362.5526	427.0804	378.1039	-1.5608	1.72E-14	1.32E-13	DAAM1	chr14	+	59655364	59838123	5806
ENSG00000(	6.214751	14.45145	5.277655	40.45008	37.73771	31.23467	-1.9889	0.000288	0.000877	ISM2	chr14	-	77940740	77965210	3042
ENSG00000(	871.101	875.5172	1146.571	760.3117	748.3112	661.6818	0.41232	0.005127	0.012677	SPTLC2	chr14	-	77972340	78083116	8170
ENSG00000(	502.3591	480.5108	427.4901	686.9023	589.0765	558.9361	-0.37779	0.011999	0.027393	RIN3	chr14	+	92980118	93155339	4079
ENSG00000(	1549.545	1428.285	1489.618	1443.469	1103.598	1203.357	0.25128	0.056295	0.10768	LGMN	chr14	-	93170152	93215047	2115
ENSG00000(	142.9393	152.9445	171.5238	270.4163	249.4371	217.8207	-0.65769	0.00097	0.002725	ALKBH1	chr14	-	78138747	78174363	2594
ENSG00000(	803.7745	806.8728	680.8175	929.6028	820.1049	843.336	-0.1774	0.18754	0.29225	SNW1	chr14	-	78183942	78227550	2163
ENSG00000(	3.107376	0	0	20.22504	6.443024	10.68554	-2.8845	0.003888	0.009851	CHGA	chr14	+	93389425	93401638	2063
ENSG00000(	617.332	492.5537	515.8908	653.943	560.5431	618.9396	-0.17199	0.24918	0.36643	ITPK1	chr14	-	93403259	93582665	6066
ENSG00000(	1111.405	1117.579	1004.074	680.1606	560.5431	675.6552	0.75216	2.51E-08	1.22E-07	DHRS7	chr14	-	60610838	60636574	2322

ENSG00000(	494.0727	499.7794	672.901	463.6778	514.5215	410.1605	0.2614	0.11932	0.20281	PPM1A	chr14	+	60712470	60765805	8184
ENSG00000(	498.2159	533.4995	587.1391	268.9181	287.1748	268.7825	0.96896	2.80E-10	1.60E-09	SIX4	chr14	-	61176246	61191066	6285
ENSG00000(	22.78742	13.24716	21.11062	11.23613	11.04518	13.15144	0.65824	0.2555	0.37375	GALNT16	chr14	+	69725994	69821183	5548
ENSG00000(	0	0	0	4.494453	0.920432	0	-1.4809	0.27346	NA	ASB2	chr14	-	94400499	94443137	2842
ENSG00000(	99.43602	115.6116	93.67838	226.2208	242.0736	241.6577	-1.1932	1.36E-08	6.78E-08	CEP128	chr14	-	80943330	81425861	4662
ENSG00000(	1327.885	1500.542	1361.635	2618.019	2339.738	2953.32	-0.91528	2.60E-13	1.86E-12	ERH	chr14	-	69846848	69865344	1116
ENSG00000(	8610.538	9002.051	10263.72	3713.917	3472.79	3070.039	1.4396	1.91E-34	3.37E-33	HIF1A	chr14	+	62162231	62214976	3922
ENSG00000(	732.3049	716.5512	671.5816	253.9366	323.9921	216.1768	1.414	4.40E-17	3.87E-16	KIAA0247	chr14	+	70078313	70181859	5388
ENSG00000(	2465.185	2901.129	2541.191	3153.608	3107.378	3185.114	-0.25623	0.020644	0.044604	SRSF5	chr14	+	70193617	70238722	3044
ENSG00000(	0	6.021439	10.55531	1.498151	8.283888	2.465895	0.35374	0.73291	0.8214	SLC10A1	chr14	-	70242134	70264006	2049
ENSG00000(	2581.193	2746.98	2773.408	4641.272	4628.853	4364.634	-0.75017	3.06E-13	2.18E-12	EIF5	chr14	+	1.04E+08	1.04E+08	5945
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	SERPINA4	chr14	+	95027428	95036250	2012
ENSG00000(	1.035792	0	0	7.490755	13.80648	8.219649	-3.4636	0.002047	0.005448	SLC8A3	chr14	-	70510934	70655787	5268
ENSG00000(	605.9383	575.6495	769.2182	1534.856	1890.567	1510.772	-1.3363	2.80E-19	2.75E-18	DICER1	chr14	-	95552565	95624347	10331
ENSG00000(	528.2539	557.5852	478.9472	1127.359	1061.258	1180.342	-1.1032	4.78E-17	4.19E-16	ZFYVE21	chr14	+	1.04E+08	1.04E+08	4453
ENSG00000(	939.4633	882.7429	1037.059	2186.552	2026.791	1904.493	-1.0958	3.56E-19	3.47E-18	MTHFD1	chr14	+	64854749	64926725	3448
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	TCL1A	chr14	-	96176304	96180533	1395
ENSG00000(	670.1574	592.5096	754.7047	907.1305	823.7866	769.3592	-0.30974	0.02997	0.062113	ZC3H14	chr14	+	89029253	89079853	4194
ENSG00000(	755.0923	851.4314	678.1787	1495.904	1503.986	1685.028	-1.0331	3.70E-15	2.95E-14	TELO2	chr16	+	1543345	1560458	3314
ENSG00000(	866.9578	851.4314	1274.554	558.8104	600.1217	583.5951	0.77643	2.27E-06	9.06E-06	PCNX	chr14	+	71374122	71582099	12919
ENSG00000(	14.50109	15.65574	9.235896	0	0	0	4.9624	1.48E-05	5.39E-05	BDKRB1	chr14	+	96722161	96735304	1687
ENSG00000(	191.6215	237.2447	236.1751	447.1981	408.6718	483.3154	-1.0091	4.32E-09	2.24E-08	GSKIP	chr14	+	96829814	96853625	3834
ENSG00000(	146.0467	127.6545	130.622	1044.96	816.4232	816.2112	-2.7146	1.36E-56	4.38E-55	VRK1	chr14	+	97263641	97398059	1745
ENSG00000(	1651.052	1824.496	1529.201	2863.716	2460.315	2698.511	-0.67945	1.43E-08	7.09E-08	PSMC1	chr14	+	90722839	90738968	2246
ENSG00000(	959.1433	1028.462	862.8966	13.48336	20.2495	24.65895	5.5807	2.19E-131	2.67E-129	PAPLN	chr14	+	73704205	73741348	5912
ENSG00000(	1.035792	1.204288	11.87472	17.97781	25.7721	29.59074	-2.233	0.002375	0.006246	RPS6KA5	chr14	-	91336799	91526980	4202
ENSG00000(	1152.836	1145.278	1352.399	1575.306	1743.298	1519.813	-0.40605	0.001173	0.003253	SMEK1	chr14	-	91923955	91976898	4108
ENSG00000(	148.1182	132.4716	127.9831	79.40201	62.58938	66.57916	0.96036	0.000153	0.000487	C14orf93	chr14	-	23456110	23479375	2361
ENSG00000(	4055.125	4051.224	3690.4	3662.23	3704.739	4339.975	0.011159	0.92186	0.95272	PSMB5	chr14	-	23485752	23504439	1294
ENSG00000(	1699.735	1800.41	1823.43	1963.327	2054.404	1771.334	-0.12087	0.29152	0.41564	YY1	chr14	+	1.01E+08	1.01E+08	6697
ENSG00000(	6956.378	6862.031	6868.868	4005.307	5564.932	5535.112	0.45281	0.0006	0.001742	ACIN1	chr14	-	23527773	23564823	4935
ENSG00000(	1105.19	1157.32	957.8944	1931.866	1396.295	1438.439	-0.56407	0.000151	0.000481	CCNB1IP1	chr14	-	20779527	20801471	1631
ENSG00000(	755.0923	684.0354	977.6856	513.8658	602.883	509.6182	0.56903	0.00039	0.001164	TRIP11	chr14	-	92432335	92507240	9996
ENSG00000(	6327.653	5960.02	5305.363	4732.659	4421.755	4836.442	0.33013	0.002696	0.007028	APEX1	chr14	+	20923350	20925927	1803
ENSG00000(	1172.516	1253.664	1200.667	1286.912	1431.272	2379.588	-0.4889	0.00818	0.019383	PABPN1	chr14	+	23790498	23795394	2768
ENSG00000(	794.4524	734.6155	639.9157	412.7406	596.4399	582.7731	0.44675	0.007596	0.018153	EFS	chr14	-	23825611	23834961	3118
ENSG00000(	657.7279	633.4553	891.9237	1262.941	1527.917	1061.157	-0.81705	1.09E-06	4.51E-06	ARHGAP5	chr14	+	32545320	32628934	9604
ENSG00000(	828.6335	822.5285	674.2204	671.1717	664.5519	590.9928	0.27171	0.055071	0.10574	CINP	chr14	-	1.03E+08	1.03E+08	2346
ENSG00000(	39.36009	50.58008	22.43003	28.46487	21.16994	18.90519	0.69339	0.12997	0.2172	DHRS2	chr14	+	24099324	24114848	5318
ENSG00000(	1061.687	1139.256	1112.266	1349.834	1146.858	1182.808	-0.15175	0.21924	0.33085	SRP54	chr14	+	35451163	35498773	2327
ENSG00000(	0	0	6.597069	0	0	0	1.83	0.17508	0.27674	CPNE6	chr14	+	24540046	24547309	4540
ENSG00000(	1528.829	1455.984	1654.545	1689.914	1950.395	1663.657	-0.1927	0.1115	0.19164	CHD8	chr14	-	21853353	21924285	8229
ENSG00000(	209.23	262.5347	205.8285	613.4929	400.3879	475.9177	-1.1324	5.21E-09	2.68E-08	PCK2	chr14	+	24563262	24579807	2505
ENSG00000(	1.035792	7.225726	6.597069	0.749076	0	0.821965	2.302	0.053747	0.10347	KIAA0391	chr14	+	35591052	35743271	2615

ENSG0000(	581.0793	556.3809	548.8761	429.9694	443.6482	410.1605	0.3932	0.005082	0.012574	DCAF11	chr14	+	24583404	24594451	4299
ENSG0000(	45.57484	50.58008	36.94359	37.45378	25.7721	53.42772	0.18504	0.64132	0.74899	PSMA6	chr14	+	35747839	35786699	4730
ENSG0000(	1149.729	1007.989	973.7274	704.131	621.2916	509.6182	0.76891	2.90E-07	1.27E-06	NFKBIA	chr14	-	35870717	35873955	1558
ENSG0000(	123.2592	126.4502	83.12307	131.0882	193.2907	232.6161	-0.73068	0.005643	0.013838	EMC9	chr14	-	24608174	24610797	953
ENSG0000(	1261.595	1024.849	1035.74	692.1458	570.6678	785.7985	0.69538	4.74E-06	1.83E-05	PSME2	chr14	-	24612574	24616779	2754
ENSG0000(	281.7354	234.8361	245.411	346.822	269.6866	263.0288	-0.2058	0.27179	0.39245	BRMS1L	chr14	+	36295524	36401531	2657
ENSG0000(	72.50543	97.54731	42.22124	80.15108	92.96363	97.81383	-0.34207	0.28247	0.40514	REC8	chr14	+	24641062	24649463	2717
ENSG0000(	78.72018	77.07441	91.03955	58.42789	63.50981	87.95025	0.22976	0.4376	0.56721	TM9SF1	chr14	-	24658349	24682679	2740
ENSG0000(	2583.265	2622.939	3265.549	1931.866	1986.292	1723.66	0.58481	4.75E-06	1.83E-05	SEC23A	chr14	-	39501123	39578850	4215
ENSG0000(	724.0185	810.4856	753.3853	945.3333	997.7483	980.6041	-0.35321	0.004608	0.011499	GMPR2	chr14	+	24701628	24708448	2160
ENSG0000(	1322.706	1406.608	1290.387	2268.201	2174.981	2242.32	-0.73276	2.42E-11	1.50E-10	PNN	chr14	+	39644387	39652422	3576
ENSG0000(	465.0706	527.478	323.2564	590.2715	347.9233	367.4183	0.010932	0.96023	0.97686	RABGGTA	chr14	-	24734744	24740945	2265
ENSG0000(	2299.458	2548.273	1881.484	128.841	130.7013	152.8855	4.0155	7.85E-150	1.21E-147	NFATC4	chr14	+	24834879	24848810	5700
ENSG0000(	7174.931	7158.286	6073.262	1695.907	1564.734	1520.635	2.0898	1.03E-74	4.90E-73	PLTP	chr20	-	44527399	44540794	2255
ENSG0000(	534.4686	529.8866	490.8219	528.8473	413.274	462.7662	0.14548	0.33913	0.46779	PCIF1	chr20	+	44563267	44576662	2747
ENSG0000(	1152.836	1274.136	1113.585	946.8315	898.3416	974.8504	0.32746	0.007565	0.018082	GSS	chr20	-	33516236	33543620	1919
ENSG0000(	671.1932	635.8639	555.4732	52.43529	31.29469	29.59074	4.0004	2.49E-74	1.17E-72	MMP9	chr20	+	44637547	44645200	2336
ENSG0000(	2160.662	2059.332	2075.438	1767.818	1481.896	1615.161	0.37091	0.001376	0.003773	TRPC4AP	chr20	-	33590207	33680674	3226
ENSG0000(	10857.17	9985.954	9428.531	3084.693	3181.013	3446.499	1.6377	1.40E-52	4.12E-51	PYGB	chr20	+	25228705	25278650	4134
ENSG0000(	1654.16	1440.328	1486.979	1616.505	1378.807	1501.73	0.026865	0.82556	0.88756	ABHD12	chr20	-	25275379	25371619	2117
ENSG0000(	592.473	658.7454	575.2644	63.67142	79.15715	70.68898	3.0872	3.69E-65	1.44E-63	PROCR	chr20	+	33759876	33765165	1348
ENSG0000(	271.3775	207.1375	258.6051	2398.54	2095.824	2284.241	-3.1912	1.88E-114	1.81E-112	GINS1	chr20	+	25388363	25433264	3249
ENSG0000(	648.4057	638.2725	522.4879	238.206	357.1276	373.1721	0.89992	1.18E-06	4.86E-06	NINL	chr20	-	25433341	25566153	4969
ENSG0000(	24.85901	18.06432	13.19414	0.749076	10.12475	4.109825	1.7789	0.017075	0.037676	CD40	chr20	+	44746911	44758502	1733
ENSG0000(	958.1075	906.8287	935.4644	765.5552	717.937	729.9048	0.33855	0.006005	0.014647	UQCC	chr20	-	33890369	33999944	3638
ENSG0000(	1293.704	1095.902	1256.082	858.4406	1029.043	831.8285	0.42278	0.001837	0.004928	ZMYND8	chr20	-	45837859	45985567	5362
ENSG0000(	7.250543	7.225726	2.638828	5.992604	0	6.575719	0.37001	0.70961	0.80381	SGK2	chr20	+	42187608	42216877	2395
ENSG0000(	626.6541	638.2725	616.1662	638.9614	501.6354	542.4968	0.15892	0.27352	0.39457	IFT52	chr20	+	42219571	42275936	1757
ENSG0000(	421.5673	464.8551	411.6571	7544.689	7357.013	7294.939	-4.0888	3.39E-292	2.34E-289	MYBL2	chr20	+	42295754	42345136	2639
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	HNF4A	chr20	+	42984340	43060030	3340
ENSG0000(	999.5392	887.56	835.1889	632.2198	576.1904	567.1558	0.61559	5.58E-06	2.13E-05	NDRG3	chr20	-	35280169	35374481	2978
ENSG0000(	3.107376	0	2.638828	1.498151	0	4.109825	0.022305	0.98595	0.99155	SLA2	chr20	-	35240721	35274619	2757
ENSG0000(	176.0846	127.6545	186.0373	187.2689	289.0156	257.275	-0.57692	0.011141	0.025631	C20orf24	chr20	+	35234137	35240960	1170
ENSG0000(	8.286335	21.67718	11.87472	53.93344	101.2475	79.7306	-2.4284	3.65E-08	1.75E-07	NFATC2	chr20	-	50003494	50179168	7525
ENSG0000(	59.04014	66.23582	39.58241	11.98521	17.48821	30.4127	1.4267	0.001205	0.003336	RIMS4	chr20	-	43380449	43438979	5203
ENSG0000(	353.205	374.5335	282.3545	649.4485	582.6335	648.5303	-0.89213	1.55E-08	7.67E-08	PABPC1L	chr20	+	43538703	43587676	2223
ENSG0000(	889.7452	850.2271	899.8402	1456.203	1257.31	1134.312	-0.54269	4.41E-05	0.000151	STK4	chr20	+	43595115	43708600	6342
ENSG0000(	7.250543	1.204288	1.319414	473.4157	562.384	434.8194	-6.8915	1.80E-48	4.78E-47	SALL4	chr20	-	50400581	50419059	3497
ENSG0000(	1682.126	1698.046	1874.887	1675.682	1856.511	1598.722	0.034305	0.77113	0.84949	ADNP	chr20	-	49505453	49547958	6234
ENSG0000(	327.3102	350.4477	253.3274	897.3925	669.1541	794.8401	-1.3361	3.75E-15	2.99E-14	PFDN4	chr20	+	52824386	52844591	1462
ENSG0000(	136.7245	130.0631	145.1355	100.3761	113.2131	90.41614	0.43574	0.064477	0.12084	DOK5	chr20	+	53092136	53267710	1963
ENSG0000(	356.3124	441.9736	414.2959	631.4707	549.4979	566.3338	-0.52754	0.000537	0.001569	CSTF1	chr20	+	54967427	54979518	2383
ENSG0000(	2.071584	1.204288	5.277655	1685.42	1804.967	1782.842	-8.9794	2.64E-76	1.32E-74	BMP7	chr20	-	55743804	55841685	4013
ENSG0000(	633.9046	563.6067	584.5003	1041.964	877.1717	895.9418	-0.6578	1.46E-06	5.93E-06	RAE1	chr20	+	55926066	55954267	3251

ENSG00000(	2528.368	2639.799	2454.11	2802.292	2108.71	2452.743	0.049312	0.69562	0.79266	TPD52L2	chr20	+	62496643	62522898	2362
ENSG00000(	1936.931	1902.775	2101.826	1710.889	1915.419	2072.174	0.06009	0.61462	0.72785	DNAJC5	chr20	+	62526518	62567384	5287
ENSG00000(	1002.647	904.4201	919.6314	1582.048	1170.789	1382.545	-0.54763	7.99E-05	0.000264	NELFCD	chr20	+	57556263	57570188	3581
ENSG00000(	228.91	178.2346	164.9267	764.8061	700.4487	941.1498	-2.0591	6.39E-31	1.00E-29	CTSZ	chr20	-	57570240	57582302	1495
ENSG00000(	1637.587	1678.777	1457.952	1807.519	1657.698	1709.687	-0.11579	0.31891	0.44602	PRPF6	chr20	+	62612488	62664453	3044
ENSG00000(	3.107376	9.634302	0	8.988907	9.20432	9.863579	-0.99004	0.26766	0.38792	TUBB1	chr20	+	57594309	57601709	3496
ENSG00000(	615.2604	668.3797	696.6505	1177.547	1041.009	1004.441	-0.70238	1.05E-07	4.83E-07	SLMO2	chr20	-	57608200	57617964	2626
ENSG00000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	HRH3	chr20	-	60790026	60795323	2659
ENSG00000(	447.4621	525.0694	477.6278	650.1976	545.8162	643.5985	-0.34363	0.020134	0.043634	GTPBP5	chr20	+	60758085	60778624	2929
ENSG00000(	2869.144	2589.219	2638.828	5103.452	4054.503	4922.748	-0.79662	3.83E-11	2.34E-10	PSMA7	chr20	-	60711791	60718496	1023
ENSG00000(	9.322127	13.24716	5.277655	25.46857	22.09037	27.94681	-1.3633	0.018935	0.041308	SLCO4A1	chr20	+	61273797	61317137	3092
ENSG00000(	21.75163	8.430014	15.83297	0	0	0	5.1771	4.99E-06	1.92E-05	NTSR1	chr20	+	61340189	61394123	4132
ENSG00000(	469.2137	446.7907	399.7824	434.4638	506.2376	494.0009	-0.12227	0.42034	0.5511	MRGBP	chr20	+	61427805	61431945	1636
ENSG00000(	208.1942	240.8575	171.5238	124.3465	136.2239	134.8022	0.64854	0.002448	0.00642	TCFL5	chr20	-	61472467	61493115	2456
ENSG00000(	1662.446	1435.511	1683.572	1095.148	1707.401	1414.602	0.18135	0.24359	0.35957	DIDO1	chr20	-	61509090	61569304	8544
ENSG00000(	616.2962	623.821	608.2498	880.1638	895.5803	826.8967	-0.49244	0.000108	0.000351	GID8	chr20	+	61569471	61576996	1566
ENSG00000(	1.035792	3.612863	0	0.749076	0.920432	1.64393	0.3166	0.80804	0.87542	SLC17A9	chr20	+	61584052	61599949	3992
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	BIRC7	chr20	+	61867235	61871859	1368
ENSG00000(	12.4295	8.430014	10.55531	64.4205	34.05598	46.03004	-2.1232	1.76E-05	6.32E-05	NKAIN4	chr20	-	61872136	61904046	1430
ENSG00000(	3398.433	3482.8	2749.658	1397.026	1713.844	2174.097	0.86331	3.21E-08	1.55E-07	ARFGAP1	chr20	+	61904137	61921142	3467
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AVP	chr20	-	3063202	3065370	619
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	COL20A1	chr20	+	61924538	61966203	8097
ENSG00000(	29.00217	38.53721	31.66593	113.8595	84.67974	95.34793	-1.5485	1.87E-06	7.52E-06	EEF1A2	chr20	-	62119366	62130505	1843
ENSG00000(	29.00217	20.47289	21.11062	15.73059	18.40864	34.52253	0.043718	0.93164	0.9589	PTK6	chr20	-	62159778	62168723	2495
ENSG00000(	579.0077	533.4995	468.3919	536.3381	596.4399	633.735	-0.15764	0.28894	0.41256	GMEB2	chr20	-	62218955	62258394	4559
ENSG00000(	2126.481	1812.453	1665.1	1476.428	1011.555	1183.629	0.60793	6.50E-05	0.000217	C20orf27	chr20	-	3734155	3749034	1886
ENSG00000(	6.214751	9.634302	7.916483	7.490755	3.681728	4.109825	0.55956	0.49789	0.62625	SPEF1	chr20	-	3758151	3762095	1925
ENSG00000(	8349.519	7837.504	7052.267	925.8574	883.6147	808.8135	3.1442	1.72E-164	3.37E-162	CDC25B	chr20	+	3767578	3786762	3594
ENSG00000(	81.82756	107.1816	68.60952	93.63444	99.40666	85.48435	-0.10945	0.69281	0.7905	ISM1	chr20	+	13202418	13281298	2592
ENSG00000(	476.4643	474.4894	605.6109	163.2985	164.7573	143.8439	1.7133	2.12E-22	2.37E-21	RNF24	chr20	-	3912068	3996229	3341
ENSG00000(	691.909	670.7883	573.945	558.8104	558.7022	641.9546	0.13917	0.33393	0.46203	ARFRP1	chr20	-	62329996	62339355	2965
ENSG00000(	205.0868	178.2346	182.0791	228.468	161.996	209.6011	-0.08613	0.6789	0.77985	NDUFAF5	chr20	+	13765596	13799067	2409
ENSG00000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	SEL1L2	chr20	-	13829893	13977089	2348
ENSG00000(	275.5206	270.9647	242.7721	725.1051	436.2848	506.3304	-1.0741	3.63E-08	1.74E-07	TRIB3	chr20	+	361261	378203	2499
ENSG00000(	46.61064	44.55865	36.94359	567.0502	629.5755	603.3223	-3.7818	1.31E-73	6.04E-72	RASSF2	chr20	-	4760669	4804291	5427
ENSG00000(	2353.319	2342.34	2524.039	3034.505	3073.322	2764.268	-0.29704	0.006087	0.014831	CSNK2A1	chr20	-	459116	524482	4416
ENSG00000(	0	0	0	5.243529	0.920432	0	-1.642	0.22589	0.33863	SLC52A3	chr20	-	740724	749131	3060
ENSG00000(	0	1.204288	3.958241	0	1.840864	0.821965	0.5701	0.6678	0.77106	RPS10L	chr20	-	820090	820620	531
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	ANGPT4	chr20	-	853296	896977	1922
ENSG00000(	0	2.408575	0	5.992604	1.840864	0.821965	-1.2152	0.34357	0.4728	RSPO4	chr20	-	939095	982907	2707
ENSG00000(	834.8483	935.7316	1059.489	1232.229	1220.493	1013.483	-0.2929	0.036262	0.073418	CDS2	chr20	+	5107432	5178533	9298
ENSG00000(	5231.785	5294.049	4860.72	4201.565	2880.952	3362.658	0.55716	4.31E-05	0.000148	HM13	chr20	+	30102231	30157370	1992
ENSG00000(	150.1898	145.7188	154.3714	51.68621	31.29469	49.3179	1.7412	3.22E-10	1.83E-09	SNPH	chr20	+	1246960	1289972	5533
ENSG00000(	7.250543	6.021439	7.916483	20.22504	20.2495	16.4393	-1.3422	0.035752	0.072498	MYLK2	chr20	+	30407111	30422492	2956

ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	SIRPB1	chr20	-	1544167	1600707	3241
ENSG00000(	758.1997	735.8198	808.8006	1570.062	1323.581	1058.691	-0.77745	3.14E-07	1.38E-06	SEC23B	chr20	+	18488137	18542059	3411
ENSG00000(	35.21692	36.12863	10.55531	567.0502	529.2484	530.1674	-4.2445	3.60E-62	1.32E-60	FERMT1	chr20	-	6055492	6104191	5151
ENSG00000(	0	0	0	0.749076	4.60216	1.64393	-1.9321	0.1526	0.24764	XKR7	chr20	+	30555805	30586256	2910
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	HAO1	chr20	-	7863628	7921121	1777
ENSG00000(	0	0	0	1.498151	6.443024	0	-1.9753	0.14478	0.23706	CCM2L	chr20	+	30598245	30619984	2596
ENSG00000(	35.21692	42.15007	48.81831	189.5161	213.5402	153.7074	-2.1265	7.82E-15	6.11E-14	PLCB4	chr20	+	9049410	9461889	5833
ENSG00000(	1430.429	1147.686	1231.013	3324.397	3769.169	4446.83	-1.5943	2.53E-31	4.02E-30	MYL9	chr20	+	35169887	35178228	1199
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	HCK	chr20	+	30639991	30689659	2217
ENSG00000(	2481.757	2469.994	2551.746	1531.859	1491.1	1301.17	0.79362	4.29E-12	2.81E-11	TM9SF4	chr20	+	30697309	30755061	4032
ENSG00000(	2.071584	9.634302	2.638828	0	0.920432	0.821965	2.2159	0.063596	0.11946	TLDC2	chr20	+	35504524	35522638	2083
ENSG00000(	407.0662	449.1993	456.5172	564.803	633.2572	503.0425	-0.37312	0.014035	0.03159	CRNKL1	chr20	-	20015012	20036690	4406
ENSG00000(	2004.257	1838.947	1976.482	1423.244	1378.807	1435.151	0.45706	3.45E-05	0.00012	POFUT1	chr20	+	30795683	30826470	5235
ENSG00000(	341.8113	337.2006	349.6447	117.6049	116.8949	111.7872	1.5634	1.14E-17	1.04E-16	SAMHD1	chr20	-	35518632	35580246	4784
ENSG00000(	0	0	0	1.498151	2.761296	3.28786	-2.0751	0.1224	0.20728	PAK7	chr20	-	9518036	9819689	4780
ENSG00000(	1839.566	1818.474	1893.359	836.7174	924.1137	802.2378	1.1133	2.80E-21	2.99E-20	KIF3B	chr20	+	30865467	30922814	6103
ENSG00000(	21.75163	21.67718	25.06886	41.94823	29.45382	32.05663	-0.58403	0.18735	0.29203	MROH8	chr20	-	35729629	35807991	3425
ENSG00000(	2415.467	2344.748	2050.369	6009.833	4638.057	5244.958	-1.2197	4.36E-22	4.80E-21	NOP56	chr20	+	2632791	2639039	2400
ENSG00000(	719.8754	765.927	659.7069	903.3851	796.1737	973.2065	-0.31619	0.021202	0.045728	MANBAL	chr20	+	35918041	35945663	1915
ENSG00000(	1252.272	1130.826	1067.406	1343.092	1271.117	1497.62	-0.25177	0.046627	0.091342	IDH3B	chr20	-	2639041	2644865	1620
ENSG00000(	2104.729	1984.666	2229.809	4989.592	4518.401	4345.729	-1.1308	2.56E-24	3.09E-23	MAPRE1	chr20	+	31407699	31438211	2623
ENSG00000(	640.1194	587.6924	657.0681	1299.646	1781.956	1186.917	-1.1747	1.37E-13	9.95E-13	JAG1	chr20	-	10618332	10654694	5987
ENSG00000(	315.9165	332.3834	259.9245	632.9688	570.6678	651.8182	-1.0257	7.28E-11	4.36E-10	CDK5RAP1	chr20	-	31946645	31989367	2650
ENSG00000(	556.2203	561.1981	481.586	110.1141	107.6905	104.3895	2.3023	1.79E-40	3.76E-39	SNTA1	chr20	-	31995761	32031698	2342
ENSG00000(	285.8786	270.9647	310.0622	764.0571	687.5627	590.1708	-1.2328	8.83E-15	6.88E-14	TTI1	chr20	-	36611409	36661870	3958
ENSG00000(	155.3688	97.54731	102.9143	739.3376	651.6659	747.9881	-2.5663	1.30E-41	2.82E-40	E2F1	chr20	-	32263489	32274210	2503
ENSG00000(	349.0619	376.9421	424.8512	659.1865	567.9065	599.2124	-0.66676	1.02E-05	3.79E-05	RPRD1B	chr20	+	36661948	36720768	3874
ENSG00000(	14.50109	18.06432	6.597069	8.239831	21.16994	16.4393	-0.19995	0.75458	0.83769	PXMP4	chr20	-	32294512	32308125	1732
ENSG00000(	2129.588	2050.902	1745.584	1948.346	1859.273	2077.105	0.010579	0.93025	0.95814	CHMP4B	chr20	+	32399110	32442172	1646
ENSG00000(	0	3.612863	1.319414	0	0	0	1.6005	0.2346	NA	BPI	chr20	+	36888551	36965907	2857
ENSG00000(	11875.35	11407.01	8270.086	3364.847	2392.203	2443.702	1.9372	9.95E-35	1.77E-33	CST3	chr20	-	23608534	23619110	2095
ENSG00000(	1.035792	6.021439	7.916483	4.494453	3.681728	7.397684	-0.06982	0.94063	0.96418	ASIP	chr20	+	32782375	32857150	610
ENSG00000(	119.1161	105.9773	118.7472	207.4939	160.1552	187.408	-0.68767	0.001937	0.005174	ACTR5	chr20	+	37377085	37400834	2236
ENSG00000(	0	0	0	364.7998	334.1168	390.4333	-8.9919	1.42E-21	1.54E-20	WFDC2	chr20	+	44098346	44110172	818
ENSG00000(	3708.135	3506.886	3415.962	5140.156	4408.869	4512.587	-0.40279	0.000244	0.000751	AHCY	chr20	-	32868074	32899608	2366
ENSG00000(	0	2.408575	0	1.498151	0.920432	0.821965	-0.23946	0.85934	NA	PPP1R16B	chr20	+	37434348	37551667	6251
ENSG00000(	254.8048	220.3847	245.411	1371.557	974.7375	1016.771	-2.2141	2.85E-40	5.93E-39	FAM83D	chr20	+	37554955	37581703	2429
ENSG00000(	184.371	209.5461	236.1751	216.4828	191.4499	202.2034	0.042449	0.82721	0.88863	DHX35	chr20	+	37590942	37668366	3325
ENSG00000(	418.4599	350.4477	356.2417	592.5188	567.9065	600.8564	-0.64284	1.47E-05	5.36E-05	DNTTIP1	chr20	+	44420576	44440066	1290
ENSG00000(	695.0164	617.7996	522.4879	121.3502	133.4626	144.6658	2.1931	1.04E-35	1.90E-34	MAP1LC3A	chr20	+	33134658	33148149	1574
ENSG00000(	38.3243	48.17151	36.94359	129.5901	114.1336	120.8288	-1.5452	1.04E-07	4.78E-07	SYNDIG1	chr20	+	24449835	24647252	2522
ENSG00000(	564.5066	606.961	480.2666	652.4448	431.6826	440.5732	0.1142	0.52935	0.65409	PIGU	chr20	-	33148346	33264910	1632
ENSG00000(	0	6.021439	1.319414	0	4.60216	0	0.43918	0.73661	0.82369	TNNC2	chr20	-	44451853	44462384	780
ENSG00000(	272.4133	258.9219	207.148	232.2134	208.0176	221.9305	0.15846	0.40178	0.53295	ACOT8	chr20	-	44470360	44486045	3059

ENSG00000(	2671.307	2620.53	2564.94	2420.263	2290.955	2340.956	0.15565	0.13332	0.22195	APMAP	chr20	-	24943561	24973615	2430
ENSG00000(	5.17896	6.021439	2.638828	4.494453	7.363456	1.64393	0.043357	0.9639	0.97911	CELF4	chr18	-	34823010	35146000	4052
ENSG00000(	1132.121	1171.772	1461.91	404.5008	582.6335	441.3952	1.3943	1.22E-17	1.10E-16	ZNF516	chr18	-	74069644	74207146	8619
ENSG00000(	0	12.04288	2.638828	5.243529	3.681728	2.465895	0.28792	0.78409	0.85786	CDH20	chr18	+	59000815	59223006	3882
ENSG00000(	422.6031	443.1779	555.4732	843.4591	931.4772	811.2794	-0.86297	7.86E-09	3.98E-08	ADNP2	chr18	+	77866915	77905406	5393
ENSG00000(	193.6931	191.4817	162.2879	136.3317	131.6218	148.7757	0.39275	0.060942	0.11512	RBFA	chr18	+	77794358	77806397	1587
ENSG00000(	1295.776	1183.815	1351.08	2473.447	2042.439	2015.458	-0.76854	1.38E-09	7.49E-09	USP14	chr18	+	158383	214622	4914
ENSG00000(	2396.822	2178.556	2312.932	2983.568	2473.201	2467.539	-0.20189	0.09146	0.16297	VAPA	chr18	+	9913999	9960018	6815
ENSG00000(	162.6193	137.2888	170.2044	202.9995	183.166	192.3398	-0.29866	0.14388	0.2358	METTL4	chr18	-	2537524	2571508	5190
ENSG00000(	776.8439	832.1628	968.4497	377.5341	450.0912	393.7212	1.0743	3.65E-13	2.58E-12	LPIN2	chr18	-	2916992	3013313	6229
ENSG00000(	905.2821	769.5399	1258.721	885.4073	1074.144	817.0331	0.078452	0.65445	0.75998	SMCHD1	chr18	+	2655737	2805015	8821
ENSG00000(	31.07376	22.88147	42.22124	14.98151	7.363456	28.76877	0.86675	0.1065	0.18471	MYOM1	chr18	-	3066805	3220106	5847
ENSG00000(	2063.297	2034.042	2068.841	3550.618	3117.503	3707.884	-0.7497	2.36E-11	1.47E-10	MYL12A	chr18	+	3247479	3256234	1229
ENSG00000(	38.3243	44.55865	42.22124	180.5272	137.1444	133.9803	-1.8357	8.85E-11	5.26E-10	CEP76	chr18	-	12661832	12702776	3309
ENSG00000(	16.57267	10.83859	19.79121	46.44268	18.40864	29.59074	-0.96926	0.066018	0.1234	ST8SIA5	chr18	-	44259081	44339220	2716
ENSG00000(	374.9567	379.3506	448.6007	467.4231	658.1089	422.49	-0.36206	0.04912	0.095586	CEP192	chr18	+	12991361	13125051	8635
ENSG00000(	680.5153	645.4982	804.8424	555.8141	556.8614	468.52	0.42827	0.004033	0.010181	RNMT	chr18	+	13726659	13764557	6250
ENSG00000(	158.4762	126.4502	197.9121	368.5452	441.8074	406.0507	-1.328	1.26E-11	7.94E-11	SMAD7	chr18	-	46446223	46477081	3087
ENSG00000(	127.4024	138.4931	167.5656	250.1912	364.4911	327.964	-1.116	1.20E-07	5.46E-07	LIPG	chr18	+	47087069	47119276	4161
ENSG00000(	261.0196	317.932	407.6989	1056.197	1369.603	1091.569	-1.8298	3.72E-26	4.82E-25	LAMA1	chr18	-	6941743	7117813	10374
ENSG00000(	55.93276	71.05298	64.65128	80.15108	46.0216	54.24968	0.078996	0.81202	0.8781	RNF125	chr18	+	29598335	29653176	6020
ENSG00000(	529.2897	616.5953	690.0534	292.8885	265.0844	287.6877	1.1121	2.52E-12	1.68E-11	ANKRD12	chr18	+	9136226	9285206	10459
ENSG00000(	0	0	1.319414	0.749076	14.72691	6.575719	-2.8796	0.016283	0.036066	NOL4	chr18	-	31431064	31804916	3957
ENSG00000(	568.6498	555.1766	630.6798	379.0322	372.775	342.7594	0.67793	3.52E-06	1.37E-05	POLI	chr18	+	51795774	51847636	6131
ENSG00000(	1268.845	1301.835	1931.622	986.5325	1215.891	848.2678	0.55879	0.001404	0.00384	MIB1	chr18	+	19284918	19450918	9576
ENSG00000(	183.3352	160.1703	196.5927	886.9054	729.9026	673.1893	-2.0772	3.08E-34	5.39E-33	RBBP8	chr18	+	20378224	20606451	3293
ENSG00000(	861.7789	1042.913	884.0072	762.5589	668.2336	592.6367	0.46074	0.001556	0.004223	RIOK3	chr18	+	21032787	21066567	4038
ENSG00000(	249.6258	234.8361	263.8828	635.9651	599.2012	656.75	-1.3348	1.07E-18	1.02E-17	CSTF2	chrX	+	1E+08	1E+08	2305
ENSG00000(	9648.402	9586.13	12307.49	733.345	1112.802	738.9465	3.5975	2.58E-112	2.37E-110	MXRA5	chrX	-	3226606	3264682	9793
ENSG00000(	2.071584	0	0	0	0	2.465895	-0.09123	0.94581	NA	VSIG1	chrX	+	1.07E+08	1.07E+08	3236
ENSG00000(	657.7279	639.4768	684.7758	643.4559	512.6806	587.7049	0.18282	0.19916	0.30675	PSMD10	chrX	-	1.07E+08	1.07E+08	1546
ENSG00000(	125.3308	116.8159	110.8308	185.0217	152.7917	161.1051	-0.4954	0.025486	0.053885	ATG4A	chrX	+	1.07E+08	1.07E+08	2501
ENSG00000(	205.0868	215.5675	236.1751	295.8848	303.7426	252.3432	-0.37504	0.038926	0.078131	STS	chrX	+	7137497	7272851	6521
ENSG00000(	1140.407	1086.268	1285.109	994.0233	1058.497	822.7869	0.28755	0.037494	0.075651	TBL1X	chrX	+	9431335	9687780	5866
ENSG00000(	5.17896	3.612863	5.277655	205.9958	142.667	168.5028	-5.0355	3.04E-27	4.12E-26	GPR143	chrX	-	9693386	9754337	1762
ENSG00000(	4290.25	4188.513	4204.972	2749.856	2345.261	2471.649	0.74378	7.22E-12	4.64E-11	PGRMC1	chrX	+	1.18E+08	1.18E+08	1911
ENSG00000(	174.013	138.4931	170.2044	486.15	494.272	424.1339	-1.5332	5.89E-18	5.42E-17	POLA1	chrX	+	24712036	25015103	5486
ENSG00000(	625.6183	578.0581	712.4834	2713.152	2956.428	2506.171	-2.0893	9.79E-60	3.38E-58	MID1	chrX	-	10413350	10851773	6463
ENSG00000(	333.525	362.4906	320.6175	358.0581	337.7985	303.3051	0.024839	0.87907	0.92447	NKAP	chrX	-	1.19E+08	1.19E+08	2345
ENSG00000(	0	0	0	0.749076	6.443024	0	-1.8192	0.17996	0.28279	RHOXF1	chrX	-	1.19E+08	1.19E+08	769
ENSG00000(	120.1519	143.3102	150.4132	113.8595	110.4518	94.52597	0.37061	0.11752	0.20041	NXT2	chrX	+	1.09E+08	1.09E+08	2692
ENSG00000(	0	3.612863	1.319414	0	0	0	1.6005	0.2346	NA	GUCY2F	chrX	-	1.09E+08	1.09E+08	3714
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	ATP1B4	chrX	+	1.19E+08	1.2E+08	3868
ENSG00000(	20.71584	18.06432	10.55531	17.97781	21.16994	20.54912	-0.25258	0.64196	0.74952	RP3-324O1	chr20	+	30135307	30135852	546

ENSG0000(	557.256	484.1237	572.6256	438.2092	377.3771	402.7628	0.40348	0.007406	0.017738	ALG13	chrX	+	1.11E+08	1.11E+08	4071
ENSG0000(	333.525	317.932	287.6322	582.0317	497.0333	424.1339	-0.67523	6.86E-05	0.000228	PRPS2	chrX	+	12809474	12842341	2511
ENSG0000(	239.2679	223.9975	230.8974	259.9292	258.6414	189.8739	-0.02865	0.88309	0.92688	MOSPD1	chrX	-	1.34E+08	1.34E+08	2364
ENSG0000(	180.2278	169.8046	279.7157	369.2942	361.7298	286.0438	-0.69129	0.001216	0.003364	AMMECR1	chrX	-	1.09E+08	1.1E+08	5504
ENSG0000(	109.7939	80.68728	98.95603	41.19916	35.89685	38.63235	1.305	2.13E-05	7.59E-05	CHRDL1	chrX	-	1.1E+08	1.1E+08	3935
ENSG0000(	1021.291	1027.257	873.4519	903.3851	594.5991	759.4956	0.37026	0.020765	0.044852	WDR13	chrX	+	48448430	48463581	2612
ENSG0000(	149.154	97.54731	101.5949	385.0248	261.4027	378.1039	-1.5406	1.89E-11	1.18E-10	SUV39H1	chrX	+	48553945	48567403	2871
ENSG0000(	0	0	0	17.22874	24.85166	8.219649	-4.9005	1.32E-05	4.84E-05	PAGE4	chrX	+	49593863	49598576	1494
ENSG0000(	3017.262	2964.956	2685.007	986.5325	844.9566	781.6886	1.7257	7.12E-43	1.61E-41	SRPX	chrX	-	38008589	38080696	1874
ENSG0000(	1.035792	0	2.638828	14.98151	12.88605	9.041614	-2.8402	0.003083	0.007945	GLRA2	chrX	+	14547420	14749934	3216
ENSG0000(	1063.758	1139.256	1290.387	831.4739	832.991	804.7037	0.49857	8.99E-05	0.000295	XIAP	chrX	+	1.23E+08	1.23E+08	8591
ENSG0000(	899.0674	1035.687	1190.111	1021.739	1247.185	923.0666	-0.0311	0.83764	0.89625	STAG2	chrX	+	1.23E+08	1.24E+08	6045
ENSG0000(	682.5869	622.6168	922.2702	338.5821	381.9793	328.786	1.0811	2.12E-10	1.22E-09	ATP11C	chrX	-	1.39E+08	1.39E+08	6924
ENSG0000(	0	0	0	0	1.840864	3.28786	-1.4188	0.29365	NA	MCF2	chrX	-	1.39E+08	1.39E+08	3945
ENSG0000(	174.013	136.0845	141.1773	70.4131	110.4518	83.01846	0.77373	0.002583	0.006749	ABCD1	chrX	+	1.53E+08	1.53E+08	3664
ENSG0000(	225.8026	232.4275	180.7597	301.8774	232.8693	286.0438	-0.3587	0.06468	0.12117	CCDC22	chrX	+	49091927	49106987	2319
ENSG0000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	CACNA1F	chrX	-	49061523	49089833	6070
ENSG0000(	25.8948	33.72006	15.83297	10.48706	24.85166	27.12484	0.2711	0.60977	0.7236	SYP	chrX	-	49044269	49056718	2486
ENSG0000(	1647.945	1584.843	1279.831	435.962	273.3683	332.8958	2.104	4.19E-35	7.52E-34	PLP2	chrX	+	49028273	49031588	1079
ENSG0000(	3618.021	3647.788	4274.901	5603.085	5642.248	5037.823	-0.49606	1.31E-05	4.78E-05	PLS3	chrX	+	1.15E+08	1.15E+08	3327
ENSG0000(	287.9501	308.2977	208.4674	336.3349	217.222	335.3617	-0.14248	0.50842	0.63588	NAA10	chrX	-	1.53E+08	1.53E+08	1772
ENSG0000(	4.143168	4.817151	0	6.74168	3.681728	8.219649	-0.87159	0.37985	0.5105	RENBP	chrX	-	1.53E+08	1.53E+08	1388
ENSG0000(	739.5554	620.2082	691.3728	451.6926	400.3879	374.816	0.73903	6.49E-07	2.74E-06	ELF4	chrX	-	1.29E+08	1.29E+08	4165
ENSG0000(	2678.558	2450.726	2834.101	1665.944	1793.002	1512.415	0.67854	1.07E-08	5.38E-08	SMARCA1	chrX	-	1.29E+08	1.29E+08	4099
ENSG0000(	2.071584	0	9.235896	9.737982	12.88605	4.93179	-1.1309	0.2267	0.33967	MTMR8	chrX	-	63444187	63615333	2639
ENSG0000(	31.07376	34.92434	39.58241	26.21764	34.97642	25.48091	0.27776	0.50597	0.63359	ASB9	chrX	-	15253410	15288589	1947
ENSG0000(	8.286335	10.83859	3.958241	35.95563	58.90765	55.07165	-2.5787	7.59E-07	3.19E-06	ZC3H12B	chrX	+	64708615	64727767	7256
ENSG0000(	1471.86	1430.694	1426.286	2663.713	2128.039	2395.206	-0.73017	1.61E-09	8.65E-09	RBBP7	chrX	-	16857406	16888537	4031
ENSG0000(	200.9436	109.5902	116.1084	71.16218	79.15715	90.41614	0.8223	0.003843	0.009742	KCND1	chrX	-	48818639	48827976	4437
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	UBE2NL	chrX	+	1.43E+08	1.43E+08	1183
ENSG0000(	321.0955	348.0392	286.3128	208.243	182.2455	194.8057	0.70357	8.60E-05	0.000283	SLC25A14	chrX	+	1.29E+08	1.3E+08	1621
ENSG0000(	561.3992	519.048	568.6673	2468.953	3269.374	2717.416	-2.352	1.35E-67	5.62E-66	FMR1	chrX	+	1.47E+08	1.47E+08	4333
ENSG0000(	104.615	107.1816	89.72014	184.2726	129.7809	185.7641	-0.72345	0.002903	0.007515	PIM2	chrX	-	48770459	48776301	2075
ENSG0000(	40.39588	46.96722	64.65128	96.63075	104.9292	80.55256	-0.88746	0.004165	0.010486	SCML2	chrX	-	18257434	18372847	4200
ENSG0000(	1028.541	967.043	996.1574	764.0571	787.8898	848.2678	0.3175	0.010148	0.02356	SLC35A2	chrX	-	48760459	48769235	2619
ENSG0000(	773.7366	773.1527	704.567	712.3708	620.3712	872.1048	0.030033	0.84278	0.89968	PQBP1	chrX	+	48755195	48760420	1428
ENSG0000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RS1	chrX	-	18658030	18690229	2810
ENSG0000(	809.9893	686.444	556.7926	208.243	160.1552	183.2982	1.8869	1.41E-25	1.78E-24	PCSK1N	chrX	-	48689504	48694035	1050
ENSG0000(	1628.265	1539.08	1345.802	1361.819	1433.113	1535.43	0.060371	0.62487	0.73629	EMD	chrX	+	1.54E+08	1.54E+08	1379
ENSG0000(	185.4068	150.536	133.2608	253.1875	207.0972	247.4114	-0.5862	0.004965	0.012306	TAZ	chrX	+	1.54E+08	1.54E+08	2286
ENSG0000(	1.035792	0	1.319414	0	0.920432	0	0.55201	0.67753	NA	RAB40AL	chrX	+	1.02E+08	1.02E+08	1029
ENSG0000(	14044.3	14706.76	12796.99	7463.04	6340.856	6880.668	1.0045	5.46E-20	5.52E-19	PGK1	chrX	+	77320685	77384793	4887
ENSG0000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	GATA1	chrX	+	48644962	48652718	1497
ENSG0000(	1926.573	1924.452	2049.05	1439.723	1516.872	1256.784	0.48482	4.84E-05	0.000165	MAGT1	chrX	-	77081861	77151090	4047

ENSG00000(	1705.949	1736.583	1646.628	8045.071	6722.835	6907.793	-2.087	1.40E-76	7.05E-75	SMS	chrX	+	21958691	22025798	1837
ENSG00000(	50.7538	45.76293	38.263	4.494453	11.04518	1.64393	2.8639	3.85E-07	1.67E-06	PHEX	chrX	+	22050559	22269427	6172
ENSG00000(	330.4176	370.9206	361.5194	749.8246	683.881	705.2459	-1.0077	1.50E-12	1.01E-11	UBL4A	chrX	-	1.54E+08	1.54E+08	2382
ENSG00000(	2435.147	2229.137	2240.365	318.3571	404.9901	313.9906	2.7303	6.03E-91	3.91E-89	CD99L2	chrX	-	1.5E+08	1.5E+08	4935
ENSG00000(	472.3211	484.1237	688.734	428.4712	485.0677	387.9674	0.33521	0.057846	0.11027	EEA1	chr12	-	93164413	93323107	9875
ENSG00000(	0	0	0	7.490755	4.60216	4.93179	-3.3096	0.008127	0.019276	GPR50	chrX	+	1.5E+08	1.5E+08	1951
ENSG00000(	431.9252	392.5978	387.9077	420.9805	472.1816	387.9674	-0.07744	0.61895	0.73133	RP2	chrX	+	46696375	46741793	3803
ENSG00000(	128.4382	113.203	145.1355	384.2758	382.8997	308.2368	-1.4692	7.65E-14	5.62E-13	PHF16	chrX	+	46771711	46920641	4931
ENSG00000(	2968.58	2746.98	2413.208	3355.109	3195.74	3143.194	-0.25314	0.02802	0.058541	CDK16	chrX	+	47077259	47089396	3158
ENSG00000(	1538.151	1369.275	1340.524	1105.636	976.5783	916.4909	0.50149	9.21E-05	0.000302	USP11	chrX	+	47092089	47107727	3515
ENSG00000(	117.0445	105.9773	141.1773	142.3244	158.3143	144.6658	-0.28953	0.20502	0.31356	PCYT1B	chrX	-	24576204	24690794	5307
ENSG00000(	1050.293	962.2259	1026.504	1167.809	1179.994	1077.596	-0.17205	0.15262	0.24765	HTATSF1	chrX	+	1.36E+08	1.36E+08	3019
ENSG00000(	0	0	0	489.1463	428.9213	420.0241	-9.2521	3.25E-23	3.74E-22	VGLL1	chrX	+	1.36E+08	1.36E+08	1215
ENSG00000(	8386.807	8280.682	6525.821	1603.771	1087.03	1391.587	2.4981	1.12E-63	4.27E-62	TIMP1	chrX	+	47441712	47446188	1415
ENSG00000(	1058.579	1145.278	1366.913	246.4459	245.7553	169.3248	2.4223	3.81E-46	9.37E-45	KLHL4	chrX	+	86772752	86925050	5818
ENSG00000(	102.5434	126.4502	67.2901	23.97042	34.05598	13.15144	2.0243	1.25E-07	5.66E-07	GABRE	chrX	-	1.51E+08	1.51E+08	6176
ENSG00000(	0	0	1.319414	45.69361	95.72493	50.13986	-6.0409	3.70E-11	2.26E-10	PCDH11X	chrX	+	91034260	91878229	9176
ENSG00000(	1122.798	1166.955	1062.128	611.2456	722.5391	678.943	0.73521	1.19E-08	5.92E-08	FGD1	chrX	-	54471887	54522599	4275
ENSG00000(	469.2137	480.5108	411.6571	276.4089	407.7514	599.2124	0.085709	0.69872	0.79519	PIN4	chrX	+	71401203	71522776	1780
ENSG00000(	242.3753	203.5246	211.1062	49.43899	29.45382	38.63235	2.4522	2.76E-21	2.95E-20	PORCN	chrX	+	48367350	48379202	2112
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	ITIH6	chrX	-	54775332	54824673	4968
ENSG00000(	7135.57	7131.792	6561.445	3836.765	3377.065	3167.031	1.0029	4.01E-19	3.90E-18	MAGED2	chrX	+	54834032	54842445	2189
ENSG00000(	4780.18	5268.759	4321.08	4378.347	3771.01	4410.664	0.19381	0.10219	0.17852	RBM3	chrX	+	48432837	48437454	2162
ENSG00000(	0	0	0	256.1838	285.3339	267.1386	-8.6149	2.41E-19	2.38E-18	KLF8	chrX	+	56258854	56314322	8964
ENSG00000(	1709.057	1717.314	1865.651	80.15108	41.41944	49.3179	4.9147	6.83E-156	1.11E-153	SRPX2	chrX	+	99899215	99926296	2138
ENSG00000(	374.9567	388.9849	356.2417	44.94453	60.74851	55.07165	2.7902	9.88E-41	2.09E-39	SYTL4	chrX	-	99929488	99987110	4847
ENSG00000(	0	12.04288	1.319414	41.19916	24.85166	23.83698	-2.5445	0.000539	0.001575	ZDHHC15	chrX	-	74588262	74743337	6012
ENSG00000(	132.5814	125.2459	172.8432	459.1833	509.9193	484.9593	-1.7515	6.16E-22	6.74E-21	CENPI	chrX	+	1E+08	1E+08	3262
ENSG00000(	40.39588	21.67718	56.73479	11.98521	20.2495	16.4393	1.247	0.011031	0.025407	DRP2	chrX	+	1E+08	1.01E+08	7277
ENSG00000(	0	7.225726	0	6.74168	6.443024	9.041614	-1.3305	0.20304	0.31105	TAF7L	chrX	-	1.01E+08	1.01E+08	2341
ENSG00000(	418.4599	329.9748	325.8952	542.3307	500.715	475.9177	-0.49557	0.002162	0.005726	PBDC1	chrX	+	75392771	75398039	1201
ENSG00000(	684.6584	626.2296	573.945	940.0898	999.5891	992.1117	-0.63417	1.34E-06	5.49E-06	GLA	chrX	-	1.01E+08	1.01E+08	1318
ENSG00000(	1824.03	1981.053	2162.519	767.8024	945.2837	997.0434	1.1361	4.00E-17	3.53E-16	ARMCX3	chrX	+	1.01E+08	1.01E+08	3730
ENSG00000(	280.6996	332.3834	286.3128	480.9065	510.8398	570.4437	-0.79407	6.29E-07	2.67E-06	BEX4	chrX	+	1.02E+08	1.02E+08	1328
ENSG00000(	6.214751	1.204288	3.958241	17.22874	32.21512	16.4393	-2.3097	0.001454	0.003962	KIAA0226L	chr13	-	46916139	47012325	3975
ENSG00000(	25.8948	24.08575	35.62417	16.47966	13.80648	13.9734	0.91206	0.067934	0.12651	NALCN	chr13	-	1.02E+08	1.02E+08	6816
ENSG00000(	45.57484	36.12863	32.98534	0	0	0	6.5002	6.43E-10	3.58E-09	FGF14	chr13	-	1.02E+08	1.03E+08	3902
ENSG00000(	88.04231	93.93444	141.1773	0	0	0	7.8567	2.77E-15	2.23E-14	HTR2A	chr13	-	47407513	47471169	3564
ENSG00000(	599.7235	561.1981	679.4981	862.935	960.931	791.5522	-0.50604	0.000351	0.001057	NDFIP2	chr13	+	80055287	80130210	4625
ENSG00000(	3.107376	4.817151	5.277655	0.749076	4.60216	4.109825	0.40463	0.69113	0.7894	TNFSF13B	chr13	+	1.09E+08	1.09E+08	2582
ENSG00000(	1388.997	1460.801	1840.582	1410.509	1633.767	1394.053	0.078939	0.56756	0.68671	FNDC3A	chr13	+	49550048	49783915	6286
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	MLNR	chr13	+	49794474	49796513	1390
ENSG00000(	146.0467	162.5788	124.0249	70.4131	55.22592	79.7306	1.0634	4.58E-05	0.000156	CDADC1	chr13	+	49822047	49867618	3383
ENSG00000(	217.5163	120.4288	183.3985	318.3571	283.4931	253.9872	-0.70804	0.00148	0.004026	CAB39L	chr13	-	49882786	50018262	3676

ENSG0000(	133.6172	143.3102	110.8308	595.5151	480.4655	449.6148	-1.9645	5.07E-25	6.27E-24	KLF5	chr13	+	73629114	73651676	3562
ENSG0000(	1007.826	865.8829	1052.892	2968.586	2753.012	2532.474	-1.4929	5.73E-33	9.60E-32	STK24	chr13	-	99102455	99230194	4345
ENSG0000(	5.17896	0	9.235896	7.490755	12.88605	8.219649	-0.87623	0.31844	0.44545	ACP5	chr19	-	11685475	11689823	1699
ENSG0000(	1021.291	1082.655	965.8109	807.5034	912.1481	743.8783	0.31742	0.016365	0.036223	DNAJC3	chr13	+	96329393	96447243	5591
ENSG0000(	701.2311	768.3356	977.6856	533.3418	471.2612	394.5432	0.80171	1.61E-06	6.54E-06	UGGT2	chr13	-	96453834	96705736	4832
ENSG0000(	1785.705	1754.647	1987.037	1274.178	1368.682	1181.164	0.53038	9.42E-06	3.51E-05	ARHGEF7	chr13	+	1.12E+08	1.12E+08	5525
ENSG0000(	5.17896	2.408575	6.597069	20.22504	23.0108	33.70056	-2.2877	0.000524	0.001535	FGF9	chr13	+	22245522	22278637	4220
ENSG0000(	2.071584	16.86003	13.19414	20.97412	24.85166	20.54912	-1.0032	0.11593	0.19821	SGCG	chr13	+	23755091	23899304	1624
ENSG0000(	945.678	885.1515	1130.738	1157.322	1088.871	872.1048	-0.07499	0.6144	0.72768	PARP4	chr13	-	24995064	25086948	5474
ENSG0000(	652.5489	603.3481	762.6212	1129.606	935.1589	912.3811	-0.56042	0.000124	0.0004	SUPT20H	chr13	-	37583449	37633850	3811
ENSG0000(	256.8764	214.3632	187.3568	452.4416	297.2995	381.3917	-0.77439	0.000123	0.000395	MRPS31	chr13	-	41303432	41345309	1293
ENSG0000(	171.9415	166.1917	176.8014	286.1469	373.6954	328.786	-0.93542	5.82E-07	2.47E-06	SLC25A15	chr13	+	41363548	41384247	1586
ENSG0000(	709.5175	782.787	924.9091	1314.628	1157.903	1078.418	-0.55508	9.71E-05	0.000318	KPNA3	chr13	-	50273447	50367057	4470
ENSG0000(	284.8428	223.9975	303.4652	377.5341	416.9557	295.9074	-0.42235	0.026971	0.056657	FLT1	chr13	-	28874489	29069265	7084
ENSG0000(	986.0739	1042.913	821.9948	272.6635	203.4155	228.5062	2.0076	1.43E-35	2.59E-34	RGCC	chr13	+	42031695	42045018	960
ENSG0000(	279.6638	255.309	333.8117	319.1062	372.775	279.4681	-0.16077	0.3824	0.51309	VWA8	chr13	-	42140973	42535256	7147
ENSG0000(	122.2234	96.34302	162.2879	49.43899	80.99802	58.35951	1.0028	0.000721	0.00207	DGKH	chr13	+	42614176	42830714	4422
ENSG0000(	446.4263	364.8992	489.5025	485.401	453.773	361.6646	-0.0007	0.99676	0.99808	KATNAL1	chr13	-	30776767	30881621	7551
ENSG0000(	447.4621	415.4793	506.6549	408.9952	393.9449	332.8958	0.26803	0.095686	0.1691	INTS6	chr13	-	51928213	52028400	3767
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	IRG1	chr13	+	77522632	77532777	2165
ENSG0000(	72.50543	87.913	77.84541	96.63075	66.2711	91.23811	-0.09631	0.73599	0.82343	DHRS12	chr13	-	52342129	52378293	1970
ENSG0000(	0	0	0	5.992604	0	0.821965	-1.772	0.19153	0.29714	MEDAG	chr13	+	31480328	31499709	2374
ENSG0000(	4178.385	4039.181	4402.884	674.9171	755.6747	632.913	2.6085	7.03E-112	6.40E-110	TSC22D1	chr13	-	45007655	45151283	4820
ENSG0000(	561.3992	627.4339	663.6651	328.0951	365.4115	296.7293	0.9005	5.03E-09	2.60E-08	CLN5	chr13	+	77564795	77576652	4064
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	OLFM4	chr13	+	53602894	53626192	2897
ENSG0000(	3.107376	13.24716	3.958241	1.498151	4.60216	3.28786	0.95955	0.31508	0.44164	MSLN	chr16	+	810762	818865	2418
ENSG0000(	2023.937	2046.085	1903.914	1787.294	1785.638	2082.037	0.07917	0.49714	0.62558	MGRN1	chr16	+	4666494	4740975	6425
ENSG0000(	597.6519	585.2838	662.3457	255.4348	595.5195	381.3917	0.58034	0.010082	0.023427	ZNF629	chr16	-	30789778	30798523	6079
ENSG0000(	305.5586	337.2006	257.2857	107.1178	131.6218	140.556	1.2425	1.08E-09	5.91E-09	TRADD	chr16	-	67188083	67194201	1877
ENSG0000(	24.85901	48.17151	23.74945	1.498151	3.681728	7.397684	2.7735	1.68E-05	6.06E-05	HSF4	chr16	+	67197288	67203848	2604
ENSG0000(	183.3352	168.6003	134.5802	46.44268	33.13555	67.40112	1.7051	4.45E-09	2.31E-08	CORO1A	chr16	+	30194148	30200397	2891
ENSG0000(	1859.246	1894.345	1519.965	746.8283	704.1305	707.7118	1.286	2.70E-23	3.12E-22	MAPK3	chr16	-	30125426	30134827	2567
ENSG0000(	42.46747	69.84869	42.22124	28.46487	19.32907	25.48091	1.0461	0.010556	0.024403	GDPD3	chr16	-	30116131	30125177	1397
ENSG0000(	41.43168	67.44011	38.263	85.39461	66.2711	94.52597	-0.73319	0.027842	0.058223	ELMO3	chr16	+	67233014	67237932	2531
ENSG0000(	496.1443	441.9736	492.1413	1161.816	921.3524	882.7903	-1.0494	2.44E-12	1.62E-11	PHKB	chr16	+	47495034	47735434	5603
ENSG0000(	435.0326	414.275	381.3106	436.711	400.3879	399.475	-0.0062	0.9673	0.98074	LYRM1	chr16	+	20911190	20936328	1695
ENSG0000(	689.8374	637.0682	593.7362	666.6772	1000.51	901.6955	-0.41624	0.010328	0.023939	NUTF2	chr16	+	67880635	67906470	2321
ENSG0000(	681.5511	629.8425	708.5252	2117.637	1690.834	1720.373	-1.4497	3.22E-27	4.36E-26	NUP93	chr16	+	56764017	56880792	2875
ENSG0000(	732.3049	791.217	563.3897	1062.938	851.3996	980.6041	-0.46999	0.002429	0.006376	CENPT	chr16	-	67862060	67881714	2957
ENSG0000(	45.57484	39.74149	58.05421	24.71949	22.09037	32.05663	0.83882	0.036094	0.073121	TSNAXIP1	chr16	+	67840668	67866051	2517
ENSG0000(	1366.21	1712.497	1886.762	576.7882	1722.128	1197.603	0.49217	0.26837	0.38867	NFAT5	chr16	+	69598997	69738569	14219
ENSG0000(	1136.264	1188.632	1212.541	1206.012	1004.191	900.0516	0.1844	0.17842	0.28093	LONP2	chr16	+	48278207	48397033	8199
ENSG0000(	656.6921	783.9913	742.83	735.5922	708.7326	675.6552	0.041414	0.75861	0.84043	N4BP1	chr16	-	48572637	48654059	7106
ENSG0000(	59.04014	66.23582	81.80365	73.4094	105.8497	134.8022	-0.59585	0.050351	0.097732	CBLN1	chr16	-	49311828	49315742	2435

ENSG00000(	274.4849	322.7491	372.0747	407.4971	283.4931	309.8808	-0.05001	0.79435	0.86553	ARL2BP	chr16	+	57279010	57287516	2099
ENSG00000(	0	0	0	0	0.920432	4.93179	-1.5674	0.24723	NA	PLLP	chr16	-	57290004	57318599	1517
ENSG00000(	857.6357	703.304	845.7442	410.4934	518.2032	392.0773	0.86429	3.58E-08	1.72E-07	ZNF423	chr16	-	49521435	49891830	7660
ENSG00000(	236.1606	240.8575	189.9956	311.6154	254.0392	357.5547	-0.46556	0.016976	0.037468	DHODH	chr16	+	72042487	72058954	2209
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CCL17	chr16	+	57438679	57449974	615
ENSG00000(	672.2289	557.5852	624.0827	1040.466	1053.895	982.2481	-0.72817	3.39E-08	1.63E-07	CTCF	chr16	+	67596310	67673086	3939
ENSG00000(	305.5586	308.2977	222.9809	540.0835	411.4331	470.1639	-0.75953	2.86E-05	0.0001	ACD	chr16	-	67691415	67694713	2526
ENSG00000(	784.0945	792.4213	745.4688	1731.863	1334.626	1651.328	-1.0205	3.66E-14	2.75E-13	POLR2C	chr16	+	57496299	57505922	2057
ENSG00000(	7.250543	8.430014	6.597069	53.93344	38.65814	47.67397	-2.5541	7.36E-07	3.09E-06	PARD6A	chr16	+	67694849	67696681	1281
ENSG00000(	160.5477	157.7617	105.5531	117.6049	130.7013	123.2947	0.1932	0.42244	0.55293	ZNF821	chr16	-	71893583	71929239	1954
ENSG00000(	307.6302	304.6848	282.3545	1577.553	1701.879	1687.494	-2.4658	4.12E-81	2.27E-79	MMP15	chr16	+	58059470	58080805	4250
ENSG00000(	615.2604	575.6495	539.6402	1606.018	1483.736	1440.083	-1.3842	3.92E-28	5.53E-27	USB1	chr16	+	58033450	58055522	3888
ENSG00000(	1692.484	1810.044	1671.697	3259.228	2844.135	2834.135	-0.78733	4.61E-12	3.01E-11	CYB5B	chr16	+	69458428	69500169	4358
ENSG00000(	15.53688	12.04288	15.83297	47.19176	28.53339	49.3179	-1.4802	0.001894	0.005066	CCDC113	chr16	+	58265061	58317740	5272
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	PRSS54	chr16	-	58313901	58328951	1810
ENSG00000(	497.1801	429.9307	329.8534	245.6968	161.996	199.7375	1.0426	3.89E-07	1.68E-06	NME3	chr16	-	1820287	1821731	1069
ENSG00000(	411.2094	434.7479	439.3648	154.3096	190.5294	216.1768	1.1919	2.74E-11	1.69E-10	NDRG4	chr16	+	58496750	58547532	5116
ENSG00000(	679.4795	623.821	726.997	1300.395	1152.381	1180.342	-0.8384	8.10E-11	4.83E-10	PSMD7	chr16	+	74330673	74340186	1670
ENSG00000(	92.18548	68.6444	102.9143	167.0438	199.7337	212.0669	-1.1254	2.94E-06	1.16E-05	SETD6	chr16	+	58549383	58554431	2769
ENSG00000(	721.947	796.0342	725.6776	713.1199	740.9478	690.4505	0.065129	0.61402	0.72738	SLC38A7	chr16	-	58699013	58719008	4549
ENSG00000(	773.7366	740.6369	701.9281	1118.37	1020.759	1152.395	-0.56894	6.38E-06	2.42E-05	VAC14	chr16	-	70721342	70835064	3609
ENSG00000(	32.10955	25.29004	21.11062	75.65663	115.054	105.2115	-1.8699	8.41E-08	3.89E-07	HAS3	chr16	+	69139467	69152622	4220
ENSG00000(	249.6258	163.7831	242.7721	188.767	187.7681	178.3664	0.24116	0.2541	0.37218	TANGO6	chr16	+	68877507	69119083	4816
ENSG00000(	1152.836	1257.276	1109.627	1265.938	960.931	923.0666	0.15907	0.27405	0.39516	COG4	chr16	-	70514471	70557468	3488
ENSG00000(	22.78742	21.67718	22.43003	19.47596	15.64734	45.20807	-0.25546	0.62288	0.73468	SMPD3	chr16	-	68392231	68482591	5450
ENSG00000(	98.40023	103.5687	108.1919	128.0919	121.497	108.4994	-0.20742	0.38863	0.5193	SLC7A6OS	chr16	-	68318406	68344849	4180
ENSG00000(	282.7712	252.9004	339.0893	277.158	369.0932	262.2068	-0.054	0.78099	0.85574	SLC7A6	chr16	+	68298433	68335722	6308
ENSG00000(	462.999	385.3721	395.8241	219.4791	192.3703	212.0669	0.99206	5.64E-09	2.90E-08	PLA2G15	chr16	+	68279207	68294961	3121
ENSG00000(	7.250543	1.204288	9.235896	785.7803	864.2856	1026.634	-7.0926	2.19E-76	1.10E-74	ESRP2	chr16	-	68263014	68272005	3793
ENSG00000(	0	0	0	3.745378	3.681728	1.64393	-2.3426	0.077905	0.14208	FA2H	chr16	-	74746853	74808729	2424
ENSG00000(	695.0164	769.5399	654.4292	612.7438	559.6227	547.4286	0.30018	0.029907	0.062005	WDR59	chr16	-	74907468	75034071	3695
ENSG00000(	625.6183	572.0367	616.1662	725.8542	821.9458	690.4505	-0.30177	0.028041	0.05857	MON1B	chr16	+	77224732	77236302	6091
ENSG00000(	139.8319	116.8159	102.9143	397.7591	250.3575	331.2519	-1.4331	1.38E-10	8.10E-10	CMC2	chr16	-	81009698	81053875	2087
ENSG00000(	753.0207	721.3683	629.3604	873.4221	877.1717	837.5823	-0.29695	0.024202	0.051492	AXIN1	chr16	-	337440	402673	6340
ENSG00000(	1694.556	1622.176	1327.33	478.6593	399.4675	536.7431	1.7092	2.93E-30	4.49E-29	HCFC1R1	chr16	-	3072621	3074287	1365
ENSG00000(	1429.393	1460.801	1191.431	992.5251	783.2876	829.3626	0.64582	4.04E-06	1.57E-05	NPRL3	chr16	-	134273	188859	3008
ENSG00000(	80.79177	90.32158	71.24834	120.6012	138.9852	149.5976	-0.74665	0.002996	0.007742	MLYCD	chr16	+	83932731	83949787	4489
ENSG00000(	855.5641	810.4856	716.4417	417.9842	445.4891	408.5166	0.90448	1.10E-10	6.50E-10	MPG	chr16	+	127006	135852	1205
ENSG00000(	16.57267	15.65574	5.277655	13.48336	1.840864	13.15144	0.36225	0.63121	0.74124	NECAB2	chr16	+	84002237	84036381	2064
ENSG00000(	498.2159	432.3393	465.7531	391.7665	431.6826	410.9825	0.1786	0.23041	0.3438	HSDL1	chr16	-	84155886	84178797	3519
ENSG00000(	692.9448	665.9711	569.9868	587.2752	554.1001	640.3107	0.11519	0.42179	0.55232	TAF1C	chr16	-	84211458	84220669	4637
ENSG00000(	262.0554	309.5019	273.1187	172.2874	161.0756	206.3132	0.64185	0.000768	0.002195	NAGPA	chr16	-	5074845	5084142	3286
ENSG00000(	7.250543	0	3.958241	2.996302	0	1.64393	0.92076	0.444	0.57364	WFDC1	chr16	+	84328252	84363450	4177
ENSG00000(	4.143168	0	0	2.247227	0	0.821965	0.25195	0.8517	0.90543	SEC14L5	chr16	+	5008318	5069159	6459

ENSG00000(	9875.24	8983.986	8527.371	17202.52	14182.02	14457.54	-0.74179	1.32E-10	7.76E-10	COTL1	chr16	-	84599200	84651683	5330
ENSG00000(	909.4253	898.3986	808.8006	1837.482	1729.492	1420.355	-0.92772	5.85E-12	3.79E-11	USP10	chr16	+	84733584	84813528	3070
ENSG00000(	632.8689	593.7138	604.2915	71.91125	67.19154	55.07165	3.2215	1.41E-69	6.09E-68	CRISPLD2	chr16	+	84853590	84954374	4584
ENSG00000(	2345.033	2209.868	2022.661	1389.535	1445.999	1435.973	0.62232	4.17E-08	1.99E-07	TSC2	chr16	+	2097466	2138716	6156
ENSG00000(	336.6324	348.0392	291.5904	378.2832	279.8113	345.2253	-0.03981	0.82198	0.88508	ZNF500	chr16	-	4798240	4817625	5880
ENSG00000(	4468.406	4388.424	3504.363	2018.759	1730.412	1911.89	1.1242	7.83E-19	7.52E-18	NME4	chr16	+	446725	460367	1861
ENSG00000(	1063.758	1081.45	1133.376	690.6477	746.4703	604.9662	0.68158	2.24E-07	9.96E-07	ABCC1	chr16	+	16043434	16236931	6594
ENSG00000(	111.8655	114.4073	196.5927	83.89646	132.5422	109.3213	0.37058	0.18725	0.29194	NOMO3	chr16	+	16326352	16388668	4353
ENSG00000(	732.3049	663.5625	616.1662	280.9033	295.4587	327.964	1.1516	2.36E-14	1.79E-13	LMF1	chr16	-	903634	1031318	3358
ENSG00000(	24.85901	34.92434	46.17948	8.988907	9.20432	4.93179	2.0986	0.000118	0.000379	FOXF1	chr16	+	86544133	86548076	2568
ENSG00000(	348.0261	320.3405	319.2981	429.9694	491.5107	588.5269	-0.60881	0.000264	0.00081	NARFL	chr16	-	779753	791329	3212
ENSG00000(	251.6974	263.739	317.9787	316.859	259.5618	286.0438	-0.05275	0.7697	0.84862	MTHFSD	chr16	-	86563782	86588841	3623
ENSG00000(	863.8504	887.56	847.0636	534.8399	537.5323	631.2691	0.60757	6.35E-06	2.41E-05	CLCN7	chr16	-	1494935	1525581	4720
ENSG00000(	239.2679	246.879	226.9392	126.5938	78.23672	102.7456	1.2002	9.58E-08	4.40E-07	HAGHL	chr16	+	776936	785525	2199
ENSG00000(	203.0152	250.4918	167.5656	358.0581	327.6738	325.4981	-0.69874	0.000237	0.000732	FAM173A	chr16	+	770581	772601	1686
ENSG00000(	2572.907	2474.811	2100.507	16028.72	14587.01	16057.91	-2.7017	2.12E-125	2.35E-123	SLC7A5	chr16	-	87863629	87903094	4537
ENSG00000(	1716.307	1451.167	1141.293	733.345	675.5971	780.0447	0.97469	2.32E-10	1.34E-09	METRN	chr16	+	765115	769655	3325
ENSG00000(	630.7973	563.6067	588.4585	376.0359	343.3211	316.4565	0.78104	1.64E-07	7.37E-07	FBXO31	chr16	-	87360593	87425748	5934
ENSG00000(	1374.496	1126.009	955.2556	786.5293	822.8662	1087.46	0.35752	0.030152	0.062457	STUB1	chr16	+	730224	732799	1853
ENSG00000(	43.50326	81.89156	29.0271	34.45748	18.40864	60.8254	0.42635	0.36075	0.4903	RHBDL1	chr16	+	725666	728268	1566
ENSG00000(	114.9729	133.6759	122.7055	104.1215	134.3831	152.0635	-0.07158	0.76739	0.84668	NUBP1	chr16	+	10837643	10863208	1228
ENSG00000(	2254.919	2162.901	1868.29	2408.278	2462.156	2766.734	-0.27976	0.020342	0.044031	UBE2I	chr16	+	1355548	1377019	3253
ENSG00000(	1.035792	2.408575	2.638828	5.243529	0	0.821965	-0.0224	0.98554	0.99136	MEFV	chr16	-	3292028	3306627	3710
ENSG00000(	2.071584	4.817151	0	7.490755	3.681728	13.15144	-1.5196	0.12407	0.20939	CRYM	chr16	-	21250195	21314404	1507
ENSG00000(	1277.131	1246.438	1170.32	576.7882	572.5087	635.3789	1.0476	5.71E-17	4.99E-16	EEF2K	chr16	+	22217603	22298554	5289
ENSG00000(	1049.257	1057.365	778.4541	1388.786	1537.121	1596.256	-0.64521	6.08E-06	2.31E-05	SOLH	chr16	+	577717	604636	4744
ENSG00000(	1849.924	1678.777	1564.825	2538.617	3042.948	3323.204	-0.80333	7.54E-10	4.17E-09	PIEZO1	chr16	-	88781751	88851619	8072
ENSG00000(	2603.981	2554.294	2890.836	5215.064	4446.607	3998.859	-0.76183	1.03E-09	5.66E-09	GSPT1	chr16	-	11961985	12009939	7105
ENSG00000(	120.1519	122.8373	133.2608	154.3096	133.4626	137.2681	-0.17731	0.42767	0.55787	ZNF174	chr16	+	3451235	3459370	2260
ENSG00000(	251.6974	273.3733	237.4945	199.2541	186.8477	158.6392	0.48283	0.01156	0.026486	CLUAP1	chr16	+	3550924	3589048	5126
ENSG00000(	2462.077	2055.719	2574.176	1927.371	2058.086	1952.167	0.25586	0.034394	0.070082	UBFD1	chr16	+	23568392	23585710	5110
ENSG00000(	584.1866	569.6281	497.419	704.131	807.2189	646.8864	-0.38342	0.008855	0.02083	EARS2	chr16	-	23533335	23569052	3961
ENSG00000(	2810.103	2532.617	2025.3	2016.511	1470.85	1948.057	0.4376	0.003947	0.009987	TCEB2	chr16	-	2821415	2827298	997
ENSG00000(	1245.022	1254.868	1190.111	1285.414	1221.413	1203.357	-0.00779	0.94588	0.96733	GGA2	chr16	-	23474863	23533316	5973
ENSG00000(	0	2.408575	1.319414	0	0	3.28786	0.089264	0.9473	0.9682	AQP8	chr16	+	25227052	25240261	1359
ENSG00000(	286.9144	289.0291	320.6175	567.7993	363.5706	351.801	-0.51679	0.009515	0.022243	CPPED1	chr16	-	12756919	12897874	3010
ENSG00000(	168.8341	150.536	241.4527	298.1321	366.3319	263.8507	-0.72495	0.000805	0.002292	USP31	chr16	-	23072727	23160591	10699
ENSG00000(	989.1813	805.6685	744.1494	1671.188	1330.945	1481.181	-0.81685	1.65E-08	8.17E-08	HMOX2	chr16	+	4524691	4560348	2147
ENSG00000(	1105.19	1047.73	1067.406	1370.059	1284.923	1513.237	-0.37146	0.002208	0.005839	DNAJA3	chr16	+	4475806	4506776	3351
ENSG00000(	1256.416	1304.244	1349.76	1561.823	1439.556	1337.337	-0.15022	0.20706	0.31625	BFAR	chr16	+	14726672	14763093	3039
ENSG00000(	688.8016	608.1653	628.041	562.5557	694.9262	600.0344	0.053065	0.71169	0.80522	SALL1	chr16	-	51169886	51185278	5253
ENSG00000(	1.035792	1.204288	3.958241	20.22504	11.96562	5.753754	-2.3054	0.010955	0.025246	TOX3	chr16	-	52471917	52581714	3414
ENSG00000(	0	2.408575	0	2.996302	0	0.821965	-0.36191	0.78935	0.8622	RRN3P2	chr16	+	29086163	29128039	2132
ENSG00000(	569.6855	519.048	653.1098	389.5193	453.773	352.623	0.54081	0.000738	0.002115	RBL2	chr16	+	53467889	53525561	4906

ENSG0000(	3240.993	3219.061	3124.372	2193.293	1718.447	2013.814	0.69197	7.95E-09	4.02E-08	QPRT	chr16	+	29690329	29710020	2343
ENSG0000(	1324.778	1117.579	1744.265	110.8632	103.0884	101.1017	3.7141	1.12E-95	7.98E-94	XYLT1	chr16	-	17195626	17564738	9891
ENSG0000(	14.50109	28.90291	18.47179	20.97412	16.56778	35.34449	-0.23297	0.65692	0.76183	PYCARD	chr16	-	31212806	31214771	1137
ENSG0000(	452.6411	446.7907	486.8637	227.719	299.1404	257.275	0.82059	7.86E-07	3.29E-06	RPGRIP1L	chr16	-	53631595	53737850	8195
ENSG0000(	482.679	461.2422	324.5758	773.046	576.1904	426.5998	-0.48137	0.021532	0.046338	MAZ	chr16	+	29817427	29823649	2698
ENSG0000(	827.5977	788.8085	566.0285	402.2536	345.162	520.3038	0.78067	2.54E-05	8.97E-05	STX4	chr16	+	31044210	31054296	1588
ENSG0000(	1830.244	1687.207	1530.52	1153.576	1004.191	1098.145	0.63148	3.81E-07	1.65E-06	CDIPT	chr16	-	29869678	29875057	2353
ENSG0000(	1589.941	1518.607	1162.404	1173.801	714.2552	747.1661	0.69305	0.000156	0.000494	BCKDK	chr16	+	31117428	31124110	2558
ENSG0000(	425.7105	437.1564	390.5465	721.3598	607.4851	628.8032	-0.64136	1.17E-05	4.31E-05	KAT8	chr16	+	31127075	31142714	2500
ENSG0000(	2730.347	2435.07	2805.074	1791.04	1631.926	1465.563	0.70362	7.56E-09	3.84E-08	NOMO1	chr16	+	14927538	14990017	4355
ENSG0000(	1.035792	0	7.916483	0	1.840864	0	1.3995	0.28807	0.41168	IL21R	chr16	+	27413483	27462115	3365
ENSG0000(	1.035792	4.817151	0	71.16218	49.70333	46.852	-4.4795	6.93E-11	4.15E-10	SYT17	chr16	+	19179293	19279652	5092
ENSG0000(	12.4295	2.408575	5.277655	101.8743	78.23672	82.19649	-3.541	1.47E-13	1.07E-12	TMC5	chr16	+	19421818	19510435	4917
ENSG0000(	321.0955	301.0719	383.9494	591.7697	757.5155	644.4205	-0.9839	1.40E-09	7.55E-09	CCP110	chr16	+	19535133	19564730	5549
ENSG0000(	1119.691	979.0859	1039.698	868.1786	783.2876	790.7303	0.36116	0.004342	0.010884	C16orf62	chr16	+	19566562	19718115	3855
ENSG0000(	0	0	0	19.47596	15.64734	18.90519	-5.0433	5.16E-06	1.98E-05	SLC6A2	chr16	+	55689516	55740104	3551
ENSG0000(	2682.701	2460.36	2320.849	2126.625	2391.282	2791.393	0.030591	0.81165	0.87789	RNF40	chr16	+	30773066	30787628	5634
ENSG0000(	210.2658	152.9445	179.4403	483.9028	517.2828	549.0726	-1.5048	7.95E-18	7.27E-17	KNOP1	chr16	-	19714902	19729557	4786
ENSG0000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	AQP9	chr15	+	58430368	58478110	3034
ENSG0000(	639.0836	535.908	600.3333	1032.226	1129.37	1169.656	-0.90482	1.11E-11	7.02E-11	AAGAB	chr15	-	67493371	67547533	2841
ENSG0000(	16.57267	14.45145	19.79121	19.47596	12.88605	10.68554	0.22121	0.70227	0.7976	IQCH	chr15	+	67547138	67794598	4208
ENSG0000(	166.7625	169.8046	170.2044	226.2208	241.1532	201.3814	-0.39781	0.040521	0.080967	LACTB	chr15	+	63413999	63434260	2023
ENSG0000(	1038.899	961.0216	1155.806	203.7485	134.3831	111.7872	2.7919	3.62E-48	9.46E-47	CORO2B	chr15	+	68871308	69020145	3611
ENSG0000(	1339.279	1276.545	1146.571	2191.046	2160.254	2054.09	-0.76543	4.19E-11	2.55E-10	CSK	chr15	+	75074398	75095539	2767
ENSG0000(	741.627	674.4011	911.7149	588.7734	828.3888	576.1974	0.22314	0.19469	0.30095	HERC1	chr15	-	63900817	64126141	15137
ENSG0000(	427.7821	364.8992	416.9348	473.4157	367.2524	468.52	-0.11456	0.4861	0.61524	TRIP4	chr15	+	64679947	64747502	2045
ENSG0000(	187.4783	163.7831	133.2608	277.158	182.2455	205.4912	-0.45197	0.046296	0.090776	MTFMT	chr15	-	65294845	65321977	1739
ENSG0000(	7.250543	1.204288	0	22.47227	22.09037	18.08323	-2.5449	0.001206	0.003337	RASL12	chr15	-	65345679	65369028	2636
ENSG0000(	12.4295	10.83859	11.87472	26.96672	27.61296	39.45432	-1.3642	0.008722	0.020558	AP3B2	chr15	-	83328033	83378666	3736
ENSG0000(	2.071584	4.817151	5.277655	2.247227	4.60216	0	0.65458	0.55563	0.67625	ACSBG1	chr15	-	78459810	78538030	6357
ENSG0000(	2168.948	2115.934	2261.475	92.13629	116.8949	83.84042	4.4744	3.51E-199	9.81E-197	IGDCC4	chr15	-	65673802	65715410	6508
ENSG0000(	1899.642	1920.839	2361.751	3592.566	3139.594	3189.224	-0.68173	4.55E-08	2.16E-07	RAB11A	chr15	+	66018392	66184329	4930
ENSG0000(	64.2191	78.2787	62.01245	62.17327	60.74851	80.55256	0.006825	0.98212	0.98984	CTSH	chr15	-	79213400	79241916	2190
ENSG0000(	0	3.612863	3.958241	0	0	0.821965	1.7382	0.19455	0.30076	GOLGA8UP	chr15	+	31083776	31094062	1755
ENSG0000(	400.8515	414.275	374.7135	235.2097	226.4263	219.4646	0.80213	8.13E-07	3.40E-06	TTC23	chr15	-	99676528	99791428	3849
ENSG0000(	4881.687	4435.392	4774.958	4172.351	4191.647	4458.338	0.13609	0.18597	0.29052	CD276	chr15	+	73976307	74006859	3469
ENSG0000(	618.3678	705.7126	562.0703	388.7702	316.6286	361.6646	0.81814	1.75E-07	7.82E-07	FAH	chr15	+	80444832	80479288	3427
ENSG0000(	3151.915	2821.646	5021.689	10.48706	32.21512	25.48091	7.1059	2.08E-50	5.79E-49	KIAA1199	chr15	+	81071684	81244117	7357
ENSG0000(	630.7973	639.4768	604.2915	1023.986	1079.667	1033.21	-0.74066	2.33E-09	1.24E-08	RPAP1	chr15	-	41809374	41836467	5897
ENSG0000(	71.46964	71.05298	59.37362	77.90386	68.11197	76.44274	-0.13699	0.63892	0.74707	HOMER2	chr15	-	83509838	83654661	6201
ENSG0000(	701.2311	591.3053	563.3897	1265.189	1441.397	1429.397	-1.1511	1.99E-17	1.78E-16	EHD4	chr15	-	42190950	42264776	3603
ENSG0000(	450.5695	482.9194	502.6967	417.9842	386.5814	304.127	0.37086	0.025067	0.053094	TMEM87A	chr15	-	42502730	42565861	3109
ENSG0000(	3040.049	3016.741	3799.912	1020.99	1291.366	974.0284	1.5806	8.95E-29	1.30E-27	ZNF106	chr15	-	42705021	42783321	10460
ENSG0000(	133.6172	139.6974	143.8161	242.7005	246.6758	198.0935	-0.71757	0.000441	0.001305	CEP152	chr15	-	49005125	49103343	5635

ENSG00000(	0	0	1.319414	9.737982	34.97642	12.32947	-4.3137	3.48E-05	0.000121	ATP8B4	chr15	-	50150435	50475014	5783
ENSG00000(	101.5076	77.07441	98.95603	11.23613	8.283888	13.15144	3.0146	9.90E-15	7.69E-14	OCA2	chr15	-	28000021	28344504	3186
ENSG00000(	235.1248	280.599	270.4798	364.0507	273.3683	269.6045	-0.20823	0.26935	0.38973	DTWD1	chr15	+	49913177	49937333	2680
ENSG00000(	0	0	0	5.992604	0	0	-1.4779	0.2718	0.39245	TGM5	chr15	-	43524793	43559055	2767
ENSG00000(	120.1519	139.6974	154.3714	172.2874	135.3035	147.9537	-0.14122	0.5317	0.65633	FAM189A1	chr15	-	29412457	29862927	4705
ENSG00000(	404.9946	355.2649	434.0871	704.131	620.3712	606.6101	-0.69208	4.12E-06	1.60E-05	GABPB1	chr15	-	50569389	50647605	3016
ENSG00000(	1832.316	1801.614	2572.857	2340.861	2389.441	1988.333	-0.11461	0.44122	0.57099	TJP1	chr15	-	29991571	30261068	7950
ENSG00000(	84.93494	98.75159	69.92893	140.8262	223.665	163.571	-1.0437	5.99E-05	0.000201	BMF	chr15	-	40380091	40401093	4687
ENSG00000(	262.0554	295.0505	403.7406	148.317	215.3811	164.393	0.85788	7.73E-05	0.000256	DMXL2	chr15	-	51739908	51915030	10672
ENSG00000(	0	1.204288	2.638828	99.62705	104.9292	101.1017	-5.8757	1.50E-16	1.28E-15	SCG3	chr15	+	51973550	52013223	3310
ENSG00000(	157.4404	155.3531	122.7055	211.2393	160.1552	183.2982	-0.34572	0.11504	0.1969	DNAJC17	chr15	-	41060067	41099675	1341
ENSG00000(	1205.662	1329.534	1319.414	2547.606	2106.869	2187.249	-0.82687	1.30E-11	8.23E-11	EIF3J	chr15	+	44829255	44855227	2569
ENSG00000(	768.5576	783.9913	948.6585	554.3159	624.9733	519.4818	0.55608	0.000132	0.000423	SPG11	chr15	-	44854894	44955876	7774
ENSG00000(	6.214751	16.86003	10.55531	53.18436	63.50981	74.79881	-2.4483	1.02E-07	4.68E-07	RHOV	chr15	-	41164412	41166487	1705
ENSG00000(	804.8103	620.2082	758.6629	1148.333	1193.8	1033.21	-0.62586	7.87E-06	2.96E-05	VPS18	chr15	+	41186628	41196173	3895
ENSG00000(	41.43168	22.88147	36.94359	255.4348	176.7229	225.2184	-2.6643	1.20E-20	1.25E-19	OIP5	chr15	-	41601466	41624819	1236
ENSG00000(	146.0467	119.2245	146.4549	60.67512	57.06678	59.18147	1.2069	2.94E-06	1.16E-05	SLC30A4	chr15	-	45771809	45815005	7157
ENSG00000(	1076.188	1112.762	1150.529	856.1934	758.436	683.8748	0.53685	4.73E-05	0.000162	BLOC1S6	chr15	+	45879321	45908197	4037
ENSG00000(	34.18113	28.90291	52.77655	624.729	777.765	595.9246	-4.0919	4.18E-71	1.85E-69	MYEF2	chr15	-	48431625	48470714	5563
ENSG00000(	51.7896	32.51577	50.13772	149.066	138.0648	114.2531	-1.5576	1.08E-07	4.95E-07	SGK3	chr8	+	67624653	67774257	4135
ENSG00000(	567.614	437.1564	372.0747	75.65663	57.98722	69.86702	2.7388	5.15E-37	9.76E-36	PDGFRL	chr8	+	17433942	17501580	1905
ENSG00000(	265.1627	299.8676	253.3274	220.9773	261.4027	207.1352	0.24761	0.17994	0.28279	CSPP1	chr8	+	67974661	68108498	4367
ENSG00000(	135.6887	172.2131	186.0373	580.5336	499.7946	514.55	-1.6894	2.18E-21	2.34E-20	ZDHHC2	chr8	+	17013538	17082308	6377
ENSG00000(	114.9729	136.0845	138.5384	96.63075	120.5766	123.2947	0.1922	0.42143	0.55206	BRF2	chr8	-	37700786	37707422	2603
ENSG00000(	514.7886	539.5209	571.3062	451.6926	471.2612	528.5234	0.16231	0.26219	0.38162	TRIM35	chr8	-	27142404	27168836	4229
ENSG00000(	402.9231	437.1564	323.2564	550.5705	369.0932	434.8194	-0.21869	0.23755	0.35228	ZFAND1	chr8	-	82613569	82645138	2719
ENSG00000(	0	0	0	0.749076	0	3.28786	-1.135	0.39451	NA	RP1	chr8	+	55528627	55543394	7100
ENSG00000(	17.60846	7.225726	19.79121	101.1252	85.60018	106.0335	-2.6569	1.26E-11	7.96E-11	CA2	chr8	+	86376081	86393722	1717
ENSG00000(	71.46964	85.50443	94.99779	487.6482	573.4291	420.846	-2.5472	9.02E-36	1.65E-34	FZD3	chr8	+	28351729	28431775	13726
ENSG00000(	254.8048	185.4603	303.4652	484.6519	404.0696	397.0091	-0.78767	5.14E-05	0.000175	INTS9	chr8	-	28625178	28747759	2759
ENSG00000(	199.9078	189.0732	184.7179	477.9102	353.4459	383.0357	-1.0772	4.18E-09	2.17E-08	RIPK2	chr8	+	90769975	90803291	2584
ENSG00000(	37.28851	49.3758	64.65128	268.9181	302.8221	240.0138	-2.4151	4.11E-22	4.54E-21	EYA1	chr8	-	72109668	72274467	4326
ENSG00000(	499.2517	535.908	649.1516	606.7512	519.1236	512.9061	0.03698	0.81167	0.87789	NBN	chr8	-	90945564	91015456	4907
ENSG00000(	1.035792	3.612863	1.319414	7.490755	0	2.465895	-0.56538	0.63287	0.74266	TRPA1	chr8	-	72932152	72987852	5223
ENSG00000(	528.2539	494.9623	492.1413	309.3682	271.5274	286.0438	0.80265	1.40E-07	6.32E-07	CPQ	chr8	+	97657455	98161882	1947
ENSG00000(	864.8862	920.0758	746.7882	347.5711	316.6286	323.8542	1.3535	1.14E-20	1.19E-19	DECR1	chr8	+	91013633	91064320	1766
ENSG00000(	6.214751	7.225726	1.319414	4.494453	0.920432	4.93179	0.42821	0.67035	0.77309	CALB1	chr8	-	91070836	91107703	5392
ENSG00000(	1618.943	1728.153	2027.939	1547.59	1648.494	1389.943	0.22799	0.077639	0.14167	IMPAD1	chr8	-	57870492	57906403	7199
ENSG00000(	4054.09	3757.378	5003.217	7173.897	7811.706	6367.762	-0.73515	2.00E-08	9.78E-08	SFRP1	chr8	-	41119481	41167016	4488
ENSG00000(	4171.134	4135.524	3921.298	4620.298	3598.889	3714.459	0.034929	0.77422	0.85182	LAPTM4B	chr8	+	98787285	98865241	3173
ENSG00000(	250.6616	320.3405	349.6447	355.8109	337.7985	340.2935	-0.17016	0.33161	0.45954	UBE2W	chr8	-	74692332	74791145	8426
ENSG00000(	378.064	354.0606	406.3794	633.7179	642.4615	532.6333	-0.66629	1.17E-05	4.29E-05	POP1	chr8	+	99129525	99172062	4719
ENSG00000(	261.0196	332.3834	324.5758	116.1067	87.44104	69.04505	1.7347	2.55E-14	1.93E-13	NIPAL2	chr8	-	99202061	99306621	4581
ENSG00000(	773.7366	676.8097	766.5794	436.711	368.1728	473.4518	0.79112	1.24E-07	5.63E-07	IKBKB	chr8	+	42128820	42189973	5002

ENSG00000(	3353.894	2978.204	3105.9	579.0354	549.4979	650.1743	2.4027	9.35E-89	5.73E-87	PLAT	chr8	-	42032236	42065242	3462
ENSG00000(	17.60846	27.69862	14.51355	219.4791	242.0736	163.571	-3.3353	1.41E-25	1.79E-24	JPH1	chr8	-	75146935	75233563	4378
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	DKK4	chr8	-	42231586	42234750	894
ENSG00000(	250.6616	274.5776	292.9099	526.6001	482.3064	378.1039	-0.76024	1.63E-05	5.91E-05	STK3	chr8	-	99413631	99955055	5333
ENSG00000(	101.5076	96.34302	113.4696	276.4089	295.4587	266.3166	-1.4224	1.90E-12	1.28E-11	GDAP1	chr8	+	75233365	75401107	3666
ENSG00000(	2423.753	2237.567	2529.316	1953.589	1878.602	1741.744	0.36661	0.001176	0.003261	RAB2A	chr8	+	61429416	61536186	3848
ENSG00000(	7881.341	8557.669	7416.425	6718.459	4814.78	5084.675	0.52014	0.00011	0.000357	EIF3E	chr8	-	1.09E+08	1.09E+08	1990
ENSG00000(	357.3482	401.0278	415.6153	510.1204	457.4547	489.8911	-0.31323	0.037486	0.075647	EMC2	chr8	+	1.09E+08	1.09E+08	2734
ENSG00000(	0	0	0	1498.9	1594.188	1332.405	-10.773	1.61E-34	2.85E-33	ESRP1	chr8	+	95653302	95719694	3770
ENSG00000(	131.5456	73.46155	125.3443	2.247227	0.920432	0	6.1667	3.47E-20	3.54E-19	WISP1	chr8	+	1.34E+08	1.34E+08	3844
ENSG00000(	4609.274	4947.214	4051.92	241.2023	247.5962	267.1386	4.1613	1.48E-235	6.45E-233	NDRG1	chr8	-	1.34E+08	1.34E+08	3983
ENSG00000(	96.32865	128.8588	182.0791	89.13999	88.36147	70.68898	0.70145	0.012321	0.028061	ZC2HC1A	chr8	+	79578282	79629935	1287
ENSG00000(	54.89697	65.03154	91.03955	104.8706	47.86246	59.18147	-0.01632	0.96309	0.97854	IL7	chr8	-	79587978	79717758	2076
ENSG00000(	583.1508	557.5852	614.8468	2423.259	1824.296	1613.517	-1.7342	4.08E-29	5.99E-28	STMN2	chr8	+	80523049	80578410	2223
ENSG00000(	505.4664	556.3809	496.0996	807.5034	710.5735	593.4587	-0.43761	0.004419	0.011061	ARMC1	chr8	-	66514694	66546442	3029
ENSG00000(	1162.159	1138.052	1566.144	287.645	427.0804	319.7444	1.8956	1.73E-27	2.38E-26	TRPS1	chr8	-	1.16E+08	1.17E+08	9990
ENSG00000(	2.071584	0	1.319414	195.5087	218.1424	161.1051	-6.7617	5.29E-23	6.04E-22	SPAG1	chr8	+	1.01E+08	1.01E+08	3852
ENSG00000(	402.9231	446.7907	399.7824	916.8685	683.881	732.3707	-0.89892	8.03E-09	4.06E-08	CHRAC1	chr8	+	1.42E+08	1.42E+08	2488
ENSG00000(	93.22127	54.19295	59.37362	59.17697	79.15715	53.42772	0.1161	0.72594	0.81625	NCALD	chr8	-	1.03E+08	1.03E+08	3808
ENSG00000(	119.1161	154.1488	196.5927	92.88537	118.7357	114.2531	0.52059	0.038213	0.076937	SNX16	chr8	-	82711816	82755101	3452
ENSG00000(	1641.73	1820.883	2191.546	1104.886	1357.637	943.6157	0.72872	2.32E-06	9.23E-06	UBR5	chr8	-	1.03E+08	1.03E+08	10297
ENSG00000(	3.107376	1.204288	7.916483	26.21764	19.32907	36.98842	-2.5907	0.000169	0.000533	GSDMD	chr8	+	1.45E+08	1.45E+08	3462
ENSG00000(	1264.702	1172.976	1009.352	1637.479	1266.514	1545.294	-0.36685	0.008798	0.020716	TSTA3	chr8	-	1.45E+08	1.45E+08	2220
ENSG00000(	297.2723	239.6533	266.5216	270.4163	255.8801	322.2102	-0.07741	0.67129	0.77386	PYCRL	chr8	-	1.45E+08	1.45E+08	2678
ENSG00000(	5150.993	5129.061	4256.429	3896.691	3792.18	4630.95	0.23837	0.055068	0.10574	EEF1D	chr8	-	1.45E+08	1.45E+08	3718
ENSG00000(	3025.548	2972.182	3359.227	1725.121	1677.948	1436.795	0.94899	1.75E-15	1.42E-14	SQLE	chr8	+	1.26E+08	1.26E+08	2961
ENSG00000(	91.14969	69.84869	60.69303	1296.65	1317.138	1225.55	-4.0842	7.20E-123	7.76E-121	SH2D4A	chr8	+	19171128	19253729	3352
ENSG00000(	606.9741	611.7782	663.6651	834.4702	686.6423	709.3557	-0.24552	0.07878	0.14343	INTS10	chr8	+	19674651	19709594	2804
ENSG00000(	315.9165	340.8134	390.5465	704.8801	691.2444	687.9846	-0.99241	1.29E-11	8.16E-11	ERI1	chr8	+	8859657	8974256	5033
ENSG00000(	1105.19	983.9031	1319.414	1418.749	1388.011	1337.337	-0.28201	0.035078	0.071279	SLC39A14	chr8	+	22224762	22291642	4641
ENSG00000(	336.6324	356.4692	436.726	454.6889	396.7062	348.5131	-0.08916	0.60611	0.72079	MTMR9	chr8	+	11141925	11185646	7472
ENSG00000(	388.422	468.4679	419.5736	704.131	647.0637	645.2425	-0.64473	8.31E-06	3.12E-05	LEPROTL1	chr8	+	29952914	30034724	3173
ENSG00000(	172.9772	197.5032	179.4403	327.346	206.1768	234.26	-0.48126	0.025235	0.053418	DCTN6	chr8	+	30013813	30041156	1127
ENSG00000(	469.2137	464.8551	372.0747	516.8621	518.2032	509.6182	-0.23933	0.11542	0.19752	R3HCC1	chr8	+	23127633	23153792	1773
ENSG00000(	1420.071	1330.738	1074.003	1710.139	1817.853	1803.391	-0.47678	0.000259	0.000794	GSR	chr8	-	30535583	30585443	3114
ENSG00000(	249.6258	211.9546	237.4945	492.1426	415.1148	452.9027	-0.95649	9.47E-09	4.75E-08	TNFRSF10A	chr8	-	23047965	23082639	2714
ENSG00000(	252.7332	289.0291	224.3003	301.1284	193.2907	251.5213	0.036527	0.85914	0.91045	UBXN8	chr8	+	30589764	30624522	1623
ENSG00000(	1501.898	1601.703	1613.643	2537.119	2004.701	2119.848	-0.49755	6.76E-05	0.000226	PPP2CB	chr8	-	30631973	30671830	2006
ENSG00000(	497.1801	449.1993	439.3648	336.3349	379.218	427.4218	0.27852	0.079464	0.14452	ERICH1	chr8	-	564746	688106	3630
ENSG00000(	402.9231	335.9963	348.3252	82.39831	109.5314	115.8971	1.8146	2.42E-19	2.38E-18	NEFM	chr8	+	24770525	24776607	4020
ENSG00000(	2321.21	2462.768	2389.458	1759.578	1480.975	1635.71	0.55533	1.33E-06	5.47E-06	TUSC3	chr8	+	15274724	15624158	3683
ENSG00000(	731.2691	743.0455	744.1494	820.2377	732.6639	596.7465	0.044857	0.76083	0.84189	NEFL	chr8	-	24808468	24814624	4083
ENSG00000(	1184.946	1172.976	1242.888	973.7982	1050.213	1025.812	0.2392	0.041459	0.082581	ARHGEF10	chr8	+	1772142	1906807	5648
ENSG00000(	291.0575	303.4805	288.9516	419.4823	555.0205	639.4887	-0.86476	1.35E-06	5.52E-06	KLHDC4	chr16	-	87730091	87799598	4572

ENSG00000(	1532.972	1557.144	1735.029	7734.205	6663.007	6509.962	-2.1121	5.05E-74	2.36E-72	MCM4	chr8	+	48872745	48890720	4183
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	ADAM2	chr8	-	39601254	39695808	2672
ENSG00000(	538.6118	479.3065	564.7091	701.8838	786.9694	637.8448	-0.42478	0.003599	0.009174	KCTD9	chr8	-	25285366	25315992	3398
ENSG00000(	0	6.021439	7.916483	0.749076	0	2.465895	1.5153	0.20748	0.31679	FGL1	chr8	-	17721889	17767874	1967
ENSG00000(	685.6942	658.7454	753.3853	1655.457	1354.876	1385.011	-1.0656	1.47E-15	1.20E-14	ASAH1	chr8	-	17913934	17942494	2609
ENSG00000(	1801.242	1893.14	1927.664	316.859	326.7534	237.5479	2.6665	5.99E-78	3.13E-76	BNIP3L	chr8	+	26240414	26363152	3610
ENSG00000(	1597.191	1600.498	1459.272	996.2705	863.3652	798.1279	0.80713	3.63E-10	2.06E-09	MAN2B1	chr19	-	12757325	12777556	3685
ENSG00000(	14.50109	13.24716	5.277655	140.0771	134.3831	175.9005	-3.6651	3.66E-22	4.05E-21	KCNN4	chr19	-	44270685	44285409	2240
ENSG00000(	0	0	0	2.996302	2.761296	0.821965	-1.8697	0.16674	0.26571	TULP2	chr19	-	49384222	49401990	1754
ENSG00000(	6163.998	6162.34	5034.883	2177.563	2244.934	2539.05	1.316	3.08E-27	4.17E-26	NUCB1	chr19	+	49403307	49426629	2668
ENSG00000(	0	0	1.319414	0	0.920432	0.821965	-0.17431	0.89516	NA	DHDH	chr19	+	49436939	49448226	1081
ENSG00000(	3098.054	3264.824	2347.237	2488.429	2130.8	2084.503	0.37691	0.007048	0.01696	GYS1	chr19	-	49471382	49496567	3574
ENSG00000(	0	0	5.277655	11.23613	3.681728	0.821965	-1.2194	0.29857	0.42355	MAP4K1	chr19	-	39078281	39109522	2700
ENSG00000(	581.0793	656.3368	455.1978	582.0317	376.4567	379.7478	0.33652	0.084861	0.15309	ECH1	chr19	-	39306062	39322645	1411
ENSG00000(	2829.783	2568.746	2955.487	3731.894	4463.175	4316.138	-0.5815	6.19E-07	2.63E-06	HNRNPL	chr19	-	39327028	39342987	3094
ENSG00000(	525.1465	454.0165	432.7677	680.1606	697.6875	736.4806	-0.57893	4.81E-05	0.000164	NFKBIB	chr19	+	39390340	39399533	2203
ENSG00000(	1.035792	2.408575	3.958241	1.498151	6.443024	9.041614	-1.0015	0.33104	0.45896	LHB	chr19	-	49519237	49520338	514
ENSG00000(	5.17896	1.204288	1.319414	0	0.920432	1.64393	1.0931	0.38846	0.51927	TUBB4A	chr19	-	6494330	6502859	2552
ENSG00000(	19.68005	13.24716	19.79121	8.988907	11.04518	27.94681	0.12959	0.83003	0.891	SARS2	chr19	-	39405906	39440495	2057
ENSG00000(	4.143168	3.612863	2.638828	0.749076	0	0	2.3251	0.070304	0.13021	KCNA7	chr19	-	49570675	49576198	4372
ENSG00000(	6072.848	6298.425	4983.426	5128.92	5729.689	7137.943	-0.05208	0.70843	0.80296	SNRNP70	chr19	+	49588676	49611862	3221
ENSG00000(	3817.929	3479.187	3414.643	3087.689	2576.289	2727.28	0.35156	0.002281	0.00602	CLPTM1	chr19	+	45457842	45496599	2732
ENSG00000(	479.5717	441.9736	385.2688	155.8077	156.4734	124.1167	1.5768	7.69E-18	7.03E-17	RELB	chr19	+	45504688	45541452	2294
ENSG00000(	789.2734	821.3242	559.4314	916.8685	759.3564	982.2481	-0.2909	0.078414	0.1429	CLASRP	chr19	+	45542298	45574214	2769
ENSG00000(	63.18331	57.80581	54.09597	43.44638	36.81728	23.83698	0.73609	0.045878	0.0901	LIN7B	chr19	+	49617581	49621717	1057
ENSG00000(	1145.586	1144.073	1019.907	1059.193	1003.271	1311.856	-0.02761	0.84169	0.89882	PPP1R37	chr19	+	45594654	45651335	5943
ENSG00000(	1026.47	1154.912	866.8549	202.2504	133.4626	180.8323	2.5467	1.67E-47	4.28E-46	FCGRT	chr19	+	50010073	50029590	2681
ENSG00000(	726.0901	635.8639	556.7926	1030.728	964.6127	1016.771	-0.64716	2.95E-06	1.16E-05	PIH1D1	chr19	-	49949555	49956754	1192
ENSG00000(	0	9.634302	3.958241	0	0	0	3.08	0.019816	0.043043	CKM	chr19	-	45809672	45826235	1657
ENSG00000(	496.1443	484.1237	488.1831	420.2314	427.0804	542.4968	0.079242	0.61219	0.72568	ARHGEF18	chr19	+	7459999	7537363	5733
ENSG00000(	175.0488	134.8802	106.8725	895.1453	788.8102	887.7221	-2.6052	9.47E-48	2.45E-46	PPP1R13L	chr19	-	45882892	45909607	3118
ENSG00000(	30.03797	21.67718	11.87472	24.71949	21.16994	32.05663	-0.27205	0.59089	0.70742	PEX11G	chr19	-	7541761	7562335	1345
ENSG00000(	837.9557	759.9056	707.2058	1014.997	916.7503	917.3128	-0.30412	0.020428	0.044193	ERCC2	chr19	-	45853095	45874176	4153
ENSG00000(	1113.476	1244.029	1005.393	1439.723	1763.548	1652.149	-0.52787	6.87E-05	0.000229	DOT1L	chr19	+	2164148	2232577	7436
ENSG00000(	1385.89	1191.041	1141.293	2597.794	2136.323	2682.893	-0.99325	6.29E-14	4.66E-13	PLEKHJ1	chr19	-	2230093	2237703	2858
ENSG00000(	2.071584	3.612863	7.916483	0	0	0	3.2517	0.011877	0.027148	SLC17A7	chr19	-	49932658	49945617	2973
ENSG00000(	325.2387	351.652	219.0227	1176.049	966.4536	958.4111	-1.7811	2.85E-24	3.43E-23	RNASEH2A	chr19	+	12917394	12924452	1487
ENSG00000(	1.035792	3.612863	2.638828	26.21764	16.56778	36.98842	-3.1819	2.17E-05	7.73E-05	KLC3	chr19	+	45836692	45854778	2006
ENSG00000(	415.3526	449.1993	428.8095	32.95932	78.23672	64.11326	2.8707	2.41E-32	3.93E-31	CD37	chr19	+	49838428	49846592	3172
ENSG00000(	1989.756	1818.474	1438.161	1944.6	2102.267	2243.964	-0.26029	0.056731	0.10843	SF3A2	chr19	+	2236520	2248713	1981
ENSG00000(	142.9393	152.9445	94.99779	280.9033	224.5854	260.5629	-0.96083	1.57E-05	5.69E-05	AMH	chr19	+	2248666	2252072	2465
ENSG00000(	30.03797	21.67718	10.55531	2.996302	11.96562	5.753754	1.507	0.026282	0.055383	DKKL1	chr19	+	49865040	49878373	1222
ENSG00000(	7.250543	10.83859	6.597069	1.498151	0.920432	0	2.6965	0.009883	0.023015	LYL1	chr19	-	13209847	13213975	1547
ENSG00000(	5711.357	5513.229	4608.712	6660.031	4402.426	5544.153	-0.06862	0.64015	0.74807	OAZ1	chr19	+	2269519	2273487	2828

ENSG00000(	1314.42	1281.362	1100.391	1301.144	1091.632	1492.688	-0.07164	0.61524	0.72835	TRMT1	chr19	-	13215716	13228381	2579
ENSG00000(	892.8526	797.2385	676.8593	497.3862	410.5127	593.4587	0.65463	8.54E-05	0.000281	STX10	chr19	-	13254872	13261197	1241
ENSG00000(	699.1595	785.1956	527.7655	635.2161	671.9154	700.3141	0.004716	0.97633	0.98632	DMPK	chr19	-	46272975	46285810	3357
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RSPH6A	chr19	-	46298968	46318577	2456
ENSG00000(	777.8797	697.2826	662.3457	503.3788	436.2848	465.2321	0.60404	2.15E-05	7.67E-05	TBC1D17	chr19	+	50380682	50392005	2831
ENSG00000(	9.322127	9.634302	11.87472	4.494453	1.840864	9.041614	0.89655	0.26361	0.3834	IL4I1	chr19	-	50392911	50432796	2407
ENSG00000(	2.071584	0	0	0	4.60216	0	-0.53557	0.69303	0.7906	TLE6	chr19	+	2977444	2995177	2095
ENSG00000(	490.9654	572.0367	385.2688	442.7036	344.2416	418.3801	0.26375	0.13863	0.22897	CCDC130	chr19	+	13842574	13874110	1922
ENSG00000(	1223.27	1217.535	964.4915	505.626	608.4055	783.3326	0.84157	5.46E-07	2.33E-06	PTOV1	chr19	+	50353992	50364001	1880
ENSG00000(	1535.044	1516.198	1345.802	1203.015	1071.383	1376.791	0.26764	0.042545	0.084458	AES	chr19	-	3052908	3063105	3274
ENSG00000(	2.071584	3.612863	6.597069	0	0.920432	0	2.4713	0.049861	0.096869	NOVA2	chr19	-	46436992	46476804	7803
ENSG00000(	1920.358	1900.366	1708.641	3614.29	2677.537	2698.511	-0.69948	3.36E-07	1.47E-06	SGTA	chr19	-	2754712	2783369	2330
ENSG00000(	832.7767	886.3558	687.4146	955.0713	851.3996	876.2146	-0.15573	0.26315	0.38291	MED25	chr19	+	50321539	50342073	3339
ENSG00000(	808.9535	639.4768	606.9303	433.7147	382.8997	360.8426	0.80191	5.56E-07	2.37E-06	SNAPC2	chr19	+	7985201	7988135	1542
ENSG00000(	1826.101	1694.433	1274.554	1703.398	1399.977	1878.19	-0.05434	0.72469	0.81523	C19orf53	chr19	+	13884982	13889276	873
ENSG00000(	1031.649	1004.376	804.8424	1492.158	1293.207	1575.707	-0.61589	9.63E-06	3.59E-05	TIMM44	chr19	-	7991603	8008805	2227
ENSG00000(	147.0825	179.4389	94.99779	152.0623	114.1336	176.7225	-0.06948	0.79391	0.86525	CCDC61	chr19	+	46498339	46524576	1825
ENSG00000(	19.68005	16.86003	15.83297	65.91865	52.46462	41.09825	-1.5615	0.000274	0.000838	IL27RA	chr19	+	14142560	14163743	2677
ENSG00000(	167.7983	127.6545	164.9267	994.7723	820.1049	798.9499	-2.4948	2.34E-48	6.18E-47	ASF1B	chr19	-	14230321	14247768	2059
ENSG00000(	26.93059	25.29004	27.70769	2.247227	7.363456	3.28786	2.4988	9.90E-05	0.000323	TNNT1	chr19	-	55644162	55660722	1163
ENSG00000(	504.4307	481.7151	456.5172	600.0095	486.9085	521.9477	-0.157	0.29184	0.41595	VRK3	chr19	-	50479724	50529203	2197
ENSG00000(	1279.203	1263.298	1033.101	1777.556	1510.429	1477.071	-0.41277	0.002116	0.005613	FAM32A	chr19	+	16296191	16302857	1455
ENSG00000(	2227.988	2044.881	2062.244	2182.057	2307.523	2422.331	-0.1251	0.25562	0.37382	PPP6R1	chr19	-	55741148	55770363	3961
ENSG00000(	129.474	169.8046	126.6637	134.8336	92.96363	109.3213	0.33135	0.18186	0.28515	C19orf44	chr19	+	16607122	16632163	3427
ENSG00000(	157.4404	148.1274	162.2879	149.066	140.8261	146.3098	0.099673	0.63487	0.74397	MED26	chr19	-	16685718	16739873	3871
ENSG00000(	1853.032	2001.526	1461.91	44.94453	35.89685	51.78379	5.294	6.33E-175	1.35E-172	OLFM2	chr19	-	9964394	10047228	2019
ENSG00000(	0	1.204288	2.638828	0	0	0	1.2853	0.33195	NA	RASAL3	chr19	-	15562438	15575377	4270
ENSG00000(	680.5153	633.4553	597.6944	925.8574	866.1265	848.2678	-0.46392	0.000377	0.001131	AKAP8	chr19	-	15464196	15490612	3700
ENSG00000(	1.035792	10.83859	1.319414	10.48706	12.88605	7.397684	-1.0796	0.21992	0.33162	EPHX3	chr19	-	15337730	15344246	1822
ENSG00000(	1521.578	1549.918	1303.581	1061.44	1128.45	1394.874	0.2872	0.039083	0.078419	ILVBL	chr19	-	15225795	15236596	4248
ENSG00000(	168.8341	150.536	145.1355	95.13259	69.95283	69.04505	0.97818	8.36E-05	0.000275	ZNF419	chr19	+	57999079	58006048	5542
ENSG00000(	1327.885	1185.019	1109.627	835.9683	707.8122	692.9164	0.694	3.18E-07	1.39E-06	SYDE1	chr19	+	15218214	15225799	3832
ENSG00000(	0	0	0	162.5494	167.5186	152.0635	-7.9596	5.41E-16	4.53E-15	SLC1A6	chr19	-	15060846	15133802	3264
ENSG00000(	8.286335	9.634302	11.87472	8.988907	4.60216	3.28786	0.73202	0.34893	0.47862	AURKC	chr19	+	57742377	57746916	1610
ENSG00000(	532.397	519.048	472.3501	725.8542	579.8722	618.1176	-0.33532	0.02339	0.049904	POP4	chr19	+	30094924	30108144	3385
ENSG00000(	46.61064	28.90291	65.97069	247.944	221.8241	264.6727	-2.36	1.74E-18	1.64E-17	CCNE1	chr19	+	30302805	30315215	2043
ENSG00000(	1024.398	897.1944	1060.809	1241.218	950.8063	988.8238	-0.09346	0.51228	0.63928	URI1	chr19	+	30414551	30506611	2540
ENSG00000(	1067.901	1089.88	882.6878	1240.469	1109.121	1487.757	-0.33439	0.021397	0.046095	PDCD5	chr19	+	33071974	33078358	3463
ENSG00000(	396.7083	411.8664	434.0871	465.1759	483.2268	423.3119	-0.14271	0.338	0.46658	ANKRD27	chr19	-	33087913	33167028	4450
ENSG00000(	24477.83	23186.15	17322.58	16942.59	15173.32	17763.48	0.38082	0.0045	0.011251	RPS16	chr19	-	39923847	39926588	2389
ENSG00000(	1300.955	1191.041	1048.934	2432.997	1772.752	2356.573	-0.88714	9.24E-10	5.08E-09	TIMM50	chr19	+	39971052	39984422	2576
ENSG00000(	4072.734	3963.311	3146.802	5299.71	4341.678	5467.711	-0.43287	0.001178	0.003264	FBL	chr19	-	40325098	40337054	1400
ENSG00000(	848.3136	799.647	666.304	325.8479	326.7534	335.3617	1.2256	1.66E-16	1.42E-15	DYRK1B	chr19	-	40315990	40324841	2724
ENSG00000(	13.46529	7.225726	6.597069	1.498151	2.761296	3.28786	1.6393	0.06609	0.12351	CNTD2	chr19	-	40728115	40732597	1817

ENSG00000(	5194.496	4919.515	4381.773	2952.856	2527.506	2665.632	0.82996	7.59E-13	5.23E-12	GPI	chr19	+	34850385	34893061	4000
ENSG00000(	3326.964	3426.199	2951.529	2620.266	3123.026	3698.02	0.03989	0.76909	0.84812	AKT2	chr19	-	40736224	40791443	5300
ENSG00000(	15748.18	15550.97	12884.08	10708.78	8533.325	8721.048	0.65854	1.64E-07	7.37E-07	PLD3	chr19	+	40854363	40886346	2180
ENSG00000(	221.6595	202.3203	211.1062	71.91125	120.5766	100.2797	1.1141	2.21E-06	8.84E-06	PRX	chr19	-	40899675	40919273	5502
ENSG00000(	676.3721	641.8854	616.1662	984.2853	1035.486	1274.046	-0.76504	6.04E-08	2.83E-07	PIAS4	chr19	+	4007644	4039384	3159
ENSG00000(	1286.454	1197.062	1031.782	367.047	384.7406	434.8194	1.5636	5.16E-28	7.22E-27	NUMBL	chr19	-	41172596	41196877	2775
ENSG00000(	22.78742	22.88147	22.43003	60.67512	34.97642	41.09825	-0.98402	0.021106	0.045548	EBI3	chr19	+	4229495	4237528	1186
ENSG00000(	297.2723	255.309	240.1333	488.3973	375.5363	499.7547	-0.778	1.18E-05	4.34E-05	CCDC94	chr19	+	4247076	4269087	1434
ENSG00000(	0	0	0	9.737982	9.20432	9.863579	-4.118	0.000466	0.001375	SHD	chr19	+	4278598	4290721	2577
ENSG00000(	2295.315	2207.459	1907.872	2000.032	1584.984	1910.246	0.22179	0.08822	0.15808	TBCB	chr19	+	36605191	36616849	1473
ENSG00000(	306.5944	284.2119	207.148	170.0401	151.8713	142.1999	0.77923	0.00019	0.000595	FSD1	chr19	+	4304597	4323840	1831
ENSG00000(	61.11172	31.31148	36.94359	69.66403	29.45382	55.89361	-0.25267	0.53903	0.66271	POLR2I	chr19	-	36604612	36606248	993
ENSG00000(	0	3.612863	1.319414	6.74168	4.60216	4.109825	-1.3242	0.22724	0.34033	OVOL3	chr19	+	36602104	36604613	806
ENSG00000(	1614.8	1530.65	1472.466	90.63814	101.2475	90.41614	4.0229	5.01E-164	9.56E-162	CLIP3	chr19	-	36505562	36524245	3370
ENSG00000(	4.143168	0	5.277655	9.737982	11.96562	9.863579	-1.5327	0.082774	0.14976	ZFR2	chr19	-	3804022	3869030	4756
ENSG00000(	5238	5242.264	4569.13	5826.31	4800.053	5498.123	-0.09934	0.39363	0.52449	SLC1A5	chr19	-	47278140	47291851	2882
ENSG00000(	647.3699	641.8854	583.1809	799.2636	809.9802	792.3742	-0.35736	0.005693	0.013945	PRKD2	chr19	-	47177532	47220384	3321
ENSG00000(	22.78742	2.408575	1.319414	202.9995	197.8929	213.7109	-3.9234	1.53E-05	5.56E-05	TJP3	chr19	+	3708107	3750811	3350
ENSG00000(	882.4947	856.2486	874.7713	85.39461	102.168	87.95025	3.2382	7.94E-91	5.09E-89	APLP1	chr19	+	36358801	36370693	2495
ENSG00000(	387.3862	445.5865	415.6153	479.4084	543.0549	711.8216	-0.47247	0.006009	0.014655	CACTIN	chr19	-	3610639	3626813	3612
ENSG00000(	776.8439	864.6786	630.6798	408.9952	578.9517	796.484	0.34769	0.087385	0.15693	CCDC9	chr19	+	47759237	47775210	2093
ENSG00000(	5097.132	5124.244	4723.501	5776.871	7289.821	8320.751	-0.51571	0.000108	0.000351	HNRNPUL1	chr19	+	41768401	41813503	3555
ENSG00000(	1309.241	1393.361	1068.725	1388.786	1557.371	1830.516	-0.33922	0.018648	0.040745	FZR1	chr19	+	3506271	3538328	5212
ENSG00000(	464.0348	454.0165	348.3252	420.2314	465.7386	582.7731	-0.21092	0.23185	0.3454	BBC3	chr19	-	47724081	47736023	1838
ENSG00000(	1250.201	985.1074	936.7838	1057.695	767.6403	882.7903	0.22766	0.14776	0.24089	TGFB1	chr19	-	41807492	41859816	2769
ENSG00000(	279.6638	272.169	261.2439	250.1912	233.7897	271.2484	0.10621	0.54079	0.66382	DENND3	chr8	+	1.42E+08	1.42E+08	5482
ENSG00000(	1097.939	1012.806	947.3391	1635.981	1277.56	1383.367	-0.48927	0.000274	0.000839	ATP5SL	chr19	-	41937223	41946622	2317
ENSG00000(	3105.304	3167.277	2890.836	1404.517	1424.829	1200.069	1.1833	5.28E-24	6.29E-23	PLIN3	chr19	-	4838353	4867780	2333
ENSG00000(	0	0	2.638828	2.996302	8.283888	12.32947	-2.5004	0.024423	0.051895	MYH14	chr19	+	50691443	50813802	6910
ENSG00000(	382.2072	463.6508	353.6029	777.5404	641.5411	658.3939	-0.79005	5.88E-07	2.50E-06	MRPL4	chr19	+	10362577	10370721	1620
ENSG00000(	13.46529	7.225726	7.916483	8.239831	0	9.863579	0.57667	0.50899	0.63644	CD79A	chr19	+	42381190	42385439	1258
ENSG00000(	37479.09	35640.9	22633.22	30142.8	24756.86	26954.7	0.22552	0.15663	0.25264	RPS19	chr19	+	42363988	42376994	2359
ENSG00000(	8831.162	8825.02	6756.718	4171.602	4090.4	4724.654	0.90873	1.24E-12	8.44E-12	GLTSCR2	chr19	+	48248779	48260315	4185
ENSG00000(	0	1.204288	0	0	2.761296	0	-0.43954	0.74062	NA	NKG7	chr19	-	51874860	51875969	843
ENSG00000(	137.7603	183.0517	175.482	2.247227	0.920432	4.93179	5.6996	9.53E-31	1.48E-29	ICAM5	chr19	+	10400657	10407454	3000
ENSG00000(	99.43602	74.66584	73.88717	69.66403	93.88406	85.48435	0.000789	0.99779	0.99864	ETFB	chr19	-	51848423	51869672	3551
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	CD33	chr19	+	51728320	51747115	4728
ENSG00000(	201.9794	168.6003	199.2315	291.3904	235.6306	301.6611	-0.53835	0.005283	0.013028	BABAM1	chr19	+	17378159	17392058	1472
ENSG00000(	1646.909	1578.821	1460.591	1126.61	1131.211	1457.344	0.33452	0.013638	0.030778	TYK2	chr19	-	10461209	10491352	4347
ENSG00000(	3.107376	0	0	0	0.920432	0	0.70943	0.5938	NA	SULT2A1	chr19	-	48373723	48389654	1987
ENSG00000(	8442.74	7664.087	6195.967	6884.004	5783.995	7222.606	0.16485	0.21945	0.33106	CDC37	chr19	-	10501810	10530797	1608
ENSG00000(	1461.502	1330.738	1348.441	1464.443	1178.153	1288.019	0.074735	0.5548	0.67555	NAPA	chr19	-	47990894	48018497	3898
ENSG00000(	4448.726	4116.255	3313.048	1346.838	970.1353	1228.838	1.7386	3.52E-32	5.72E-31	RABAC1	chr19	-	42460833	42463542	821
ENSG00000(	10.35792	6.021439	13.19414	2.247227	7.363456	9.041614	0.60802	0.44307	0.57272	ATP1A3	chr19	-	42470734	42501649	3818

ENSG00000(	1556.795	1547.51	1228.374	77.90386	68.11197	85.48435	4.2078	1.34E-139	1.80E-137	MEIS3	chr19	-	47906316	47922780	2195
ENSG00000(	5504.198	5131.47	5352.862	806.7544	1053.895	940.3279	2.509	1.07E-93	7.30E-92	PTPRS	chr19	-	5158506	5340814	7350
ENSG00000(	7.250543	13.24716	2.638828	38.20285	53.38506	19.72716	-2.1365	0.000372	0.001115	CNFN	chr19	-	42891171	42894439	523
ENSG00000(	3766.139	3728.475	3798.592	1432.232	2629.674	2709.196	0.73509	4.70E-05	0.000161	MEGF8	chr19	+	42829761	42882921	10966
ENSG00000(	8798.016	8840.676	7403.231	5174.614	4824.905	5216.189	0.71765	1.06E-10	6.29E-10	KDELR1	chr19	-	48885827	48894810	1594
ENSG00000(	786.1661	858.6571	724.3582	621.7327	684.8014	827.7187	0.15077	0.31002	0.43619	CYTH2	chr19	+	48972289	48985571	4652
ENSG00000(	1114.512	942.9573	961.8526	2405.282	1954.077	2038.473	-1.0803	1.38E-16	1.19E-15	GRWD1	chr19	+	48949030	48960279	5571
ENSG00000(	76.6486	66.23582	60.69303	51.68621	62.58938	67.40112	0.16696	0.58874	0.70579	GRIN2D	chr19	+	48898132	48948188	5093
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	SYNGR4	chr19	+	48867652	48879633	1000
ENSG00000(	7.250543	8.430014	13.19414	29.21395	15.64734	21.37109	-1.1518	0.055382	0.1062	CLEC11A	chr19	+	51226586	51228974	1419
ENSG00000(	1.035792	6.021439	5.277655	8.239831	0	9.863579	-0.47871	0.64071	0.74846	CCDC114	chr19	-	48799714	48825130	3215
ENSG00000(	409.1378	427.5221	422.2124	342.3275	286.2544	289.3317	0.45254	0.004574	0.01142	CARD8	chr19	-	48684027	48759203	5263
ENSG00000(	458.8558	452.8122	339.0893	1250.956	1320.82	1380.079	-1.6522	7.98E-30	1.21E-28	LIG1	chr19	-	48618702	48673860	4102
ENSG00000(	0	0	0	4.494453	6.443024	9.863579	-3.606	0.003241	0.008331	SIGLEC6	chr19	-	52022779	52035110	1940
ENSG00000(	162.6193	163.7831	179.4403	80.90016	84.67974	87.95025	0.98891	1.41E-05	5.14E-05	ZNF175	chr19	+	52074551	52092991	3742
ENSG00000(	5.17896	16.86003	1.319414	16.47966	1.840864	4.93179	-0.00304	0.99732	0.99833	PLA2G4C	chr19	-	48551100	48614074	2496
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	SIGLEC5	chr19	-	52114781	52150151	2498
ENSG00000(	1.035792	0	6.597069	6.74168	0.920432	2.465895	-0.3415	0.76872	0.8478	HAS1	chr19	-	52216365	52227247	2110
ENSG00000(	42.46747	22.88147	17.15238	128.841	227.3467	185.7641	-2.649	4.53E-15	3.59E-14	RAB3D	chr19	-	11432722	11456946	4273
ENSG00000(	36.25272	26.49433	32.98534	12.73428	6.443024	16.4393	1.3645	0.009133	0.021431	DBP	chr19	-	49133287	49140695	5756
ENSG00000(	16.57267	28.90291	21.11062	47.94084	30.37426	36.16646	-0.76785	0.088105	0.15791	TMEM205	chr19	-	11453452	11457194	1310
ENSG00000(	109.7939	137.2888	101.5949	65.16957	73.63456	84.66239	0.63689	0.017233	0.037985	CAPS	chr19	+	5911718	5915888	3515
ENSG00000(	1910	1679.981	1443.439	51.68621	38.65814	34.52253	5.2997	2.46E-173	5.20E-171	DKFZP761J	chr19	+	11466062	11476374	2727
ENSG00000(	4.143168	13.24716	5.277655	13.48336	24.85166	23.01502	-1.3483	0.041061	0.081899	FAM83E	chr19	-	49104067	49118111	1926
ENSG00000(	12.4295	22.88147	18.47179	27.7158	13.80648	20.54912	-0.20981	0.70006	0.7961	RASIP1	chr19	-	49223844	49243978	3308
ENSG00000(	0	0	2.638828	0	0.920432	1.64393	0.005124	0.99699	NA	FGF21	chr19	+	49258816	49261587	1312
ENSG00000(	616.2962	551.5638	476.3084	436.711	332.276	336.1837	0.57091	0.000767	0.002194	BCAT2	chr19	-	49298319	49314286	2254
ENSG00000(	420.5315	397.4149	385.2688	434.4638	347.0029	325.4981	0.11934	0.47509	0.60436	MIER2	chr19	-	305575	344798	2764
ENSG00000(	1777.419	1687.207	1364.274	52.43529	58.90765	69.86702	4.719	1.11E-160	2.02E-158	PLEKHA4	chr19	-	49340354	49371889	3088
ENSG00000(	7529.171	7218.501	6951.991	6260.024	5386.368	5047.687	0.37764	0.000891	0.002519	PPP2R1A	chr19	+	52693292	52730687	3281
ENSG00000(	2526.296	2746.98	2632.23	2421.761	2877.27	3002.638	-0.07031	0.55414	0.67501	TNPO2	chr19	-	12810008	12834825	5122
ENSG00000(	127.4024	138.4931	143.8161	135.5827	88.36147	155.3514	0.10623	0.67597	0.7777	WDR83OS	chr19	-	12778885	12782170	2562
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	CACNG7	chr19	+	54412589	54447195	2688
ENSG00000(	306.5944	297.4591	270.4798	411.9916	425.2396	466.8761	-0.57294	0.000312	0.000946	GCDH	chr19	+	13001840	13025021	1956
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	LILRB5	chr19	-	54754263	54761164	5545
ENSG00000(	205.0868	196.2989	141.1773	238.9551	189.609	220.2866	-0.25422	0.23111	0.34447	DNASE2	chr19	-	12986025	12992282	1955
ENSG00000(	25.8948	19.2686	17.15238	14.98151	14.72691	18.90519	0.34963	0.51106	0.63824	MAST1	chr19	+	12944765	12985765	4833
ENSG00000(	227.8742	232.4275	157.0102	100.3761	126.0992	205.4912	0.51266	0.055241	0.10601	LENG1	chr19	-	54658899	54663620	1542
ENSG00000(	714.6964	682.8311	547.5567	1047.957	852.32	951.8354	-0.54955	0.000201	0.000628	PRPF31	chr19	+	54618837	54635140	2126
ENSG00000(	295.2007	296.2548	250.6886	264.4237	320.3103	397.831	-0.2194	0.25201	0.36969	TFPT	chr19	-	54610320	54619055	1205
ENSG00000(	62.14751	56.60152	59.37362	20.22504	19.32907	16.4393	1.6345	2.64E-05	9.30E-05	JAK3	chr19	-	17935589	17958880	5432
ENSG00000(	29034.28	28776.46	18333.25	22567.4	16854.03	17566.21	0.41658	0.010837	0.025	RPL18A	chr19	+	17970685	17974962	1391
ENSG00000(	4.143168	0	0	0.749076	0	0	1.0202	0.44849	NA	CTB-52I2.8	chr19	+	18062111	18109930	2657
ENSG00000(	226.8384	195.0946	135.8996	16.47966	5.522592	16.4393	3.7731	1.08E-26	1.42E-25	ARRDC2	chr19	+	18111941	18124911	3748

ENSG00000(	4.143168	3.612863	0	0	0.920432	0	1.7606	0.18718	0.29187	PIK3R2	chr19	+	18263626	18281350	4335
ENSG00000(	112.9013	126.4502	69.92893	38.20285	24.85166	19.72716	1.8644	1.95E-07	8.69E-07	RAB3A	chr19	-	18307594	18314884	1528
ENSG00000(	12.4295	10.83859	9.235896	2.996302	7.363456	4.93179	1.0063	0.19184	0.29751	PDE4C	chr19	-	18318771	18366229	5979
ENSG00000(	412.2452	364.8992	323.2564	2713.152	2004.701	2099.298	-2.6207	1.73E-66	6.96E-65	ISYNA1	chr19	-	18545198	18549111	2039
ENSG00000(	203.0152	251.6961	155.6908	188.767	197.8929	291.7975	-0.14987	0.52198	0.64756	ELL	chr19	-	18553473	18632937	4027
ENSG00000(	521.0033	487.7365	422.2124	344.5748	335.0372	344.4033	0.48262	0.001821	0.004891	CRTC1	chr19	+	18794487	18893004	6790
ENSG00000(	1652.088	1501.747	1597.81	1307.886	1534.36	1762.293	0.045672	0.73187	0.82071	WBP7	chr19	+	36208921	36229779	8469
ENSG00000(	8.286335	8.430014	6.597069	0	0.920432	0.821965	2.9621	0.006389	0.015503	COMP	chr19	-	18893583	18902123	2707
ENSG00000(	4.143168	4.817151	0	7.490755	4.60216	0	-0.32343	0.777	0.85319	UPK1A	chr19	+	36157715	36169367	1223
ENSG00000(	1629.301	1669.143	1299.623	1620.999	1012.475	1314.322	0.21887	0.18495	0.28944	COPE	chr19	-	19010323	19030206	1770
ENSG00000(	1440.787	1331.942	1124.141	1534.107	1244.424	1301.992	-0.06583	0.63278	0.7426	DDX49	chr19	+	19030484	19039436	1882
ENSG00000(	72.50543	45.76293	56.73479	5.243529	24.85166	6.575719	2.1959	1.90E-05	6.82E-05	ETV2	chr19	+	36132647	36135773	1571
ENSG00000(	2.071584	0	3.958241	0.749076	4.60216	4.93179	-0.58558	0.6143	0.72765	ATP4A	chr19	-	36040945	36054560	3709
ENSG00000(	828.6335	783.9913	668.9428	1552.085	1049.292	1216.508	-0.73994	3.03E-06	1.19E-05	ARMC6	chr19	+	19144384	19170563	2488
ENSG00000(	771.665	824.9371	719.0805	1024.735	617.6099	845.8019	-0.10416	0.5432	0.6657	TMEM147	chr19	+	36036497	36038428	1783
ENSG00000(	3.107376	1.204288	2.638828	2.247227	0.920432	0.821965	0.57209	0.63784	0.74623	GAPDHS	chr19	+	36024314	36036218	1489
ENSG00000(	0	2.408575	0	0	0	1.64393	0.21935	0.86915	NA	AC104537.	chr19	+	2538108	2538786	363
ENSG00000(	77.68439	48.17151	68.60952	23.22134	21.16994	10.68554	1.7769	1.92E-05	6.86E-05	TMEM59L	chr19	+	18718240	18731849	1717
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	HAMP	chr19	+	35771619	35776046	2624
ENSG00000(	1126.942	1177.793	915.6732	1316.875	1026.282	1303.636	-0.1787	0.2213	0.33304	USF2	chr19	+	35759881	35770718	2742
ENSG00000(	29.00217	31.31148	22.43003	2618.019	2325.932	2592.477	-6.461	2.95E-210	9.76E-208	LSR	chr19	+	35739233	35758866	2480
ENSG00000(	588.3298	716.5512	534.3626	847.9535	667.3132	715.1095	-0.27767	0.076366	0.13978	KXD1	chr19	+	18668572	18680197	2738
ENSG00000(	9164.687	9108.028	6862.271	6083.243	5274.075	6369.406	0.50265	0.000152	0.000485	FKBP8	chr19	-	18642568	18654863	1774
ENSG00000(	599.7235	662.3582	575.2644	801.5108	761.1973	783.3326	-0.35179	0.007739	0.018462	SUGP1	chr19	-	19386827	19432123	2425
ENSG00000(	0	1.204288	1.319414	38.20285	45.10117	38.63235	-4.9492	5.17E-09	2.67E-08	HPN	chr19	+	35531410	35557475	2363
ENSG00000(	83.89914	62.62296	93.67838	95.88167	65.35067	84.66239	-0.03737	0.89917	0.93744	ZNF14	chr19	-	19821280	19843906	2949
ENSG00000(	199.9078	191.4817	137.219	26.96672	19.32907	35.34449	2.658	7.71E-19	7.42E-18	SCN1B	chr19	+	35521588	35531352	3460
ENSG00000(	5.17896	3.612863	3.958241	19.47596	6.443024	9.041614	-1.3107	0.10602	0.18401	PBX4	chr19	-	19672516	19729725	1730
ENSG00000(	1497.755	1411.425	1415.731	1516.129	1722.128	2395.206	-0.37984	0.014957	0.033399	ERF	chr19	-	42751724	42759309	2698
ENSG00000(	1057.544	1076.633	870.8131	1608.265	1401.818	1530.499	-0.59353	5.31E-06	2.03E-05	GSK3A	chr19	-	42734338	42746777	3524
ENSG00000(	2680.629	2555.499	2264.114	1624.745	1388.932	1304.458	0.79479	4.02E-10	2.27E-09	ATP13A1	chr19	-	19756007	19774502	4729
ENSG00000(	263.0911	311.9105	275.7575	580.5336	402.2288	327.964	-0.62157	0.002576	0.006731	ZNF574	chr19	+	42572629	42585701	3598
ENSG00000(	3.107376	1.204288	9.235896	5.243529	4.60216	7.397684	-0.31832	0.73382	0.82196	GRIK5	chr19	-	42502473	42573650	3493
ENSG00000(	708.4817	684.0354	664.9845	464.4268	920.432	734.8366	-0.04118	0.83391	0.89355	SIPA1L3	chr19	+	38397868	38699012	7987
ENSG00000(	51.7896	45.76293	44.86007	185.7707	193.2907	204.6693	-2.0136	9.66E-16	7.96E-15	ZNF85	chr19	+	21106028	21133503	2652
ENSG00000(	118.0803	87.913	80.48424	735.5922	393.9449	572.0876	-2.546	1.80E-27	2.47E-26	ETHE1	chr19	-	44010871	44031396	1052
ENSG00000(	121.1877	116.8159	106.8725	871.9239	879.933	1150.751	-3.0577	9.99E-68	4.18E-66	CADM4	chr19	-	44126520	44143991	2178
ENSG00000(	581.0793	564.8109	550.1955	874.9202	730.823	846.6239	-0.53084	0.000103	0.000336	SMG9	chr19	-	44235301	44259142	2387
ENSG00000(	925.998	787.6042	946.0197	477.9102	570.6678	419.2021	0.85584	2.53E-08	1.23E-07	AVL9	chr7	+	32535038	33078516	7937
ENSG00000(	2.071584	1.204288	13.19414	6.74168	7.363456	4.93179	-0.20355	0.8258	0.8877	RUNDC3B	chr7	+	87256864	87461611	4099
ENSG00000(	14.50109	38.53721	27.70769	15.73059	17.48821	13.9734	0.73879	0.163	0.26106	C7orf63	chr7	+	89874488	89940377	6966
ENSG00000(	230.9816	272.169	257.2857	400.7554	370.0137	373.1721	-0.58889	0.000372	0.001115	GTPBP10	chr7	+	89964537	90020769	7531
ENSG00000(	38.3243	34.92434	36.94359	3.745378	7.363456	11.50751	2.1972	5.12E-05	0.000174	RASA4	chr7	-	1.02E+08	1.02E+08	5605
ENSG00000(	1394.176	1378.909	2006.828	2453.222	2895.679	2216.017	-0.66077	2.64E-05	9.31E-05	CDK6	chr7	-	92234235	92465908	11612

ENSG00000(	861.7789	977.8816	873.4519	1131.104	902.9438	1021.702	-0.17202	0.20228	0.31008	PMPCB	chr7	+	1.03E+08	1.03E+08	2472
ENSG00000(	437.1042	446.7907	349.6447	614.991	495.1924	474.2738	-0.35911	0.031514	0.064901	DNAJC2	chr7	-	1.03E+08	1.03E+08	3033
ENSG00000(	241.3395	166.1917	166.2461	241.2023	164.7573	208.7791	-0.09699	0.66865	0.77174	TFPI2	chr7	-	93514709	93520303	2444
ENSG00000(	315.9165	270.9647	317.9787	286.1469	217.222	237.5479	0.28531	0.1197	0.20329	BET1	chr7	-	93592074	93633694	3586
ENSG00000(	1632.408	1633.014	1754.82	1319.122	1210.368	1103.077	0.46533	0.000115	0.000371	NAMPT	chr7	-	1.06E+08	1.06E+08	4582
ENSG00000(	327.3102	285.4162	336.4505	632.9688	475.8633	465.2321	-0.72792	2.56E-05	9.03E-05	TWISTNB	chr7	-	19735085	19748710	3942
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	PON3	chr7	-	94989256	95025680	2433
ENSG00000(	1243.986	1260.889	1390.662	1597.029	1292.287	1409.67	-0.14286	0.25998	0.37886	PON2	chr7	-	95034175	95064510	1779
ENSG00000(	18.64425	38.53721	44.86007	11.98521	29.45382	13.9734	0.8495	0.10138	0.17747	ITGB8	chr7	+	20370325	20450419	5573
ENSG00000(	334.5608	332.3834	368.1164	191.7633	168.4391	124.9387	1.0858	4.25E-08	2.02E-07	HBP1	chr7	+	1.07E+08	1.07E+08	2829
ENSG00000(	74.57702	78.2787	58.05421	167.7929	136.2239	113.4312	-0.97291	0.00032	0.00097	DUS4L	chr7	+	1.07E+08	1.07E+08	2280
ENSG00000(	104.615	83.09585	97.63662	63.67142	117.8153	68.22309	0.19604	0.51718	0.64348	SP4	chr7	+	21467652	21554440	6126
ENSG00000(	367.7061	311.9105	389.2271	134.0845	193.2907	221.1086	0.95872	3.82E-06	1.49E-05	WDR91	chr7	-	1.35E+08	1.35E+08	4588
ENSG00000(	76.6486	66.23582	67.2901	22.47227	19.32907	7.397684	2.0426	1.11E-06	4.59E-06	DNAH11	chr7	+	21582833	21941457	14188
ENSG00000(	191.6215	195.0946	267.841	256.1838	329.5147	229.3282	-0.31606	0.13252	0.22077	CBLL1	chr7	+	1.07E+08	1.07E+08	2349
ENSG00000(	2.071584	0	2.638828	2364.832	2310.284	2137.109	-9.9095	1.20E-66	4.89E-65	DLX5	chr7	-	96649704	96654409	1688
ENSG00000(	1806.421	1686.003	2443.554	976.7945	1744.219	1121.982	0.62449	0.001088	0.003035	MTPN	chr7	-	1.36E+08	1.36E+08	3738
ENSG00000(	137.7603	143.3102	127.9831	31.46117	21.16994	18.08323	2.4905	1.52E-15	1.24E-14	STEAP1B	chr7	-	22459063	22672544	1515
ENSG00000(	1921.394	1975.032	1588.574	3085.442	2764.978	3178.538	-0.71716	6.83E-09	3.48E-08	PTN	chr7	-	1.37E+08	1.37E+08	1614
ENSG00000(	153.2972	173.4174	222.9809	309.3682	360.8093	290.1536	-0.8042	5.20E-05	0.000176	MPP6	chr7	+	24612887	24729159	3848
ENSG00000(	418.4599	358.8777	451.2395	447.1981	454.6934	433.1755	-0.11993	0.43681	0.5665	DFNA5	chr7	-	24737972	24809244	4182
ENSG00000(	0	0	0	0	2.761296	3.28786	-1.6293	0.2296	0.34285	ATP6V0A4	chr7	-	1.38E+08	1.38E+08	3135
ENSG00000(	302.4512	264.9433	263.8828	1131.853	1306.093	1079.24	-2.0725	6.21E-46	1.52E-44	ZC3HAV1	chr7	-	1.39E+08	1.39E+08	7100
ENSG00000(	191.6215	202.3203	183.3985	241.9514	186.8477	157.8173	-0.02416	0.91031	0.94496	TTC26	chr7	+	1.39E+08	1.39E+08	4299
ENSG00000(	1664.518	1602.907	1617.601	2519.141	2301.08	2341.778	-0.55114	3.87E-07	1.68E-06	OGDH	chr7	+	44646171	44748665	4181
ENSG00000(	10.35792	1.204288	0	11.98521	10.12475	18.90519	-1.5645	0.072194	0.13322	ADAP1	chr7	-	937540	995043	2363
ENSG00000(	3.107376	4.817151	0	20.22504	11.96562	6.575719	-1.9914	0.023809	0.050736	TFEC	chr7	-	1.16E+08	1.16E+08	6628
ENSG00000(	1148.693	1012.806	1118.863	2250.972	2170.379	2305.612	-1.0341	1.46E-19	1.45E-18	H2AFV	chr7	-	44866390	44887682	3804
ENSG00000(	297.2723	391.3935	428.8095	1098.894	721.6187	748.81	-1.1985	2.31E-10	1.33E-09	CAV2	chr7	+	1.16E+08	1.16E+08	3301
ENSG00000(	5877.083	5566.218	6097.011	4900.452	3597.048	3453.897	0.55183	5.51E-05	0.000186	CAV1	chr7	+	1.16E+08	1.16E+08	2704
ENSG00000(	324.2029	291.4376	411.6571	1299.646	1410.102	1023.346	-1.8563	1.15E-28	1.67E-27	MET	chr7	+	1.16E+08	1.16E+08	6635
ENSG00000(	40.39588	25.29004	21.11062	22.47227	20.2495	26.30288	0.32815	0.48671	0.61585	RNF32	chr7	+	1.56E+08	1.56E+08	2260
ENSG00000(	540.6834	573.241	707.2058	856.9424	920.432	733.1927	-0.46314	0.002384	0.006268	LMBR1	chr7	-	1.56E+08	1.57E+08	4911
ENSG00000(	0	1.204288	1.319414	0	1.840864	2.465895	-0.45422	0.73462	0.82247	NHP2P1	chr10	+	93976089	93976550	462
ENSG00000(	0	0	0	24.71949	19.32907	24.65895	-5.3838	7.14E-07	3.00E-06	WNT2	chr7	-	1.17E+08	1.17E+08	2907
ENSG00000(	17.60846	25.29004	18.47179	47.94084	42.33987	33.70056	-0.98993	0.024098	0.051301	HOXA1	chr7	-	27132612	27135615	2517
ENSG00000(	1979.398	1846.173	2166.477	2793.303	2813.761	2723.992	-0.47493	1.93E-05	6.91E-05	DNAJB6	chr7	+	1.57E+08	1.57E+08	7992
ENSG00000(	9.322127	10.83859	13.19414	13.48336	17.48821	13.15144	-0.38447	0.53609	0.66026	HOXA2	chr7	-	27139721	27142430	2066
ENSG00000(	113.9371	91.52587	96.31721	77.90386	79.15715	78.08667	0.3592	0.17309	0.27445	HOXA3	chr7	-	27145803	27192200	3263
ENSG00000(	15.53688	26.49433	36.94359	76.40571	78.23672	50.96182	-1.3646	0.00064	0.001851	LFNG	chr7	+	2552163	2568811	2377
ENSG00000(	111.8655	122.8373	89.72014	6.74168	8.283888	8.219649	3.7241	1.68E-20	1.73E-19	HOXA5	chr7	-	27180671	27183287	1657
ENSG00000(	23.82321	31.31148	51.45714	0	0	3.28786	4.4996	1.20E-08	5.99E-08	HOXA6	chr7	-	27185015	27192217	989
ENSG00000(	825.5261	687.6483	612.208	1101.89	921.3524	974.8504	-0.49351	0.000803	0.002288	BRAT1	chr7	-	2577511	2595361	5360
ENSG00000(	703.3027	810.4856	790.3289	398.5082	585.3947	509.6182	0.62431	0.000109	0.000354	IQCE	chr7	+	2598632	2654368	6844

ENSG00000(	0	0	0	2.247227	9.20432	5.753754	-3.2864	0.008952	0.021044	VIPR2	chr7	-	1.59E+08	1.59E+08	3944
ENSG00000(	17.60846	22.88147	31.66593	420.9805	427.0804	383.0357	-4.0769	1.37E-55	4.29E-54	TSPAN12	chr7	-	1.2E+08	1.2E+08	2796
ENSG00000(	977.7876	1060.977	944.7003	2095.164	1591.427	1934.083	-0.91189	1.03E-11	6.57E-11	SSBP1	chr7	+	1.41E+08	1.41E+08	2620
ENSG00000(	420.5315	460.0379	496.0996	0	0	2.465895	8.4453	8.22E-39	1.65E-37	HOXA13	chr7	-	27233122	27239725	4376
ENSG00000(	159.512	156.5574	188.6762	25.46857	47.86246	31.23467	2.2547	6.39E-15	5.01E-14	CPED1	chr7	+	1.21E+08	1.21E+08	5340
ENSG00000(	1.035792	0	0	0	0	2.465895	-0.37334	0.77636	NA	EVX1	chr7	+	27282164	27290112	2712
ENSG00000(	583.1508	488.9408	511.9325	357.309	281.6522	292.6195	0.76248	3.01E-06	1.19E-05	HIBADH	chr7	-	27565061	27702614	1990
ENSG00000(	1075.152	1040.505	1146.571	1026.234	787.8898	732.3707	0.35526	0.016181	0.035867	TAX1BP1	chr7	+	27778950	27880938	2890
ENSG00000(	73.54123	56.60152	65.97069	925.8574	695.8466	661.6818	-3.518	1.75E-66	7.04E-65	CPVL	chr7	-	29034847	29235067	2213
ENSG00000(	18.64425	14.45145	27.70769	163.2985	204.3359	164.393	-3.0961	3.18E-22	3.53E-21	CHN2	chr7	+	29161956	29553944	3530
ENSG00000(	1575.439	1613.746	1626.837	909.3777	984.8622	883.6123	0.79267	8.44E-12	5.40E-11	GRB10	chr7	-	50657760	50861159	5432
ENSG00000(	145.0109	143.3102	114.789	563.3048	481.3859	593.4587	-2.0106	7.86E-29	1.14E-27	ABHD11	chr7	-	73150424	73153197	1562
ENSG00000(	2.071584	0	0	289.1432	348.8437	312.3467	-7.7971	1.15E-26	1.51E-25	COBL	chr7	-	51083909	51384515	7697
ENSG00000(	1529.865	1737.787	1951.413	558.0613	566.9861	484.9593	1.6919	3.25E-35	5.87E-34	FKBP14	chr7	-	30050203	30066300	4960
ENSG00000(	103.5792	87.913	157.0102	143.8225	269.6866	169.3248	-0.73525	0.008815	0.020747	PLEKHA8	chr7	+	30067020	30170096	3050
ENSG00000(	169.8699	190.2775	125.3443	107.8669	83.75931	106.8554	0.69594	0.004786	0.011898	STX1A	chr7	-	73113536	73134002	2095
ENSG00000(	265.1627	326.362	258.6051	208.243	266.0048	220.2866	0.2919	0.12296	0.20806	NOD1	chr7	-	30464143	30518400	4610
ENSG00000(	4535.733	4617.239	4537.464	4489.21	3440.575	3469.514	0.26341	0.034722	0.070647	GARS	chr7	+	30634297	30673649	2634
ENSG00000(	0	0	3.958241	0	1.840864	0	0.51729	0.70257	NA	CRHR2	chr7	-	30692200	30739745	2530
ENSG00000(	26.93059	28.90291	29.0271	126.5938	173.9616	249.8773	-2.6602	1.15E-16	9.90E-16	EPHB6	chr7	+	1.43E+08	1.43E+08	4406
ENSG00000(	7.250543	4.817151	0	0	1.840864	1.64393	1.3226	0.27429	0.39542	FAM188B	chr7	+	30811033	30932002	3573
ENSG00000(	0	2.408575	1.319414	0.749076	0.920432	0	0.60573	0.65463	NA	GHRHR	chr7	+	30978284	31032869	1613
ENSG00000(	4.143168	10.83859	15.83297	9.737982	25.7721	33.70056	-1.1114	0.086438	0.15547	NSUN5P2	chr7	-	72418120	72425329	1789
ENSG00000(	542.755	507.0051	518.5296	1231.48	1184.596	969.0966	-1.1067	2.93E-15	2.35E-14	CASP2	chr7	+	1.43E+08	1.43E+08	5769
ENSG00000(	2370.928	2351.974	1709.96	2344.606	2005.621	2261.225	-0.03897	0.78213	0.85651	CHCHD2	chr7	-	56169262	56174269	901
ENSG00000(	7811.943	7020.997	5127.242	1491.409	1205.766	1300.349	2.3127	1.42E-53	4.25E-52	HSPB1	chr7	+	75931861	75933612	1455
ENSG00000(	412.2452	433.5436	424.8512	131.0882	133.4626	109.3213	1.7575	5.27E-23	6.03E-22	NPTX2	chr7	+	98246609	98259180	2700
ENSG00000(	3309.355	3160.051	3137.566	3061.472	3587.844	4780.548	-0.24977	0.08945	0.15998	PDAP1	chr7	-	98989671	99006452	2546
ENSG00000(	651.5131	750.2712	601.6527	591.7697	770.4016	699.4921	-0.03997	0.79227	0.86423	BUD31	chr7	+	99006264	99017239	1139
ENSG00000(	8.286335	24.08575	18.47179	41.94823	39.57858	49.3179	-1.3353	0.004696	0.0117	PTCD1	chr7	-	99014362	99063820	5582
ENSG00000(	31.07376	22.88147	21.11062	19.47596	29.45382	13.15144	0.27459	0.58863	0.70573	CYP3A5	chr7	-	99245817	99277621	3320
ENSG00000(	2252.847	2301.394	2778.685	809.0016	1210.368	999.5093	1.277	4.69E-17	4.12E-16	ZKSCAN1	chr7	+	99613204	99639312	9418
ENSG00000(	5079.523	5125.449	4554.616	6826.325	6359.265	6495.167	-0.41441	6.79E-05	0.000226	EIF3B	chr7	+	2393721	2420380	3745
ENSG00000(	825.5261	846.6143	815.3977	802.2599	889.1373	1209.11	-0.22067	0.16206	0.25979	SNX8	chr7	-	2291405	2393953	4727
ENSG00000(	204.051	267.3519	228.2586	280.9033	324.9125	490.7131	-0.64484	0.003089	0.007958	NUDT1	chr7	+	2281857	2290781	872
ENSG00000(	3.107376	1.204288	0	29.21395	26.69253	13.9734	-3.4897	2.91E-05	0.000102	PTPRZ1	chr7	+	1.22E+08	1.22E+08	8175
ENSG00000(	664.9784	535.908	563.3897	623.2309	702.2896	749.632	-0.23169	0.11586	0.1981	TAF6	chr7	-	99704693	99717464	2727
ENSG00000(	928.0695	887.56	1100.391	673.4189	999.5891	729.0829	0.27923	0.087512	0.15709	WASL	chr7	-	1.23E+08	1.23E+08	4435
ENSG00000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	HYAL4	chr7	+	1.23E+08	1.24E+08	2407
ENSG00000(	0	0	0	14.98151	12.88605	7.397684	-4.4058	0.000139	0.000444	SPAM1	chr7	+	1.24E+08	1.24E+08	2349
ENSG00000(	291.0575	290.2333	269.1604	773.046	593.6786	591.8147	-1.1991	2.67E-13	1.90E-12	AIMP2	chr7	+	6048876	6063465	1225
ENSG00000(	18.64425	54.19295	18.47179	16.47966	10.12475	6.575719	1.38	0.019574	0.042558	TFR2	chr7	-	1E+08	1E+08	3131
ENSG00000(	3.107376	1.204288	3.958241	3.745378	5.522592	2.465895	-0.41133	0.69442	0.79168	FSCN3	chr7	+	1.27E+08	1.27E+08	2238
ENSG00000(	501.3233	467.2636	374.7135	274.1617	237.4715	189.0519	0.93514	7.21E-07	3.03E-06	MOSPD3	chr7	+	1E+08	1E+08	1191

ENSG00000(	10216.02	11242.03	7977.176	886.1564	595.5195	583.5951	3.8179	3.93E-119	4.08E-117	PCOLCE	chr7	+	1E+08	1E+08	1702
ENSG00000(	13.46529	13.24716	9.235896	1.498151	8.283888	5.753754	1.1198	0.15146	0.24599	FBXO24	chr7	+	1E+08	1E+08	2276
ENSG00000(	461.9632	388.9849	427.4901	763.308	765.7994	781.6886	-0.85069	8.94E-10	4.92E-09	RBM28	chr7	-	1.28E+08	1.28E+08	2808
ENSG00000(	370.8135	295.0505	406.3794	346.822	440.8869	338.6495	-0.06997	0.69897	0.79531	USP42	chr7	+	6144515	6201195	5155
ENSG00000(	1956.611	1633.014	1527.881	1829.992	1457.964	1648.862	0.052071	0.70208	0.79743	IMPDH1	chr7	-	1.28E+08	1.28E+08	2881
ENSG00000(	464.0348	369.7163	349.6447	230.7153	251.2779	231.7941	0.72934	3.24E-05	0.000113	AGFG2	chr7	+	1E+08	1E+08	4796
ENSG00000(	415.3526	494.9623	381.3106	1292.155	1072.303	1224.728	-1.4702	8.91E-24	1.05E-22	LSM5	chr7	-	32524951	32534895	2251
ENSG00000(	8560.82	8226.489	8110.437	570.0465	322.1512	383.8576	4.2681	3.86E-152	5.97E-150	SERPINE1	chr7	+	1.01E+08	1.01E+08	3190
ENSG00000(	3022.441	3180.524	2683.688	3070.461	3289.624	4321.07	-0.26446	0.058258	0.11095	AP1S1	chr7	+	1.01E+08	1.01E+08	1306
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	MOGAT3	chr7	-	1.01E+08	1.01E+08	2132
ENSG00000(	510.6454	619.0039	713.8029	982.038	961.8514	840.8701	-0.59545	8.47E-05	0.000279	C1GALT1	chr7	+	7196565	7288251	6208
ENSG00000(	5343.65	5015.858	4376.496	3165.593	2528.427	2789.749	0.79484	1.77E-10	1.03E-09	PLOD3	chr7	-	1.01E+08	1.01E+08	2920
ENSG00000(	151.2256	144.5145	131.9414	363.3016	296.3791	413.4484	-1.3191	2.11E-11	1.31E-10	RPA3	chr7	-	7676149	7758238	2020
ENSG00000(	2907.468	2685.562	2042.453	1853.213	1434.033	1713.797	0.60882	4.00E-05	0.000138	ZNHIT1	chr7	+	1.01E+08	1.01E+08	3958
ENSG00000(	174.013	152.9445	150.4132	143.0734	136.2239	201.3814	-0.00873	0.96955	0.9821	CLDN15	chr7	-	1.01E+08	1.01E+08	2131
ENSG00000(	140.8677	192.686	192.6344	89.88907	83.75931	76.44274	1.0609	9.97E-06	3.70E-05	GLCCI1	chr7	+	8008425	8133902	4743
ENSG00000(	588.3298	696.0783	637.2769	928.1046	852.32	775.1129	-0.41115	0.003033	0.007828	PHF14	chr7	+	11013499	11209250	4276
ENSG00000(	189.5499	180.6432	215.0644	323.6006	373.6954	369.8842	-0.86381	1.13E-06	4.67E-06	NRF1	chr7	+	1.29E+08	1.29E+08	3528
ENSG00000(	506.5022	441.9736	591.0974	779.0386	764.879	681.4089	-0.53094	0.000416	0.001238	TMEM106B	chr7	+	12250867	12276886	6432
ENSG00000(	249.6258	195.0946	257.2857	1097.396	927.7955	961.699	-2.0825	3.31E-40	6.87E-39	EZH2	chr7	-	1.49E+08	1.49E+08	3641
ENSG00000(	218.5521	239.6533	292.9099	333.3386	262.3231	270.4265	-0.20864	0.2738	0.39492	CEP41	chr7	-	1.3E+08	1.3E+08	3750
ENSG00000(	399.8157	443.1779	395.8241	125.8447	163.8369	150.4196	1.4892	1.57E-16	1.34E-15	ZNF862	chr7	+	1.5E+08	1.5E+08	6950
ENSG00000(	1846.817	1866.646	1760.098	779.0386	673.7562	581.1292	1.4242	2.38E-26	3.10E-25	SFRP4	chr7	-	37945543	38065297	2957
ENSG00000(	3600.413	3933.204	3835.536	5921.442	4738.384	5062.482	-0.46712	6.28E-05	0.00021	MEST	chr7	+	1.3E+08	1.3E+08	2465
ENSG00000(	760.2713	733.4112	726.997	0	0	0.821965	9.815	1.36E-36	2.55E-35	MEOX2	chr7	-	15650837	15726437	2500
ENSG00000(	353.205	368.512	386.5882	506.3751	467.5795	392.8992	-0.30263	0.05919	0.11238	ANKMY2	chr7	-	16639401	16685442	2599
ENSG00000(	0	0	0	2.247227	0.920432	2.465895	-1.668	0.21871	NA	ACTR3C	chr7	-	1.5E+08	1.5E+08	5697
ENSG00000(	3.107376	0	0	8.988907	11.04518	8.219649	-2.5068	0.015383	0.034254	POU6F2	chr7	+	39017598	39532694	5925
ENSG00000(	108.7581	108.3859	117.4278	683.906	508.9989	553.1824	-2.3749	3.79E-37	7.24E-36	TSPAN13	chr7	+	16793160	16824161	2093
ENSG00000(	0	1.204288	0	4573.106	4252.396	5765.262	-11.838	3.21E-58	1.07E-56	RARRES2	chr7	-	1.5E+08	1.5E+08	1905
ENSG00000(	2.071584	0	0	0	1.840864	0.821965	-0.14076	0.91727	NA	AGR2	chr7	-	16831435	16873057	1778
ENSG00000(	2242.489	2079.805	2534.594	834.4702	817.3436	721.6852	1.5269	1.73E-33	2.95E-32	AHR	chr7	+	17338246	17385776	6276
ENSG00000(	946.7138	1100.719	963.1721	1751.339	1688.993	1892.163	-0.8234	1.53E-11	9.58E-11	CHCHD3	chr7	-	1.32E+08	1.33E+08	1598
ENSG00000(	0	0	0	0.749076	1.840864	0	-0.68825	0.58858	NA	TMEM176B	chr7	-	1.5E+08	1.5E+08	1430
ENSG00000(	1810.564	1767.894	2192.866	1250.956	1796.683	1329.939	0.39778	0.00882	0.020758	GLI3	chr7	-	42000548	42277469	8208
ENSG00000(	39.36009	46.96722	32.98534	93.63444	64.43024	60.8254	-0.86146	0.013028	0.029504	PSMA2	chr7	-	42956460	42971822	4251
ENSG00000(	688.8016	716.5512	575.2644	785.7803	653.5067	742.2343	-0.13866	0.33941	0.46804	MRPL32	chr7	+	42971799	42988557	2734
ENSG00000(	753.0207	809.2813	770.5376	773.046	746.4703	784.1545	0.017701	0.88777	0.93022	COA1	chr7	-	43648055	43769316	3223
ENSG00000(	620.4394	582.8753	531.7238	173.0365	150.0304	184.1201	1.7671	9.10E-27	1.21E-25	BLVRA	chr7	+	43798279	43846939	1159
ENSG00000(	497.1801	467.2636	394.5047	436.711	317.549	440.5732	0.1849	0.29153	0.41564	URGCP	chr7	-	43915493	43966010	5658
ENSG00000(	1827.137	1840.152	1922.386	1783.549	1603.393	1509.95	0.19011	0.1018	0.17801	TMEM248	chr7	+	66386212	66423538	4229
ENSG00000(	66.29068	84.30014	100.2754	179.0291	140.8261	163.571	-0.94616	0.000168	0.000531	STAG3L4	chr7	+	66767608	66786513	2143
ENSG00000(	630.7973	641.8854	546.2373	2468.953	2049.802	2236.567	-1.8878	2.82E-48	7.39E-47	RHEB	chr7	-	1.51E+08	1.51E+08	2075
ENSG00000(	121.1877	136.0845	163.6073	1067.433	854.1609	854.0216	-2.7164	1.37E-55	4.30E-54	PRKAG2	chr7	-	1.51E+08	1.52E+08	3305

ENSG0000(	11501.43	11044.52	9605.332	667.4263	791.5715	687.1627	3.8985	2.63E-233	1.10E-230	AEBP1	chr7	+	44143960	44154161	4081
ENSG0000(	3302.105	3249.168	2652.022	3452.489	2598.38	2909.756	0.038495	0.77655	0.85305	POLD2	chr7	-	44154286	44163957	2158
ENSG0000(	2.071584	0	0	86.89276	73.63456	120.0069	-6.1226	1.06E-14	8.18E-14	MYL7	chr7	-	44178463	44180931	791
ENSG0000(	66.29068	81.89156	68.60952	0	0.920432	0.821965	6.2177	5.09E-15	4.02E-14	GCK	chr7	-	44183872	44237769	2729
ENSG0000(	556.2203	552.7681	469.7113	934.0972	763.9586	777.5788	-0.64659	1.01E-05	3.75E-05	BCL7B	chr7	-	72950686	72972332	1975
ENSG0000(	4281.964	3762.195	4352.746	3373.836	3416.644	3692.266	0.24157	0.028038	0.058569	YKT6	chr7	+	44240567	44253893	2696
ENSG0000(	1317.527	1224.761	1114.905	791.7729	695.8466	719.2193	0.72729	1.80E-08	8.89E-08	TBL2	chr7	-	72983990	72993121	2430
ENSG0000(	3136.378	2945.688	2948.89	193.2615	248.5166	241.6577	3.7183	3.40E-175	7.40E-173	CLIP2	chr7	+	73703805	73820273	5563
ENSG0000(	10297.84	9681.269	9940.463	7974.658	9052.449	9948.241	0.14928	0.18163	0.28484	EIF4H	chr7	+	73588575	73611431	2679
ENSG0000(	595.5803	528.6823	505.3355	661.4337	605.6443	800.5938	-0.34154	0.025892	0.054631	LIMK1	chr7	+	73497263	73536855	3374
ENSG0000(	1.035792	3.612863	10.55531	17.22874	21.16994	13.9734	-1.6713	0.025853	0.054557	SPATA6L	chr9	-	4553386	4666674	4073
ENSG0000(	152.2614	148.1274	205.8285	14.98151	18.40864	20.54912	3.189	1.55E-24	1.88E-23	SLC1A1	chr9	+	4490444	4587469	3722
ENSG0000(	3.107376	6.021439	3.958241	2.996302	4.60216	0.821965	0.52819	0.60859	0.72266	LHX2	chr9	+	1.27E+08	1.27E+08	2554
ENSG0000(	457.82	473.2851	655.7486	364.7998	291.7769	306.5929	0.71399	7.14E-05	0.000237	FKTN	chr9	+	1.08E+08	1.08E+08	7364
ENSG0000(	90.1139	113.203	166.2461	118.3539	78.23672	83.84042	0.38531	0.18251	0.28607	FSD1L	chr9	+	1.08E+08	1.08E+08	7623
ENSG0000(	132.5814	132.4716	191.315	61.42419	52.46462	59.18147	1.3799	2.33E-07	1.03E-06	CNTNAP3	chr9	-	39072764	39288312	5064
ENSG0000(	1311.313	1439.124	1669.058	1507.889	1621.801	1354.598	-0.02161	0.8702	0.91845	SPIN1	chr9	+	91003334	91093609	4484
ENSG0000(	359.4198	334.792	312.7011	382.7776	308.3447	357.5547	-0.05834	0.72572	0.81607	NMRK1	chr9	-	77675489	77703133	2050
ENSG0000(	886.6379	914.0544	1155.806	1212.004	1359.478	1131.024	-0.32463	0.021969	0.04718	TMEM245	chr9	-	1.12E+08	1.12E+08	7980
ENSG0000(	2153.411	2243.588	2842.017	56.18067	92.0432	73.97684	5.0136	1.71E-177	3.85E-175	PRUNE2	chr9	-	79226292	79521003	12587
ENSG0000(	317.9881	248.0833	340.4088	178.28	256.8005	152.0635	0.62467	0.00465	0.011594	MEGF9	chr9	-	1.23E+08	1.23E+08	6298
ENSG0000(	33.14534	37.33292	50.13772	59.92604	74.55499	77.2647	-0.80465	0.018131	0.039717	TRIM14	chr9	-	1.01E+08	1.01E+08	4454
ENSG0000(	14.50109	12.04288	14.51355	545.327	596.4399	487.4252	-5.2453	4.50E-72	2.03E-70	CORO2A	chr9	-	1.01E+08	1.01E+08	5635
ENSG0000(	614.2246	561.1981	815.3977	1347.587	1768.15	1380.079	-1.172	5.18E-13	3.62E-12	TGFBR1	chr9	+	1.02E+08	1.02E+08	6516
ENSG0000(	2440.326	2460.36	1971.204	1458.45	1420.227	2151.082	0.44884	0.005329	0.013132	SEC61B	chr9	+	1.02E+08	1.02E+08	687
ENSG0000(	23.82321	43.35436	51.45714	158.804	150.9508	126.5826	-1.8697	1.25E-09	6.77E-09	C5	chr9	-	1.24E+08	1.24E+08	5462
ENSG0000(	137.7603	217.9761	130.622	1.498151	7.363456	0.821965	5.5137	2.54E-28	3.62E-27	OGN	chr9	-	95146249	95166978	2971
ENSG0000(	65.25489	83.09585	72.56776	5.243529	3.681728	4.109825	3.9297	1.17E-15	9.60E-15	ASPN	chr9	-	95218487	95244788	2470
ENSG0000(	34.18113	38.53721	65.97069	5.992604	11.96562	4.93179	2.5072	1.94E-06	7.79E-06	ECM2	chr9	-	95256365	95298937	3253
ENSG0000(	1721.486	1581.23	1918.428	1120.617	1239.822	863.8851	0.69341	2.59E-06	1.03E-05	TLE4	chr9	+	82186688	82341658	4845
ENSG0000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	LHX6	chr9	-	1.25E+08	1.25E+08	3587
ENSG0000(	704.3385	674.4011	626.7215	1091.403	1066.781	1040.608	-0.67124	7.91E-08	3.66E-07	PTGR1	chr9	-	1.14E+08	1.14E+08	2298
ENSG0000(	151.2256	142.106	139.8579	329.5932	404.0696	303.3051	-1.2504	1.03E-10	6.10E-10	SUSD1	chr9	-	1.15E+08	1.15E+08	3124
ENSG0000(	15.53688	6.021439	0	0	2.761296	8.219649	0.80213	0.45455	0.58424	AMBP	chr9	-	1.17E+08	1.17E+08	1434
ENSG0000(	296.2365	397.4149	263.8828	606.7512	733.5843	671.5453	-1.0657	8.14E-10	4.49E-09	AKNA	chr9	-	1.17E+08	1.17E+08	7380
ENSG0000(	0	0	0	7.490755	0	2.465895	-2.3194	0.084332	0.15224	TNFSF8	chr9	-	1.18E+08	1.18E+08	1906
ENSG0000(	3036.942	2832.485	2365.709	220.9773	207.0972	207.1352	3.6867	3.98E-158	6.77E-156	DNM1	chr9	+	1.31E+08	1.31E+08	3286
ENSG0000(	4975.944	4522.1	4625.865	125.8447	104.0088	124.1167	5.3017	0	0	ENG	chr9	-	1.31E+08	1.31E+08	3059
ENSG0000(	191.6215	169.8046	127.9831	21.72319	34.97642	30.4127	2.4706	1.31E-16	1.13E-15	AK1	chr9	-	1.31E+08	1.31E+08	2266
ENSG0000(	213.3731	279.3948	246.7304	228.468	189.609	166.8589	0.33361	0.10026	0.17584	CDC37L1	chr9	+	4679559	4708398	3502
ENSG0000(	1.035792	0	0	31.46117	34.05598	33.70056	-5.185	7.05E-08	3.28E-07	RLN2	chr9	-	5299868	5304969	1177
ENSG0000(	0	0	0	2.247227	7.363456	6.575719	-3.2021	0.01126	0.02588	RLN1	chr9	-	5334969	5339873	1068
ENSG0000(	117.0445	107.1816	105.5531	384.2758	350.6846	362.4865	-1.7244	4.94E-20	5.00E-19	PLGRKT	chr9	-	5357973	5437878	932
ENSG0000(	798.5956	720.1641	790.3289	624.729	669.1541	682.2309	0.22462	0.085881	0.15472	TBC1D13	chr9	+	1.32E+08	1.32E+08	3906

ENSG00000(	591.4372	684.0354	1043.656	733.345	842.1953	552.3604	0.12216	0.54379	0.66614	KIAA1432	chr9	+	5629025	5776557	6774
ENSG00000(	399.8157	351.652	449.9201	162.5494	186.8477	128.2265	1.3249	8.72E-12	5.57E-11	KDM4C	chr9	+	6720863	7175648	4655
ENSG00000(	0	1.204288	1.319414	264.4237	439.0461	309.0588	-7.862	6.60E-27	8.82E-26	DOCK8	chr9	+	214854	465259	9277
ENSG00000(	383.243	413.0707	523.8073	743.832	779.6059	715.9314	-0.76245	6.82E-07	2.87E-06	KANK1	chr9	+	470291	746105	7193
ENSG00000(	194.7289	164.9874	282.3545	2044.976	2449.27	1748.319	-3.2707	1.28E-72	5.83E-71	ELAVL2	chr9	-	23690102	23826335	3805
ENSG00000(	4874.437	4508.853	4335.594	1829.242	1962.361	1916.822	1.2634	2.39E-32	3.90E-31	NCS1	chr9	+	1.33E+08	1.33E+08	4991
ENSG00000(	390.4935	405.845	332.4923	263.6746	219.0628	222.7525	0.67503	0.000109	0.000353	TESK1	chr9	+	35605367	35610038	2421
ENSG00000(	0	4.817151	0	3.745378	4.60216	4.109825	-1.0319	0.37822	0.50892	KCNT1	chr9	+	1.39E+08	1.39E+08	4830
ENSG00000(	223.7311	248.0833	141.1773	0	10.12475	3.28786	4.7478	3.44E-07	1.50E-06	CA9	chr9	+	35673853	35681156	1618
ENSG00000(	1655.195	1645.057	1959.329	1298.897	1791.161	1825.584	0.097339	0.50837	0.63585	FUBP3	chr9	+	1.33E+08	1.34E+08	3124
ENSG00000(	2.071584	4.817151	3.958241	3.745378	1.840864	0	0.72006	0.52973	0.65448	TYRP1	chr9	+	12685439	12710290	2851
ENSG00000(	1072.045	1027.257	1116.224	1152.078	887.2964	1071.842	0.046509	0.72996	0.81912	CREB3	chr9	+	35732332	35737001	1832
ENSG00000(	757.1639	746.6584	778.4541	332.5895	636.9389	563.046	0.57314	0.003288	0.008444	RGP1	chr9	+	35749203	35758572	7018
ENSG00000(	603.8667	651.5197	821.9948	734.8431	1001.43	761.1395	-0.26532	0.10791	0.18669	MPDZ	chr9	-	13105703	13279589	7722
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	LHX3	chr9	-	1.39E+08	1.39E+08	2403
ENSG00000(	150.1898	114.4073	172.8432	298.8811	333.1964	209.6011	-0.93795	4.52E-05	0.000155	DDX58	chr9	-	32455300	32526322	4621
ENSG00000(	4274.713	4101.804	3480.614	2003.028	2554.199	3845.152	0.49488	0.006355	0.015423	EDF1	chr9	-	1.4E+08	1.4E+08	809
ENSG00000(	0	0	2.638828	26.21764	23.0108	12.32947	-3.9276	2.96E-05	0.000104	PIP5K1B	chr9	+	71320575	71624092	3335
ENSG00000(	3765.104	3801.936	4657.531	66.66772	70.87326	43.56414	6.0551	4.75E-280	3.10E-277	GLIS3	chr9	-	3824127	4348392	6667
ENSG00000(	740.5912	706.9169	653.1098	1096.647	1003.271	1016.771	-0.56727	8.14E-06	3.05E-05	BAG1	chr9	-	33247818	33264761	3865
ENSG00000(	1326.849	1221.148	1353.719	1367.812	1980.77	1688.316	-0.36682	0.010629	0.024551	RAPGEF1	chr9	-	1.34E+08	1.35E+08	6256
ENSG00000(	772.7008	621.4125	489.5025	794.7692	567.9065	678.943	-0.11451	0.52492	0.64984	NPDC1	chr9	-	1.4E+08	1.4E+08	2187
ENSG00000(	669.1216	673.1968	814.0783	85.39461	126.0992	94.52597	2.809	1.16E-52	3.42E-51	APBA1	chr9	-	72042446	72287222	6534
ENSG00000(	1036.828	1116.375	1385.384	829.9757	917.6707	687.1627	0.53706	0.000455	0.001345	SETX	chr9	-	1.35E+08	1.35E+08	11103
ENSG00000(	2.071584	9.634302	1.319414	329.5932	369.0932	261.3848	-6.0229	7.00E-40	1.44E-38	SH3GL2	chr9	+	17579080	17797127	2565
ENSG00000(	237.1963	243.2661	189.9956	0	0.920432	0	8.2149	1.72E-23	2.00E-22	PTGDS	chr9	+	1.4E+08	1.4E+08	989
ENSG00000(	1082.403	1030.87	857.619	69.66403	66.2711	54.24968	3.9482	1.88E-108	1.63E-106	ABCA2	chr9	-	1.4E+08	1.4E+08	8154
ENSG00000(	244.4469	231.2232	201.8703	309.3682	300.0608	338.6495	-0.48058	0.006378	0.015477	SHB	chr9	-	37919131	38069210	2783
ENSG00000(	2100.586	2111.116	2066.202	2183.555	1970.645	1913.534	0.048872	0.65933	0.76383	UBE2R2	chr9	+	33817565	33920402	4075
ENSG00000(	273.4491	314.3191	325.8952	458.4342	493.3516	393.7212	-0.55777	0.000777	0.002218	ABHD17B	chr9	-	74477368	74525847	2614
ENSG00000(	189.5499	196.2989	168.885	400.7554	367.2524	440.5732	-1.1177	1.87E-10	1.09E-09	EXOSC3	chr9	-	37766975	37801434	1625
ENSG00000(	3748.531	3650.196	3956.922	3250.239	3028.221	2547.269	0.36275	0.002476	0.006488	ZFAND5	chr9	-	74966341	74980163	5728
ENSG00000(	1631.372	1517.403	1287.748	1397.775	1405.5	1725.304	-0.02882	0.83349	0.89318	DVL1	chr1	-	1270656	1284730	3239
ENSG00000(	855.5641	882.7429	728.3164	6709.47	4879.21	5210.436	-2.7597	1.12E-85	6.60E-84	PDLIM1	chr10	-	96997329	97050781	1452
ENSG00000(	224.7668	217.9761	274.4381	692.8949	856.0018	690.4505	-1.6384	2.80E-23	3.23E-22	CCNJ	chr10	+	97803151	97820627	4115
ENSG00000(	2.071584	7.225726	3.958241	1338.598	1195.641	1112.941	-7.9253	2.49E-79	1.33E-77	GATA3	chr10	+	8095567	8117161	3078
ENSG00000(	186.4425	254.1047	225.6198	50.18806	69.95283	55.89361	1.9078	4.93E-15	3.90E-14	ATRNL1	chr10	+	1.17E+08	1.18E+08	8479
ENSG00000(	1419.035	1242.825	1190.111	1115.373	932.3976	1015.127	0.33014	0.011428	0.026209	HPS1	chr10	-	1E+08	1E+08	3703
ENSG00000(	209.23	228.8147	217.7033	162.5494	124.2583	122.4728	0.67303	0.001329	0.003659	PHYH	chr10	-	13319796	13344412	1829
ENSG00000(	39.36009	30.10719	26.38828	749.8246	661.7906	654.2841	-4.3836	7.07E-86	4.19E-84	RASSF4	chr10	+	45454855	45490172	4350
ENSG00000(	1137.3	991.1288	1238.93	791.7729	772.2424	654.2841	0.60023	1.71E-05	6.18E-05	DNMBP	chr10	-	1.02E+08	1.02E+08	6472
ENSG00000(	178.1562	211.9546	254.6469	257.682	261.4027	201.3814	-0.16257	0.4282	0.55842	RAB11FIP2	chr10	-	1.2E+08	1.2E+08	6061
ENSG00000(	151.2256	185.4603	130.622	1990.294	2093.062	1901.205	-3.6656	9.97E-134	1.25E-131	CXCL12	chr10	-	44793038	44881941	3532
ENSG00000(	808.9535	899.6029	938.1032	1298.148	1269.276	1074.308	-0.46027	0.000507	0.00149	ERLIN1	chr10	-	1.02E+08	1.02E+08	5792

ENSG00000(	8368.163	7646.023	8749.033	3976.093	6099.703	4740.272	0.73918	2.61E-07	1.15E-06	EIF3A	chr10	-	1.21E+08	1.21E+08	5472
ENSG00000(	44.53905	63.82725	75.20659	12.73428	9.20432	5.753754	2.6349	1.27E-08	6.32E-08	CUBN	chr10	-	16865963	17171830	11949
ENSG00000(	79.75598	90.32158	108.1919	149.066	125.1788	120.8288	-0.50699	0.043157	0.085527	TRDMT1	chr10	-	17184253	17244053	8230
ENSG00000(	0	0	0	4.494453	1.840864	2.465895	-2.3009	0.084026	0.15172	RBP3	chr10	-	48381487	48390991	4276
ENSG00000(	8.286335	0	0	2.247227	4.60216	6.575719	-0.50253	0.6575	0.76231	GDF10	chr10	-	48425815	48438976	2458
ENSG00000(	974.6802	882.7429	876.0908	820.9868	688.4831	734.8366	0.28371	0.032498	0.066658	DDX50	chr10	+	70661034	70706603	2538
ENSG00000(	446.4263	425.1136	493.4608	534.0909	476.7838	431.5316	-0.08062	0.60053	0.71593	MAPK8	chr10	+	49514698	49647403	5796
ENSG00000(	867.9936	868.2914	1109.627	1086.909	945.2837	904.9834	-0.04691	0.74438	0.82968	SEC23IP	chr10	+	1.22E+08	1.22E+08	4656
ENSG00000(	159.512	169.8046	259.9245	295.1358	280.7318	225.2184	-0.44483	0.043734	0.086518	ATE1	chr10	-	1.23E+08	1.24E+08	4900
ENSG00000(	157.4404	204.7289	193.9538	732.5959	597.3604	558.1142	-1.7597	3.89E-23	4.46E-22	NSMCE4A	chr10	-	1.24E+08	1.24E+08	2399
ENSG00000(	456.7842	540.7252	569.9868	459.9324	435.3643	418.3801	0.25203	0.095796	0.16926	PLEKHA1	chr10	+	1.24E+08	1.24E+08	8619
ENSG00000(	128.4382	130.0631	163.6073	62.17327	61.66894	48.49593	1.2777	1.45E-06	5.92E-06	PALD1	chr10	+	72238577	72328205	4555
ENSG00000(	3232.707	3181.728	3241.8	930.3518	1258.231	1139.243	1.5343	6.67E-33	1.11E-31	UNC5B	chr10	+	72972327	73062621	6841
ENSG00000(	2937.506	2975.795	2797.157	8.239831	5.522592	24.65895	7.505	1.54E-45	3.75E-44	CDH23	chr10	+	73156691	73575702	10085
ENSG00000(	66.29068	93.93444	101.5949	229.2171	206.1768	171.7907	-1.2109	7.05E-07	2.97E-06	C10orf54	chr10	-	73507316	73533255	4689
ENSG00000(	36.25272	44.55865	71.24834	31.46117	23.0108	25.48091	0.89496	0.029149	0.060647	SPOCK2	chr10	-	73818793	73848790	5445
ENSG00000(	745.7702	699.6912	763.9406	530.3455	470.3408	462.7662	0.59194	1.68E-05	6.07E-05	MICU1	chr10	-	74127098	74385899	2425
ENSG00000(	1199.447	1372.888	1378.787	753.57	688.4831	622.2274	0.93342	1.66E-12	1.12E-11	PPP3CB	chr10	-	75196186	75255782	3501
ENSG00000(	648.4057	720.1641	854.9801	913.1231	997.7483	741.4124	-0.25461	0.10216	0.17851	CCSER2	chr10	+	86088342	86278273	7664
ENSG00000(	571.7571	593.7138	733.5941	913.1231	881.7739	782.5106	-0.4411	0.00242	0.006355	BMPR1A	chr10	+	88516407	88684945	3605
ENSG00000(	395.6725	395.0064	406.3794	432.2166	347.9233	324.6761	0.11384	0.4921	0.62113	MINPP1	chr10	+	89264632	89313217	2415
ENSG00000(	1054.436	1068.203	1051.573	3300.427	3424.927	3211.417	-1.6437	3.53E-53	1.04E-51	ACTA2	chr10	-	90694831	90751147	1756
ENSG00000(	6325.581	6565.777	7357.051	651.6957	589.9969	477.5616	3.549	8.54E-160	1.52E-157	LIPA	chr10	-	90973326	91174314	2782
ENSG00000(	0	0	0	39.701	23.93123	27.12484	-5.7625	6.99E-08	3.26E-07	TLX1	chr10	+	1.03E+08	1.03E+08	3910
ENSG00000(	261.0196	227.6104	229.578	475.663	539.3732	528.5234	-1.0974	7.93E-12	5.09E-11	C10orf2	chr10	+	1.03E+08	1.03E+08	3175
ENSG00000(	3157.094	2925.215	2529.316	2116.888	2018.507	2205.332	0.44118	0.000216	0.000671	LZTS2	chr10	+	1.03E+08	1.03E+08	5741
ENSG00000(	2057.083	2103.891	1866.971	530.3455	462.0569	435.6414	2.0723	2.37E-58	7.90E-57	SFXN3	chr10	+	1.03E+08	1.03E+08	3095
ENSG00000(	126.3666	171.0089	174.1626	28.46487	29.45382	36.16646	2.2965	1.28E-15	1.05E-14	KAZALD1	chr10	+	1.03E+08	1.03E+08	1913
ENSG00000(	259.9838	313.1148	273.1187	333.3386	335.0372	464.4102	-0.41954	0.024435	0.05191	FBXW4	chr10	-	1.03E+08	1.03E+08	3183
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	FGF8	chr10	-	1.04E+08	1.04E+08	1197
ENSG00000(	1010.933	986.3116	874.7713	1083.163	828.3888	1210.754	-0.12023	0.43075	0.56066	NPM3	chr10	-	1.04E+08	1.04E+08	877
ENSG00000(	1051.329	1260.889	1542.395	901.1379	1076.905	734.0147	0.50475	0.002692	0.007019	TNKS2	chr10	+	93558069	93625033	6157
ENSG00000(	4.143168	0	0	0	0	0.821965	0.9919	0.46158	NA	PITX3	chr10	-	1.04E+08	1.04E+08	1391
ENSG00000(	2497.294	2220.707	2246.962	1609.014	2099.505	1650.506	0.37805	0.004081	0.010294	GBF1	chr10	+	1.04E+08	1.04E+08	6403
ENSG00000(	2298.422	2142.428	2823.545	1442.72	1472.691	1305.28	0.78116	2.78E-09	1.46E-08	ARHGAP21	chr10	-	24872538	25012597	7167
ENSG00000(	13.46529	18.06432	17.15238	17.97781	9.20432	11.50751	0.30391	0.61151	0.72525	CPEB3	chr10	-	93806449	94050844	7664
ENSG00000(	153.2972	156.5574	79.16483	146.8188	114.1336	109.3213	0.073744	0.79089	0.86313	FBXL15	chr10	+	1.04E+08	1.04E+08	2362
ENSG00000(	1445.965	1401.791	1187.472	779.7876	769.4811	844.158	0.75255	5.72E-09	2.94E-08	CUEDC2	chr10	-	1.04E+08	1.04E+08	1191
ENSG00000(	1237.771	1253.664	1345.802	677.9134	788.8102	734.8366	0.80019	1.54E-10	8.97E-10	SUFU	chr10	+	1.04E+08	1.04E+08	5001
ENSG00000(	228.91	205.9332	267.841	250.1912	242.0736	189.0519	0.042835	0.82931	0.89049	ANKRD26	chr10	-	27280843	27389421	6591
ENSG00000(	293.1291	298.6634	399.7824	373.7887	356.2072	384.6796	-0.17118	0.32378	0.45117	ACBD5	chr10	-	27484146	27531059	3918
ENSG00000(	174.013	133.6759	121.3861	100.3761	97.56579	98.63579	0.53244	0.028327	0.059105	LHPP	chr10	+	1.26E+08	1.26E+08	1622
ENSG00000(	1125.906	1098.31	1351.08	1600.025	1726.73	1460.632	-0.42079	0.001264	0.003488	LARP4B	chr10	-	855484	977564	5640
ENSG00000(	1032.685	1058.569	1070.045	2024.002	1924.623	1905.315	-0.88776	1.68E-15	1.37E-14	GTPBP4	chr10	+	1034338	1065876	4696

ENSG00000(	307.6302	280.599	407.6989	503.3788	466.659	418.3801	-0.47989	0.006664	0.016092	C10orf137	chr10	+	1.27E+08	1.27E+08	4387
ENSG00000(	719.8754	812.8942	697.9699	1482.421	1340.149	1367.75	-0.90776	5.53E-13	3.85E-12	BCCIP	chr10	+	1.28E+08	1.28E+08	2338
ENSG00000(	325.2387	372.1249	298.1875	541.5816	524.6462	438.1073	-0.59288	0.0003	0.000912	MTPAP	chr10	-	30598730	30663377	5947
ENSG00000(	35.21692	6.021439	6.597069	150.5642	143.5874	122.4728	-2.8741	5.33E-05	0.00018	NEURL	chr10	+	1.05E+08	1.05E+08	4314
ENSG00000(	4955.228	4919.515	5632.577	185.0217	321.2308	286.0438	4.279	1.30E-152	2.04E-150	SH3PXD2A	chr10	-	1.05E+08	1.06E+08	11468
ENSG00000(	1505.006	1454.78	1688.85	1315.377	1163.426	1009.373	0.41266	0.002091	0.00555	PITRM1	chr10	-	3179920	3215003	3457
ENSG00000(	355.2766	313.1148	333.8117	204.4976	171.2004	210.423	0.76962	1.64E-05	5.94E-05	OBFC1	chr10	-	1.06E+08	1.06E+08	1417
ENSG00000(	100.4718	87.913	112.1502	181.2763	191.4499	201.3814	-0.92871	2.91E-05	0.000102	MAP3K8	chr10	+	30722866	30750762	3096
ENSG00000(	170.9057	161.3746	196.5927	373.0396	323.0716	416.7362	-1.0707	8.38E-09	4.22E-08	DKK1	chr10	+	54074056	54077802	1790
ENSG00000(	322.1313	360.082	456.5172	86.14369	173.0412	138.0901	1.5107	1.87E-10	1.09E-09	EBF3	chr10	-	1.32E+08	1.32E+08	4375
ENSG00000(	1348.601	1327.125	1169.001	2650.229	2141.845	2342.6	-0.88977	1.48E-12	1.00E-11	GLRX3	chr10	+	1.32E+08	1.32E+08	1921
ENSG00000(	5.17896	2.408575	3.958241	137.8299	158.3143	109.3213	-4.9209	2.26E-22	2.52E-21	SORCS1	chr10	-	1.08E+08	1.09E+08	7272
ENSG00000(	801.7029	851.4314	1132.057	1103.388	1293.207	1000.331	-0.28648	0.068072	0.12669	FAM208B	chr10	+	5726801	5805703	8626
ENSG00000(	2032.224	2042.472	2059.605	1223.989	913.0685	851.5557	1.0337	5.51E-13	3.84E-12	XPNPEP1	chr10	-	1.12E+08	1.12E+08	4384
ENSG00000(	710.5532	827.3457	885.3266	1177.547	1287.684	1174.588	-0.58673	8.31E-06	3.11E-05	SMC3	chr10	+	1.12E+08	1.12E+08	4114
ENSG00000(	655.6563	626.2296	849.7025	506.3751	521.8849	405.2287	0.56929	0.000558	0.001626	SHOC2	chr10	+	1.13E+08	1.13E+08	3943
ENSG00000(	524.1107	452.8122	537.0014	1471.184	1486.498	1429.397	-1.5316	3.89E-33	6.57E-32	TFAM	chr10	+	60144782	60158981	5414
ENSG00000(	2163.769	2176.148	2596.606	1659.951	2111.471	1589.68	0.37079	0.007289	0.017483	CCDC6	chr10	-	61548521	61666414	5811
ENSG00000(	596.6161	591.3053	684.7758	1017.245	803.5371	780.0447	-0.47397	0.001502	0.004082	CUL2	chr10	-	35297479	35379570	4440
ENSG00000(	1569.225	1425.877	1593.852	1761.826	1688.072	1613.517	-0.1418	0.21548	0.3262	CCNY	chr10	+	35535953	35860852	3960
ENSG00000(	1600.298	1384.931	1290.387	6264.519	4962.049	5991.302	-2.0044	3.23E-54	9.78E-53	UBE2S	chr19	-	55912652	55919145	1009
ENSG00000(	20641.26	19977.93	13948.84	13684.11	10052.04	10756.23	0.65964	1.91E-05	6.85E-05	RPL28	chr19	+	55896713	55914612	5620
ENSG00000(	2004.257	1995.505	2130.853	1588.789	2516.461	2110.806	-0.01949	0.89744	0.93634	ZMIZ1	chr10	+	80828792	81076276	7546
ENSG00000(	137.7603	157.7617	105.5531	2.996302	0.920432	2.465895	5.6739	9.22E-26	1.18E-24	DNAJC12	chr10	-	69556427	69597924	1197
ENSG00000(	1114.512	1113.966	961.8526	1732.612	1492.02	1529.677	-0.5739	5.11E-06	1.96E-05	PPIF	chr10	+	81107225	81115093	2190
ENSG00000(	141.9035	177.0303	166.2461	70.4131	101.2475	85.48435	0.91054	0.000202	0.000629	PBLD	chr10	-	70042417	70092684	2587
ENSG00000(	2549.084	2356.791	2553.066	2922.893	2979.438	2760.158	-0.2154	0.042816	0.08493	TSPAN14	chr10	+	82213922	82282387	5691
ENSG00000(	0	1.204288	0	3.745378	1.840864	1.64393	-1.5288	0.24703	0.36383	LGI1	chr10	+	95517566	95557916	2290
ENSG00000(	250.6616	245.6747	248.0498	131.8373	123.3379	105.2115	1.0403	2.20E-07	9.75E-07	TBC1D12	chr10	+	96162261	96295687	5272
ENSG00000(	0	0	0	0	1.840864	2.465895	-1.2108	0.36631	NA	CYP2C18	chr10	+	96443251	96495947	2418
ENSG00000(	0	0	2.638828	29.96302	18.40864	27.94681	-4.2546	2.66E-06	1.05E-05	KRT23	chr17	-	39078948	39093886	1987
ENSG00000(	1.035792	6.021439	2.638828	0	0.920432	0	2.1206	0.10223	0.17857	CRYBA1	chr17	+	27573881	27581512	783
ENSG00000(	1662.446	1818.474	2438.277	1703.398	2657.287	1869.97	-0.07384	0.67122	0.77383	NUFIP2	chr17	-	27582854	27621136	10850
ENSG00000(	1348.601	1375.297	1273.234	1698.154	1554.61	1734.346	-0.31865	0.005611	0.013769	GIT1	chr17	-	27900487	27921072	3768
ENSG00000(	261.0196	246.879	246.7304	370.7924	346.0824	388.7894	-0.54871	0.000832	0.002363	TADA2A	chr17	+	35766965	35839835	4253
ENSG00000(	1018.183	945.3659	942.0614	1155.824	1016.157	1139.243	-0.18806	0.12814	0.21482	AATF	chr17	+	35306175	35414171	2141
ENSG00000(	60.07593	72.25726	64.65128	158.804	166.5982	174.2566	-1.3335	5.14E-08	2.43E-07	DHRS11	chr17	+	34948228	34957235	4505
ENSG00000(	430.8894	349.2434	390.5465	484.6519	427.0804	440.5732	-0.20685	0.18609	0.29063	ZNHIT3	chr17	+	34842473	34855154	4421
ENSG00000(	1126.942	1087.472	1039.698	376.0359	589.0765	606.6101	1.0474	8.18E-10	4.51E-09	MLLT6	chr17	+	36861795	36886056	7578
ENSG00000(	1315.456	1354.824	1089.836	2862.218	2035.075	2387.808	-0.95124	5.70E-11	3.44E-10	PSMB3	chr17	+	36908989	36920484	773
ENSG00000(	332.4892	334.792	298.1875	326.5969	295.4587	353.4449	-0.01455	0.93008	0.95802	CWC25	chr17	-	36957340	36981734	2581
ENSG00000(	28367.23	28303.17	21159.44	17678.18	14865.9	16877.41	0.65368	5.65E-07	2.41E-06	RPL19	chr17	+	37356536	37360980	1303
ENSG00000(	90.1139	56.60152	122.7055	41.19916	63.50981	33.70056	0.94618	0.008241	0.019516	FBXL20	chr17	-	37415384	37558776	2445
ENSG00000(	4.143168	7.225726	1.319414	6.74168	8.283888	4.93179	-0.55961	0.53651	0.6605	RUNDC3A	chr17	+	42385781	42396039	3686

ENSG00000(	2324.317	2193.008	2268.072	2235.991	2722.638	2717.416	-0.17721	0.13562	0.22487	UBTF	chr17	-	42282401	42298994	4997
ENSG00000(	2756.242	2867.409	2673.132	4122.163	3969.823	4381.895	-0.5874	1.95E-08	9.56E-08	PSMD3	chr17	+	38137050	38154213	2888
ENSG00000(	1394.176	1458.392	1457.952	1548.339	1486.498	1516.525	-0.07868	0.47643	0.60575	CASC3	chr17	+	38296571	38328436	4116
ENSG00000(	193.6931	184.256	158.3297	92.13629	68.11197	99.45776	1.0365	1.57E-05	5.69E-05	RAPGEFL1	chr17	+	38333263	38351908	3727
ENSG00000(	2.071584	10.83859	5.277655	7.490755	22.09037	10.68554	-1.0478	0.1776	0.27987	RGS9	chr17	+	63133549	63223821	2387
ENSG00000(	3.107376	1.204288	0	613.4929	825.6275	710.1777	-8.3127	5.68E-44	1.32E-42	RNF43	chr17	-	56429861	56494956	5575
ENSG00000(	23.82321	22.88147	22.43003	108.616	88.36147	72.33291	-1.9267	7.02E-08	3.27E-07	WNT3	chr17	-	44839872	44910520	3355
ENSG00000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	ASPA	chr17	+	3375668	3406713	5431
ENSG00000(	145.0109	157.7617	146.4549	644.954	544.8957	574.5535	-1.9672	1.13E-31	1.82E-30	RAD51C	chr17	+	56769934	56811703	2077
ENSG00000(	23.82321	34.92434	40.90183	1.498151	6.443024	3.28786	2.9916	2.34E-06	9.31E-06	4-Sep	chr17	-	56597611	56618179	3544
ENSG00000(	1194.268	944.1616	1308.858	677.1643	936.9998	768.5372	0.53173	0.000876	0.002481	MTMR4	chr17	-	56566898	56595266	5839
ENSG00000(	395.6725	393.8021	494.7802	636.7142	689.4036	547.4286	-0.54437	0.000627	0.001814	TRIM37	chr17	-	57059999	57184282	4391
ENSG00000(	555.1845	631.0468	616.1662	653.1939	591.8378	492.357	0.051722	0.73375	0.82196	DHX40	chr17	+	57642886	57685706	3724
ENSG00000(	63.18331	63.82725	59.37362	255.4348	208.0176	210.423	-1.84	5.72E-15	4.50E-14	TUBD1	chr17	-	57936851	57970304	2472
ENSG00000(	6576.243	6237.006	6800.259	6758.16	8487.303	7567.831	-0.21754	0.057206	0.10923	KPNB1	chr17	+	45726842	45762871	6139
ENSG00000(	280.6996	269.7604	298.1875	223.9736	237.4715	230.1502	0.29396	0.0884	0.15836	GOSR2	chr17	+	45000483	45105003	2202
ENSG00000(	11.39371	33.72006	26.38828	19.47596	34.97642	32.8786	-0.28393	0.57443	0.69309	PNPO	chr17	+	46018872	46025654	2397
ENSG00000(	537.576	579.2624	645.1933	555.8141	606.5647	517.0159	0.068246	0.63807	0.74635	RPS6KB1	chr17	+	57970447	58027925	5375
ENSG00000(	333.525	354.0606	281.0351	195.5087	166.5982	192.3398	0.80097	1.37E-05	4.98E-05	TRIM16L	chr17	+	18601311	18639431	3189
ENSG00000(	2.071584	2.408575	3.958241	13.48336	5.522592	3.28786	-1.2163	0.20161	0.30921	ZNF29P	chr17	+	15578790	15578957	168
ENSG00000(	670.1574	667.1754	584.5003	483.9028	464.8182	567.9778	0.3411	0.020355	0.044052	CDK5RAP3	chr17	+	46045176	46059140	2759
ENSG00000(	2698.238	2976.999	2793.199	2898.922	3390.871	3492.529	-0.20763	0.07292	0.13429	CBX1	chr17	-	46147414	46178883	2422
ENSG00000(	499.2517	522.6609	420.893	447.1981	463.8977	430.7096	0.10583	0.48398	0.61311	RECQL5	chr17	-	73622925	73663269	3710
ENSG00000(	148.1182	150.536	141.1773	196.2578	130.7013	260.5629	-0.41551	0.096648	0.17053	PIGL	chr17	+	16120523	16252115	1345
ENSG00000(	437.1042	380.5549	328.534	180.5272	160.1552	147.1317	1.2276	5.32E-11	3.21E-10	GALK1	chr17	-	73747675	73761792	1866
ENSG00000(	245.4827	275.7819	364.1582	320.6043	358.048	238.3698	-0.05245	0.79926	0.86912	INTS2	chr17	-	59942731	60005377	5878
ENSG00000(	486.8222	552.7681	453.8783	317.608	321.2308	386.3235	0.54117	0.000784	0.002237	CAMTA2	chr17	-	4871287	4890960	4777
ENSG00000(	787.2018	762.3141	1114.905	695.1421	856.9222	589.3488	0.3134	0.076699	0.1402	MED13	chr17	-	60019966	60142643	10465
ENSG00000(	17.60846	3.612863	18.47179	138.579	148.1896	144.6658	-3.369	5.34E-19	5.18E-18	HOXB6	chr17	-	46671639	46682354	3434
ENSG00000(	29.00217	49.3758	26.38828	47.94084	44.18074	79.7306	-0.69901	0.081284	0.1474	ENO3	chr17	+	4851387	4860426	1521
ENSG00000(	7739.437	7786.924	6331.867	19896.2	13378.48	15706.11	-1.1607	7.99E-16	6.61E-15	PFN1	chr17	-	4848947	4852356	1291
ENSG00000(	1658.303	1743.809	1389.343	2232.994	2376.555	2917.975	-0.64953	2.39E-06	9.51E-06	RNF167	chr17	+	4843303	4848517	1915
ENSG00000(	981.9307	836.98	827.2724	1222.491	925.0342	1175.41	-0.32737	0.024064	0.051234	SLC25A11	chr17	-	4840425	4843546	2176
ENSG00000(	41.43168	27.69862	30.34652	16.47966	8.283888	14.79537	1.2777	0.011361	0.026075	RASD1	chr17	-	17397751	17399709	1746
ENSG00000(	1.035792	4.817151	2.638828	1.498151	0.920432	0.821965	0.99461	0.41035	0.5411	CHRNE	chr17	-	4801069	4806369	2455
ENSG00000(	997.4676	898.3986	874.7713	877.9165	1584.984	1590.502	-0.54529	0.003623	0.009231	RAI1	chr17	+	17584787	17714767	7662
ENSG00000(	453.6769	399.8235	451.2395	1235.975	956.3288	879.5025	-1.2315	5.91E-15	4.65E-14	NUP88	chr17	-	5264258	5323480	2916
ENSG00000(	2446.54	2345.952	2125.576	5338.661	4437.403	4506.012	-1.0435	1.54E-18	1.46E-17	C1QBP	chr17	-	5336097	5352150	1169
ENSG00000(	1.035792	0	10.55531	46.44268	26.69253	38.63235	-3.0977	8.91E-06	3.33E-05	SLC6A4	chr17	-	28521337	28563020	6543
ENSG00000(	896.9958	869.4957	821.9948	1426.24	1304.252	1357.064	-0.65749	3.81E-08	1.82E-07	BLMH	chr17	-	28575218	28619074	2360
ENSG00000(	1993.899	1806.432	2629.592	1028.481	1286.764	1010.195	0.94817	9.62E-10	5.28E-09	CPD	chr17	+	28705923	28797007	9394
ENSG00000(	1054.436	1027.257	953.9362	1379.797	1094.394	1069.376	-0.22276	0.10497	0.18252	GOSR1	chr17	+	28804380	28854610	6039
ENSG00000(	1482.218	1564.37	1719.196	1551.335	1587.745	1551.87	0.022211	0.84684	0.90246	CCDC47	chr17	-	61822610	61853711	3466
ENSG00000(	42.46747	52.98866	68.60952	68.91495	59.82808	72.33291	-0.29744	0.35982	0.48944	MED31	chr17	-	6546635	6554954	1654

ENSG0000(	786.1661	881.5386	612.208	826.9794	714.2552	819.499	-0.04955	0.7486	0.83297	DRG2	chr17	+	17991200	18011285	5342
ENSG0000(	1493.612	1447.554	1361.635	1587.291	1966.043	1857.641	-0.32911	0.007931	0.018866	FTSJ3	chr17	-	61896793	61907372	3559
ENSG0000(	404.9946	354.0606	456.5172	435.2129	447.33	357.5547	-0.02929	0.86078	0.91151	AKAP10	chr17	-	19807615	19881656	4072
ENSG0000(	2.071584	0	0	0.749076	0	1.64393	-0.07972	0.95303	NA	ALDH3A1	chr17	-	19641297	19652256	2144
ENSG0000(	1310.277	1299.426	1263.998	1485.417	1529.758	1579.817	-0.24566	0.027815	0.058171	SMARCD2	chr17	-	61909444	61920425	2716
ENSG0000(	61.11172	44.55865	83.12307	1470.435	1065.86	1084.994	-4.2445	4.68E-93	3.15E-91	SYNGR2	chr17	+	76164639	76169608	3036
ENSG0000(	199.9078	245.6747	176.8014	119.8521	116.8949	105.2115	0.85884	9.07E-05	0.000298	B9D1	chr17	-	19240867	19281495	1353
ENSG0000(	997.4676	969.4516	903.7984	1492.908	1110.041	1290.485	-0.4387	0.001501	0.00408	UTP6	chr17	-	30187923	30228784	4387
ENSG0000(	6517.203	6027.46	7796.416	7631.582	7669.96	7659.069	-0.17461	0.13545	0.22472	DDX5	chr17	-	62495734	62504317	3558
ENSG0000(	124.295	131.2674	109.5113	210.4902	233.7897	221.9305	-0.86035	3.04E-05	0.000106	C17orf75	chr17	-	30651584	30677042	1642
ENSG0000(	657.7279	681.6268	712.4834	326.5969	368.1728	422.49	0.87438	6.18E-09	3.16E-08	CYTH1	chr17	-	76670130	76778379	4423
ENSG0000(	1192.196	1033.279	1209.902	4123.661	3502.244	3801.588	-1.7307	3.99E-47	1.01E-45	PSMD11	chr17	+	30771279	30810336	4098
ENSG0000(	299.3439	376.9421	306.104	83.14739	81.91845	67.40112	2.0665	5.02E-23	5.75E-22	LGALS3BP	chr17	-	76967320	76976191	2405
ENSG0000(	0	0	1.319414	1.498151	25.7721	8.219649	-3.5398	0.001825	0.004902	ASIC2	chr17	-	31340105	32501983	3443
ENSG0000(	9.322127	6.021439	1.319414	0	0	0	3.5644	0.005108	0.012633	CCL7	chr17	+	32597240	32599261	810
ENSG0000(	187.4783	164.9874	164.9267	185.7707	147.2691	141.378	0.12411	0.56337	0.68302	CCL2	chr17	+	32582237	32584222	996
ENSG0000(	0	6.021439	0	0	0	0.821965	1.3469	0.32084	0.44795	CCL8	chr17	+	32646055	32648421	1261
ENSG0000(	109.7939	90.32158	114.789	75.65663	72.71413	69.04505	0.52867	0.04711	0.092172	PEX12	chr17	-	33901814	33905882	2675
ENSG0000(	1.035792	1.204288	0	0.749076	0	0.821965	0.23857	0.86007	NA	HNF1B	chr17	-	36046434	36105237	3481
ENSG0000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	KRT32	chr17	-	39616063	39623681	1750
ENSG0000(	3.107376	10.83859	7.916483	1.498151	0	0	2.8609	0.011503	0.026367	DHX58	chr17	-	40253422	40264751	2617
ENSG0000(	674.3005	659.9497	589.778	833.7211	634.1776	727.439	-0.18991	0.1974	0.30446	KAT2A	chr17	-	40265126	40273376	3109
ENSG0000(	1193.232	1142.869	993.5186	1294.403	1223.254	1781.198	-0.36693	0.017739	0.038974	RAB5C	chr17	-	40276994	40307035	1771
ENSG0000(	647.3699	649.1111	602.9721	274.1617	216.3015	256.4531	1.3404	7.77E-18	7.11E-17	NAGLU	chr17	+	40688190	40696467	2544
ENSG0000(	51.7896	50.58008	25.06886	15.73059	11.04518	14.79537	1.565	0.00106	0.002962	HSD17B1P1	chr17	+	40698782	40700724	955
ENSG0000(	97.36444	84.30014	75.20659	68.91495	71.7937	84.66239	0.19039	0.49753	0.62596	HSD17B1	chr17	+	40701232	40707231	4982
ENSG0000(	787.2018	664.7668	668.9428	606.0021	543.9753	595.1026	0.28129	0.044527	0.08782	MLX	chr17	+	40719086	40725257	2586
ENSG0000(	1628.265	1546.305	1421.009	233.7116	198.8133	217.8207	2.8122	1.06E-93	7.25E-92	CNTNAP1	chr17	+	40834631	40851832	5276
ENSG0000(	1.035792	0	0	9.737982	5.522592	14.79537	-3.4838	0.00195	0.005205	ABI3	chr17	+	47287589	47300587	2109
ENSG0000(	384.2788	397.4149	296.8681	138.579	179.4842	219.4646	1.0015	1.43E-06	5.84E-06	EZH1	chr17	-	40852293	40897071	4623
ENSG0000(	4.143168	0	0	5.992604	1.840864	10.68554	-1.6169	0.15183	0.24654	DLX4	chr17	+	48046334	48052321	2032
ENSG0000(	3535.158	3441.854	3175.829	1182.041	1546.326	1726.126	1.1859	2.85E-17	2.53E-16	PPP1R9B	chr17	-	48211104	48227991	4158
ENSG0000(	411964.5	399074.5	375495.9	1238.222	1484.657	1402.272	8.1558	0	0	COL1A1	chr17	-	48260650	48278993	6727
ENSG0000(	10.35792	4.817151	5.277655	0	0	0	3.9369	0.001417	0.00387	SGCA	chr17	+	48241575	48253292	1432
ENSG0000(	956.0359	912.8501	667.6234	982.038	942.5224	1119.516	-0.26094	0.089889	0.16063	MRPL27	chr17	-	48445218	48450575	2441
ENSG0000(	11068.47	10719.36	10056.57	6654.787	6699.825	7193.015	0.63128	3.59E-10	2.04E-09	VAT1	chr17	-	41166622	41177140	2734
ENSG0000(	3633.558	3433.424	3674.567	3388.069	3302.51	3084.834	0.13573	0.1933	0.29916	LRRC59	chr17	-	48452420	48474914	2910
ENSG0000(	32.10955	38.53721	23.74945	140.8262	133.4626	208.7791	-2.3191	1.09E-13	7.97E-13	RND2	chr17	+	41177258	41184057	4154
ENSG0000(	70.43385	77.07441	51.45714	28.46487	36.81728	22.19305	1.1698	0.001555	0.004221	ALOX12	chr17	+	6899384	6914055	2358
ENSG0000(	836.9199	824.9371	697.9699	423.9768	416.9557	430.7096	0.8905	2.27E-10	1.31E-09	HDAC5	chr17	-	42154114	42201070	5326
ENSG0000(	32.10955	15.65574	42.22124	5.992604	5.522592	5.753754	2.2527	0.000189	0.000591	ABCC3	chr17	+	48712138	48769613	5716
ENSG0000(	2252.847	2397.737	2203.421	2754.351	1910.817	2264.513	-0.01625	0.90625	0.94215	LUC7L3	chr17	+	48796905	48833574	7040
ENSG0000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	PPY	chr17	-	42018172	42019836	563
ENSG0000(	130.5098	103.5687	108.1919	32.95932	42.33987	42.74218	1.523	2.43E-07	1.07E-06	MPP2	chr17	-	41952725	41987068	4414

ENSG00000(	480.6074	466.0593	635.9574	1286.912	1083.348	978.1383	-1.0795	1.51E-11	9.50E-11	SMURF2	chr17	-	62538413	62658186	5892
ENSG00000(	1007.826	1092.289	1219.138	1187.285	1241.663	1142.531	-0.10629	0.39594	0.52694	DUSP3	chr17	-	41843489	41856356	4110
ENSG00000(	0	0	0	0.749076	1.840864	0	-0.68825	0.58858	NA	CACNG1	chr17	+	65040706	65052909	1262
ENSG00000(	2117.159	1942.516	1910.511	3464.474	2720.797	2682.072	-0.56941	1.01E-05	3.73E-05	EFTUD2	chr17	-	42927311	42977030	4548
ENSG00000(	7.250543	9.634302	9.235896	0.749076	7.363456	0.821965	1.3573	0.14836	0.24167	HLF	chr17	+	53342373	53402426	5547
ENSG00000(	12.4295	19.2686	26.38828	59.92604	64.43024	81.37453	-1.7994	8.89E-06	3.32E-05	SLC16A6	chr17	-	66263167	66287408	3807
ENSG00000(	7740.473	7420.821	8784.657	3394.81	4304.86	3508.968	1.093	1.41E-18	1.33E-17	PRKAR1A	chr17	+	66409764	66547460	4256
ENSG00000(	396.7083	408.2535	337.7699	284.6487	270.607	292.6195	0.42985	0.008761	0.02064	EFNB3	chr17	+	7608520	7614696	3222
ENSG00000(	2580.158	2532.617	2301.058	211.9884	203.4155	245.7675	3.4785	2.23E-154	3.52E-152	FAM20A	chr17	-	66531254	66597530	3668
ENSG00000(	10477.04	10301.48	10106.71	14091.61	13326.93	12714.98	-0.37739	0.000119	0.000382	YWHAE	chr17	-	1247566	1303672	2211
ENSG00000(	7.250543	7.225726	1.319414	8.988907	4.60216	6.575719	-0.30055	0.73241	0.82109	AC016292.	chr17	-	1761333	1761740	408
ENSG00000(	1028.541	989.9245	1270.595	758.8135	717.0165	694.5604	0.59704	1.53E-05	5.58E-05	MMD	chr17	-	53469974	53499353	2735
ENSG00000(	1.035792	0	2.638828	2.247227	1.840864	6.575719	-1.1429	0.33879	0.46737	RANGRF	chr17	+	8191815	8193410	1140
ENSG00000(	310.7376	266.1476	213.745	226.9699	187.7681	219.4646	0.31829	0.10943	0.1887	DPH1	chr17	+	1933404	1946724	2607
ENSG00000(	47.64643	49.3758	27.70769	101.8743	105.8497	92.88204	-1.2429	8.60E-05	0.000283	MAP2K6	chr17	+	67410839	67539472	3076
ENSG00000(	113.9371	122.8373	127.9831	331.8405	290.8565	291.7975	-1.3221	9.63E-12	6.13E-11	DHRS7B	chr17	+	21026677	21096578	2175
ENSG00000(	3117.734	3473.166	3002.986	1609.763	1843.625	1612.695	0.91993	3.55E-15	2.84E-14	WSB1	chr17	+	25621102	25640657	4187
ENSG00000(	1.035792	2.408575	0	4.494453	0	0	-0.22567	0.86659	0.91591	RCVRN	chr17	-	9799637	9808938	2819
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	MYH1	chr17	-	10395624	10421860	6024
ENSG00000(	152.2614	190.2775	164.9267	2064.452	1503.986	1578.173	-3.3321	9.48E-91	6.05E-89	SLC9A3R1	chr17	+	72744791	72765492	1969
ENSG00000(	23.82321	18.06432	35.62417	28.46487	56.14635	35.34449	-0.61294	0.17585	0.27774	MYH3	chr17	-	10531843	10560626	6037
ENSG00000(	956.0359	1073.02	909.0761	520.6075	483.2268	554.0044	0.91274	1.75E-11	1.10E-10	NAT9	chr17	-	72766686	72772506	1993
ENSG00000(	907.3537	753.8841	899.8402	577.5372	622.212	664.9696	0.45707	0.000997	0.002795	TMEM104	chr17	+	72772622	72835918	4745
ENSG00000(	12.4295	18.06432	15.83297	14.98151	24.85166	30.4127	-0.57682	0.28715	0.41072	SEBOX	chr17	-	26691290	26700110	2149
ENSG00000(	900.1032	809.2813	748.1076	1191.779	1083.348	1028.278	-0.42482	0.001295	0.00357	TNFAIP1	chr17	+	26662628	26674035	3627
ENSG00000(	296.2365	266.1476	291.5904	191.7633	207.0972	246.5895	0.40271	0.02869	0.059783	IFT20	chr17	-	26655352	26662515	1485
ENSG00000(	1675.911	1671.551	1611.004	2683.189	2186.026	2179.851	-0.50669	3.52E-05	0.000122	TMEM97	chr17	+	26646121	26655707	2564
ENSG00000(	993.3244	922.4844	816.7171	483.1537	487.829	493.179	0.89903	3.73E-11	2.28E-10	CDR2L	chr17	+	72983727	73001895	3536
ENSG00000(	3016.226	3131.148	2905.349	2441.986	1716.606	2001.485	0.55355	4.10E-05	0.000141	PMP22	chr17	-	15133095	15168643	1817
ENSG00000(	553.1129	576.8538	471.0307	465.925	373.6954	394.5432	0.37391	0.018147	0.039749	UNC119	chr17	-	26873725	26879686	4189
ENSG00000(	626.6541	733.4112	530.4043	47.94084	38.65814	36.98842	3.9069	2.96E-77	1.51E-75	ALDOC	chr17	-	26900133	26904282	1982
ENSG00000(	3699.849	3533.38	3854.008	2396.293	2698.707	2614.67	0.52348	1.15E-06	4.73E-06	SUPT6H	chr17	+	26989109	27029697	6518
ENSG00000(	3098.054	2696.4	2601.884	3936.392	3324.6	3496.639	-0.35659	0.002805	0.007282	RAB34	chr17	-	27041299	27045447	1736
ENSG00000(	741.627	645.4982	807.4812	776.0423	861.5243	775.9349	-0.13683	0.32159	0.44883	PHF12	chr17	-	27232268	27278789	7679
ENSG00000(	838.9914	846.6143	930.1867	1622.498	1506.747	1415.424	-0.79615	8.46E-11	5.03E-10	TMEM33	chr4	+	41937137	41962589	7482
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	GABRA4	chr4	-	46920917	46996424	11973
ENSG00000(	0	0	6.597069	5.243529	10.12475	4.109825	-1.2828	0.23751	0.35225	GNRHR	chr4	-	68605046	68620078	2164
ENSG00000(	738.5196	720.1641	895.882	721.3598	613.0077	576.1974	0.29893	0.045066	0.088711	SLAIN2	chr4	+	48343339	48428229	6299
ENSG00000(	1757.739	1855.807	1741.626	1821.003	1341.069	1457.344	0.21208	0.11404	0.19537	OCIAD1	chr4	+	48807229	48863834	1916
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	UGT2B10	chr4	+	69681711	69696914	1931
ENSG00000(	0	0	0	0.749076	1.840864	1.64393	-1.2986	0.33698	NA	CWH43	chr4	+	48988264	49064098	2472
ENSG00000(	788.2376	956.2044	1060.809	754.3191	887.2964	618.1176	0.31031	0.05594	0.1071	DCUN1D4	chr4	+	52709166	52783003	4840
ENSG00000(	467.1421	426.3179	622.7633	705.6292	781.4468	614.8298	-0.47078	0.005222	0.012895	USP46	chr4	-	53460340	53525502	4752
ENSG00000(	59.04014	84.30014	42.22124	0	0	0	7.128	4.08E-12	2.68E-11	SULT1E1	chr4	-	70676498	70725870	1780

ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	ODAM	chr4	+	71062213	71070293	1319
ENSG00000(	205.0868	222.7932	168.885	87.64184	87.44104	89.59418	1.1663	2.01E-07	8.96E-07	CHIC2	chr4	-	54875956	54930857	1194
ENSG00000(	1.035792	0	0	12.73428	11.04518	7.397684	-3.5485	0.001439	0.003923	NMU	chr4	-	56461396	56502865	816
ENSG00000(	598.6877	484.1237	716.4417	170.7892	417.8761	277.0022	1.0493	1.67E-05	6.04E-05	KIAA1211	chr4	+	57036361	57194791	4628
ENSG00000(	537.576	627.4339	558.112	928.1046	665.4723	778.4008	-0.46092	0.003001	0.007755	LAMTOR3	chr4	-	1.01E+08	1.01E+08	4226
ENSG00000(	375.9925	385.3721	447.2813	665.9282	670.0745	605.7881	-0.68367	3.03E-06	1.19E-05	NFKB1	chr4	+	1.03E+08	1.04E+08	4085
ENSG00000(	0	0	0	31.46117	41.41944	35.34449	-6.0082	1.25E-08	6.25E-08	AREG	chr4	+	75310851	75320726	1240
ENSG00000(	624.5825	649.1111	662.3457	1845.722	1845.466	1668.589	-1.4667	2.73E-34	4.79E-33	MANBA	chr4	-	1.04E+08	1.04E+08	7429
ENSG00000(	4169.062	4428.166	4384.412	6596.359	5874.197	5794.853	-0.4921	3.05E-06	1.20E-05	UBE2D3	chr4	-	1.04E+08	1.04E+08	4819
ENSG00000(	35.21692	20.47289	26.38828	38.95193	36.81728	21.37109	-0.23075	0.6125	0.72591	MAPK10	chr4	-	86936276	87515284	4107
ENSG00000(	351.1335	392.5978	468.3919	382.0285	451.9321	331.2519	0.055573	0.7533	0.83679	ELF2	chr4	-	1.4E+08	1.4E+08	4012
ENSG00000(	557.256	641.8854	504.0161	463.6778	487.829	517.8379	0.2131	0.1544	0.24993	NDUFC1	chr4	-	1.4E+08	1.4E+08	1257
ENSG00000(	0	0	0	11.23613	9.20432	11.50751	-4.2727	0.000242	0.000745	UCP1	chr4	-	1.41E+08	1.41E+08	1462
ENSG00000(	789.2734	747.8627	844.4248	913.1231	1220.493	925.5325	-0.35964	0.014432	0.032374	TBC1D9	chr4	-	1.42E+08	1.42E+08	5306
ENSG00000(	486.8222	454.0165	463.1142	567.7993	497.9537	569.6217	-0.21967	0.12638	0.21249	ZNF330	chr4	+	1.42E+08	1.42E+08	1899
ENSG00000(	656.6921	531.0909	894.5625	257.682	309.2652	262.2068	1.3219	2.92E-12	1.93E-11	INPP4B	chr4	-	1.43E+08	1.44E+08	8831
ENSG00000(	342.8471	432.3393	490.8219	430.7184	368.1728	326.3201	0.16624	0.35605	0.48557	GAB1	chr4	+	1.44E+08	1.44E+08	7981
ENSG00000(	169.8699	187.8689	159.6491	299.6302	353.4459	375.638	-0.98553	1.13E-07	5.14E-07	KLHL2	chr4	+	1.66E+08	1.66E+08	3134
ENSG00000(	4898.26	5042.353	4649.614	1219.495	1132.131	963.3429	2.1336	4.08E-71	1.81E-69	CPE	chr4	+	1.66E+08	1.66E+08	2421
ENSG00000(	15111.17	15434.15	10796.76	7253.299	7041.305	9030.929	0.82337	1.85E-08	9.11E-08	RPL34	chr4	+	1.1E+08	1.1E+08	2627
ENSG00000(	598.6877	650.3154	571.3062	582.0317	571.5883	527.7015	0.11448	0.40776	0.53855	WFS1	chr4	+	6271576	6304992	3655
ENSG00000(	8.286335	6.021439	5.277655	2.247227	0	0	2.3632	0.035066	0.071266	ANXA10	chr4	+	1.69E+08	1.69E+08	1417
ENSG00000(	759.2355	851.4314	767.8988	989.5288	928.7159	1102.255	-0.34431	0.008674	0.020455	GRPEL1	chr4	-	7060633	7069924	2775
ENSG00000(	675.3363	751.4755	766.5794	764.0571	827.4684	1034.854	-0.25974	0.080129	0.14563	GAR1	chr4	+	1.11E+08	1.11E+08	1224
ENSG00000(	397.7441	390.1892	314.0205	525.851	402.2288	480.8495	-0.35246	0.0372	0.075136	FRG1	chr4	+	1.91E+08	1.91E+08	1074
ENSG00000(	1478.075	1331.942	1741.626	1034.473	1139.495	955.1232	0.5391	8.11E-05	0.000268	CLCN3	chr4	+	1.71E+08	1.71E+08	6692
ENSG00000(	290.0217	393.8021	325.8952	417.2351	424.3192	369.0622	-0.26192	0.12414	0.20948	AADAT	chr4	-	1.71E+08	1.71E+08	2261
ENSG00000(	330.4176	286.6205	405.06	547.5742	600.1217	476.7397	-0.66696	0.000103	0.000337	GALNT7	chr4	+	1.74E+08	1.74E+08	4307
ENSG00000(	2438.254	2260.448	2769.45	3313.91	3260.17	3027.297	-0.36215	0.001879	0.005032	DHX15	chr4	-	24519064	24586173	3028
ENSG00000(	223.7311	175.826	160.9685	11.98521	20.2495	5.753754	3.8378	4.18E-28	5.88E-27	SOD3	chr4	+	24791534	24802464	1526
ENSG00000(	105.6508	80.68728	105.5531	98.87797	110.4518	109.3213	-0.124	0.62651	0.73775	SEPSECS	chr4	-	25121627	25162204	5496
ENSG00000(	49.71801	60.21439	40.90183	1.498151	6.443024	3.28786	3.609	2.52E-10	1.44E-09	CPZ	chr4	+	8594387	8621488	3718
ENSG00000(	525.1465	580.4667	736.2329	259.9292	370.9341	273.7143	1.0216	2.99E-08	1.44E-07	TRIM2	chr4	+	1.54E+08	1.54E+08	6735
ENSG00000(	5.17896	6.021439	6.597069	3.745378	11.04518	3.28786	-0.01177	0.98922	0.9937	SLC2A9	chr4	-	9772777	10056560	2175
ENSG00000(	656.6921	616.5953	762.6212	417.2351	449.1708	427.4218	0.6517	7.24E-06	2.73E-05	FBXW7	chr4	-	1.53E+08	1.53E+08	4977
ENSG00000(	51.7896	60.21439	72.56776	264.4237	206.1768	252.3432	-1.9627	3.29E-16	2.78E-15	NEIL3	chr4	+	1.78E+08	1.78E+08	2408
ENSG00000(	375.9925	438.3607	461.7948	92.88537	102.168	108.4994	2.0616	2.55E-28	3.63E-27	TBC1D19	chr4	+	26578059	26756973	2263
ENSG00000(	714.6964	832.1628	876.0908	3047.988	3731.431	3276.352	-2.0497	9.96E-57	3.21E-55	WHSC1	chr4	+	1873151	1983934	8568
ENSG00000(	1491.54	1418.651	1686.211	709.3745	752.9134	641.9546	1.1246	3.80E-18	3.53E-17	SH3D19	chr4	-	1.52E+08	1.52E+08	5284
ENSG00000(	392.5651	321.5448	443.323	436.711	513.6011	427.4218	-0.25041	0.13767	0.22766	STIM2	chr4	+	26859300	27027003	5178
ENSG00000(	19.68005	9.634302	15.83297	0	0.920432	12.32947	1.5527	0.080891	0.14675	NKX3-2	chr4	-	13542454	13546674	2801
ENSG00000(	2053.975	1884.71	1666.42	2032.242	1315.297	1595.434	0.18058	0.24427	0.36043	MFSD10	chr4	-	2932288	2936586	2173
ENSG00000(	26.93059	32.51577	23.74945	30.7121	18.40864	13.15144	0.39887	0.4232	0.55368	GLRB	chr4	+	1.58E+08	1.58E+08	3126
ENSG00000(	48.68222	50.58008	46.17948	149.066	115.054	133.9803	-1.4381	2.13E-07	9.47E-07	BST1	chr4	+	15704573	15739936	1993

ENSG00000(	298.3081	255.309	376.0329	245.6968	291.7769	226.8623	0.28047	0.15031	0.24439	RAPGEF2	chr4	+	1.6E+08	1.6E+08	6949
ENSG00000(	14.50109	20.47289	2.638828	14.98151	22.09037	32.05663	-0.81488	0.1952	0.3016	HGFAC	chr4	+	3443614	3451211	2148
ENSG00000(	265.1627	239.6533	233.5362	245.6968	201.5746	165.2149	0.26806	0.18526	0.28968	SNX25	chr4	+	1.86E+08	1.86E+08	3323
ENSG00000(	36.25272	83.09585	46.17948	37.45378	18.40864	46.852	0.66311	0.12585	0.21179	LRP2BP	chr4	-	1.86E+08	1.86E+08	5164
ENSG00000(	477.5001	428.7264	434.0871	278.6561	252.1984	219.4646	0.83394	5.21E-07	2.23E-06	UFSP2	chr4	-	1.86E+08	1.86E+08	2348
ENSG00000(	1228.449	1248.846	1448.716	668.9245	735.4252	546.6067	1.006	3.22E-12	2.13E-11	KLF3	chr4	+	38665817	38702663	5122
ENSG00000(	386.3504	461.2422	455.1978	400.7554	405.9105	349.3351	0.17057	0.2804	0.40264	KLHL5	chr4	+	39046659	39128477	3425
ENSG00000(	33.14534	40.94578	52.77655	103.3724	106.7701	94.52597	-1.2562	4.57E-05	0.000156	FAM149A	chr4	+	1.87E+08	1.87E+08	2997
ENSG00000(	341.8113	267.3519	379.9912	1679.427	1774.593	1309.39	-2.2601	1.15E-43	2.64E-42	NCAPG	chr4	+	17812525	17846485	4661
ENSG00000(	1555.759	1569.187	1418.37	1322.118	1204.845	1126.092	0.31409	0.009622	0.022465	UGDH	chr4	-	39500375	39529931	3216
ENSG00000(	21.75163	28.90291	19.79121	25.46857	45.10117	17.26126	-0.3012	0.54393	0.66625	PPARGC1A	chr4	-	23756664	23905712	6318
ENSG00000(	0	1.204288	3.958241	13.48336	5.522592	1.64393	-1.6396	0.12938	0.2164	DDX25	chr11	+	1.26E+08	1.26E+08	2276
ENSG00000(	6.214751	10.83859	13.19414	10.48706	7.363456	3.28786	0.45923	0.5481	0.66982	CRYAB	chr11	-	1.12E+08	1.12E+08	1119
ENSG00000(	0	0	1.319414	0.749076	0.920432	0.821965	-0.46006	0.7339	NA	DBX1	chr11	-	20177701	20182159	1380
ENSG00000(	58.00435	52.98866	76.526	528.8473	561.4635	487.4252	-3.0625	1.89E-51	5.42E-50	HTATIP2	chr11	+	20385231	20405329	1748
ENSG00000(	3844.86	4263.179	3931.853	2009.021	1590.506	1646.396	1.1955	2.13E-22	2.37E-21	CTSC	chr11	-	88026760	88070955	6125
ENSG00000(	378.064	403.4364	358.8805	687.6514	540.2936	627.9812	-0.70097	5.10E-06	1.96E-05	CCDC34	chr11	-	27352374	27385415	2109
ENSG00000(	336.6324	420.2964	354.9223	0	10.12475	4.109825	5.5226	3.32E-10	1.89E-09	ZBTB16	chr11	+	1.14E+08	1.14E+08	4427
ENSG00000(	130.5098	119.2245	129.3026	259.9292	151.8713	153.7074	-0.57465	0.022488	0.048151	ELP4	chr11	+	31531297	31805546	1961
ENSG00000(	928.0695	870.7	795.6065	1031.477	836.6727	983.892	-0.13608	0.31739	0.44424	ZNF259	chr11	-	1.17E+08	1.17E+08	2645
ENSG00000(	1789.848	1658.304	1775.931	2309.4	1818.774	2049.159	-0.24168	0.050641	0.098181	MTCH2	chr11	-	47638867	47664175	2587
ENSG00000(	1002.647	1038.096	1132.057	1023.986	1002.35	1031.566	0.052301	0.66408	0.76805	FNBP4	chr11	-	47738072	47788995	3969
ENSG00000(	6.214751	4.817151	13.19414	13.48336	13.80648	7.397684	-0.48951	0.50025	0.62847	TECTA	chr11	+	1.21E+08	1.21E+08	7426
ENSG00000(	863.8504	800.8513	1121.502	2024.002	1965.122	1749.963	-1.0408	3.75E-13	2.65E-12	SC5D	chr11	+	1.21E+08	1.21E+08	2456
ENSG00000(	30.03797	40.94578	35.62417	5.992604	0.920432	0	3.6022	2.46E-07	1.09E-06	CRTAM	chr11	+	1.23E+08	1.23E+08	2469
ENSG00000(	89.0781	120.4288	122.7055	44.94453	50.62376	43.56414	1.2394	2.02E-05	7.22E-05	C11orf63	chr11	+	1.23E+08	1.23E+08	2910
ENSG00000(	0	0	0	31.46117	39.57858	30.4127	-5.9202	2.29E-08	1.12E-07	B3GAT1	chr11	-	1.34E+08	1.34E+08	6160
ENSG00000(	22131.77	20751.08	22010.46	41998.42	32927.53	33134.23	-0.73432	5.39E-10	3.01E-09	HSPA8	chr11	-	1.23E+08	1.23E+08	2463
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	P2RX3	chr11	+	57105848	57138073	1831
ENSG00000(	64.2191	109.5902	77.84541	495.1389	436.2848	488.2472	-2.4865	1.35E-32	2.22E-31	VWA5A	chr11	+	1.24E+08	1.24E+08	4388
ENSG00000(	525.1465	543.1338	401.1018	278.6561	202.495	206.3132	1.0897	7.15E-09	3.64E-08	DNAJC4	chr11	+	63997750	64001758	1340
ENSG00000(	394.6367	399.8235	405.06	140.0771	177.6434	157.8173	1.3316	3.64E-14	2.73E-13	SIAE	chr11	-	1.25E+08	1.25E+08	5583
ENSG00000(	426.7463	368.512	336.4505	346.0729	297.2995	346.0472	0.19427	0.24652	0.36322	SNX15	chr11	+	64781654	64808044	4713
ENSG00000(	89.0781	114.4073	94.99779	65.16957	47.86246	47.67397	0.87804	0.002866	0.007428	LPXN	chr11	-	58294344	58345693	2099
ENSG00000(	110.8297	111.9988	118.7472	401.5045	491.5107	421.668	-1.9356	2.61E-25	3.26E-24	DTX4	chr11	+	58938903	58976060	5642
ENSG00000(	565.5424	580.4667	525.1267	412.7406	561.4635	494.8229	0.18723	0.23136	0.34481	ATG2A	chr11	-	64662007	64684722	6376
ENSG00000(	3489.583	3326.243	3121.733	3100.424	3155.241	3322.382	0.053376	0.61359	0.72697	EHD1	chr11	-	64619114	64655768	4551
ENSG00000(	1487.397	1406.608	1622.879	853.9461	1039.168	784.9765	0.75267	4.57E-08	2.17E-07	OSBP	chr11	-	59341871	59383617	5083
ENSG00000(	340.7755	279.3948	259.9245	180.5272	157.3939	198.9155	0.71073	0.000259	0.000794	UNC93B1	chr11	-	67758575	67772452	2315
ENSG00000(	230.9816	221.5889	230.8974	188.018	220.9037	166.0369	0.24967	0.20025	0.30776	PUS3	chr11	-	1.26E+08	1.26E+08	1843
ENSG00000(	207.1584	166.1917	102.9143	390.2684	257.721	354.2669	-1.06	1.19E-05	4.38E-05	DCPS	chr11	+	1.26E+08	1.26E+08	2467
ENSG00000(	584.1866	606.961	833.8695	548.3233	481.3859	467.698	0.43155	0.009106	0.021376	SUV420H1	chr11	-	67922330	67981295	5837
ENSG00000(	317.9881	325.1577	255.9663	689.8986	643.382	751.2759	-1.2072	1.18E-14	9.14E-14	FOXRED1	chr11	+	1.26E+08	1.26E+08	3045
ENSG00000(	1057.544	1001.967	1316.775	1650.213	1569.337	1408.026	-0.45464	0.000923	0.002601	PPP6R3	chr11	+	68228186	68382802	5119

ENSG00000(	4.143168	1.204288	2.638828	11.23613	11.96562	9.041614	-1.759	0.042791	0.084891	NRXN2	chr11	-	64373646	64490660	6621
ENSG00000(	0	0	0	24.71949	15.64734	17.26126	-5.1297	3.29E-06	1.29E-05	MS4A6A	chr11	-	59939081	59952139	2416
ENSG00000(	0	0	0	27.7158	22.09037	13.9734	-5.2642	1.58E-06	6.43E-06	MS4A4A	chr11	+	60048014	60076445	1676
ENSG00000(	575.9003	566.0152	476.3084	432.9657	384.7406	361.6646	0.45549	0.003319	0.00852	ST3GAL4	chr11	+	1.26E+08	1.26E+08	1967
ENSG00000(	2909.539	2672.314	3000.347	159.5531	196.9724	170.9687	4.0178	1.00E-200	3.02E-198	CPT1A	chr11	-	68522088	68611878	5232
ENSG00000(	4086.199	3676.69	4131.085	10850.36	13425.42	12896.63	-1.6409	2.80E-45	6.74E-44	CCND1	chr11	+	69455855	69469242	4307
ENSG00000(	920.819	816.5071	759.9823	1101.141	906.6255	1076.774	-0.30333	0.027793	0.058134	CCDC86	chr11	+	60609544	60618554	1893
ENSG00000(	2048.796	1979.849	1818.152	4215.048	3577.719	3990.64	-1.009	1.23E-18	1.17E-17	PRPF19	chr11	-	60658202	60674060	2157
ENSG00000(	1567.153	1628.197	1729.751	2374.569	1996.417	2046.693	-0.38187	0.001363	0.003742	TMEM109	chr11	+	60681346	60690915	2413
ENSG00000(	0	0	0	21.72319	21.16994	23.83698	-5.3441	8.93E-07	3.72E-06	CCKBR	chr11	+	6280966	6293357	2138
ENSG00000(	23.82321	32.51577	38.263	8.239831	10.12475	21.37109	1.1974	0.024372	0.051813	HPX	chr11	-	6452279	6463847	1652
ENSG00000(	482.679	364.8992	474.989	247.1949	217.222	246.5895	0.89105	3.35E-07	1.46E-06	TRIM3	chr11	-	6469843	6495689	4419
ENSG00000(	608.0098	643.0896	647.8322	1370.808	1330.945	1176.232	-1.0285	7.48E-16	6.20E-15	CHORDC1	chr11	-	89934328	89956532	5361
ENSG00000(	0	0	0	19.47596	11.96562	17.26126	-4.8884	1.24E-05	4.56E-05	FOLR1	chr11	+	71900602	71907345	1331
ENSG00000(	43.50326	86.70872	56.73479	74.90755	97.56579	70.68898	-0.37551	0.25201	0.36969	ANAPC15	chr11	-	71817424	71823826	1481
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	FOLR3	chr11	+	71825915	71850936	990
ENSG00000(	391.5293	367.3078	517.2102	324.3497	423.3987	249.0554	0.3542	0.08504	0.15335	PANX1	chr11	+	93862094	93915138	2769
ENSG00000(	1255.38	1299.426	1246.846	955.0713	1155.142	1094.035	0.24677	0.047124	0.092192	ARHGEF17	chr11	+	73019334	73080136	7853
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	APOC3	chr11	+	1.17E+08	1.17E+08	604
ENSG00000(	1700.77	1702.863	1531.839	598.5114	846.7974	873.7487	1.0875	5.97E-13	4.14E-12	CEP164	chr11	+	1.17E+08	1.17E+08	5690
ENSG00000(	648.4057	631.0468	737.5523	823.9831	787.8898	795.662	-0.25586	0.052236	0.10089	RNF141	chr11	-	10533225	10562777	5818
ENSG00000(	116.0087	111.9988	126.6637	32.95932	11.04518	30.4127	2.1995	4.78E-10	2.69E-09	KIAA1377	chr11	+	1.02E+08	1.02E+08	7039
ENSG00000(	14574.63	14066.08	17156.34	19927.66	20724.45	16916.04	-0.32942	0.006207	0.015091	EIF4G2	chr11	-	10818597	10830657	6769
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	IL10RA	chr11	+	1.18E+08	1.18E+08	5155
ENSG00000(	20.71584	21.67718	18.47179	128.0919	81.91845	101.9236	-2.3156	9.67E-11	5.73E-10	GALNT18	chr11	-	11292423	11643552	2504
ENSG00000(	1004.718	1116.375	1085.878	2012.017	1963.281	1700.645	-0.82247	1.86E-11	1.16E-10	BIRC2	chr11	+	1.02E+08	1.02E+08	4073
ENSG00000(	509.6096	437.1564	745.4688	188.018	345.162	216.9987	1.1665	4.83E-07	2.07E-06	UBE4A	chr11	+	1.18E+08	1.18E+08	6103
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	MMP12	chr11	-	1.03E+08	1.03E+08	1873
ENSG00000(	1574.404	1508.973	2279.947	841.9609	1718.447	1164.724	0.51698	0.14092	0.23206	DDX6	chr11	-	1.19E+08	1.19E+08	4538
ENSG00000(	3.107376	7.225726	7.916483	44.94453	40.49901	41.09825	-2.6967	1.23E-06	5.06E-06	UPK2	chr11	+	1.19E+08	1.19E+08	958
ENSG00000(	627.6899	653.9282	777.1347	930.3518	1291.366	949.3695	-0.6214	8.95E-05	0.000294	CBL	chr11	+	1.19E+08	1.19E+08	11465
ENSG00000(	388.422	326.362	410.3377	3776.839	5552.046	5895.954	-3.7447	1.98E-116	1.97E-114	PVRL1	chr11	-	1.19E+08	1.2E+08	5840
ENSG00000(	938.4275	964.6345	1384.065	724.3561	818.264	643.5985	0.5854	0.00041	0.001221	HIPK3	chr11	+	33278218	33378569	7408
ENSG00000(	461.9632	425.1136	634.638	195.5087	213.5402	175.9005	1.3718	3.74E-13	2.65E-12	KIAA1549L	chr11	+	33563618	33695648	11678
ENSG00000(	419.4957	439.565	493.4608	371.5415	358.9685	319.7444	0.36219	0.02086	0.04504	FBXO3	chr11	-	33762485	33796089	7410
ENSG00000(	391.5293	410.6621	390.5465	487.6482	471.2612	443.8611	-0.23353	0.11129	0.19132	PDHX	chr11	+	34937376	35042138	2503
ENSG00000(	14.50109	14.45145	30.34652	9.737982	14.72691	14.79537	0.56071	0.33698	0.46548	SLC1A2	chr11	-	35272753	35441610	11696
ENSG00000(	851.4209	797.2385	767.8988	807.5034	653.5067	696.2043	0.16312	0.23541	0.34978	COMMD9	chr11	-	36295051	36310999	1745
ENSG00000(	0	0	5.277655	1.498151	3.681728	4.109825	-0.61387	0.61495	0.72804	SLC15A3	chr11	-	60704556	60720002	4579
ENSG00000(	3.107376	2.408575	2.638828	0	6.443024	5.753754	-0.44578	0.68715	0.78614	CD5	chr11	+	60869867	60895324	3221
ENSG00000(	102.5434	74.66584	88.40072	35.20655	62.58938	60.8254	0.73992	0.021637	0.046538	ACCS	chr11	+	44087475	44105772	3373
ENSG00000(	4674.529	4582.315	3503.044	13582.24	11608.49	15438.97	-1.6663	4.13E-33	6.96E-32	MDK	chr11	+	46402306	46405375	1339
ENSG00000(	740.5912	745.4541	705.8864	568.5483	650.7454	614.0078	0.25817	0.051803	0.10016	AMBRA1	chr11	-	46417964	46615675	5351
ENSG00000(	815.1682	867.0872	745.4688	700.3856	904.7847	821.143	0.002127	0.98806	0.99282	MADD	chr11	+	47290712	47351582	6005

ENSG00000(	3.107376	9.634302	3.958241	24.71949	11.04518	23.83698	-1.7135	0.014621	0.03274	PTPMT1	chr11	+	47586982	47595013	2272
ENSG00000(	482.679	515.4351	391.8659	810.4997	734.5047	837.5823	-0.77395	2.11E-07	9.40E-07	NAA40	chr11	+	63706431	63724800	4707
ENSG00000(	1380.711	1298.222	1191.431	1087.658	884.5351	910.7371	0.42384	0.001369	0.003758	CARS	chr11	-	3022152	3078843	5732
ENSG00000(	176.0846	219.1804	162.2879	87.64184	67.19154	75.62077	1.2617	1.62E-07	7.28E-07	SLC22A18	chr11	+	2920951	2946476	2635
ENSG00000(	12507.19	13090.61	10588.3	7345.435	5359.676	6215.699	0.93311	2.36E-12	1.57E-11	CD81	chr11	+	2397407	2418649	5235
ENSG00000(	93.22127	86.70872	104.2337	1337.1	1282.162	1224.728	-3.7477	3.06E-122	3.27E-120	SLC35F2	chr11	-	1.08E+08	1.08E+08	3331
ENSG00000(	2.071584	1.204288	1.319414	0	0	0	1.6469	0.22376	NA	C11orf21	chr11	-	2316875	2324279	2956
ENSG00000(	0	0	0	72.66033	72.71413	76.44274	-6.9634	7.13E-12	4.59E-11	ELMOD1	chr11	+	1.07E+08	1.08E+08	2852
ENSG00000(	0	0	0	14.98151	6.443024	4.109825	-3.8935	0.001245	0.003439	CALCA	chr11	-	14988214	14993900	1837
ENSG00000(	54.89697	61.41867	69.92893	39.701	36.81728	43.56414	0.61912	0.066666	0.12445	SOX6	chr11	-	15987995	16761138	8925
ENSG00000(	2313.959	2331.501	2440.915	3120.649	2769.58	2987.021	-0.32493	0.00254	0.006644	C11orf58	chr11	+	16634679	16778428	4258
ENSG00000(	1985.613	1793.184	1669.058	1016.496	1058.497	1191.027	0.73725	3.99E-09	2.08E-08	PITPNM1	chr11	-	67259239	67273734	4225
ENSG00000(	14234.89	15918.28	10771.69	9599.403	9627.719	11975.21	0.39027	0.007169	0.017228	RPS13	chr11	-	17095936	17099334	777
ENSG00000(	1161.123	1116.375	936.7838	582.7808	446.4095	503.8645	1.0644	7.95E-13	5.48E-12	AIP	chr11	+	67250512	67258574	1221
ENSG00000(	1567.153	1290.996	1591.213	2402.285	2371.953	2049.159	-0.61548	1.49E-06	6.07E-06	NUP98	chr11	-	3692313	3819022	6973
ENSG00000(	1060.651	1113.966	964.4915	1592.535	1116.484	1367.75	-0.37635	0.00995	0.023152	NDUFS8	chr11	+	67798084	67804111	3072
ENSG00000(	1076.188	1020.032	852.3413	623.2309	449.1708	598.3905	0.81623	2.47E-07	1.09E-06	TCIRG1	chr11	+	67806483	67818362	2677
ENSG00000(	220.6237	239.6533	244.0915	581.2826	606.5647	499.7547	-1.2573	6.29E-15	4.95E-14	CHKA	chr11	-	67820326	67888911	2530
ENSG00000(	2.071584	14.45145	3.958241	316.1099	285.3339	248.2334	-5.278	2.66E-39	5.41E-38	EXPH5	chr11	-	1.08E+08	1.08E+08	10187
ENSG00000(	350.0977	391.3935	398.463	388.7702	405.9105	352.623	-0.01021	0.94809	0.96872	HPS5	chr11	-	18300223	18343745	4717
ENSG00000(	888.7095	942.9573	946.0197	925.1083	777.765	718.3973	0.19664	0.1529	0.248	GTF2H1	chr11	+	18343842	18388591	2982
ENSG00000(	4.143168	1.204288	1.319414	2.996302	1.840864	2.465895	-0.08641	0.9401	0.96394	PTPN5	chr11	-	18749475	18814268	3871
ENSG00000(	4.143168	1.204288	0	26.21764	64.43024	46.852	-4.1998	7.66E-09	3.89E-08	VWF	chr12	-	6058040	6233936	8838
ENSG00000(	87.00652	71.05298	73.88717	70.4131	49.70333	44.38611	0.48752	0.12382	0.20902	PSMD9	chr12	+	1.22E+08	1.22E+08	3051
ENSG00000(	3411.899	3281.684	2864.447	388.7702	349.7642	355.0888	3.1204	4.64E-138	6.12E-136	LEPREL2	chr12	+	6937564	6949018	3226
ENSG00000(	5660.603	5404.843	6240.827	3131.885	3149.718	2686.181	0.9467	1.47E-16	1.26E-15	PPFIBP1	chr12	+	27676364	27848497	6001
ENSG00000(	145.0109	161.3746	197.9121	77.15478	101.2475	138.9121	0.66108	0.011041	0.025423	PRPF40B	chr12	+	49962001	50038449	3602
ENSG00000(	929.1053	833.3671	946.0197	734.094	738.1865	647.7084	0.35266	0.007506	0.017957	PRDM4	chr12	-	1.08E+08	1.08E+08	4210
ENSG00000(	19.68005	34.92434	13.19414	0	3.681728	0	3.7686	1.36E-05	4.98E-05	CLEC2B	chr12	-	10005583	10022735	1700
ENSG00000(	365.6345	332.3834	343.0476	414.2388	360.8093	445.505	-0.22873	0.15376	0.24916	COQ5	chr12	-	1.21E+08	1.21E+08	1535
ENSG00000(	262.0554	261.3304	255.9663	77.90386	48.7829	41.09825	2.1899	2.32E-18	2.17E-17	SELPLG	chr12	-	1.09E+08	1.09E+08	2528
ENSG00000(	5501.091	5200.114	5848.961	4711.685	4442.925	4059.685	0.32409	0.002966	0.007668	CORO1C	chr12	-	1.09E+08	1.09E+08	3892
ENSG00000(	409.1378	319.1362	286.3128	26.21764	18.40864	32.8786	3.6697	1.09E-44	2.57E-43	ASIC1	chr12	+	50451331	50477394	4072
ENSG00000(	0	0	0	0.749076	0.920432	0.821965	-0.73223	0.57364	NA	DAO	chr12	+	1.09E+08	1.09E+08	2385
ENSG00000(	999.5392	979.0859	1200.667	984.2853	964.6127	999.5093	0.10753	0.40564	0.53658	CAPRIN2	chr12	-	30862486	30907885	6543
ENSG00000(	1535.044	1567.983	1443.439	436.711	480.4655	475.9177	1.7038	3.91E-43	8.90E-42	TSPAN11	chr12	+	31079362	31149534	5505
ENSG00000(	5897.799	5622.819	6050.832	2166.326	2154.731	2092.723	1.4519	6.16E-47	1.54E-45	KCTD10	chr12	-	1.1E+08	1.1E+08	5355
ENSG00000(	424.6747	463.6508	465.7531	516.1131	538.4527	473.4518	-0.17448	0.23012	0.34348	SLC11A2	chr12	-	51373184	51422349	4156
ENSG00000(	5062.951	5100.158	5831.809	3209.04	3843.724	3623.221	0.58221	5.17E-07	2.21E-06	MLEC	chr12	+	1.21E+08	1.21E+08	6626
ENSG00000(	788.2376	774.357	756.0241	746.8283	586.3152	672.3673	0.20794	0.135	0.22411	MVK	chr12	+	1.1E+08	1.1E+08	4109
ENSG00000(	813.0966	858.6571	932.8255	794.0201	924.1137	892.6539	-0.00371	0.97745	0.98685	CSRNP2	chr12	-	51454990	51477447	4469
ENSG00000(	876.28	844.2057	799.5648	543.0798	622.212	623.0494	0.49488	0.000207	0.000644	CAMKK2	chr12	-	1.22E+08	1.22E+08	5598
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	BIN2	chr12	-	51674822	51718452	2781
ENSG00000(	11.39371	24.08575	14.51355	14.98151	7.363456	14.79537	0.39523	0.52139	0.64701	IL23A	chr12	+	56732663	56734193	1041

ENSG0000(	10079.29	9893.224	9563.111	14107.34	11244.92	11921.78	-0.33517	0.003071	0.007918	ATP5B	chr12	-	57031959	57039798	1789
ENSG0000(	3071.123	3046.848	3013.541	8083.274	6533.226	6902.861	-1.2346	1.58E-27	2.17E-26	PTGES3	chr12	-	57057127	57082159	2928
ENSG0000(	0	0	0	25.46857	57.06678	39.45432	-6.1431	5.81E-09	2.98E-08	SYT10	chr12	-	33527173	33592754	4461
ENSG0000(	121.1877	107.1816	150.4132	363.3016	391.1836	344.4033	-1.5317	3.48E-15	2.78E-14	BCL7A	chr12	+	1.22E+08	1.22E+08	6245
ENSG0000(	1065.83	964.6345	882.6878	1190.281	1213.129	1222.262	-0.31379	0.011662	0.026688	RSRC2	chr12	-	1.23E+08	1.23E+08	3156
ENSG0000(	13.46529	25.29004	22.43003	25.46857	30.37426	18.90519	-0.28419	0.57271	0.69137	CYP27B1	chr12	-	58156117	58161034	2540
ENSG0000(	0	0	1.319414	2.996302	4.60216	0.821965	-1.6609	0.20397	0.31222	MYF6	chr12	+	81101277	81103253	1465
ENSG0000(	478.5359	540.7252	605.6109	34.45748	42.33987	19.72716	4.0486	3.35E-67	1.38E-65	LIN7A	chr12	-	81186299	81331704	6112
ENSG0000(	191.6215	183.0517	182.0791	26688.81	19462.53	21760.7	-6.91	0	0	KRT18	chr12	+	53342655	53346685	2088
ENSG0000(	23.82321	33.72006	19.79121	259.1801	354.3663	262.2068	-3.4593	9.15E-35	1.63E-33	ACSS3	chr12	+	81331594	81650533	4803
ENSG0000(	819.3114	833.3671	701.9281	69.66403	102.168	139.734	2.9044	4.80E-45	1.15E-43	TENC1	chr12	+	53440753	53458156	5010
ENSG0000(	122.2234	144.5145	137.219	2.996302	3.681728	4.93179	4.9729	8.11E-28	1.13E-26	GLI1	chr12	+	57853918	57866045	3613
ENSG0000(	159.512	168.6003	207.148	810.4997	1018.918	686.3407	-2.2254	6.21E-34	1.08E-32	PPM1H	chr12	-	63037762	63328817	6353
ENSG0000(	2602.945	2556.703	2393.417	2752.853	2058.086	2137.931	0.11976	0.36242	0.49205	METAP2	chr12	+	95867296	95909615	3601
ENSG0000(	1317.527	1406.608	1289.067	1219.495	1122.007	1192.671	0.1828	0.11674	0.19936	LTA4H	chr12	-	96394606	96437298	6109
ENSG0000(	906.3179	920.0758	1074.003	629.2235	686.6423	578.6633	0.61247	8.34E-06	3.12E-05	ELK3	chr12	+	96588160	96663613	4205
ENSG0000(	1.035792	1.204288	1.319414	0.749076	0	0	1.0069	0.45773	NA	SLC6A12	chr12	-	299243	323736	3571
ENSG0000(	594.5446	585.2838	588.4585	2385.057	2331.454	2630.288	-2.0508	1.60E-67	6.64E-66	WNT5B	chr12	+	1639057	1756409	2303
ENSG0000(	232.0174	287.8248	228.2586	331.8405	370.0137	375.638	-0.52384	0.002702	0.007041	MAGOHB	chr12	-	10758612	10766222	2671
ENSG0000(	47.64643	40.94578	69.92893	35.20655	45.10117	40.27628	0.38505	0.29435	0.41878	TRPV4	chr12	-	1.1E+08	1.1E+08	3247
ENSG0000(	291.0575	291.4376	306.104	294.3867	272.4479	286.8658	0.056466	0.73214	0.8209	ITFG2	chr12	+	2921788	2968957	2361
ENSG0000(	516.8602	463.6508	533.0432	1692.911	1889.647	1506.662	-1.745	7.54E-38	1.47E-36	FOXM1	chr12	-	2966847	2986206	3475
ENSG0000(	75.61281	46.96722	63.33186	65.16957	65.35067	61.64737	-0.04351	0.89088	0.93231	PRR4	chr12	-	10977559	11324212	1555
ENSG0000(	2.071584	6.021439	1.319414	1.498151	0.920432	0	1.3617	0.27157	0.39231	PRMT8	chr12	+	3490515	3703139	5899
ENSG0000(	237.1963	234.8361	250.6886	116.8558	145.4283	105.2115	0.97204	3.03E-06	1.19E-05	PARP11	chr12	-	3900213	3982608	4424
ENSG0000(	1507.077	1639.036	1331.289	2799.295	1713.844	1971.894	-0.53272	0.001238	0.00342	ARPC3	chr12	-	1.11E+08	1.11E+08	1098
ENSG0000(	258.948	215.5675	220.3421	481.6556	386.5814	409.3385	-0.87376	5.32E-07	2.28E-06	GPN3	chr12	-	1.11E+08	1.11E+08	1604
ENSG0000(	787.2018	944.1616	818.0365	1540.099	1148.699	1461.454	-0.70192	1.23E-06	5.06E-06	VPS29	chr12	-	1.11E+08	1.11E+08	1523
ENSG0000(	76.6486	74.66584	108.1919	477.9102	406.8309	430.7096	-2.3364	1.49E-30	2.31E-29	RAD51AP1	chr12	+	4647950	4669214	2235
ENSG0000(	2.071584	2.408575	1.319414	8.988907	0.920432	12.32947	-1.5957	0.12036	0.20428	CUX2	chr12	+	1.11E+08	1.12E+08	6844
ENSG0000(	866.9578	793.6256	1018.587	304.1247	267.8457	252.3432	1.6933	5.92E-28	8.27E-27	SH2B3	chr12	+	1.12E+08	1.12E+08	5406
ENSG0000(	15.53688	30.10719	25.06886	34.45748	26.69253	26.30288	-0.30654	0.51403	0.64092	AKAP3	chr12	-	4724674	4758213	3318
ENSG0000(	30.03797	30.10719	11.87472	279.4052	202.495	198.0935	-3.1766	2.37E-24	2.87E-23	MANSC1	chr12	-	12482198	12503475	2623
ENSG0000(	58.00435	73.46155	91.03955	0	1.840864	0	6.2369	4.82E-15	3.81E-14	KCNA1	chr12	+	5019071	5040527	7976
ENSG0000(	232.0174	156.5574	236.1751	247.1949	404.9901	260.5629	-0.54076	0.019174	0.041781	DUSP16	chr12	-	12628829	12715317	3568
ENSG0000(	416.3883	386.5764	424.8512	305.6228	282.5726	226.8623	0.58823	0.000613	0.001779	CREBL2	chr12	+	12764761	12798042	3754
ENSG0000(	687.7658	633.4553	585.8197	322.1025	447.33	405.2287	0.69924	1.54E-05	5.58E-05	ACAD10	chr12	+	1.12E+08	1.12E+08	4071
ENSG0000(	698.1237	764.7227	629.3604	606.7512	522.8054	626.3373	0.25189	0.081411	0.14755	ALDH2	chr12	+	1.12E+08	1.12E+08	2018
ENSG0000(	920.819	851.4314	874.7713	635.9651	725.3004	742.2343	0.33173	0.011354	0.026063	CDKN1B	chr12	+	12867992	12875305	2657
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	GPRC5D	chr12	-	13093709	13105081	1038
ENSG0000(	511.6812	576.8538	605.6109	744.5811	790.6511	614.0078	-0.34314	0.021926	0.047103	NAA25	chr12	-	1.12E+08	1.13E+08	6003
ENSG0000(	16.57267	15.65574	10.55531	2.247227	0.920432	2.465895	2.5978	0.00179	0.004814	GSG1	chr12	-	13236494	13256619	2390
ENSG0000(	43.50326	20.47289	42.22124	286.8959	312.0264	318.9224	-3.0781	3.53E-32	5.73E-31	SCNN1A	chr12	-	6456009	6486896	3545
ENSG0000(	900.1032	787.6042	742.83	93.63444	90.20234	101.9236	3.0769	3.97E-76	1.97E-74	LTBR	chr12	+	6484211	6500733	2323

ENSG00000(	17.60846	12.04288	17.15238	8.239831	5.522592	12.32947	0.78784	0.22617	0.33898	OGFOD2	chr12	+	1.23E+08	1.23E+08	2308
ENSG00000(	1410.749	1303.039	1302.261	1271.181	1228.777	951.8354	0.21815	0.11277	0.19358	CDK2AP1	chr12	-	1.24E+08	1.24E+08	1812
ENSG00000(	3.107376	2.408575	10.55531	12.73428	12.88605	7.397684	-0.95943	0.23266	0.34636	OAS3	chr12	+	1.13E+08	1.13E+08	6719
ENSG00000(	1.035792	0	2.638828	0	1.840864	0	0.50894	0.70757	NA	OAS2	chr12	+	1.13E+08	1.13E+08	4734
ENSG00000(	2.071584	0	0	4.494453	1.840864	5.753754	-1.7221	0.16067	0.25804	ART4	chr12	-	14978503	14996429	5129
ENSG00000(	242.3753	285.4162	207.148	0.749076	0	2.465895	7.3025	9.52E-32	1.53E-30	MGP	chr12	-	15034115	15038860	1405
ENSG00000(	0	0	0	4.494453	13.80648	12.32947	-4.1699	0.000409	0.001219	RASAL1	chr12	-	1.14E+08	1.14E+08	3817
ENSG00000(	175.0488	137.2888	159.6491	2181.308	1663.221	1612.695	-3.5163	7.79E-101	5.98E-99	ARHGDIB	chr12	-	15094951	15114662	1256
ENSG00000(	529.2897	576.8538	569.9868	919.1157	857.8426	889.366	-0.66923	2.34E-07	1.04E-06	GTF2H3	chr12	+	1.24E+08	1.24E+08	3329
ENSG00000(	755.0923	941.753	762.6212	1404.517	1057.576	1195.959	-0.57183	0.000112	0.000362	EIF2B1	chr12	-	1.24E+08	1.24E+08	2477
ENSG00000(	441.2474	414.275	317.9787	683.1569	607.4851	611.5419	-0.69212	1.61E-05	5.84E-05	DDX55	chr12	+	1.24E+08	1.24E+08	2767
ENSG00000(	1898.607	1779.937	2410.569	5367.875	6549.794	5388.802	-1.5036	6.16E-28	8.58E-27	SLC38A1	chr12	-	46576846	46663800	8066
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	RERGL	chr12	-	18233803	18473041	1147
ENSG00000(	0	1.204288	3.958241	12.73428	3.681728	6.575719	-1.8134	0.080445	0.14604	ENDOU	chr12	-	48103517	48119350	2413
ENSG00000(	344.9187	368.512	471.0307	777.5404	814.5823	649.3523	-0.91926	1.85E-08	9.11E-08	C12orf49	chr12	-	1.17E+08	1.17E+08	2801
ENSG00000(	218.5521	173.4174	221.6615	65.16957	79.15715	48.49593	1.6589	3.96E-11	2.41E-10	VDR	chr12	-	48235320	48336831	4773
ENSG00000(	0	0	0	48.68991	40.49901	51.78379	-6.3653	9.19E-10	5.05E-09	FZD10	chr12	+	1.31E+08	1.31E+08	3282
ENSG00000(	259.9838	301.0719	238.8139	749.0755	696.767	720.0413	-1.4321	4.57E-21	4.83E-20	RFC5	chr12	+	1.18E+08	1.18E+08	2442
ENSG00000(	1002.647	1033.279	981.6439	718.3635	684.8014	545.7847	0.62893	7.99E-06	3.00E-05	STX2	chr12	-	1.31E+08	1.31E+08	3331
ENSG00000(	0	0	0	4.494453	0.920432	1.64393	-1.9637	0.14572	0.23837	GPR133	chr12	+	1.31E+08	1.32E+08	7085
ENSG00000(	3952.582	3827.226	3516.238	2961.096	2338.818	2350.82	0.5608	7.25E-06	2.73E-05	COPZ1	chr12	+	54694986	54745633	1897
ENSG00000(	40.39588	48.17151	31.66593	61.42419	39.57858	60.00344	-0.41398	0.26318	0.38292	TBC1D30	chr12	+	65174589	65274812	7433
ENSG00000(	2056.047	2141.224	2584.732	2403.034	2694.104	2202.866	-0.10631	0.41226	0.54275	CAND1	chr12	+	67663061	67713731	11251
ENSG00000(	294.1649	242.0618	362.8388	140.8262	190.5294	184.9421	0.79605	0.000154	0.000489	RAB5B	chr12	+	56367697	56388490	3362
ENSG00000(	89.0781	72.25726	104.2337	126.5938	115.9744	106.8554	-0.39477	0.12769	0.21422	MDM1	chr12	-	68666223	68726161	2918
ENSG00000(	382.2072	404.6407	385.2688	1681.675	1416.545	1249.387	-1.8861	2.09E-38	4.14E-37	NUP107	chr12	+	69080514	69136785	3653
ENSG00000(	875.2442	800.8513	803.523	913.1231	816.4232	827.7187	-0.0442	0.72924	0.81854	CNOT2	chr12	+	70636774	70748773	4753
ENSG00000(	390.4935	373.3292	368.1164	1184.288	1384.33	1286.375	-1.7624	7.10E-40	1.46E-38	TIMELESS	chr12	-	56810903	56843187	4376
ENSG00000(	1261.595	1241.621	1353.719	2111.644	2141.845	1823.94	-0.655	4.19E-08	2.00E-07	CPSF6	chr12	+	69633317	69668138	6616
ENSG00000(	749.9133	714.1426	936.7838	562.5557	561.4635	429.0657	0.6253	0.000109	0.000353	KRR1	chr12	-	75890684	75905416	4075
ENSG00000(	1681.09	1648.67	1521.284	1429.985	1678.868	2559.599	-0.22347	0.2012	0.30879	MRPL51	chr12	-	6601150	6603007	1136
ENSG00000(	70104.47	68757.6	57886.64	47186.52	41355.93	41090.85	0.60086	1.36E-07	6.16E-07	GAPDH	chr12	+	6643093	6647537	1875
ENSG00000(	793.4166	714.1426	753.3853	1765.571	1537.121	1778.732	-1.1657	7.43E-21	7.78E-20	NOP2	chr12	-	6666029	6677857	3038
ENSG00000(	4753.249	4693.109	5145.714	4437.524	5919.298	5107.69	-0.08349	0.49967	0.62804	CHD4	chr12	-	6679249	6716642	6580
ENSG00000(	6.214751	8.430014	0	0.749076	0	1.64393	1.8828	0.11715	0.19995	ACRBP	chr12	-	6747241	6756626	1933
ENSG00000(	301.4154	320.3405	370.7553	137.8299	158.3143	129.0485	1.2169	1.50E-10	8.77E-10	UHRF1BP1l	chr12	-	1E+08	1.01E+08	5168
ENSG00000(	1685.233	1611.337	1386.704	1072.676	853.2405	891.8319	0.73099	8.59E-08	3.96E-07	COPS7A	chr12	+	6832907	6841041	2127
ENSG00000(	442.2831	382.9635	278.3963	246.4459	190.5294	272.0704	0.63578	0.002099	0.005572	ING4	chr12	-	6759446	6772314	1709
ENSG00000(	52.82539	71.05298	64.65128	42.69731	34.97642	34.52253	0.73145	0.033942	0.069257	GNB3	chr12	+	6949118	6956557	2869
ENSG00000(	267.2343	252.9004	215.0644	1291.406	995.9074	1120.338	-2.2029	4.07E-45	9.75E-44	CDCA3	chr12	-	6953957	6961230	2917
ENSG00000(	505.4664	431.135	422.2124	456.9361	382.8997	387.1455	0.14733	0.35301	0.48274	CHPT1	chr12	+	1.02E+08	1.02E+08	4342
ENSG00000(	2274.599	2350.77	2264.114	2623.263	2737.365	3173.607	-0.30827	0.007505	0.017957	USP5	chr12	+	6961292	6975796	3181
ENSG00000(	21647.02	22391.32	17790.98	11414.41	9351.589	10416.76	0.98551	8.53E-16	7.05E-15	TPI1	chr12	+	6976283	6980112	1763
ENSG00000(	496.1443	432.3393	639.9157	659.9356	668.2336	586.883	-0.28852	0.078298	0.14273	GNPTAB	chr12	-	1.02E+08	1.02E+08	5701

ENSG00000(	87.00652	90.32158	72.56776	83.89646	70.87326	110.9653	-0.08709	0.76072	0.84185	SPSB2	chr12	-	6980099	6998522	1496
ENSG00000(	1188.053	1393.361	960.5332	104.1215	124.2583	88.77221	3.4693	9.43E-83	5.34E-81	ENO2	chr12	+	7022909	7032861	2827
ENSG00000(	6243.754	6099.717	5205.087	4415.051	3985.471	3861.591	0.51631	7.43E-06	2.80E-05	ATN1	chr12	+	7033626	7051484	4293
ENSG00000(	2276.671	2336.318	1456.633	880.1638	591.8378	642.7766	1.5137	1.76E-16	1.51E-15	C12orf57	chr12	+	7052141	7055166	980
ENSG00000(	9.322127	6.021439	3.958241	282.4015	242.994	270.4265	-5.2067	1.16E-39	2.39E-38	PTPN6	chr12	+	7055631	7070479	2412
ENSG00000(	592.473	587.6924	517.2102	501.8806	485.9881	570.4437	0.1237	0.39508	0.52609	LPCAT3	chr12	-	7085348	7125814	2902
ENSG00000(	650.4773	609.3696	643.8739	573.7919	652.5863	590.1708	0.068293	0.61438	0.72768	NT5DC3	chr12	-	1.04E+08	1.04E+08	7207
ENSG00000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	NANOG	chr12	+	7940390	7948655	2101
ENSG00000(	920.819	910.4415	1063.448	1059.942	1254.549	1168.834	-0.26671	0.040785	0.081452	SUDS3	chr12	+	1.19E+08	1.19E+08	4897
ENSG00000(	786.1661	1000.763	977.6856	650.9467	632.3368	600.0344	0.55104	8.77E-05	0.000288	GOLT1B	chr12	+	21654715	21671342	3227
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	GYS2	chr12	-	21689123	21757781	3132
ENSG00000(	14389.22	14440.61	12965.88	15824.97	15252.48	15508.83	-0.15629	0.11491	0.19676	LDHB	chr12	-	21788276	21910791	1538
ENSG00000(	345.9545	298.6634	336.4505	585.7771	454.6934	436.4634	-0.58845	0.00054	0.001577	PRKAB1	chr12	+	1.2E+08	1.2E+08	4019
ENSG00000(	460.9274	529.8866	515.8908	1026.983	979.3396	1034.854	-1.0123	1.25E-14	9.65E-14	CMAS	chr12	+	22199108	22218608	1787
ENSG00000(	216.4805	236.0404	324.5758	71.91125	68.11197	60.00344	1.9395	2.06E-16	1.75E-15	HCFC2	chr12	+	1.04E+08	1.04E+08	4071
ENSG00000(	108.7581	90.32158	68.60952	18.72689	10.12475	25.48091	2.2472	7.02E-09	3.58E-08	ST8SIA1	chr12	-	22216707	22589975	2330
ENSG00000(	5.17896	3.612863	2.638828	5.243529	0.920432	2.465895	0.32491	0.75759	0.83962	CLEC4A	chr12	+	8276228	8291203	1281
ENSG00000(	343.8829	333.5877	424.8512	279.4052	366.3319	281.112	0.24912	0.16912	0.26902	C2CD5	chr12	-	22601517	22697480	4436
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AICDA	chr12	-	8754762	8765467	2819
ENSG00000(	1600.298	1560.757	1517.326	1931.866	1847.307	2248.074	-0.36467	0.002379	0.006256	RAB35	chr12	-	1.21E+08	1.21E+08	2945
ENSG00000(	368.7419	362.4906	412.9765	289.8922	402.2288	343.5813	0.14411	0.40436	0.53529	PHC1	chr12	+	9066492	9094063	5174
ENSG00000(	87.00652	83.09585	65.97069	96.63075	79.15715	67.40112	-0.04058	0.88865	0.93096	COX6A1	chr12	+	1.21E+08	1.21E+08	767
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	RFX4	chr12	+	1.07E+08	1.07E+08	3955
ENSG00000(	242.3753	303.4805	283.674	211.2393	246.6758	189.0519	0.35657	0.061271	0.11565	RIC8B	chr12	+	1.07E+08	1.07E+08	5131
ENSG00000(	3340.429	3312.996	3020.138	4250.255	3945.892	5032.069	-0.45049	0.000196	0.000613	SRSF9	chr12	-	1.21E+08	1.21E+08	1704
ENSG00000(	149.154	121.6331	109.5113	303.3756	265.0844	371.5281	-1.2934	1.12E-09	6.13E-09	RP11-22B2	chr12	+	9429831	9466684	3919
ENSG00000(	469.2137	529.8866	519.849	525.102	562.384	492.357	-0.05708	0.69164	0.7896	FGFR1OP2	chr12	+	27091316	27119583	2945
ENSG00000(	0	1.204288	0	0	9.20432	0.821965	-1.7479	0.18732	0.292	KLRB1	chr12	-	9747147	9760482	1448
ENSG00000(	18564.5	19237.29	25571.56	1831.49	2210.878	1586.392	3.4828	8.58E-123	9.21E-121	COL12A1	chr6	-	75794042	75915767	11723
ENSG00000(	256.8764	287.8248	295.5487	7.490755	3.681728	5.753754	5.4981	1.70E-50	4.75E-49	BTN3A3	chr6	+	26440700	26453643	4547
ENSG00000(	478.5359	525.0694	531.7238	598.5114	616.6894	515.372	-0.17291	0.23415	0.34819	TDP2	chr6	-	24650205	24667261	2120
ENSG00000(	4.143168	7.225726	7.916483	0	4.60216	11.50751	0.21963	0.82076	0.88422	FRK	chr6	-	1.16E+08	1.16E+08	2849
ENSG00000(	514.7886	556.3809	626.7215	542.3307	641.5411	521.1258	-0.00657	0.9653	0.9799	DSE	chr6	+	1.17E+08	1.17E+08	4255
ENSG00000(	1059.615	940.5487	996.1574	1007.507	747.3908	857.3094	0.19676	0.16584	0.26454	RWDD1	chr6	+	1.17E+08	1.17E+08	5522
ENSG00000(	5.17896	7.225726	5.277655	8.988907	17.48821	10.68554	-0.98032	0.18536	0.28975	RSPH4A	chr6	+	1.17E+08	1.17E+08	2825
ENSG00000(	49.71801	55.39724	47.4989	44.94453	67.19154	47.67397	-0.06113	0.85888	0.91034	MAK	chr6	-	10762956	10838764	3984
ENSG00000(	1897.571	1900.366	1616.282	1825.497	1487.418	1814.077	0.078499	0.54363	0.66609	TMEM14C	chr6	+	10723148	10731362	1177
ENSG00000(	358.384	354.0606	317.9787	869.6767	716.0961	759.4956	-1.1824	1.52E-15	1.24E-14	PAK1IP1	chr6	+	10694928	10710015	1800
ENSG00000(	0	1.204288	0	408.2462	415.1148	378.9258	-8.5387	4.32E-26	5.59E-25	GCNT2	chr6	+	10492456	10629601	4525
ENSG00000(	60.07593	79.48299	124.0249	97.37982	99.40666	103.5676	-0.19424	0.51054	0.6379	SMIM8	chr6	+	88032306	88052043	2434
ENSG00000(	323.1671	262.5347	368.1164	600.7586	652.5863	504.6865	-0.87921	3.44E-07	1.50E-06	NEDD9	chr6	-	11183531	11382581	4934
ENSG00000(	223.7311	207.1375	258.6051	157.3059	209.8585	160.2832	0.38534	0.061084	0.11537	CEP85L	chr6	-	1.19E+08	1.19E+08	7673
ENSG00000(	2.071584	0	0	2.996302	7.363456	6.575719	-2.1633	0.063892	0.11996	ADTRP	chr6	-	11712287	11807279	1927
ENSG00000(	249.6258	198.7075	262.5633	523.6038	356.2072	435.6414	-0.88503	3.80E-06	1.48E-05	ASF1A	chr6	+	1.19E+08	1.19E+08	2362

ENSG00000(	97.36444	59.0101	101.5949	157.3059	178.5638	161.9271	-0.93881	0.000244	0.00075	MCM9	chr6	-	1.19E+08	1.19E+08	7592
ENSG00000(	0	6.021439	1.319414	36.7047	22.09037	13.9734	-3.008	0.000168	0.000532	FAM184A	chr6	-	1.19E+08	1.19E+08	4141
ENSG00000(	337.6682	326.362	428.8095	424.7258	461.1364	396.1871	-0.23109	0.16529	0.26387	RNGTT	chr6	-	89319985	89673348	4434
ENSG00000(	1887.213	1830.517	2551.746	792.5219	902.0234	696.2043	1.3863	1.38E-19	1.37E-18	MAN1A1	chr6	-	1.19E+08	1.2E+08	5014
ENSG00000(	15.53688	3.612863	3.958241	3.745378	4.60216	6.575719	0.57634	0.50908	0.63644	GABRR2	chr6	-	89966927	90025018	1691
ENSG00000(	3180.917	3145.6	3368.463	1608.265	1368.682	1241.989	1.1974	4.06E-22	4.49E-21	SERINC1	chr6	-	1.23E+08	1.23E+08	3382
ENSG00000(	589.3656	710.5298	538.3208	1218.746	935.1589	1150.751	-0.84377	3.44E-08	1.65E-07	HDDC2	chr6	-	1.26E+08	1.26E+08	1615
ENSG00000(	68.36227	57.80581	27.70769	1348.336	1052.974	1112.941	-4.4632	1.03E-95	7.35E-94	TPD52L1	chr6	+	1.25E+08	1.26E+08	2489
ENSG00000(	204.051	191.4817	196.5927	405.2499	495.1924	538.387	-1.2742	3.85E-13	2.72E-12	HINT3	chr6	+	1.26E+08	1.26E+08	3311
ENSG00000(	136.7245	173.4174	222.9809	831.4739	984.8622	841.6921	-2.3143	3.56E-38	7.00E-37	NCOA7	chr6	+	1.26E+08	1.26E+08	5521
ENSG00000(	325.2387	348.0392	434.0871	108.616	126.0992	106.0335	1.6913	8.41E-18	7.67E-17	FAM65B	chr6	-	24797601	25042238	5471
ENSG00000(	925.998	939.3444	1153.168	562.5557	669.1541	514.55	0.78711	1.62E-07	7.29E-07	SASH1	chr6	+	1.49E+08	1.49E+08	7711
ENSG00000(	523.0749	549.1552	631.9992	129.5901	121.497	115.0751	2.2077	3.93E-38	7.73E-37	UST	chr6	+	1.49E+08	1.49E+08	4198
ENSG00000(	80.79177	77.07441	84.44248	29.96302	23.0108	21.37109	1.6718	1.26E-06	5.17E-06	ULBP1	chr6	+	1.5E+08	1.5E+08	3140
ENSG00000(	267.2343	266.1476	240.1333	868.9276	788.8102	710.1777	-1.6079	5.72E-26	7.33E-25	FBXO5	chr6	-	1.53E+08	1.53E+08	2600
ENSG00000(	373.9209	302.2762	331.1729	404.5008	432.603	403.5848	-0.29754	0.062147	0.1171	MTRF1L	chr6	-	1.53E+08	1.53E+08	3676
ENSG00000(	1145.586	1160.933	1079.28	566.3011	583.5539	608.254	0.94394	2.64E-14	2.00E-13	PPARD	chr6	+	35310335	35395968	3774
ENSG00000(	193.6931	183.0517	159.6491	332.5895	266.9253	272.8924	-0.69696	0.000283	0.000865	FANCE	chr6	+	35420138	35434880	2554
ENSG00000(	3.107376	3.612863	7.916483	10.48706	10.12475	38.63235	-1.8637	0.013777	0.031067	TULP1	chr6	-	35465651	35480715	2162
ENSG00000(	0	3.612863	1.319414	3.745378	2.761296	3.28786	-0.75947	0.51716	0.64348	SLC26A8	chr6	-	35911291	35992645	3653
ENSG00000(	1074.116	964.6345	1070.045	960.3149	1039.168	965.8088	0.068471	0.57632	0.69458	MAPK14	chr6	+	35995488	36079013	4319
ENSG00000(	1258.487	1362.049	1431.564	1895.91	1804.047	1725.304	-0.42102	0.000281	0.000858	KCTD20	chr6	+	36410544	36458920	5619
ENSG00000(	1252.272	1275.341	1360.316	984.2853	939.7611	898.4077	0.46058	0.000107	0.000348	STK38	chr6	-	36461669	36515247	3576
ENSG00000(	3291.747	3381.64	3415.962	7356.671	6745.846	7063.145	-1.0676	1.61E-26	2.11E-25	SRSF3	chr6	+	36562145	36571209	2054
ENSG00000(	2453.791	2311.028	1903.914	1247.96	1217.732	1210.754	0.85782	9.68E-12	6.16E-11	SOD2	chr6	-	1.6E+08	1.6E+08	4302
ENSG00000(	836.9199	821.3242	597.6944	1118.37	1071.383	1222.262	-0.59357	7.16E-05	0.000238	MRPL18	chr6	+	1.6E+08	1.6E+08	1075
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	IL17F	chr6	-	52101479	52109335	926
ENSG00000(	587.294	516.6394	569.9868	4172.351	3894.348	3776.107	-2.817	7.51E-129	8.73E-127	MCM3	chr6	-	52128807	52149679	3169
ENSG00000(	311.7734	357.6735	345.6864	393.2647	341.4803	333.7178	-0.07557	0.6436	0.75092	RNF8	chr6	+	37321748	37362514	5631
ENSG00000(	49.71801	52.98866	47.4989	25.46857	53.38506	42.74218	0.30537	0.42397	0.5545	PHACTR1	chr6	+	12717893	13288645	4784
ENSG00000(	610.0814	659.9497	633.3186	53.18436	58.90765	62.46933	3.433	1.28E-79	6.86E-78	MDGA1	chr6	-	37598455	37667082	10736
ENSG00000(	372.8851	340.8134	486.8637	269.6672	271.5274	201.3814	0.68815	0.000377	0.001129	ICK	chr6	-	52866077	52926600	6227
ENSG00000(	673.2647	676.8097	786.3706	776.0423	629.5755	684.6968	0.029613	0.83564	0.89487	FBXO9	chr6	+	52916789	52965671	4559
ENSG00000(	143.9751	163.7831	91.03955	55.43159	38.65814	27.94681	1.6814	2.58E-07	1.14E-06	CD83	chr6	+	14117872	14137149	2471
ENSG00000(	963.2865	843.0014	1208.583	1157.322	1658.618	1105.543	-0.37781	0.029351	0.060996	MDN1	chr6	-	90352218	90529442	18413
ENSG00000(	263.0911	239.6533	193.9538	122.8484	92.96363	146.3098	0.93718	4.31E-05	0.000148	SAYSD1	chr6	-	39071840	39082965	2020
ENSG00000(	11.39371	18.06432	18.47179	211.2393	242.0736	229.3282	-3.7976	1.27E-33	2.17E-32	BMP5	chr6	-	55618443	55740362	3952
ENSG00000(	50.7538	43.35436	34.30476	247.944	365.4115	252.3432	-2.7161	2.93E-25	3.66E-24	BACH2	chr6	-	90636248	91006627	9113
ENSG00000(	210.2658	256.5133	273.1187	59.92604	37.73771	40.27628	2.3927	2.43E-21	2.60E-20	RBM24	chr6	+	17281577	17294106	2703
ENSG00000(	170.9057	192.686	300.8263	543.0798	482.3064	497.2888	-1.1957	2.61E-09	1.38E-08	CAP2	chr6	+	17393447	17558023	3316
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	TREML2	chr6	-	41158015	41168932	3302
ENSG00000(	619.4036	593.7138	725.6776	677.1643	577.1109	517.8379	0.12775	0.40617	0.53704	ZNF451	chr6	+	56951642	57035105	9478
ENSG00000(	804.8103	1054.956	891.9237	1149.082	916.7503	969.9186	-0.1425	0.33001	0.45781	BAG2	chr6	+	57037124	57049735	1755
ENSG00000(	1481.182	1500.542	1712.599	488.3973	471.2612	381.3917	1.8022	3.37E-38	6.64E-37	RAB23	chr6	-	57053607	57087078	2986

ENSG00000(	0	0	0	0	4.60216	0.821965	-1.4643	0.27877	NA	TSPO2	chr6	+	41010293	41012076	958
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	FHL5	chr6	+	97010424	97064512	2031
ENSG00000(	27.96638	51.78437	54.09597	55.43159	65.35067	62.46933	-0.45328	0.20482	0.31333	GPR63	chr6	-	97245888	97285353	2198
ENSG00000(	0	1.204288	0	4.494453	2.761296	4.109825	-2.1085	0.095431	0.16873	KHDRBS2	chr6	-	62390139	62996132	2058
ENSG00000(	241.3395	256.5133	236.1751	152.8114	193.2907	105.2115	0.69894	0.002246	0.00593	FBXL4	chr6	-	99321334	99395849	3115
ENSG00000(	706.4101	739.4327	977.6856	1592.535	1147.779	1377.613	-0.76407	1.91E-06	7.69E-06	CCNC	chr6	-	99990256	1E+08	2473
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	PRDM13	chr6	+	1E+08	1E+08	3234
ENSG00000(	403.9588	402.2321	403.7406	632.9688	596.4399	623.0494	-0.61319	1.04E-05	3.84E-05	E2F3	chr6	+	20402398	20493941	4744
ENSG00000(	2241.454	2297.781	2622.995	3792.57	3753.522	3508.968	-0.62564	2.25E-08	1.10E-07	PTP4A1	chr6	+	64231666	64293492	5088
ENSG00000(	1213.948	1188.632	1723.154	1534.856	1447.84	1204.179	-0.02215	0.88874	0.93098	ASCC3	chr6	-	1.01E+08	1.01E+08	8146
ENSG00000(	162.6193	160.1703	205.8285	260.6783	233.7897	216.9987	-0.42972	0.031526	0.064919	BVES	chr6	-	1.06E+08	1.06E+08	5567
ENSG00000(	1.035792	0	0	0.749076	0.920432	1.64393	-0.70513	0.60322	NA	COL9A1	chr6	-	70924764	71012786	4761
ENSG00000(	470.2495	428.7264	635.9574	441.9546	439.0461	312.3467	0.35999	0.058337	0.11106	MED23	chr6	-	1.32E+08	1.32E+08	5245
ENSG00000(	563.4708	491.3494	539.6402	563.3048	510.8398	475.0957	0.041402	0.77711	0.85323	WASF1	chr6	-	1.1E+08	1.11E+08	3220
ENSG00000(	1.035792	0	3.958241	9.737982	7.363456	14.79537	-2.3036	0.016778	0.037066	GPLD1	chr6	-	24424793	24495433	3489
ENSG00000(	15.53688	12.04288	17.15238	60.67512	58.90765	43.56414	-1.8186	3.06E-05	0.000107	ALDH5A1	chr6	+	24495080	24537435	5248
ENSG00000(	145.0109	189.0732	241.4527	105.6197	115.054	115.0751	0.76785	0.001233	0.003406	AIM1	chr6	+	1.07E+08	1.07E+08	7544
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	VNN1	chr6	-	1.33E+08	1.33E+08	3106
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	VNN2	chr6	-	1.33E+08	1.33E+08	2118
ENSG00000(	368.7419	355.2649	314.0205	335.5858	321.2308	354.2669	0.039033	0.8085	0.87565	ACOT13	chr6	+	24667263	24705293	4391
ENSG00000(	142.9393	134.8802	105.5531	128.0919	129.7809	115.8971	0.040066	0.86476	0.91464	SMAP1	chr6	+	71377479	71571718	3333
ENSG00000(	16279.54	16860.03	11323.21	15195	12944.96	15662.54	0.021585	0.88201	0.92636	RPS12	chr6	+	1.33E+08	1.33E+08	639
ENSG00000(	3606.627	3652.605	3751.093	2088.423	2347.102	2080.393	0.75582	2.10E-12	1.41E-11	C6orf62	chr6	-	24705089	24721064	4134
ENSG00000(	33.14534	19.2686	40.90183	1.498151	1.840864	9.863579	2.6314	9.06E-05	0.000297	B3GAT2	chr6	-	71566382	71666741	6565
ENSG00000(	228.91	210.7504	245.411	1552.834	1198.402	1306.102	-2.5595	1.57E-63	5.94E-62	GMNN	chr6	+	24775159	24786327	1262
ENSG00000(	52.82539	44.55865	76.526	89.88907	116.8949	64.11326	-0.63258	0.055462	0.10632	EYA4	chr6	+	1.34E+08	1.34E+08	5699
ENSG00000(	884.5663	732.2069	849.7025	47.94084	97.56579	108.4994	3.2643	3.34E-49	9.07E-48	SOBP	chr6	+	1.08E+08	1.08E+08	5231
ENSG00000(	0	0	0	2.247227	2.761296	0.821965	-1.7061	0.20822	NA	NR2E1	chr6	+	1.08E+08	1.09E+08	3212
ENSG00000(	3522.728	3801.936	3302.493	2413.521	2078.335	2106.696	0.6861	2.92E-09	1.53E-08	SNX3	chr6	-	1.09E+08	1.09E+08	1755
ENSG00000(	1101.047	967.043	1126.779	948.3296	885.4556	803.8817	0.27559	0.03528	0.071653	HBS1L	chr6	-	1.35E+08	1.35E+08	7163
ENSG00000(	506.5022	423.9093	473.6695	180.5272	221.8241	163.571	1.308	1.85E-13	1.33E-12	TRIM38	chr6	+	25963030	25985348	3255
ENSG00000(	41.43168	46.96722	54.09597	87.64184	60.74851	82.19649	-0.69151	0.032513	0.066678	PEX7	chr6	+	1.37E+08	1.37E+08	1539
ENSG00000(	227.8742	213.1589	216.3839	422.4786	307.4243	345.2253	-0.70725	0.000116	0.000375	ZBTB24	chr6	-	1.1E+08	1.1E+08	5519
ENSG00000(	219.5879	243.2661	224.3003	250.9403	206.1768	196.4496	0.070178	0.71325	0.80626	FIG4	chr6	+	1.1E+08	1.1E+08	3011
ENSG00000(	1711.128	1620.971	1810.236	7142.435	6186.223	6043.908	-1.9104	4.36E-63	1.63E-61	PERP	chr6	-	1.38E+08	1.38E+08	2009
ENSG00000(	7.250543	15.65574	6.597069	89.88907	124.2583	82.19649	-3.242	5.81E-14	4.31E-13	KIAA1244	chr6	+	1.38E+08	1.39E+08	14877
ENSG00000(	3.107376	2.408575	1.319414	97.37982	91.12277	61.64737	-4.8538	4.45E-15	3.53E-14	SLC16A10	chr6	+	1.11E+08	1.12E+08	2508
ENSG00000(	422.6031	354.0606	468.3919	238.9551	268.7661	250.6993	0.71255	3.18E-05	0.000111	HECA	chr6	+	1.39E+08	1.4E+08	5614
ENSG00000(	2.071584	10.83859	3.958241	1641.974	1838.103	1360.352	-8.0186	1.49E-95	1.05E-93	GPR126	chr6	+	1.43E+08	1.43E+08	7026
ENSG00000(	233.0532	283.0076	344.367	343.0766	376.4567	288.5097	-0.23006	0.22918	0.3426	PHACTR2	chr6	+	1.44E+08	1.44E+08	9531
ENSG00000(	52.82539	36.12863	65.97069	65.16957	77.31629	87.12828	-0.56101	0.088355	0.1583	EPM2A	chr6	-	1.46E+08	1.46E+08	3633
ENSG00000(	5684.426	5827.548	5309.321	2292.92	2394.964	2988.664	1.1295	9.07E-20	9.08E-19	SLC39A7	chr6	+	33168222	33172216	2409
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	CCR6	chr6	+	1.68E+08	1.68E+08	4018
ENSG00000(	0	0	0	3.745378	0	1.64393	-1.4934	0.26982	NA	UNC93A	chr6	+	1.68E+08	1.68E+08	2116

ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	SLC22A2	chr6	-	1.61E+08	1.61E+08	3737
ENSG00000(	743.6986	790.0127	708.5252	576.7882	574.3496	646.8864	0.31791	0.01808	0.039621	PHF1	chr6	+	33378176	33384230	2330
ENSG00000(	3143.628	2975.795	2648.063	2908.66	2067.29	2345.066	0.25931	0.060853	0.11502	CUTA	chr6	-	33384219	33386094	1378
ENSG00000(	7.250543	6.021439	6.597069	0.749076	0	2.465895	2.0964	0.049483	0.096213	PACRG	chr6	+	1.63E+08	1.64E+08	1619
ENSG00000(	2802.853	2798.765	3404.088	2495.171	2823.885	2273.555	0.24554	0.054959	0.10554	QKI	chr6	+	1.64E+08	1.64E+08	9463
ENSG00000(	2.071584	3.612863	3.958241	11.23613	12.88605	4.93179	-1.4141	0.10515	0.18274	C6orf118	chr6	-	1.66E+08	1.66E+08	1838
ENSG00000(	138.7961	136.0845	201.8703	244.1986	319.3899	247.4114	-0.76441	0.000447	0.001324	PDE10A	chr6	-	1.66E+08	1.66E+08	8233
ENSG00000(	1333.064	1198.266	1088.516	2793.303	2428.1	3019.899	-1.1835	5.39E-20	5.46E-19	MDFI	chr6	+	41604620	41621984	1629
ENSG00000(	60.07593	80.68728	68.60952	32.95932	43.2603	50.96182	0.70852	0.035561	0.072154	TFEB	chr6	-	41651716	41703997	2595
ENSG00000(	2.071584	0	1.319414	75.65663	68.11197	68.22309	-5.3747	3.41E-13	2.41E-12	SMOC2	chr6	+	1.69E+08	1.69E+08	3150
ENSG00000(	1778.455	1602.907	1629.476	821.7359	851.3996	863.8851	0.98065	4.97E-17	4.35E-16	CCND3	chr6	-	41902671	42018095	2394
ENSG00000(	554.1487	497.3708	507.9743	1064.436	775.9242	983.892	-0.85423	1.72E-08	8.49E-08	BYSL	chr6	+	41888926	41900784	2029
ENSG00000(	622.5109	711.734	828.5919	458.4342	513.6011	410.1605	0.64295	4.30E-05	0.000148	FAM120B	chr6	+	1.71E+08	1.71E+08	5155
ENSG00000(	268.2701	232.4275	226.9392	483.9028	354.3663	450.4368	-0.82033	5.00E-06	1.92E-05	TBP	chr6	+	1.71E+08	1.71E+08	1903
ENSG00000(	13.46529	9.634302	11.87472	14.23244	2.761296	1.64393	0.80253	0.32361	0.451	GUCA1B	chr6	-	42152139	42162654	1113
ENSG00000(	96.32865	99.95588	87.08131	0	6.443024	0.821965	5.1287	2.88E-19	2.82E-18	PRPH2	chr6	-	42664340	42690312	2974
ENSG00000(	211.3015	220.3847	175.482	83.89646	107.6905	101.1017	1.0496	2.82E-06	1.11E-05	GLTSCR1L	chr6	+	42749765	42836298	6530
ENSG00000(	1548.509	1370.479	1403.856	1251.705	1219.572	1076.774	0.28479	0.020546	0.044408	PPP2R5D	chr6	+	42952237	42980080	3044
ENSG00000(	396.7083	461.2422	350.9641	493.6408	500.715	630.4471	-0.42429	0.011092	0.025528	MRPL2	chr6	-	43021767	43027544	1588
ENSG00000(	4627.918	4730.442	4174.625	3553.614	5055.013	4889.047	0.004073	0.97644	0.98634	PTK7	chr6	+	43044006	43129457	5282
ENSG00000(	1452.18	1436.715	1516.006	1737.106	2112.391	2245.608	-0.46737	0.000237	0.000732	SRF	chr6	+	43139037	43149243	4200
ENSG00000(	311.7734	298.6634	312.7011	182.0254	296.3791	255.6311	0.3316	0.096833	0.17081	CUL9	chr6	+	43149913	43192325	8150
ENSG00000(	192.6573	150.536	245.411	149.8151	195.1316	206.3132	0.093289	0.68398	0.78385	NUDT3	chr6	-	34255997	34360451	1364
ENSG00000(	502.3591	581.671	436.726	147.5679	221.8241	326.3201	1.1215	1.29E-06	5.28E-06	DNPH1	chr6	-	43193367	43197222	834
ENSG00000(	216.4805	189.0732	209.7868	415.7369	346.0824	358.3767	-0.86095	9.39E-07	3.91E-06	DUSP22	chr6	+	291630	351355	3824
ENSG00000(	286.9144	376.9421	461.7948	711.6218	694.0057	562.224	-0.80564	9.32E-06	3.48E-05	EXOC2	chr6	-	485133	693117	4449
ENSG00000(	1929.68	1952.15	1591.213	1997.784	1812.331	2165.878	-0.1262	0.32216	0.44947	COX7A2	chr6	-	75947391	75960039	914
ENSG00000(	4146.275	4229.458	5463.692	3787.326	4580.99	4164.896	0.14252	0.28149	0.40403	TMEM30A	chr6	-	75962640	75994684	4594
ENSG00000(	460.9274	492.5537	378.6718	311.6154	197.8929	300.8392	0.71194	0.000281	0.00086	GMDS	chr6	-	1624041	2245926	1752
ENSG00000(	1228.449	1422.264	1426.286	1342.343	1231.538	1136.777	0.13465	0.28696	0.41051	SENP6	chr6	+	76311225	76427997	6645
ENSG00000(	1.035792	4.817151	3.958241	11.23613	12.88605	7.397684	-1.5113	0.078817	0.14347	IMPG1	chr6	-	76630832	76782395	5795
ENSG00000(	2482.793	2944.483	2260.156	403.7517	428.0009	373.994	2.6665	5.70E-86	3.39E-84	VEGFA	chr6	+	43737921	43754224	12167
ENSG00000(	1018.183	1030.87	1190.111	1276.425	1390.773	1169.656	-0.24425	0.058071	0.11064	PRPF4B	chr6	+	4021501	4065217	6775
ENSG00000(	167.7983	173.4174	166.2461	853.9461	691.2444	643.5985	-2.1011	3.31E-35	5.97E-34	TTK	chr6	+	80713604	80752244	3725
ENSG00000(	208.1942	180.6432	201.8703	937.8426	679.2788	780.0447	-2.013	1.64E-32	2.70E-31	SLC29A1	chr6	+	44187242	44201888	2485
ENSG00000(	6.214751	0	2.638828	2.996302	4.60216	4.109825	-0.30253	0.77916	0.85467	WISP3	chr6	+	1.12E+08	1.12E+08	2512
ENSG00000(	590.4014	578.0581	550.1955	370.0433	280.7318	372.3501	0.74437	3.36E-06	1.31E-05	BTN2A1	chr6	+	26458150	26476849	3113
ENSG00000(	4888.938	4631.691	5370.014	20.97412	29.45382	18.08323	7.7369	0	0	LAMA4	chr6	-	1.12E+08	1.13E+08	6547
ENSG00000(	2266.313	2516.961	2729.867	363.3016	411.4331	325.4981	2.7655	4.29E-94	2.94E-92	FAM46A	chr6	-	82201156	82462491	5664
ENSG00000(	0	0	2.638828	18.72689	25.7721	27.94681	-4.1785	4.53E-06	1.75E-05	CLIC5	chr6	-	45868045	46048132	2713
ENSG00000(	1329.957	1207.901	1050.253	1987.297	1736.855	1782.842	-0.61582	1.70E-06	6.88E-06	FBRSL1	chr12	+	1.33E+08	1.33E+08	5568
ENSG00000(	0	0	0	20.22504	17.48821	21.37109	-5.1713	2.49E-06	9.88E-06	ENPP5	chr6	-	46126924	46138708	3834
ENSG00000(	0	0	0	0.749076	1.840864	0	-0.68825	0.58858	NA	LY86	chr6	+	6588341	6655216	1197
ENSG00000(	6.214751	2.408575	2.638828	117.6049	115.9744	96.99186	-4.6377	2.74E-19	2.69E-18	PRSS16	chr6	+	27215480	27224403	3411

ENSG00000(	715.7322	691.2612	928.8673	24.71949	18.40864	11.50751	5.3605	7.19E-103	5.75E-101	TBX18	chr6	-	85444157	85474237	4408
ENSG00000(	911.4969	940.5487	1121.502	835.9683	1123.847	826.0747	0.09379	0.54203	0.66469	ERBB2IP	chr5	+	65222303	65378377	8647
ENSG00000(	1698.699	1614.95	1903.914	531.8436	517.2828	475.0957	1.7709	4.80E-44	1.12E-42	PCDHB2	chr5	+	1.4E+08	1.4E+08	2736
ENSG00000(	588.3298	486.5322	551.515	354.3127	474.0225	452.9027	0.34481	0.034404	0.070092	HARS2	chr5	+	1.4E+08	1.4E+08	2483
ENSG00000(	143.9751	174.6217	213.745	141.5753	172.1208	129.8705	0.25909	0.25728	0.37585	NUDT12	chr5	-	1.03E+08	1.03E+08	3492
ENSG00000(	99.43602	86.70872	101.5949	180.5272	263.2436	223.5745	-1.2029	1.88E-07	8.38E-07	CEP72	chr5	+	612387	667283	2434
ENSG00000(	1594.084	1718.519	2171.755	1381.295	1705.56	1266.648	0.33185	0.027541	0.057716	MAN2A1	chr5	+	1.09E+08	1.09E+08	5599
ENSG00000(	1489.469	1460.801	1870.929	477.9102	523.7258	418.3801	1.7584	1.18E-33	2.03E-32	SEMA5A	chr5	-	9035138	9546187	11762
ENSG00000(	729.1975	756.2927	810.1201	0.749076	6.443024	3.28786	7.6557	2.92E-77	1.49E-75	C7	chr5	+	40909354	40983041	4257
ENSG00000(	742.6628	806.8728	662.3457	797.7655	708.7326	689.6286	0.010407	0.94029	0.96401	PAPD7	chr5	+	6714718	6757161	3861
ENSG00000(	75.61281	63.82725	76.526	17.97781	11.96562	17.26126	2.1408	3.03E-08	1.46E-07	GHR	chr5	+	42423879	42721979	4560
ENSG00000(	2988.26	2708.443	3941.089	1236.724	1705.56	1444.192	1.1321	4.14E-13	2.91E-12	HMGCS1	chr5	-	43289497	43313614	3506
ENSG00000(	4624.811	4404.08	4486.007	2556.595	2175.901	2105.874	0.98085	8.02E-18	7.33E-17	DAP	chr5	-	10679342	10761384	2339
ENSG00000(	8.286335	4.817151	5.277655	29.21395	19.32907	30.4127	-1.9746	0.00141	0.003853	NME5	chr5	-	1.37E+08	1.37E+08	1193
ENSG00000(	912.5327	835.7757	928.8673	893.6471	808.1393	810.4574	0.091082	0.47315	0.60223	BRD8	chr5	-	1.37E+08	1.38E+08	4388
ENSG00000(	692.9448	714.1426	800.8842	2421.012	2382.998	2199.578	-1.6633	1.16E-43	2.66E-42	KIF20A	chr5	+	1.38E+08	1.38E+08	3201
ENSG00000(	841.063	973.0645	1080.6	614.991	648.9046	565.5119	0.65933	3.06E-06	1.20E-05	NNT	chr5	+	43602794	43707507	6483
ENSG00000(	621.4751	687.6483	678.1787	1122.864	724.38	728.2609	-0.37392	0.031194	0.064327	MRPS30	chr5	+	44809027	44820530	4331
ENSG00000(	3790.998	3544.219	3846.091	6648.045	6310.482	6085.828	-0.76723	7.03E-14	5.18E-13	HSPA9	chr5	-	1.38E+08	1.38E+08	3321
ENSG00000(	1857.175	1717.314	1695.447	2049.471	1850.068	1561.733	-0.0512	0.69115	0.7894	MRPS27	chr5	-	71515236	71616473	4435
ENSG00000(	648.4057	588.8967	525.1267	1319.871	926.875	993.7556	-0.87508	4.24E-08	2.02E-07	PFDN1	chr5	-	1.4E+08	1.4E+08	1352
ENSG00000(	68.36227	73.46155	84.44248	200.7522	126.0992	120.8288	-0.97956	0.000417	0.001239	HBEGF	chr5	-	1.4E+08	1.4E+08	2386
ENSG00000(	0	2.408575	7.916483	0	0	0	2.6457	0.048962	0.095311	SLC4A9	chr5	+	1.4E+08	1.4E+08	3343
ENSG00000(	5790.077	6147.889	6156.385	1274.927	1016.157	967.4527	2.4672	2.32E-86	1.39E-84	LOX	chr5	-	1.21E+08	1.21E+08	5102
ENSG00000(	246.5185	345.6306	233.5362	132.5864	118.7357	128.2265	1.1132	1.87E-07	8.36E-07	APBB3	chr5	-	1.4E+08	1.4E+08	2801
ENSG00000(	95.29286	128.8588	79.16483	167.0438	151.8713	175.0785	-0.69709	0.004406	0.011036	TMCO6	chr5	+	1.4E+08	1.4E+08	1953
ENSG00000(	131749.6	131464.9	120054.8	30433.44	26028.9	25107.74	2.2286	2.53E-91	1.65E-89	SPARC	chr5	-	1.51E+08	1.51E+08	3701
ENSG00000(	1430.429	1462.005	1384.065	1327.362	1454.283	1420.355	0.025731	0.82075	0.88422	IK	chr5	+	1.4E+08	1.4E+08	1964
ENSG00000(	2347.104	2449.521	2959.445	2447.23	2590.096	2275.199	0.084349	0.49675	0.62528	HMGCR	chr5	+	74632154	74657929	4585
ENSG00000(	547.9339	562.4024	679.4981	596.2641	796.1737	566.3338	-0.12977	0.43327	0.56311	COL4A3BP	chr5	-	74664311	74807963	5651
ENSG00000(	1518.471	1342.781	1651.906	1319.122	1406.42	1208.288	0.19772	0.12033	0.20425	FAF2	chr5	+	1.76E+08	1.76E+08	4515
ENSG00000(	0	0	0	8914.748	8467.054	8327.327	-13.043	1.23E-57	4.06E-56	HAND1	chr5	-	1.54E+08	1.54E+08	1738
ENSG00000(	103.5792	120.4288	126.6637	43.44638	39.57858	23.01502	1.6992	6.89E-08	3.21E-07	PCDHB3	chr5	+	1.4E+08	1.4E+08	3173
ENSG00000(	136.7245	145.7188	178.1209	465.1759	373.6954	392.0773	-1.4164	5.71E-14	4.24E-13	PCDHB5	chr5	+	1.41E+08	1.41E+08	2904
ENSG00000(	16.57267	9.634302	32.98534	6.74168	3.681728	4.109825	1.8621	0.008071	0.019158	PCDHB6	chr5	+	1.41E+08	1.41E+08	3030
ENSG00000(	24.85901	19.2686	34.30476	7.490755	1.840864	2.465895	2.5216	0.000172	0.000543	PCDHB7	chr5	+	1.41E+08	1.41E+08	3715
ENSG00000(	87.00652	78.2787	85.7619	42.69731	64.43024	27.12484	0.89361	0.009865	0.022977	PDE8B	chr5	+	76506274	76725632	5956
ENSG00000(	364.5988	391.3935	362.8388	256.9329	184.0864	192.3398	0.81448	9.98E-06	3.71E-05	CLK4	chr5	-	1.78E+08	1.78E+08	3722
ENSG00000(	352.1692	261.3304	394.5047	106.3687	99.40666	92.06007	1.7469	1.69E-16	1.45E-15	PCDHB15	chr5	+	1.41E+08	1.41E+08	2653
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	HAVCR1	chr5	-	1.56E+08	1.56E+08	1845
ENSG00000(	0	0	0	0	6.443024	9.041614	-2.9523	0.024019	0.051142	GRM6	chr5	-	1.78E+08	1.78E+08	6143
ENSG00000(	903.2105	856.2486	872.1325	651.6957	427.0804	400.2969	0.82629	2.82E-06	1.11E-05	RNF130	chr5	-	1.79E+08	1.79E+08	9945
ENSG00000(	482.679	497.3708	415.6153	306.3719	279.8113	289.3317	0.67083	2.17E-05	7.74E-05	THG1L	chr5	+	1.57E+08	1.57E+08	3107
ENSG00000(	591.4372	573.241	684.7758	573.7919	543.0549	515.372	0.17849	0.21007	0.31976	ARSB	chr5	-	78073032	78281910	5327

ENSG00000(	1484.29	1564.37	1733.71	1748.342	1573.939	1474.605	-0.00518	0.96644	0.98027	CLINT1	chr5	-	1.57E+08	1.57E+08	3987
ENSG00000(	19.68005	36.12863	21.11062	14.23244	10.12475	22.19305	0.68963	0.20077	0.30831	THBS4	chr5	+	79287134	79379110	3222
ENSG00000(	912.5327	953.7959	1186.153	1266.687	1568.416	1415.424	-0.47708	0.000744	0.002131	CNOT6	chr5	+	1.8E+08	1.8E+08	6303
ENSG00000(	0	1.204288	0	3.745378	0	2.465895	-1.2708	0.34576	0.47523	IL12B	chr5	-	1.59E+08	1.59E+08	2761
ENSG00000(	757.1639	808.0771	723.0388	1175.3	922.2729	956.7672	-0.416	0.002854	0.0074	TTC1	chr5	+	1.59E+08	1.59E+08	1467
ENSG00000(	277.5922	304.6848	246.7304	426.9731	362.6502	343.5813	-0.44896	0.009568	0.022351	MSH3	chr5	+	79950467	80172279	4092
ENSG00000(	25.8948	18.06432	25.06886	865.1823	929.6363	893.4759	-5.2389	1.03E-110	9.21E-109	RASGRF2	chr5	+	80256491	80525975	8167
ENSG00000(	0	0	0	2.996302	7.363456	0	-2.364	0.07798	0.1422	GABRG2	chr5	+	1.61E+08	1.62E+08	4056
ENSG00000(	5831.508	6137.05	6517.904	4096.694	3227.035	2994.418	0.83903	1.02E-10	6.05E-10	CCNG1	chr5	+	1.63E+08	1.63E+08	2458
ENSG00000(	116.0087	150.536	129.3026	243.4496	182.2455	237.5479	-0.74319	0.000669	0.001929	POLR3G	chr5	+	89767565	89810370	3285
ENSG00000(	980.8949	881.5386	1022.546	1255.451	1434.953	1214.864	-0.43563	0.000698	0.002009	DROSHA	chr5	-	31400604	31532303	5305
ENSG00000(	29.00217	54.19295	51.45714	255.4348	410.5127	279.4681	-2.7935	2.20E-24	2.66E-23	CDH6	chr5	+	31193857	31329253	8476
ENSG00000(	816.204	718.9598	799.5648	3849.499	3990.993	3619.112	-2.2908	5.27E-89	3.26E-87	LMNB1	chr5	+	1.26E+08	1.26E+08	3475
ENSG00000(	1142.478	1204.288	1322.053	425.4749	493.3516	376.4599	1.4984	9.26E-26	1.18E-24	ARRDC3	chr5	-	90664541	90679176	4188
ENSG00000(	1626.193	1498.134	1559.547	1771.564	1748.821	1604.476	-0.12936	0.25336	0.37126	GOLPH3	chr5	-	32124810	32174456	2721
ENSG00000(	2338.818	2413.393	2385.5	2730.38	2085.699	2495.485	-0.03511	0.77686	0.85319	SUB1	chr5	+	32531739	32604185	4273
ENSG00000(	1726.665	1738.991	2385.5	116.1067	247.5962	182.4762	3.4058	4.53E-61	1.63E-59	NPR3	chr5	+	32689176	32791819	7337
ENSG00000(	614.2246	602.1439	679.4981	286.8959	312.0264	265.4947	1.1298	5.84E-14	4.33E-13	FAM172A	chr5	-	92953775	93447404	4312
ENSG00000(	11.39371	3.612863	11.87472	2114.64	2708.831	2312.187	-7.9302	1.65E-137	2.15E-135	SLC27A6	chr5	+	1.28E+08	1.28E+08	3219
ENSG00000(	3454.366	3322.63	3285.34	4770.862	4068.309	3843.508	-0.33333	0.003947	0.009987	TARS	chr5	+	33440802	33469644	4314
ENSG00000(	0	0	0	44.19546	44.18074	54.24968	-6.3803	8.16E-10	4.50E-09	IRX4	chr5	-	1877541	1887350	2538
ENSG00000(	371.8493	386.5764	552.8344	202.9995	445.4891	184.1201	0.63838	0.14307	0.23473	LNPEP	chr5	+	96271098	96373219	12752
ENSG00000(	557.256	585.2838	631.9992	632.9688	737.266	530.9893	-0.09925	0.52242	0.64784	PDE4D	chr5	-	58264865	59817947	8232
ENSG00000(	297.2723	279.3948	278.3963	684.6551	510.8398	514.55	-0.99634	3.95E-09	2.06E-08	RAD1	chr5	-	34905369	34919094	5770
ENSG00000(	212.3373	234.8361	208.4674	1281.668	679.2788	729.9048	-2.0253	2.65E-21	2.84E-20	BRIX1	chr5	+	34915481	34926101	2380
ENSG00000(	1.035792	3.612863	0	0	0	0	1.5346	0.25314	NA	AGXT2	chr5	-	34998206	35048198	2364
ENSG00000(	117.0445	105.9773	248.0498	226.9699	262.3231	159.4612	-0.4609	0.11292	0.19377	PRLR	chr5	-	35048861	35230794	11680
ENSG00000(	190.5857	125.2459	150.4132	345.3238	357.1276	361.6646	-1.1798	1.61E-09	8.68E-09	SLC12A7	chr5	-	1050499	1112150	5272
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	IL4	chr5	+	1.32E+08	1.32E+08	616
ENSG00000(	550.0055	538.3166	687.4146	630.7216	729.9026	572.0876	-0.12254	0.43287	0.56272	RAD50	chr5	+	1.32E+08	1.32E+08	6597
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	IL5	chr5	-	1.32E+08	1.32E+08	905
ENSG00000(	13.46529	24.08575	29.0271	83.14739	51.54419	65.75719	-1.5709	0.000116	0.000376	ST8SIA4	chr5	-	1E+08	1E+08	3585
ENSG00000(	717.8038	787.6042	881.3684	1350.583	1318.979	1269.114	-0.72253	1.48E-08	7.32E-08	GNPDA1	chr5	-	1.41E+08	1.41E+08	2980
ENSG00000(	32.10955	31.31148	21.11062	19.47596	11.96562	20.54912	0.67602	0.17462	0.27638	PCDH12	chr5	-	1.41E+08	1.41E+08	6562
ENSG00000(	3903.9	4098.191	3524.154	4006.056	2972.995	3453.897	0.14328	0.26705	0.38717	SKP1	chr5	-	1.33E+08	1.34E+08	2033
ENSG00000(	588.3298	566.0152	712.4834	2068.947	1856.511	1626.669	-1.5696	1.15E-28	1.66E-27	NUP155	chr5	-	37288239	37371283	8143
ENSG00000(	1182.874	1209.105	1269.276	3317.656	2086.619	2370.547	-1.0835	4.52E-12	2.95E-11	PPP2CA	chr5	-	1.34E+08	1.34E+08	4649
ENSG00000(	42.46747	27.69862	35.62417	253.9366	297.2995	273.7143	-2.9285	1.09E-30	1.69E-29	FGF1	chr5	-	1.42E+08	1.42E+08	3660
ENSG00000(	882.4947	876.7215	1137.335	220.9773	219.9832	171.7907	2.2317	4.21E-41	8.95E-40	NR3C1	chr5	-	1.43E+08	1.43E+08	7286
ENSG00000(	1256.416	1293.405	1382.746	1687.667	1382.489	1387.477	-0.18129	0.15416	0.24966	C5orf15	chr5	-	1.33E+08	1.33E+08	2350
ENSG00000(	325.2387	403.4364	372.0747	567.7993	520.9645	474.2738	-0.50596	0.00136	0.003734	PPWD1	chr5	+	64859063	64883376	2166
ENSG00000(	2362.641	2108.708	3303.812	243.4496	379.218	243.3016	3.1533	8.28E-63	3.07E-61	LIFR	chr5	-	38475065	38608456	10089
ENSG00000(	251.6974	208.3418	279.7157	125.0956	163.8369	133.1583	0.8064	0.000125	0.000403	TRIM23	chr5	-	64885507	64921802	4186
ENSG00000(	199.9078	228.8147	225.6198	223.9736	226.4263	216.1768	-0.02807	0.87855	0.92417	TRAPPC13	chr5	+	64920543	64962060	5994

ENSG00000(	3.107376	2.408575	5.277655	0	0.920432	0	2.3025	0.071172	0.13167	C9	chr5	-	39284364	39424970	2713
ENSG00000(	671.1932	638.2725	979.005	539.3344	604.7238	484.1373	0.48803	0.005305	0.013079	SEC24A	chr5	+	1.34E+08	1.34E+08	6299
ENSG00000(	1093.796	1000.763	1081.919	528.0983	547.657	544.1408	0.96979	1.28E-14	9.83E-14	TXNDC15	chr5	+	1.34E+08	1.34E+08	3548
ENSG00000(	122.2234	72.25726	170.2044	97.37982	107.6905	82.19649	0.33823	0.25902	0.37776	TTC33	chr5	-	40714577	40756077	2612
ENSG00000(	1941.074	2082.213	1963.288	2946.114	2527.506	2453.565	-0.40463	0.000543	0.001586	RARS	chr5	+	1.68E+08	1.68E+08	2146
ENSG00000(	71.46964	69.84869	59.37362	1054.698	1141.336	1159.793	-4.041	1.24E-119	1.30E-117	WWC1	chr5	+	1.68E+08	1.68E+08	7130
ENSG00000(	1194.268	1050.139	1296.984	3097.427	3170.888	2945.1	-1.3771	5.40E-31	8.46E-30	H2AFY	chr5	-	1.35E+08	1.35E+08	10982
ENSG00000(	1068.937	1152.503	1223.097	1582.048	1663.221	1452.412	-0.44732	0.000224	0.000693	TCERG1	chr5	+	1.46E+08	1.46E+08	4654
ENSG00000(	423.6389	376.9421	447.2813	1134.849	1405.5	1059.513	-1.5236	4.25E-24	5.08E-23	DPYSL3	chr5	-	1.47E+08	1.47E+08	5476
ENSG00000(	1180.803	1085.063	1467.188	903.3851	1095.314	858.1314	0.38465	0.010211	0.023692	SMAD5	chr5	+	1.35E+08	1.36E+08	7011
ENSG00000(	2330.532	2131.589	2786.602	1587.291	2313.046	1551.048	0.40992	0.010558	0.024406	CSNK1A1	chr5	-	1.49E+08	1.49E+08	6067
ENSG00000(	1567.153	1521.015	1647.948	1125.111	1143.177	1131.024	0.47749	2.25E-05	7.99E-05	HMGXB3	chr5	+	1.49E+08	1.49E+08	5275
ENSG00000(	7780.869	7753.204	6371.449	2280.186	2571.687	2669.742	1.5395	2.06E-37	3.94E-36	ERGIC1	chr5	+	1.72E+08	1.72E+08	5687
ENSG00000(	3089.767	3068.525	2855.211	242.7005	215.3811	224.3964	3.714	1.62E-199	4.63E-197	PDGFRB	chr5	-	1.49E+08	1.5E+08	5717
ENSG00000(	2.071584	0	0	0	3.681728	4.93179	-1.2241	0.35032	0.47995	CDX1	chr5	+	1.5E+08	1.5E+08	1757
ENSG00000(	2702.381	2812.012	2438.277	2280.186	1730.412	1914.356	0.42338	0.001081	0.003017	ATP6V0E1	chr5	+	1.72E+08	1.72E+08	1433
ENSG00000(	100.4718	162.5788	108.1919	211.9884	150.0304	136.4462	-0.42427	0.10442	0.18171	BNIP1	chr5	+	1.73E+08	1.73E+08	1339
ENSG00000(	5959.947	6094.9	6140.552	1765.571	1806.808	1968.606	1.7128	2.40E-61	8.69E-60	STC2	chr5	-	1.73E+08	1.73E+08	5353
ENSG00000(	285.8786	276.9862	542.2791	205.9958	261.4027	168.5028	0.78915	0.001544	0.004194	CPEB4	chr5	+	1.73E+08	1.73E+08	9483
ENSG00000(	26.93059	37.33292	30.34652	1.498151	0.920432	13.15144	2.4157	0.000458	0.001354	HRH2	chr5	+	1.75E+08	1.75E+08	3095
ENSG00000(	9302.447	9186.307	8412.582	7772.408	8065.746	8655.291	0.1352	0.18992	0.29517	DBN1	chr5	-	1.77E+08	1.77E+08	3072
ENSG00000(	352.1692	337.2006	267.841	335.5858	327.6738	307.4149	-0.01774	0.91781	0.95016	ZNF346	chr5	+	1.76E+08	1.77E+08	2774
ENSG00000(	46.61064	39.74149	36.94359	0.749076	0	2.465895	4.7622	1.72E-10	1.00E-09	UNC5A	chr5	+	1.76E+08	1.76E+08	3812
ENSG00000(	24.85901	24.08575	25.06886	71.91125	69.95283	77.2647	-1.5384	1.73E-05	6.22E-05	EHHADH	chr3	-	1.85E+08	1.85E+08	3850
ENSG00000(	19.68005	43.35436	30.34652	24.71949	28.53339	31.23467	0.13567	0.76443	0.84443	CNTN3	chr3	-	74311719	74570291	4948
ENSG00000(	668.0858	617.7996	1015.949	1489.911	1931.987	1232.947	-1.0119	1.13E-07	5.17E-07	SMC4	chr3	+	1.6E+08	1.6E+08	5471
ENSG00000(	456.7842	439.565	399.7824	691.3967	551.3388	801.4158	-0.65461	6.88E-05	0.000229	SELK	chr3	-	53918437	53926015	1633
ENSG00000(	483.7148	475.6936	560.7509	388.7702	451.9321	347.6912	0.35395	0.027421	0.057495	ACTR8	chr3	-	53901093	53916229	3629
ENSG00000(	175.0488	186.6646	189.9956	245.6968	186.8477	177.5444	-0.14703	0.47846	0.60751	TBCCD1	chr3	-	1.86E+08	1.86E+08	3058
ENSG00000(	976.7518	962.2259	815.3977	1412.007	1168.028	1408.026	-0.53219	8.23E-05	0.000271	TIMMDC1	chr3	+	1.19E+08	1.19E+08	2394
ENSG00000(	218.5521	213.1589	242.7721	303.3756	270.607	234.26	-0.26154	0.16032	0.25764	CRBN	chr3	-	3190676	3221394	5628
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	KNG1	chr3	+	1.86E+08	1.86E+08	3435
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	HRG	chr3	+	1.86E+08	1.86E+08	4272
ENSG00000(	1502.934	1611.337	1589.894	235.9588	207.0972	213.7109	2.8318	8.79E-102	6.86E-100	BCL6	chr3	-	1.87E+08	1.87E+08	4178
ENSG00000(	1.035792	0	1.319414	2.996302	1.840864	0	-0.61081	0.64729	0.75389	HGD	chr3	-	1.2E+08	1.2E+08	2005
ENSG00000(	4.143168	0	0	2.247227	0	0	0.43986	0.74578	0.83076	CLDN16	chr3	+	1.9E+08	1.9E+08	3273
ENSG00000(	81.82756	46.96722	96.31721	76.40571	50.62376	46.03004	0.36861	0.29081	0.41492	ARL6	chr3	+	97483365	97519953	1705
ENSG00000(	870.0652	863.4743	844.4248	577.5372	578.0313	536.7431	0.60613	2.14E-06	8.57E-06	NPHP3	chr3	-	1.32E+08	1.32E+08	7784
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CD86	chr3	+	1.22E+08	1.22E+08	2708
ENSG00000(	1340.315	1310.265	1599.13	2371.573	2649.924	2219.305	-0.76758	1.57E-09	8.43E-09	AMOTL2	chr3	-	1.34E+08	1.34E+08	4521
ENSG00000(	337.6682	286.6205	266.5216	538.5853	391.1836	628.8032	-0.80195	2.80E-05	9.81E-05	NIT2	chr3	+	1E+08	1E+08	1655
ENSG00000(	1345.494	1546.305	1006.713	420.2314	384.7406	379.7478	1.7125	2.66E-26	3.46E-25	FAM162A	chr3	+	1.22E+08	1.22E+08	3052
ENSG00000(	402.9231	440.7693	385.2688	265.9218	273.3683	262.2068	0.61505	0.00011	0.000357	OGG1	chr3	+	9791628	9829903	4977
ENSG00000(	1075.152	1009.193	1380.107	1821.003	1623.642	1435.973	-0.49404	0.000772	0.002206	KPNA1	chr3	-	1.22E+08	1.22E+08	6830

ENSG00000(	314.8807	321.5448	303.4652	614.991	611.1668	602.5003	-0.95712	3.11E-11	1.91E-10	PCCB	chr3	+	1.36E+08	1.36E+08	6090
ENSG00000(	1018.183	1012.806	1209.902	1099.643	1262.833	875.3926	0.001136	0.99403	0.99624	UBE3A	chr15	-	25582381	25684128	5179
ENSG00000(	536.5402	588.8967	621.4439	573.0428	464.8182	405.2287	0.27282	0.093083	0.1653	ARMC8	chr3	+	1.38E+08	1.38E+08	4790
ENSG00000(	135.6887	120.4288	182.0791	183.5235	174.8821	155.3514	-0.23147	0.30767	0.4334	CEP70	chr3	-	1.38E+08	1.38E+08	2732
ENSG00000(	1.035792	3.612863	2.638828	0	7.363456	7.397684	-0.8032	0.46893	0.59815	RBP2	chr3	-	1.39E+08	1.39E+08	694
ENSG00000(	5.17896	3.612863	7.916483	139.3281	129.7809	117.541	-4.4142	4.18E-22	4.61E-21	RBP1	chr3	-	1.39E+08	1.39E+08	1935
ENSG00000(	1004.718	992.3331	1327.33	827.7285	897.4212	674.8332	0.46787	0.002824	0.007327	SLC25A36	chr3	+	1.41E+08	1.41E+08	4638
ENSG00000(	0	1.204288	1.319414	0.749076	0.920432	2.465895	-0.44614	0.73696	0.82369	GRK7	chr3	+	1.41E+08	1.42E+08	3239
ENSG00000(	1551.616	1427.081	1274.554	1269.683	1151.46	1447.48	0.13686	0.30513	0.43046	RNF7	chr3	+	1.41E+08	1.41E+08	2763
ENSG00000(	591.4372	538.3166	563.3897	295.1358	335.0372	355.0888	0.77995	2.54E-07	1.12E-06	TFDP2	chr3	-	1.42E+08	1.42E+08	9911
ENSG00000(	583.1508	639.4768	836.5083	191.0143	291.7769	192.3398	1.6018	4.87E-16	4.09E-15	XRN1	chr3	-	1.42E+08	1.42E+08	10143
ENSG00000(	263.0911	240.8575	401.1018	109.365	107.6905	69.86702	1.6413	3.56E-11	2.18E-10	KAT2B	chr3	+	20081515	20195896	4833
ENSG00000(	85.97073	77.07441	92.35896	21.72319	20.2495	24.65895	1.9048	3.04E-08	1.47E-07	BCHE	chr3	-	1.65E+08	1.66E+08	2527
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	SERPINI2	chr3	-	1.67E+08	1.67E+08	1837
ENSG00000(	419.4957	340.8134	395.8241	976.7945	737.266	851.5557	-1.1462	2.49E-13	1.78E-12	PDCD10	chr3	-	1.67E+08	1.67E+08	2067
ENSG00000(	4969.73	4541.369	6529.779	907.1305	1130.29	838.4042	2.4722	6.96E-59	2.35E-57	WNT5A	chr3	-	55499743	55523973	6042
ENSG00000(	895.96	833.3671	757.3435	173.0365	196.9724	212.8889	2.0882	1.80E-41	3.86E-40	PFKFB4	chr3	-	48555117	48599448	3586
ENSG00000(	356.3124	350.4477	228.2586	124.3465	201.5746	280.29	0.62246	0.016352	0.036202	COL7A1	chr3	-	48601506	48632700	9276
ENSG00000(	175.0488	183.0517	246.7304	45.69361	44.18074	38.63235	2.2111	1.31E-17	1.19E-16	FGF12	chr3	-	1.92E+08	1.92E+08	3058
ENSG00000(	1148.693	1176.589	1380.107	985.0343	983.9418	874.5707	0.38029	0.003376	0.008654	PRKAR2A	chr3	-	48782030	48885279	6471
ENSG00000(	48.68222	45.76293	21.11062	663.6809	555.9409	541.6749	-3.8796	6.26E-61	2.25E-59	HES1	chr3	+	1.94E+08	1.94E+08	1578
ENSG00000(	669.1216	637.0682	638.5963	674.168	751.0725	629.6251	-0.07828	0.56516	0.68462	USP4	chr3	-	49315264	49378145	3541
ENSG00000(	805.8461	758.7013	1046.295	782.7839	793.4124	679.765	0.20904	0.16888	0.26872	ACAP2	chr3	-	1.95E+08	1.95E+08	7160
ENSG00000(	344.9187	289.0291	398.463	1162.565	1168.028	1019.236	-1.6941	3.39E-29	4.99E-28	ECT2	chr3	+	1.72E+08	1.73E+08	4363
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	GNAT1	chr3	+	50229045	50233949	2417
ENSG00000(	10855.1	10438.77	9300.548	5203.079	4620.569	5356.745	1.0094	1.32E-19	1.32E-18	GNAI2	chr3	+	50263724	50296787	3886
ENSG00000(	3149.843	3263.62	3074.234	3003.793	2450.19	2376.301	0.27618	0.02277	0.048664	TFG	chr3	+	1E+08	1E+08	3271
ENSG00000(	460.9274	567.2195	699.2893	341.5785	421.5579	301.6611	0.69395	0.000183	0.000574	USP9Y	chrY	+	14813160	14972764	10036
ENSG00000(	32.10955	22.88147	25.06886	12.73428	13.80648	13.9734	0.95086	0.063951	0.12003	HYAL1	chr3	-	50337320	50349812	2517
ENSG00000(	580.0435	537.1123	453.8783	1133.351	1058.497	1128.558	-1.075	5.32E-15	4.20E-14	TUSC2	chr3	-	50357458	50365682	1691
ENSG00000(	250.6616	262.5347	201.8703	190.2652	150.0304	167.6808	0.4904	0.015376	0.034242	NPRL2	chr3	-	50384761	50388522	3113
ENSG00000(	15406.37	16727.56	11234.81	10410.65	9507.142	12262.89	0.42924	0.003555	0.009066	RPL24	chr3	-	1.01E+08	1.01E+08	1857
ENSG00000(	237.1963	142.106	211.1062	210.4902	157.3939	179.1884	0.10914	0.63529	0.74431	CYB561D2	chr3	+	50388126	50395891	1533
ENSG00000(	127.4024	161.3746	108.1919	248.6931	199.7337	211.245	-0.72773	0.000999	0.0028	C3orf14	chr3	+	62304648	62321888	3525
ENSG00000(	3277.246	3175.707	3346.033	2363.333	2521.063	2220.949	0.46312	1.57E-05	5.71E-05	FXR1	chr3	+	1.81E+08	1.81E+08	3277
ENSG00000(	590.4014	621.4125	682.1369	342.3275	380.1384	323.0322	0.85451	9.13E-09	4.59E-08	CBLB	chr3	-	1.05E+08	1.06E+08	6780
ENSG00000(	653.5847	532.2952	858.9384	969.3038	1325.422	1013.483	-0.69163	9.88E-05	0.000323	BBX	chr3	+	1.07E+08	1.08E+08	8930
ENSG00000(	985.0381	956.2044	1081.919	482.4047	414.1944	410.9825	1.2046	1.91E-18	1.80E-17	IFT57	chr3	-	1.08E+08	1.08E+08	3203
ENSG00000(	663.9426	670.7883	1014.629	354.3127	532.0097	340.2935	0.93266	3.81E-06	1.48E-05	GNB4	chr3	-	1.79E+08	1.79E+08	3321
ENSG00000(	1.035792	1.204288	5.277655	0	0	0	2.3025	0.088097	0.15791	HHLA2	chr3	+	1.08E+08	1.08E+08	2666
ENSG00000(	148.1182	148.1274	130.622	68.91495	99.40666	78.90863	0.78631	0.001718	0.004628	IQCG	chr3	-	1.98E+08	1.98E+08	3250
ENSG00000(	1308.205	1340.372	1417.05	710.1236	782.3672	696.2043	0.89177	2.91E-13	2.07E-12	GBE1	chr3	-	81538850	81811312	3461
ENSG00000(	459.8916	417.8878	410.3377	1060.691	1013.396	1091.569	-1.2929	1.14E-22	1.29E-21	UMPS	chr3	+	1.24E+08	1.24E+08	2658
ENSG00000(	1663.482	1640.24	1562.186	1821.752	1615.358	1919.288	-0.13834	0.23916	0.35415	NCBP2	chr3	-	1.97E+08	1.97E+08	4161

ENSG0000(	360.4556	380.5549	439.3648	663.6809	618.5303	592.6367	-0.66779	7.11E-06	2.68E-05	SNX4	chr3	-	1.25E+08	1.25E+08	2506
ENSG0000(	76.6486	95.13873	75.20659	328.8442	337.7985	300.8392	-1.9584	3.88E-21	4.11E-20	C3orf52	chr3	+	1.12E+08	1.12E+08	3722
ENSG0000(	13.46529	10.83859	10.55531	194.0106	198.8133	130.6924	-3.8245	2.09E-25	2.63E-24	FRMD4B	chr3	-	69219141	69591734	5261
ENSG0000(	776.8439	804.4642	864.216	508.6223	409.5922	440.5732	0.84357	3.36E-09	1.76E-08	SLC41A3	chr3	-	1.26E+08	1.26E+08	3828
ENSG0000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	ROPN1B	chr3	+	1.26E+08	1.26E+08	2050
ENSG0000(	3449.187	3149.212	3389.574	1716.132	2190.628	1943.947	0.77057	2.24E-10	1.29E-09	PLXNA1	chr3	+	1.27E+08	1.27E+08	9066
ENSG0000(	879.3873	845.41	931.5061	1105.636	1000.51	924.7105	-0.1905	0.13977	0.23046	ATP6V1A	chr3	+	1.13E+08	1.14E+08	4591
ENSG0000(	161.5835	127.6545	137.219	147.5679	154.6326	153.7074	-0.09279	0.66974	0.77262	ABTB1	chr3	+	1.27E+08	1.27E+08	5061
ENSG0000(	626.6541	610.5739	585.8197	345.3238	282.5726	347.6912	0.89813	3.36E-09	1.76E-08	PODXL2	chr3	+	1.27E+08	1.27E+08	2186
ENSG0000(	12.4295	1.204288	2.638828	11.23613	15.64734	10.68554	-1.0531	0.19353	0.29943	UPK1B	chr3	+	1.19E+08	1.19E+08	2118
ENSG0000(	7.250543	24.08575	10.55531	12.73428	13.80648	18.90519	-0.11588	0.85405	0.90713	CSPG5	chr3	-	47603729	47622282	4161
ENSG0000(	265.1627	240.8575	385.2688	507.1241	491.5107	399.475	-0.64916	0.000818	0.002328	KLHL18	chr3	+	47324407	47388306	4620
ENSG0000(	1337.207	1212.718	1109.627	1767.818	1708.322	1883.122	-0.54839	6.31E-06	2.40E-05	SCAP	chr3	-	47455203	47518616	4394
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	EFCC1	chr3	+	1.29E+08	1.29E+08	2691
ENSG0000(	1.035792	0	1.319414	2.247227	7.363456	13.9734	-2.565	0.020485	0.044305	KIAA1257	chr3	-	1.29E+08	1.29E+08	6034
ENSG0000(	218.5521	183.0517	153.052	116.8558	57.06678	91.23811	1.0508	0.000116	0.000375	NEK11	chr3	+	1.31E+08	1.31E+08	2914
ENSG0000(	1841.638	1931.678	1980.44	3055.479	2359.988	2571.928	-0.4728	0.000151	0.00048	MRPL3	chr3	-	1.31E+08	1.31E+08	1706
ENSG0000(	157.4404	148.1274	160.9685	5.243529	10.12475	13.9734	3.9325	8.52E-28	1.18E-26	PLSCR4	chr3	-	1.46E+08	1.46E+08	3303
ENSG0000(	331.4534	366.1035	300.8263	262.9255	217.222	308.2368	0.33844	0.067978	0.12658	HEMK1	chr3	+	50606583	50622366	6087
ENSG0000(	90.1139	102.3645	85.7619	27.7158	38.65814	36.98842	1.4136	8.36E-06	3.13E-05	CISH	chr3	-	50643921	50649262	5042
ENSG0000(	638.0478	596.1224	563.3897	1045.709	1013.396	1148.285	-0.83245	1.76E-10	1.02E-09	MAPKAPK3	chr3	+	50648951	50686720	2988
ENSG0000(	44.53905	15.65574	18.47179	45.69361	70.87326	58.35951	-1.1032	0.011422	0.026198	ACVR2B	chr3	+	38495342	38524948	5370
ENSG0000(	374.9567	323.9534	412.9765	427.7221	388.4223	330.4299	-0.04523	0.79142	0.86367	WDR48	chr3	+	39093489	39138155	4925
ENSG0000(	426.7463	346.8349	459.156	984.2853	812.7415	863.8851	-1.1075	4.79E-13	3.36E-12	COMMD2	chr3	-	1.49E+08	1.49E+08	3706
ENSG0000(	480.6074	449.1993	497.419	647.9503	580.7926	561.402	-0.32668	0.022213	0.047642	GORASP1	chr3	-	39138150	39149854	3722
ENSG0000(	55.93276	59.0101	55.41538	11.23613	16.56778	11.50751	2.0708	9.85E-07	4.09E-06	PEX5L	chr3	-	1.8E+08	1.8E+08	9082
ENSG0000(	503.3949	433.5436	390.5465	1079.418	811.821	1006.907	-1.1212	9.99E-13	6.85E-12	RRP9	chr3	-	51967446	51975957	1578
ENSG0000(	480.6074	509.4137	605.6109	503.3788	630.4959	563.046	-0.08917	0.56607	0.6854	ABCC5	chr3	-	1.84E+08	1.84E+08	5921
ENSG0000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	AADAC	chr3	+	1.52E+08	1.52E+08	1638
ENSG0000(	441.2474	435.9522	317.9787	123.5975	70.87326	90.41614	2.0499	1.17E-19	1.17E-18	ABHD14B	chr3	-	52002526	52017425	2236
ENSG0000(	670.1574	621.4125	577.9032	716.8653	640.6207	657.5719	-0.10726	0.43335	0.56313	EIF1B	chr3	+	40351175	40353915	1010
ENSG0000(	69.39806	91.52587	62.01245	125.0956	136.2239	132.3364	-0.81127	0.001872	0.005016	ARHGEF26	chr3	+	1.54E+08	1.54E+08	5254
ENSG0000(	135.6887	157.7617	213.745	17.22874	30.37426	45.20807	2.4165	1.82E-13	1.31E-12	KLHL24	chr3	+	1.83E+08	1.83E+08	3848
ENSG0000(	2.071584	1.204288	3.958241	20.97412	31.29469	27.94681	-3.2021	1.36E-05	4.98E-05	PLCH1	chr3	-	1.55E+08	1.55E+08	6413
ENSG0000(	1.035792	1.204288	1.319414	100.3761	59.82808	83.84042	-5.559	3.47E-14	2.61E-13	VIPR1	chr3	+	42530791	42579059	3759
ENSG0000(	198.872	244.4704	219.0227	29.21395	40.49901	51.78379	2.427	2.28E-20	2.35E-19	DNAH1	chr3	+	52350335	52434507	13300
ENSG0000(	10188.05	9978.728	9792.689	8493.019	5899.969	6727.783	0.50301	0.000132	0.000423	SSR3	chr3	-	1.56E+08	1.56E+08	3716
ENSG0000(	693.9806	745.4541	547.5567	94.38352	89.2819	129.8705	2.6501	8.31E-43	1.88E-41	ZBTB47	chr3	+	42695176	42709072	5507
ENSG0000(	5.17896	14.45145	2.638828	34.45748	23.0108	41.09825	-2.0307	0.000832	0.002363	TNNC1	chr3	-	52485118	52488086	727
ENSG0000(	1778.455	1714.906	2120.298	1076.422	1259.151	1126.914	0.69552	7.47E-08	3.47E-07	NKTR	chr3	+	42642106	42690227	7964
ENSG0000(	129.474	137.2888	158.3297	185.0217	137.1444	175.9005	-0.23156	0.30061	0.42565	CLCN2	chr3	-	1.84E+08	1.84E+08	3290
ENSG0000(	1304.062	1294.609	1341.844	78.65293	104.0088	103.5676	3.7757	5.23E-130	6.17E-128	FOXP1	chr3	-	71003844	71633140	7114
ENSG0000(	9757.16	9503.034	9826.994	13693.1	18335.93	20344.45	-0.84629	4.30E-10	2.43E-09	EIF4G1	chr3	+	1.84E+08	1.84E+08	5667
ENSG0000(	986.0739	1124.805	1026.504	1095.898	1020.759	1205.823	-0.08307	0.51417	0.64099	SPCS1	chr3	+	52738971	52742182	1274

ENSG00000(	319.0239	273.3733	292.9099	432.9657	448.2504	354.2669	-0.47757	0.004699	0.011705	NEK4	chr3	-	52744800	52804965	3722
ENSG00000(	615.2604	609.3696	530.4043	383.5267	397.6266	473.4518	0.48375	0.001571	0.004259	SLC4A3	chr2	+	2.2E+08	2.21E+08	4454
ENSG00000(	187.4783	285.4162	304.7846	273.4126	330.4351	243.3016	-0.12537	0.55466	0.67542	INO80D	chr2	-	2.07E+08	2.07E+08	14136
ENSG00000(	8289.443	8295.134	6401.796	8146.197	6386.878	7417.411	0.066419	0.61766	0.73007	EEF1B2	chr2	+	2.07E+08	2.07E+08	1098
ENSG00000(	638.0478	628.6382	744.1494	116.8558	122.4175	100.2797	2.5561	3.69E-51	1.05E-49	ADAM23	chr2	+	2.07E+08	2.07E+08	6327
ENSG00000(	513.7528	422.705	447.2813	462.1796	453.773	534.2772	-0.06631	0.6673	0.77067	DGUOK	chr2	+	74153953	74186088	1144
ENSG00000(	695.0164	726.1855	865.5354	830.7248	1007.873	766.0713	-0.18773	0.21135	0.32124	MOB1A	chr2	-	74382165	74406025	2375
ENSG00000(	832.7767	715.3469	862.8966	641.9577	630.4959	584.4171	0.37566	0.006029	0.0147	KANSL3	chr2	-	97258907	97308524	5253
ENSG00000(	480.6074	420.2964	505.3355	659.1865	501.6354	660.8598	-0.37337	0.019915	0.043211	LMAN2L	chr2	-	97371666	97405801	2410
ENSG00000(	459.8916	532.2952	407.6989	1173.801	1230.618	1363.64	-1.4237	1.39E-23	1.63E-22	RTKN	chr2	-	74652963	74669549	2646
ENSG00000(	940.499	863.4743	1106.988	1188.783	1122.927	1072.664	-0.21781	0.10289	0.17956	TTL	chr2	+	1.13E+08	1.13E+08	5180
ENSG00000(	4.143168	12.04288	7.916483	7.490755	10.12475	3.28786	0.18182	0.82211	0.88519	IL1A	chr2	-	1.14E+08	1.14E+08	2124
ENSG00000(	5.17896	13.24716	1.319414	0	0	0	3.7991	0.00251	0.00657	CCL20	chr2	+	2.29E+08	2.29E+08	831
ENSG00000(	687.7658	709.3255	1055.531	433.7147	570.6678	412.6264	0.78738	2.30E-05	8.17E-05	PIKFYVE	chr2	+	2.09E+08	2.09E+08	9901
ENSG00000(	935.3201	849.0228	857.619	12.73428	9.20432	4.109825	6.5708	1.91E-113	1.80E-111	KCNIP3	chr2	+	95963052	96051825	3658
ENSG00000(	1426.285	1386.135	1256.082	360.3053	365.4115	357.5547	1.9055	7.53E-50	2.07E-48	FAHD2A	chr2	+	96068469	96082364	4757
ENSG00000(	14194.49	13736.11	13531.91	19991.33	21407.41	21847.01	-0.60833	3.51E-10	1.99E-09	NCL	chr2	-	2.32E+08	2.32E+08	4034
ENSG00000(	901.139	836.98	700.6087	976.7945	876.2513	1058.691	-0.25404	0.07357	0.13537	ACTR1B	chr2	-	98272431	98280570	2238
ENSG00000(	1033.72	1029.666	1153.168	758.8135	838.5135	735.6586	0.46225	0.000294	0.000895	SLC35F5	chr2	-	1.14E+08	1.15E+08	4412
ENSG00000(	1.035792	0	0	20.22504	30.37426	31.23467	-4.9082	6.32E-07	2.68E-06	ZAP70	chr2	+	98330023	98356325	3273
ENSG00000(	3971.226	3886.236	4532.186	6946.178	6830.526	5900.886	-0.66642	7.73E-09	3.92E-08	ACTR3	chr2	+	1.15E+08	1.15E+08	6718
ENSG00000(	1134.192	1104.332	1095.113	785.0312	851.3996	820.321	0.44009	0.00024	0.000741	STEAP3	chr2	+	1.2E+08	1.2E+08	4282
ENSG00000(	189.5499	272.169	274.4381	452.4416	517.2828	478.3836	-0.97531	6.21E-08	2.91E-07	EPB41L5	chr2	+	1.21E+08	1.21E+08	6628
ENSG00000(	0	0	0	19.47596	33.13555	33.70056	-5.6865	1.16E-07	5.29E-07	TFCP2L1	chr2	-	1.22E+08	1.22E+08	9292
ENSG00000(	1270.917	1263.298	1088.516	1609.014	1352.115	1468.851	-0.28933	0.022601	0.048369	SF3B14	chr2	-	24290454	24299313	770
ENSG00000(	864.8862	764.7227	729.6358	693.644	753.8338	1035.676	-0.0727	0.65643	0.76134	TP53I3	chr2	-	24300303	24308731	1998
ENSG00000(	71.46964	73.46155	75.20659	43.44638	78.23672	64.11326	0.24563	0.44002	0.56968	DNAJC27	chr2	-	25166505	25194963	4992
ENSG00000(	0	0	3.958241	20.97412	9.20432	9.863579	-2.8783	0.003161	0.008138	POMC	chr2	-	25383722	25391772	1426
ENSG00000(	507.538	538.3166	628.041	301.1284	273.3683	305.7709	0.92186	4.25E-09	2.21E-08	STAM2	chr2	-	1.53E+08	1.53E+08	5701
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	OTOF	chr2	-	26680071	26781566	7156
ENSG00000(	321.0955	313.1148	406.3794	774.5441	898.3416	720.8632	-1.1995	5.15E-14	3.83E-13	GPD2	chr2	+	1.57E+08	1.57E+08	6041
ENSG00000(	109.7939	104.773	105.5531	498.8843	412.3535	480.8495	-2.1105	4.40E-30	6.70E-29	CENPA	chr2	+	26987157	27023935	1452
ENSG00000(	3.107376	0	0	2.996302	0	0	0.032759	0.98073	0.98877	CYTIP	chr2	-	1.58E+08	1.58E+08	2260
ENSG00000(	712.6248	644.2939	837.8278	313.8627	289.9361	253.9872	1.3494	3.46E-17	3.06E-16	ACVR1	chr2	-	1.59E+08	1.59E+08	3045
ENSG00000(	978.8233	788.8085	1021.226	860.6878	1399.057	920.6007	-0.18785	0.29312	0.41744	TANC1	chr2	+	1.6E+08	1.6E+08	7586
ENSG00000(	12.4295	6.021439	2.638828	1.498151	0	0	2.8121	0.014028	0.031577	SLC30A3	chr2	-	27476552	27498685	3448
ENSG00000(	1036.828	1083.859	956.575	786.5293	638.7798	900.0516	0.40256	0.006397	0.015519	MPV17	chr2	-	27532360	27548547	2011
ENSG00000(	823.4546	774.357	675.5399	1316.126	1308.854	1274.868	-0.77549	9.87E-10	5.42E-09	GTF3C2	chr2	-	27548716	27579868	3992
ENSG00000(	518.9317	438.3607	506.6549	822.485	694.9262	770.1811	-0.64238	7.76E-06	2.92E-05	EIF2B4	chr2	-	27587219	27593353	4293
ENSG00000(	2887.788	2746.98	2655.98	2718.395	2022.189	2018.746	0.29365	0.029191	0.060713	NRBP1	chr2	+	27650657	27665126	2887
ENSG00000(	4.143168	3.612863	1.319414	135.5827	142.667	171.7907	-5.3529	5.78E-24	6.87E-23	ITGB6	chr2	-	1.61E+08	1.61E+08	4675
ENSG00000(	543.7907	559.9938	455.1978	32.95932	25.7721	23.83698	4.2029	3.44E-77	1.75E-75	FNDC4	chr2	-	27714750	27718112	1657
ENSG00000(	429.8536	339.6091	606.9303	76.40571	99.40666	65.75719	2.4935	3.04E-26	3.95E-25	ITGA4	chr2	+	1.82E+08	1.82E+08	4189
ENSG00000(	869.0294	899.6029	955.2556	2298.913	1911.737	1908.603	-1.1661	2.24E-20	2.31E-19	PSMD14	chr2	+	1.62E+08	1.62E+08	4890

ENSG00000(	2468.292	2459.156	2398.694	1755.084	1545.405	1772.978	0.52891	2.27E-06	9.05E-06	SNX17	chr2	+	27593389	27599995	2044
ENSG00000(	10.35792	2.408575	9.235896	11.23613	9.20432	20.54912	-0.8229	0.26117	0.38042	GPR75-ASB	chr2	-	53759810	54087170	2648
ENSG00000(	2554.263	2289.351	2338.001	4089.203	3787.578	4150.101	-0.74248	5.91E-12	3.82E-11	PPM1G	chr2	-	27604061	27632554	3752
ENSG00000(	5.17896	4.817151	3.958241	38.95193	15.64734	14.79537	-2.1463	0.00208	0.005527	PDE1A	chr2	-	1.83E+08	1.83E+08	4885
ENSG00000(	170.9057	207.1375	141.1773	74.15848	68.11197	65.75719	1.3087	1.34E-07	6.08E-07	REEP6	chr19	+	1491165	1497926	1375
ENSG00000(	66.29068	78.2787	59.37362	38.95193	13.80648	33.70056	1.2016	0.002541	0.006646	PCSK4	chr19	-	1481427	1490751	2855
ENSG00000(	509.6096	452.8122	382.63	90.63814	124.2583	111.7872	2.0364	2.68E-25	3.35E-24	APC2	chr19	+	1446300	1473243	11650
ENSG00000(	3.107376	0	6.597069	151.3133	110.4518	135.6242	-5.1599	1.53E-21	1.66E-20	IFIH1	chr2	-	1.63E+08	1.63E+08	3595
ENSG00000(	22650.7	20008.04	14464.73	18025.75	14113.9	14421.37	0.29407	0.055082	0.10575	RPS15	chr19	+	1438358	1440583	1610
ENSG00000(	15.53688	22.88147	7.916483	524.3529	445.4891	398.653	-4.8102	1.89E-59	6.52E-58	GCA	chr2	+	1.63E+08	1.63E+08	1992
ENSG00000(	719.8754	744.2498	692.6922	289.1432	237.4715	355.9108	1.2831	1.16E-14	8.93E-14	INO80B	chr2	+	74682150	74688011	2040
ENSG00000(	1318.563	1345.189	1133.376	1330.358	1631.005	1831.338	-0.33422	0.018518	0.040483	MOGS	chr2	-	74688184	74692537	2895
ENSG00000(	374.9567	357.6735	360.2	328.0951	334.1168	362.4865	0.093088	0.55008	0.67143	TTC31	chr2	+	74710200	74722013	4025
ENSG00000(	581.0793	480.5108	361.5194	454.6889	383.8201	443.8611	0.15158	0.40364	0.53472	NDUFS7	chr19	+	1383526	1395583	3743
ENSG00000(	297.2723	322.7491	232.2168	230.7153	144.5078	181.6542	0.60843	0.004929	0.012227	PCGF1	chr2	-	74732170	74735707	1792
ENSG00000(	55.93276	51.78437	81.80365	142.3244	105.8497	123.2947	-0.96795	0.000665	0.001919	GRB14	chr2	-	1.65E+08	1.65E+08	2382
ENSG00000(	269.3059	269.7604	332.4923	173.0365	140.8261	125.7606	0.97833	1.46E-06	5.96E-06	CLIP4	chr2	+	29320571	29412509	4293
ENSG00000(	2.071584	1.204288	3.958241	2.247227	0	1.64393	0.60791	0.62316	0.7349	TLX2	chr2	+	74740590	74744274	2136
ENSG00000(	7012.311	6391.155	8693.617	3871.222	5853.947	4630.95	0.62028	5.62E-05	0.000189	SPTBN1	chr2	+	54683422	54896812	9075
ENSG00000(	1887.213	1771.507	1422.328	2039.733	1361.319	1582.282	0.027954	0.85991	0.91098	AUP1	chr2	-	74753772	74757066	1695
ENSG00000(	7643.108	7154.673	7558.922	8257.809	7106.655	6685.041	0.019858	0.85982	0.91092	RTN4	chr2	-	55199325	55339757	4790
ENSG00000(	285.8786	261.3304	246.7304	292.1395	290.8565	376.4599	-0.27057	0.13541	0.22467	HTRA2	chr2	+	74756504	74760472	2367
ENSG00000(	1069.973	1046.526	1047.615	68.91495	67.19154	93.704	3.7679	4.48E-112	4.11E-110	LOXL3	chr2	-	74759541	74782817	3502
ENSG00000(	499.2517	360.082	418.2542	65.91865	81.91845	82.19649	2.4636	3.81E-33	6.45E-32	DOK1	chr2	+	74776153	74784681	2555
ENSG00000(	11.39371	12.04288	9.235896	688.4004	623.1325	530.9893	-5.7293	1.80E-74	8.48E-73	GALNT3	chr2	-	1.67E+08	1.67E+08	3868
ENSG00000(	326.2744	295.0505	263.8828	342.3275	318.4695	366.5964	-0.21228	0.20879	0.31833	POLE4	chr2	+	75185619	75197255	1248
ENSG00000(	1.035792	0	0	1.498151	5.522592	4.93179	-2.1914	0.084056	0.15177	TACR1	chr2	-	75276231	75426826	2318
ENSG00000(	941.5348	1004.376	1151.848	527.3492	502.5559	360.8426	1.1504	1.43E-12	9.70E-12	CCDC88A	chr2	-	55514978	55647057	9811
ENSG00000(	0	0	1.319414	118.3539	157.3939	142.1999	-7.1256	8.47E-17	7.34E-16	ACADL	chr2	-	2.11E+08	2.11E+08	2543
ENSG00000(	422.6031	328.7705	435.4065	120.6012	81.91845	92.88204	1.9898	1.53E-21	1.65E-20	EVA1A	chr2	-	75696428	75796848	1815
ENSG00000(	355.2766	434.7479	370.7553	739.3376	676.5175	674.8332	-0.84742	8.55E-09	4.31E-08	MRPL19	chr2	+	75873909	75917977	3479
ENSG00000(	693.9806	669.584	877.4102	782.0349	833.9114	682.2309	-0.03721	0.8045	0.87318	LANCL1	chr2	-	2.11E+08	2.11E+08	4781
ENSG00000(	762.3428	847.8186	840.4666	1658.453	1218.652	1195.959	-0.73184	9.70E-07	4.03E-06	WDR75	chr2	+	1.9E+08	1.9E+08	4297
ENSG00000(	264.1269	293.8462	252.008	340.0803	276.1296	313.9906	-0.19982	0.25249	0.37023	EFEMP1	chr2	-	56093102	56151274	3024
ENSG00000(	0	0	0	5.992604	6.443024	18.08323	-4.159	0.00044	0.001303	REG1A	chr2	+	79347488	79350545	901
ENSG00000(	136.7245	133.6759	178.1209	225.4717	235.6306	256.4531	-0.67738	0.000928	0.002613	FANCL	chr2	-	58386378	58468507	1698
ENSG00000(	350514.1	333086.7	461963.7	19441.51	22951.89	16465.6	4.2702	6.30E-188	1.61E-185	FN1	chr2	-	2.16E+08	2.16E+08	9171
ENSG00000(	878.3515	850.2271	982.9633	815.7433	926.875	752.9199	0.11943	0.38028	0.51093	STAT1	chr2	-	1.92E+08	1.92E+08	4310
ENSG00000(	867.9936	787.6042	1237.61	2656.971	2899.361	2475.758	-1.4694	7.19E-21	7.54E-20	GLS	chr2	+	1.92E+08	1.92E+08	4834
ENSG00000(	189.5499	214.3632	238.8139	250.9403	230.108	208.7791	-0.1047	0.58503	0.70253	PAPOLG	chr2	+	60983365	61029220	6074
ENSG00000(	0	0	2.638828	4.494453	0.920432	0	-0.61964	0.64445	0.75163	DNAH6	chr2	+	84743579	85046713	12795
ENSG00000(	101.5076	73.46155	75.20659	111.6123	102.168	99.45776	-0.31685	0.23557	0.34993	PECR	chr2	-	2.17E+08	2.17E+08	1853
ENSG00000(	337.6682	397.4149	397.1435	397.01	383.8201	470.1639	-0.1452	0.37159	0.50216	UNC50	chr2	+	99225042	99234978	2172
ENSG00000(	50111.61	48446.09	40180.11	10420.39	8357.523	9802.754	2.2745	7.31E-76	3.60E-74	IGFBP2	chr2	+	2.17E+08	2.18E+08	4414

ENSG00000(	312.8092	302.2762	270.4798	211.2393	266.9253	303.3051	0.18192	0.33517	0.46327	ELMOD3	chr2	+	85581517	85618875	4761
ENSG00000(	15477.84	15593.12	14898.82	221.7264	335.0372	319.7444	5.7011	0	0	IGFBP5	chr2	-	2.18E+08	2.18E+08	6215
ENSG00000(	1898.607	1918.43	2719.312	1316.126	1624.562	1183.629	0.66178	3.93E-05	0.000135	USP34	chr2	-	61414598	61697904	11357
ENSG00000(	14.50109	9.634302	6.597069	487.6482	321.2308	373.994	-5.1467	3.80E-51	1.08E-49	EFHD1	chr2	+	2.33E+08	2.34E+08	2259
ENSG00000(	8.286335	0	5.277655	3.745378	2.761296	9.041614	-0.1568	0.87552	0.92199	KCNJ13	chr2	-	2.34E+08	2.34E+08	2950
ENSG00000(	3160.201	3051.665	2918.543	5095.961	4303.02	4336.687	-0.58813	1.88E-07	8.40E-07	CCT4	chr2	-	62095224	62115939	2520
ENSG00000(	1585.797	1495.725	1671.697	838.9646	913.989	927.9984	0.82472	4.78E-12	3.12E-11	GGCX	chr2	-	85774743	85788670	3222
ENSG00000(	362.5272	358.8777	492.1413	545.327	680.1992	477.5616	-0.48797	0.007005	0.016871	EHBP1	chr2	+	62900986	63273622	5165
ENSG00000(	0	0	3.958241	37.45378	58.90765	43.56414	-4.7376	1.32E-09	7.16E-09	OTX1	chr2	+	63277192	63284971	2861
ENSG00000(	322.1313	348.0392	356.2417	656.9393	518.2032	601.6783	-0.79117	3.74E-07	1.62E-06	TXNDC9	chr2	-	99935445	99957165	1637
ENSG00000(	346.9903	345.6306	364.1582	414.9879	344.2416	319.7444	-0.03135	0.85074	0.9049	COQ10B	chr2	+	1.98E+08	1.98E+08	2239
ENSG00000(	4645.527	4788.248	5417.513	4182.838	4130.899	3344.575	0.34833	0.004648	0.011592	SF3B1	chr2	-	1.98E+08	1.98E+08	4336
ENSG00000(	96.32865	71.05298	104.2337	116.8558	89.2819	83.84042	-0.09595	0.73039	0.81952	ST3GAL5	chr2	-	86066267	86116137	3487
ENSG00000(	239.2679	208.3418	229.578	300.3793	272.4479	294.2634	-0.35503	0.043219	0.085621	CHST10	chr2	-	1.01E+08	1.01E+08	2837
ENSG00000(	239.2679	301.0719	220.3421	477.9102	408.6718	439.7512	-0.79903	4.82E-06	1.85E-05	PDCL3	chr2	+	1.01E+08	1.01E+08	1337
ENSG00000(	199.9078	220.3847	254.6469	489.8954	409.5922	465.2321	-1.0156	3.57E-09	1.87E-08	MOB4	chr2	+	1.98E+08	1.98E+08	3986
ENSG00000(	143.9751	110.7945	171.5238	334.8368	224.5854	369.8842	-1.119	1.53E-06	6.23E-06	HSPE1	chr2	+	1.98E+08	1.98E+08	950
ENSG00000(	994.3602	975.4731	1163.723	453.1907	453.773	355.9108	1.3066	1.68E-18	1.59E-17	KDM3A	chr2	+	86667770	86719839	8741
ENSG00000(	193.6931	207.1375	208.4674	191.0143	139.9057	143.8439	0.35447	0.092063	0.16381	PLCD4	chr2	+	2.19E+08	2.2E+08	4350
ENSG00000(	1123.834	1134.439	1282.47	952.8241	788.8102	837.5823	0.45474	0.00053	0.001551	CHMP3	chr2	-	86730554	86948245	3171
ENSG00000(	279.6638	352.8563	344.367	555.065	555.9409	482.4934	-0.70566	1.16E-05	4.27E-05	ZNF142	chr2	-	2.2E+08	2.2E+08	6034
ENSG00000(	26.93059	19.2686	15.83297	0	0	4.109825	3.4539	5.44E-05	0.000184	IL1R2	chr2	+	1.03E+08	1.03E+08	1578
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	PRKAG3	chr2	-	2.2E+08	2.2E+08	2326
ENSG00000(	0	0	0	6.74168	7.363456	14.79537	-4.1006	0.000527	0.001544	SMYD1	chr2	+	88367299	88412906	4433
ENSG00000(	4612.381	4647.346	5261.822	53.18436	69.95283	48.49593	6.3896	0	0	IL1R1	chr2	+	1.03E+08	1.03E+08	5143
ENSG00000(	0	0	0	543.0798	508.9989	468.52	-9.4144	2.78E-24	3.35E-23	WNT6	chr2	+	2.2E+08	2.2E+08	1703
ENSG00000(	13.46529	10.83859	9.235896	0	1.840864	0.821965	3.1031	0.001578	0.004274	IL1RL2	chr2	+	1.03E+08	1.03E+08	2615
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	IL1RL1	chr2	+	1.03E+08	1.03E+08	3994
ENSG00000(	25.8948	50.58008	27.70769	8.239831	7.363456	7.397684	2.0831	0.000138	0.000442	IL18R1	chr2	+	1.03E+08	1.03E+08	3854
ENSG00000(	4.143168	0	7.916483	2.996302	3.681728	0	0.6409	0.58282	0.7004	IL18RAP	chr2	+	1.03E+08	1.03E+08	2773
ENSG00000(	2.071584	0	6.597069	21.72319	11.04518	11.50751	-2.1195	0.013057	0.029558	SLC9A2	chr2	+	1.03E+08	1.03E+08	5410
ENSG00000(	1198.411	1217.535	1083.239	1202.266	951.7267	1046.361	0.12818	0.33253	0.4606	FHL2	chr2	-	1.06E+08	1.06E+08	4881
ENSG00000(	462.999	454.0165	515.8908	179.0291	140.8261	176.7225	1.5193	2.09E-18	1.97E-17	MLPH	chr2	+	2.38E+08	2.38E+08	3823
ENSG00000(	465.0706	437.1564	445.9619	407.4971	300.0608	387.9674	0.29692	0.072309	0.1334	CNPPD1	chr2	-	2.2E+08	2.2E+08	2073
ENSG00000(	804.8103	765.927	741.5105	1154.325	960.0106	964.9868	-0.41235	0.001915	0.005119	UXS1	chr2	-	1.07E+08	1.07E+08	2907
ENSG00000(	42.46747	24.08575	15.83297	11.98521	10.12475	8.219649	1.3825	0.015373	0.034237	ABCB6	chr2	-	2.2E+08	2.2E+08	3016
ENSG00000(	532.397	520.2523	432.7677	392.5156	272.4479	461.1223	0.39709	0.038338	0.077149	STK16	chr2	+	2.2E+08	2.2E+08	2868
ENSG00000(	0	0	0	13.48336	5.522592	1.64393	-3.5296	0.004584	0.011443	SLC5A7	chr2	+	1.09E+08	1.09E+08	5152
ENSG00000(	24899.4	23486.02	23709.87	9428.614	10549.07	9103.261	1.308	7.18E-37	1.36E-35	HDLBP	chr2	-	2.42E+08	2.42E+08	6372
ENSG00000(	991.2529	887.56	806.1618	1025.484	830.2297	960.055	-0.068	0.62548	0.7369	PPP1R7	chr2	+	2.42E+08	2.42E+08	2386
ENSG00000(	107.7224	125.2459	167.5656	382.0285	473.102	434.8194	-1.6841	4.54E-17	3.99E-16	PASK	chr2	-	2.42E+08	2.42E+08	5174
ENSG00000(	3204.74	2887.882	2753.617	4430.033	3589.685	3873.099	-0.42598	0.000394	0.001178	STK25	chr2	-	2.42E+08	2.42E+08	4619
ENSG00000(	0	0	0	5.992604	14.72691	12.32947	-4.2967	0.000231	0.000714	TPO	chr2	+	1377995	1547483	5391
ENSG00000(	2.071584	0	1.319414	0	0	2.465895	0.24177	0.8585	NA	PROC	chr2	+	1.28E+08	1.28E+08	1853

ENSG00000(	677.4079	729.7984	658.3875	1946.847	1569.337	1676.808	-1.3272	3.06E-24	3.67E-23	ID2	chr2	+	8818975	8824583	2041
ENSG00000(	196.8005	202.3203	213.745	331.0914	289.0156	305.7709	-0.5947	0.000742	0.002127	TAF1B	chr2	+	9983483	10074545	2387
ENSG00000(	177.1204	172.2131	175.482	2301.909	1640.21	1780.376	-3.435	4.22E-102	3.34E-100	HPCAL1	chr2	+	10443015	10567743	4781
ENSG00000(	838.9914	763.5184	829.9113	4890.714	3823.475	4007.079	-2.3815	1.45E-77	7.44E-76	ODC1	chr2	-	10580094	10588630	2653
ENSG00000(	1032.685	883.9472	1402.537	1110.13	1150.54	874.5707	0.081182	0.6338	0.74338	BIRC6	chr2	+	32582096	32843966	15703
ENSG00000(	404.9946	410.6621	407.6989	592.5188	577.1109	458.6564	-0.41125	0.00839	0.019837	NOL10	chr2	-	10710892	10830101	3333
ENSG00000(	1488.433	1454.78	1671.697	2241.983	2365.51	2101.764	-0.53921	3.70E-06	1.44E-05	PLEKHB2	chr2	+	1.32E+08	1.32E+08	4307
ENSG00000(	2045.689	2008.752	2021.342	2062.205	1988.133	1993.265	0.007616	0.94229	0.96521	GORASP2	chr2	+	1.72E+08	1.72E+08	3173
ENSG00000(	431.9252	331.1791	642.5545	495.888	563.3044	443.8611	-0.09749	0.63634	0.74502	STRN	chr2	-	37070783	37193615	8168
ENSG00000(	416.3883	488.9408	558.112	761.0608	692.1649	577.0194	-0.4729	0.003645	0.009282	CEBPZ	chr2	-	37428755	37458856	3463
ENSG00000(	1424.214	1345.189	1876.206	643.4559	738.1865	600.0344	1.2251	7.02E-16	5.83E-15	PRKD3	chr2	-	37477645	37551951	6111
ENSG00000(	325.2387	315.5234	406.3794	429.9694	358.048	320.5663	-0.08451	0.63641	0.74507	DCAF17	chr2	+	1.72E+08	1.72E+08	5828
ENSG00000(	84.93494	89.11729	77.84541	17.97781	12.88605	30.4127	1.9949	1.21E-07	5.49E-07	QPCT	chr2	+	37571717	37600465	1739
ENSG00000(	1118.655	1073.02	1234.971	829.9757	866.1265	761.9615	0.478	0.000167	0.000527	RAB3GAP1	chr2	+	1.36E+08	1.36E+08	4914
ENSG00000(	408.102	415.4793	416.9348	253.1875	200.6542	191.5178	0.93676	7.39E-08	3.43E-07	SLC25A12	chr2	-	1.73E+08	1.73E+08	2979
ENSG00000(	69.39806	93.93444	81.80365	59.92604	33.13555	38.63235	0.87428	0.009246	0.021671	RMDN2	chr2	+	38150330	38294285	2280
ENSG00000(	30.03797	22.88147	34.30476	1546.092	1409.181	1248.565	-5.5583	8.65E-144	1.24E-141	DLX2	chr2	-	1.73E+08	1.73E+08	2453
ENSG00000(	0	0	0	5.992604	2.761296	9.041614	-3.3561	0.007264	0.017434	LCT	chr2	-	1.37E+08	1.37E+08	6279
ENSG00000(	904.2463	869.4957	935.4644	1504.144	1264.674	1106.365	-0.51555	0.00022	0.000682	DARS	chr2	-	1.37E+08	1.37E+08	2361
ENSG00000(	1183.91	1228.373	1071.364	3073.457	2719.877	2853.04	-1.3088	1.79E-29	2.67E-28	SRSF7	chr2	-	38970741	38978636	2857
ENSG00000(	1450.109	1294.609	1421.009	3253.235	3268.454	3961.049	-1.3285	2.34E-27	3.19E-26	SDC1	chr2	-	20400558	20425194	3291
ENSG00000(	36.25272	38.53721	36.94359	0	2.761296	6.575719	3.3714	2.78E-07	1.22E-06	PLCL1	chr2	+	1.99E+08	1.99E+08	6665
ENSG00000(	324.2029	311.9105	263.8828	397.7591	413.274	381.3917	-0.40202	0.013508	0.0305	SLC1A4	chr2	+	65215611	65250999	5789
ENSG00000(	633.9046	643.0896	880.049	555.8141	525.5667	461.9443	0.4795	0.003244	0.008337	SOS1	chr2	-	39208537	39351486	8517
ENSG00000(	7.250543	2.408575	1.319414	27.7158	17.48821	18.90519	-2.3003	0.001628	0.004406	KYNU	chr2	+	1.44E+08	1.44E+08	1805
ENSG00000(	3006.904	3043.235	3369.783	185.0217	210.7789	149.5976	4.1013	7.48E-187	1.89E-184	WIPF1	chr2	-	1.75E+08	1.76E+08	4587
ENSG00000(	360.4556	311.9105	332.4923	723.607	714.2552	749.632	-1.118	4.53E-15	3.59E-14	ORC2	chr2	-	2.02E+08	2.02E+08	4312
ENSG00000(	2251.812	2242.384	2023.981	1528.114	1328.183	1446.658	0.59794	2.77E-07	1.22E-06	COX7A2L	chr2	-	42560686	42596150	3056
ENSG00000(	281.7354	297.4591	266.5216	1117.621	836.6727	915.6689	-1.7571	3.14E-29	4.63E-28	PNO1	chr2	+	68384976	68403370	2286
ENSG00000(	211.3015	278.1905	248.0498	749.0755	528.328	524.4136	-1.2853	6.33E-12	4.09E-11	ORC4	chr2	-	1.49E+08	1.49E+08	3091
ENSG00000(	1.035792	0	0	6.74168	20.2495	18.90519	-4.0652	0.000141	0.00045	PLEK	chr2	+	68592305	68624585	2869
ENSG00000(	1623.086	1468.027	1918.428	1959.582	1600.631	1439.261	0.002178	0.9881	0.99282	RND3	chr2	-	1.51E+08	1.51E+08	2777
ENSG00000(	682.5869	629.8425	910.3955	551.3196	550.4183	524.4136	0.448	0.004749	0.011817	ATF2	chr2	-	1.76E+08	1.76E+08	4176
ENSG00000(	398.7799	423.9093	523.8073	496.6371	528.328	439.7512	-0.12272	0.4471	0.57681	THADA	chr2	-	43393800	43823185	6939
ENSG00000(	327.3102	264.9433	364.1582	87.64184	241.1532	185.7641	0.88848	0.001207	0.003339	AAK1	chr2	-	69688532	69901481	4499
ENSG00000(	1210.841	1174.181	1716.557	647.2013	704.1305	554.0044	1.1016	1.52E-11	9.53E-11	TRAK2	chr2	-	2.02E+08	2.02E+08	6510
ENSG00000(	145.0109	137.2888	145.1355	113.8595	88.36147	83.84042	0.57233	0.017808	0.039113	C2orf42	chr2	-	70377012	70475747	2581
ENSG00000(	1628.265	1618.563	1811.555	1224.739	1216.811	1160.614	0.4885	2.30E-05	8.15E-05	TIA1	chr2	-	70436576	70475792	4647
ENSG00000(	2490.044	2657.863	3273.466	1832.239	1956.838	1697.358	0.61637	2.20E-06	8.80E-06	PCYOX1	chr2	+	70484518	70508323	5345
ENSG00000(	0	1.204288	2.638828	8.988907	4.60216	4.93179	-1.8435	0.09017	0.16102	KISS1R	chr19	+	917287	921015	1680
ENSG00000(	943.6064	759.9056	1110.946	9347.714	13952.83	11700.67	-3.6245	5.73E-116	5.65E-114	EPAS1	chr2	+	46520806	46613836	5160
ENSG00000(	1067.901	1006.785	800.8842	5355.141	6385.037	7921.276	-2.7635	2.75E-73	1.27E-71	ARID3A	chr19	+	925781	975939	5983
ENSG00000(	1318.563	1416.242	1448.716	2424.008	2077.415	2399.316	-0.72141	9.50E-10	5.22E-09	SUMO1	chr2	-	2.03E+08	2.03E+08	1536
ENSG00000(	14.50109	39.74149	23.74945	7.490755	1.840864	17.26126	1.4411	0.030048	0.062269	GRIN3B	chr19	+	1000418	1009731	3281

ENSG00000(	3.107376	8.430014	0	1.498151	0.920432	0	1.5611	0.20852	0.31805	VAX2	chr2	+	71127720	71160576	1147
ENSG00000(	6.214751	1.204288	0	0	0	0	2.1793	0.10812	0.18693	ATP6V1B1	chr2	+	71163012	71192536	1905
ENSG00000(	1277.131	1398.178	1414.412	1603.022	1133.972	1119.516	0.083452	0.57995	0.69813	NFE2L2	chr2	-	1.78E+08	1.78E+08	2853
ENSG00000(	973.6444	843.0014	996.1574	1873.438	2426.259	1861.751	-1.1278	7.99E-16	6.61E-15	MSH6	chr2	+	48010221	48034092	4328
ENSG00000(	174.013	184.256	187.3568	128.841	130.7013	107.6774	0.56715	0.008011	0.019032	PLEKHA3	chr2	+	1.79E+08	1.79E+08	2784
ENSG00000(	141.9035	164.9874	98.95603	169.2911	164.7573	184.1201	-0.34684	0.13777	0.22779	SPR	chr2	+	73114489	73119287	1480
ENSG00000(	498.2159	376.9421	542.2791	228.468	285.3339	202.2034	0.98167	2.89E-07	1.27E-06	EPHA4	chr2	-	2.22E+08	2.22E+08	6346
ENSG00000(	30.03797	15.65574	48.81831	62.17327	88.36147	54.24968	-1.0947	0.007518	0.017981	PARD3B	chr2	+	2.05E+08	2.06E+08	8174
ENSG00000(	1021.291	986.3116	1060.809	1904.899	1614.438	1604.476	-0.73873	2.32E-09	1.23E-08	FARSB	chr2	-	2.23E+08	2.24E+08	3369
ENSG00000(	277.5922	232.4275	329.8534	294.3867	345.162	230.1502	-0.05028	0.80402	0.87283	ALMS1	chr2	+	73612886	73837920	12922
ENSG00000(	1150.765	1057.365	1157.126	641.9577	1017.077	771.0031	0.46935	0.0036	0.009174	BCL9	chr1	+	1.47E+08	1.47E+08	6278
ENSG00000(	13056.16	13477.18	16181.29	843.4591	1129.37	775.1129	3.948	1.68E-164	3.31E-162	PRRX1	chr1	+	1.71E+08	1.71E+08	4284
ENSG00000(	6457.127	5837.183	7450.73	7879.526	8150.425	7309.734	-0.24095	0.040379	0.08071	DHCR24	chr1	-	55315306	55352891	4250
ENSG00000(	473.3569	537.1123	467.0725	525.102	545.8162	435.6414	-0.02772	0.85702	0.90911	DNAJC16	chr1	+	15853308	15918874	6299
ENSG00000(	48.68222	38.53721	34.30476	192.5124	196.052	219.4646	-2.2914	2.12E-18	1.99E-17	MARK1	chr1	+	2.21E+08	2.21E+08	5230
ENSG00000(	45.57484	95.13873	62.01245	61.42419	89.2819	60.00344	-0.05563	0.87047	0.91856	MORN1	chr1	-	2252692	2323146	1907
ENSG00000(	312.8092	323.9534	299.5069	164.7966	116.8949	140.556	1.1397	5.41E-09	2.78E-08	GPX7	chr1	+	53068044	53074723	1228
ENSG00000(	985.0381	993.5374	928.8673	2969.335	2291.876	2536.584	-1.4202	1.74E-28	2.50E-27	CACYBP	chr1	+	1.75E+08	1.75E+08	2834
ENSG00000(	1440.787	1441.532	1415.731	782.0349	738.1865	857.3094	0.85227	1.87E-12	1.25E-11	SCP2	chr1	+	53392901	53517375	5204
ENSG00000(	31.07376	31.31148	35.62417	82.39831	68.11197	51.78379	-1.0304	0.004227	0.010632	PAPPA2	chr1	+	1.76E+08	1.77E+08	9685
ENSG00000(	279.6638	309.5019	393.1853	277.158	366.3319	265.4947	0.11046	0.5697	0.68877	RALGPS2	chr1	+	1.79E+08	1.79E+08	5834
ENSG00000(	270.3417	307.0934	279.7157	8.988907	11.04518	10.68554	4.7451	3.46E-53	1.03E-51	ANGPTL1	chr1	-	1.79E+08	1.79E+08	3348
ENSG00000(	533.4328	523.8652	533.0432	658.4374	642.4615	571.2656	-0.2348	0.089504	0.16001	CEP104	chr1	-	3728645	3773778	6424
ENSG00000(	1072.045	1281.362	1397.259	1194.776	1193.8	1021.702	0.13589	0.3232	0.45056	FAM20B	chr1	+	1.79E+08	1.79E+08	5984
ENSG00000(	111.8655	118.0202	125.3443	194.7596	145.4283	181.6542	-0.55461	0.013838	0.031188	TCEANC2	chr1	+	54519260	54578192	4097
ENSG00000(	1923.466	2131.589	1828.708	815.7433	741.8682	839.2262	1.2926	4.22E-26	5.46E-25	TMEM59	chr1	-	54497347	54519177	2473
ENSG00000(	544.8265	497.3708	511.9325	1244.214	1236.14	1260.072	-1.2637	2.95E-24	3.55E-23	LRRC42	chr1	+	54411750	54433841	2037
ENSG00000(	287.9501	261.3304	220.3421	632.9688	501.6354	512.9061	-1.0915	2.35E-10	1.35E-09	WRAP73	chr1	-	3547331	3569325	6089
ENSG00000(	2001.15	1937.699	1632.115	2704.163	2097.665	2249.718	-0.33899	0.011315	0.025993	MRPL37	chr1	+	54649714	54691137	1582
ENSG00000(	1517.435	1396.974	1745.584	4084.709	4572.706	4585.742	-1.5043	1.08E-35	1.98E-34	ICMT	chr1	-	6281253	6296032	4771
ENSG00000(	9020.712	9655.979	8507.58	5243.529	5569.534	7181.507	0.59388	4.99E-06	1.92E-05	RPL22	chr1	-	6241329	6269449	2279
ENSG00000(	11.39371	18.06432	6.597069	2.247227	11.96562	13.9734	0.33707	0.6526	0.75842	CHD5	chr1	-	6161853	6240183	9646
ENSG00000(	8799.052	8377.025	7870.303	1647.966	1456.123	1511.593	2.4359	2.56E-113	2.38E-111	QSOX1	chr1	+	1.8E+08	1.8E+08	9311
ENSG00000(	431.9252	440.7693	482.9054	513.8658	439.9665	420.0241	-0.02097	0.89128	0.93252	STXBP3	chr1	+	1.09E+08	1.09E+08	2536
ENSG00000(	609.0456	523.8652	674.2204	572.2937	577.1109	523.5917	0.11044	0.45347	0.58322	PHF13	chr1	+	6673745	6684093	3681
ENSG00000(	1218.091	1247.642	1246.846	3382.825	3669.762	3262.379	-1.4719	3.75E-41	7.96E-40	ERRFI1	chr1	-	8064464	8086368	3104
ENSG00000(	3866.611	3893.462	3335.478	3395.559	3536.3	4303.808	-0.01784	0.88701	0.92967	PARK7	chr1	+	8014351	8045565	1088
ENSG00000(	6.214751	6.021439	3.958241	11.98521	24.85166	12.32947	-1.4668	0.040343	0.080645	KIAA1324	chr1	+	1.1E+08	1.1E+08	5966
ENSG00000(	0	0	0	33.7084	34.05598	15.61733	-5.6271	1.86E-07	8.32E-07	OPRD1	chr1	+	29138654	29190208	1774
ENSG00000(	1722.522	1801.614	1570.102	440.4564	484.1472	557.2922	1.7777	4.58E-40	9.47E-39	AMPD2	chr1	+	1.1E+08	1.1E+08	3899
ENSG00000(	1379.675	1331.942	1332.608	2475.695	2349.863	2231.635	-0.80178	3.90E-13	2.75E-12	SRSF4	chr1	-	29474255	29508499	2387
ENSG00000(	344.9187	420.2964	303.4652	510.8695	403.1492	484.9593	-0.38727	0.025552	0.054004	MECR	chr1	-	29519385	29557454	2416
ENSG00000(	56.96855	79.48299	83.12307	139.3281	134.3831	142.1999	-0.91986	0.000371	0.001114	KCNC4	chr1	+	1.11E+08	1.11E+08	7597
ENSG00000(	704.3385	646.7025	1113.585	423.9768	431.6826	328.786	1.0504	9.43E-08	4.34E-07	EDEM3	chr1	-	1.85E+08	1.85E+08	6898

ENSG0000(	218.5521	228.8147	200.5509	1005.259	701.3692	711.8216	-1.892	1.62E-26	2.13E-25	WDR77	chr1	-	1.12E+08	1.12E+08	2576
ENSG0000(	3094.946	2928.828	2733.825	3836.016	3088.049	3531.983	-0.25521	0.031808	0.065414	ATP5F1	chr1	+	1.12E+08	1.12E+08	3156
ENSG0000(	854.5283	858.6571	847.0636	949.8278	775.9242	881.9684	-0.02718	0.83567	0.89487	RAP1A	chr1	+	1.12E+08	1.12E+08	5024
ENSG0000(	1414.892	1499.338	1465.869	1651.712	1616.279	1653.793	-0.16822	0.12503	0.21067	HDAC1	chr1	+	32757687	32799236	2409
ENSG0000(	3051.443	3061.299	3243.119	3914.669	3553.788	3305.121	-0.20347	0.066026	0.12341	CAPZA1	chr1	+	1.13E+08	1.13E+08	3020
ENSG0000(	568.6498	562.4024	504.0161	593.2678	514.5215	535.0992	-0.00667	0.96279	0.97845	S100PBP	chr1	+	33282368	33324476	4318
ENSG0000(	158.4762	192.686	211.1062	658.4374	618.5303	588.5269	-1.7285	3.65E-25	4.54E-24	RNF19B	chr1	-	33402046	33430286	2598
ENSG0000(	1675.911	1547.51	1443.439	1439.723	1026.282	1020.058	0.41923	0.005208	0.012868	SCAMP3	chr1	-	1.55E+08	1.55E+08	1537
ENSG0000(	199.9078	140.9017	200.5509	167.7929	204.3359	163.571	0.016955	0.93837	0.96259	TRIM62	chr1	-	33611003	33647660	3437
ENSG0000(	923.9264	920.0758	1349.76	334.0877	467.5795	400.2969	1.4041	3.32E-15	2.66E-14	ASH1L	chr1	-	1.55E+08	1.56E+08	11942
ENSG0000(	1.035792	3.612863	2.638828	5.992604	9.20432	12.32947	-1.6752	0.068176	0.12684	DLGAP3	chr1	-	35331037	35395186	3856
ENSG0000(	4897.224	4870.14	5337.029	9573.935	9907.53	9192.034	-0.92359	6.64E-20	6.70E-19	SFPQ	chr1	-	35641979	35658749	3747
ENSG0000(	137.7603	166.1917	127.9831	611.2456	791.5715	671.5453	-2.2527	5.93E-37	1.12E-35	RHOU	chr1	+	2.29E+08	2.29E+08	4372
ENSG0000(	678.4437	640.6811	890.6043	414.2388	582.6335	512.0841	0.54823	0.001445	0.00394	GON4L	chr1	-	1.56E+08	1.56E+08	7713
ENSG0000(	1966.969	2068.966	1670.378	1113.126	1397.216	1404.738	0.54299	6.94E-05	0.000231	ARHGEF2	chr1	-	1.56E+08	1.56E+08	4435
ENSG0000(	739.5554	641.8854	608.2498	456.187	477.7042	687.1627	0.29534	0.08988	0.16063	LAMTOR2	chr1	+	1.56E+08	1.56E+08	868
ENSG0000(	1103.118	1216.331	1079.28	307.121	406.8309	387.1455	1.6231	1.76E-28	2.53E-27	MEF2D	chr1	-	1.56E+08	1.56E+08	5965
ENSG0000(	1033.72	930.9144	1204.625	1037.47	1132.131	847.4458	0.070543	0.63553	0.74452	DOCK7	chr1	-	62920399	63153969	7110
ENSG0000(	3546.551	3370.801	2851.253	4829.29	2826.647	2968.115	-0.1207	0.48805	0.61718	SRM	chr1	-	11114641	11120081	1266
ENSG0000(	1.035792	6.021439	5.277655	0	4.60216	0.821965	0.9132	0.43104	0.56088	DLEU2L	chr1	+	64014588	64015405	703
ENSG0000(	127.4024	90.32158	138.5384	119.103	110.4518	174.2566	-0.18009	0.49777	0.62617	FBXO2	chr1	-	11708424	11715842	1560
ENSG0000(	55.93276	54.19295	31.66593	6.74168	11.96562	6.575719	2.416	1.47E-06	5.98E-06	FBXO6	chr1	+	11724181	11734411	1520
ENSG0000(	410.1736	437.1564	443.323	434.4638	457.4547	410.1605	-0.01309	0.92933	0.95737	C1orf21	chr1	+	1.84E+08	1.85E+08	10265
ENSG0000(	82.86335	111.9988	124.0249	115.3576	98.48622	92.06007	0.053278	0.83941	0.89727	SWT1	chr1	+	1.85E+08	1.85E+08	3830
ENSG0000(	647.3699	531.0909	596.375	527.3492	404.0696	492.357	0.31629	0.043952	0.086875	MAD2L2	chr1	-	11734537	11751707	1860
ENSG0000(	19.68005	13.24716	30.34652	262.1764	270.607	254.8091	-3.6096	3.22E-35	5.82E-34	DNAJC6	chr1	+	65713902	65881552	5743
ENSG0000(	270.3417	287.8248	381.3106	119.8521	95.72493	103.5676	1.5433	3.03E-13	2.16E-12	LEPR	chr1	+	65886248	66107242	8227
ENSG0000(	1039.935	1185.019	1373.51	3201.549	3297.908	3233.61	-1.4338	1.55E-30	2.39E-29	IVNS1ABP	chr1	-	1.85E+08	1.85E+08	4199
ENSG0000(	1586.833	1451.167	1347.121	2223.256	1737.776	1811.611	-0.39549	0.00283	0.007344	KIAA2013	chr1	-	11979648	11986485	2815
ENSG0000(	1490.505	1351.211	1625.518	2062.954	2462.156	2354.108	-0.62156	5.76E-07	2.45E-06	MFN2	chr1	+	12040238	12073571	4539
ENSG0000(	17.60846	25.29004	32.98534	32.95932	13.80648	25.48091	0.05361	0.91541	0.94839	PRG4	chr1	+	1.86E+08	1.86E+08	5044
ENSG0000(	381.1714	386.5764	300.8263	999.2668	673.7562	868.8169	-1.2442	7.27E-13	5.02E-12	MIIP	chr1	+	12079523	12092102	1709
ENSG0000(	1162.159	1030.87	1329.969	2346.105	2634.276	2014.636	-0.9872	1.43E-12	9.68E-12	SMG7	chr1	+	1.83E+08	1.84E+08	5970
ENSG0000(	15.53688	15.65574	6.597069	8.239831	10.12475	9.041614	0.44332	0.51389	0.64083	NCF2	chr1	-	1.84E+08	1.84E+08	2276
ENSG0000(	2.071584	0	2.638828	1.498151	0.920432	2.465895	-0.0403	0.97458	0.98524	PDC	chr1	-	1.86E+08	1.86E+08	1242
ENSG0000(	281.7354	293.8462	341.7282	316.859	427.0804	379.7478	-0.29183	0.098461	0.17313	SLC35D1	chr1	-	67465015	67519782	6162
ENSG0000(	220.6237	255.309	296.8681	34.45748	51.54419	20.54912	2.8343	1.37E-23	1.61E-22	PLA2G4A	chr1	+	1.87E+08	1.87E+08	2875
ENSG0000(	1539.187	1535.467	1531.839	1486.915	1442.317	1739.278	-0.01935	0.87231	0.91977	GADD45A	chr1	+	68150744	68154021	1496
ENSG0000(	1.035792	0	0	1.498151	0.920432	0	-0.39626	0.76684	NA	PRAMEF1	chr1	+	12851546	12856777	2160
ENSG0000(	3.107376	0	0	0	2.761296	2.465895	-0.40632	0.76089	0.84192	PRAMEF12	chr1	+	12834984	12838049	1786
ENSG0000(	5629.529	5363.898	6194.648	3388.818	3805.986	3601.028	0.66988	8.07E-10	4.45E-09	WLS	chr1	-	68564142	68698803	2748
ENSG0000(	1236.736	1288.588	1336.566	757.3154	1054.815	875.3926	0.52238	0.000223	0.000691	PRDM2	chr1	+	14026693	14151574	7957
ENSG0000(	263.0911	281.8033	315.3399	110.1141	66.2711	86.30632	1.6925	5.40E-14	4.02E-13	RGS2	chr1	+	1.93E+08	1.93E+08	1344
ENSG0000(	14.50109	9.634302	10.55531	1.498151	0	0.821965	3.2146	0.001025	0.002869	RPE65	chr1	-	68894505	68915642	2610

ENSG00000(	1061.687	1244.029	1125.46	1037.47	1089.791	884.4343	0.18756	0.15887	0.25566	TROVE2	chr1	+	1.93E+08	1.93E+08	7848
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AMPD1	chr1	-	1.15E+08	1.15E+08	2392
ENSG00000(	327.3102	358.8777	312.7011	886.1564	794.3328	788.2644	-1.3018	1.11E-19	1.11E-18	UCHL5	chr1	-	1.93E+08	1.93E+08	1911
ENSG00000(	324.2029	367.3078	308.7428	913.1231	639.7002	718.3973	-1.1793	2.11E-12	1.41E-11	BCAS2	chr1	-	1.15E+08	1.15E+08	1299
ENSG00000(	2372.999	2444.704	2909.307	2353.595	2361.829	2197.934	0.15972	0.17889	0.28157	SRSF11	chr1	+	70671365	70718735	4008
ENSG00000(	145.0109	143.3102	126.6637	141.5753	104.0088	95.34793	0.28006	0.25302	0.37084	CTH	chr1	+	70876901	70905534	2044
ENSG00000(	15.53688	19.2686	15.83297	26.96672	21.16994	43.56414	-0.8287	0.10023	0.17583	AGMAT	chr1	-	15898848	15911605	2500
ENSG00000(	4492.229	4696.722	4016.296	1198.521	1221.413	1195.137	1.8661	1.13E-63	4.29E-62	OLFML3	chr1	+	1.15E+08	1.15E+08	2063
ENSG00000(	2.071584	1.204288	2.638828	0	0	0	1.9938	0.14152	NA	CFHR3	chr1	+	1.97E+08	1.97E+08	1965
ENSG00000(	1845.781	1661.917	1736.349	1369.31	1417.465	1538.718	0.27767	0.016336	0.036173	PLEKHM2	chr1	+	16010827	16061264	4122
ENSG00000(	514.7886	454.0165	589.778	828.4776	693.0853	690.4505	-0.50503	0.000906	0.002558	CRYZ	chr1	-	75171170	75199092	2899
ENSG00000(	394.6367	388.9849	514.5714	340.0803	385.661	381.3917	0.22749	0.17399	0.27552	PHTF1	chr1	-	1.14E+08	1.14E+08	4314
ENSG00000(	770.6292	582.8753	577.9032	497.3862	481.3859	527.7015	0.35901	0.021236	0.045793	ZBTB17	chr1	-	16268364	16302627	2770
ENSG00000(	125.3308	115.6116	101.5949	178.28	110.4518	148.7757	-0.35049	0.16197	0.25967	CD58	chr1	-	1.17E+08	1.17E+08	1328
ENSG00000(	14.50109	22.88147	6.597069	16.47966	20.2495	23.83698	-0.43177	0.45814	0.58771	TFAP2E	chr1	+	36038971	36060929	2189
ENSG00000(	203.0152	244.4704	253.3274	651.6957	626.8142	614.8298	-1.4325	8.45E-20	8.47E-19	TTF2	chr1	+	1.18E+08	1.18E+08	4879
ENSG00000(	0	0	0	4.494453	1.840864	6.575719	-2.8639	0.026703	0.056165	NR5A2	chr1	+	2E+08	2E+08	5086
ENSG00000(	113.9371	111.9988	125.3443	77.90386	128.8605	92.06007	0.23431	0.37708	0.5077	KIF21B	chr1	-	2.01E+08	2.01E+08	9895
ENSG00000(	1257.451	1274.136	1064.767	1352.081	1096.235	1424.465	-0.10645	0.44392	0.57357	TMEM9	chr1	-	2.01E+08	2.01E+08	2892
ENSG00000(	422.6031	416.6836	406.3794	801.5108	645.2228	821.9649	-0.86274	7.02E-09	3.57E-08	ADPRHL2	chr1	+	36554476	36559533	1668
ENSG00000(	4892.045	4384.812	3859.285	5950.656	5429.628	5886.091	-0.39339	0.000775	0.002216	MAP7D1	chr1	+	36621180	36646450	3456
ENSG00000(	395.6725	388.9849	370.7553	260.6783	219.9832	258.9189	0.64036	0.00011	0.000357	WARS2	chr1	-	1.2E+08	1.2E+08	2811
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	HAO2	chr1	+	1.2E+08	1.2E+08	1668
ENSG00000(	169.8699	228.8147	92.35896	98.1289	57.98722	69.86702	1.1029	0.000462	0.001365	RP11-268J:	chr1	+	36789335	36794822	1838
ENSG00000(	101.5076	108.3859	94.99779	78.65293	77.31629	74.79881	0.39861	0.12655	0.21266	OSCP1	chr1	-	36881428	36916086	1463
ENSG00000(	1000.575	1083.859	803.523	1701.9	1270.196	1634.888	-0.67138	1.02E-05	3.77E-05	MRPS15	chr1	-	36921319	36930038	2127
ENSG00000(	385.3146	375.7378	453.8783	286.8959	379.218	277.8241	0.36318	0.041236	0.082184	EXOC8	chr1	-	2.31E+08	2.31E+08	5100
ENSG00000(	905.2821	1054.956	1039.698	789.5256	691.2444	638.6667	0.4987	0.000303	0.00092	GNPAT	chr1	+	2.31E+08	2.31E+08	2643
ENSG00000(	413.281	355.2649	478.9472	587.2752	537.5323	495.6448	-0.37746	0.018723	0.040892	TSNAX	chr1	+	2.32E+08	2.32E+08	5629
ENSG00000(	317.9881	308.2977	273.1187	493.6408	500.715	651.8182	-0.86725	2.92E-07	1.28E-06	C1orf109	chr1	-	38147242	38157914	2570
ENSG00000(	676.3721	731.0026	799.5648	576.0391	554.1001	579.4853	0.36607	0.006837	0.016489	RRAGC	chr1	-	39303870	39325495	2732
ENSG00000(	533.4328	545.5423	494.7802	650.1976	505.3172	517.0159	-0.08815	0.56516	0.68462	TBCE	chr1	+	2.36E+08	2.36E+08	1980
ENSG00000(	11146.16	11098.72	12828.66	3059.225	3687.251	2553.845	1.9104	6.92E-45	1.65E-43	NID1	chr1	-	2.36E+08	2.36E+08	5864
ENSG00000(	183.3352	175.826	225.6198	329.5932	265.0844	231.7941	-0.49948	0.014293	0.032104	LGALS8	chr1	+	2.37E+08	2.37E+08	6420
ENSG00000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	HPCAL4	chr1	-	40144320	40157361	4856
ENSG00000(	1051.329	1009.193	1182.195	855.4443	1018.918	829.3626	0.26176	0.053293	0.10271	MTR	chr1	+	2.37E+08	2.37E+08	10529
ENSG00000(	13.46529	10.83859	21.11062	11.98521	9.20432	10.68554	0.47278	0.45129	0.58089	BMP8B	chr1	-	40222854	40254533	4822
ENSG00000(	7.250543	3.612863	5.277655	21.72319	17.48821	19.72716	-1.7354	0.009757	0.022747	MYCL1	chr1	-	40361098	40367928	3256
ENSG00000(	872.1368	668.3797	907.7567	913.1231	1225.095	965.8088	-0.34055	0.032069	0.065901	SIPA1L2	chr1	-	2.33E+08	2.33E+08	6690
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	ZP4	chr1	-	2.38E+08	2.38E+08	1799
ENSG00000(	566.5782	578.0581	593.7362	442.7036	415.1148	335.3617	0.54055	0.000484	0.001425	RLF	chr1	+	40627045	40706593	6246
ENSG00000(	10.35792	0	3.958241	3.745378	0.920432	0	1.195	0.31307	0.43952	KMO	chr1	+	2.42E+08	2.42E+08	5261
ENSG00000(	32.10955	56.60152	32.98534	32.21025	43.2603	39.45432	0.081913	0.83751	0.89622	ZNF684	chr1	+	40997233	41013841	2097
ENSG00000(	7.250543	1.204288	0	10.48706	6.443024	9.041614	-1.3353	0.16437	0.26268	KCNQ4	chr1	+	41249684	41306124	4099

ENSG00000(	16.57267	0	5.277655	38.95193	49.70333	41.92021	-2.3981	9.42E-05	0.000308	RIMS3	chr1	-	41086351	41131329	7235
ENSG00000(	389.4578	370.9206	472.3501	253.1875	304.663	204.6693	0.68988	0.000255	0.000783	AKT3	chr1	-	2.44E+08	2.44E+08	5127
ENSG00000(	530.3255	591.3053	666.304	600.0095	872.5695	741.4124	-0.30745	0.060673	0.11474	ETV3	chr1	-	1.57E+08	1.57E+08	5254
ENSG00000(	310.7376	290.2333	255.9663	538.5853	498.8741	570.4437	-0.90291	1.03E-08	5.17E-08	ACADM	chr1	+	76190036	76253260	2619
ENSG00000(	49.71801	43.35436	59.37362	23.97042	22.09037	16.4393	1.254	0.002078	0.005524	ST6GALNAC	chr1	+	77333126	77531396	3751
ENSG00000(	870.0652	798.4428	1112.266	2026.249	1949.475	1656.259	-1.0163	3.64E-12	2.40E-11	LPHN2	chr1	+	81771845	82458120	6302
ENSG00000(	0	0	1.319414	19.47596	41.41944	18.90519	-4.8252	1.14E-06	4.71E-06	PADI2	chr1	-	17393256	17445948	4345
ENSG00000(	674.3005	746.6584	610.8886	1173.052	841.2748	881.9684	-0.5101	0.001161	0.003225	SDHB	chr1	-	17345217	17380665	1153
ENSG00000(	1312.348	1194.653	972.408	1833.737	1434.953	1685.85	-0.50778	0.000434	0.001289	MFAP2	chr1	-	17300997	17307330	2371
ENSG00000(	326.2744	314.3191	389.2271	782.0349	515.4419	672.3673	-0.9342	1.46E-07	6.61E-07	RPF1	chr1	+	84944942	84963473	1385
ENSG00000(	2470.364	2660.272	2786.602	1855.46	2011.144	1551.87	0.54586	1.55E-05	5.64E-05	KDM5B	chr1	-	2.03E+08	2.03E+08	7438
ENSG00000(	1337.207	1256.072	1252.124	675.6661	489.6698	483.3154	1.2169	7.06E-16	5.86E-15	UAP1	chr1	+	1.63E+08	1.63E+08	2344
ENSG00000(	3.107376	0	0	0.749076	0	4.109825	-0.34632	0.79636	0.86707	ACTL8	chr1	+	18081808	18153558	1861
ENSG00000(	296.2365	361.2863	335.1311	97.37982	74.55499	73.15488	2.0012	8.97E-22	9.80E-21	CTBS	chr1	-	85018804	85040163	3082
ENSG00000(	459.8916	433.5436	674.2204	1211.255	1182.755	1269.114	-1.2225	6.76E-14	4.99E-13	RGS4	chr1	+	1.63E+08	1.63E+08	3774
ENSG00000(	588.3298	650.3154	618.8051	491.3936	613.9281	493.179	0.21672	0.14418	0.23624	KLHL12	chr1	-	2.03E+08	2.03E+08	3359
ENSG00000(	336.6324	310.7062	357.5611	891.3999	940.6815	907.4493	-1.4436	1.30E-25	1.64E-24	SSX2IP	chr1	-	85109390	85156486	5843
ENSG00000(	601.7951	623.821	686.0952	743.0829	748.3112	687.9846	-0.18956	0.15553	0.25135	ZNHIT6	chr1	-	86115106	86174116	6080
ENSG00000(	303.487	315.5234	347.0058	508.6223	415.1148	412.6264	-0.46882	0.004249	0.010682	RBBP5	chr1	-	2.05E+08	2.05E+08	4404
ENSG00000(	220.6237	181.8474	255.9663	18.72689	36.81728	34.52253	2.8479	2.39E-23	2.76E-22	GBP3	chr1	-	89472349	89488577	3678
ENSG00000(	228.91	290.2333	279.7157	4.494453	2.761296	0.821965	6.384	6.35E-42	1.39E-40	GBP1	chr1	-	89518002	89531043	3035
ENSG00000(	91.14969	119.2245	110.8308	172.2874	102.168	148.7757	-0.39976	0.12644	0.21252	PINK1-AS	chr1	-	20969150	20978686	4443
ENSG00000(	36.25272	44.55865	35.62417	33.7084	20.2495	44.38611	0.23319	0.58027	0.69841	KIF17	chr1	-	20990507	21044510	3969
ENSG00000(	164.6909	168.6003	151.7326	137.8299	96.64536	131.5144	0.40106	0.08126	0.14739	GPR89A	chr1	-	1.46E+08	1.46E+08	2699
ENSG00000(	16.57267	4.817151	7.916483	208.9921	169.3595	175.0785	-4.1146	1.48E-27	2.04E-26	CDK18	chr1	+	2.05E+08	2.06E+08	3966
ENSG00000(	286.9144	266.1476	261.2439	111.6123	92.0432	81.37453	1.5038	7.28E-13	5.03E-12	RAB7L1	chr1	-	2.06E+08	2.06E+08	3272
ENSG00000(	37.28851	54.19295	32.98534	9.737982	18.40864	10.68554	1.6362	0.000717	0.002058	CD160	chr1	-	1.46E+08	1.46E+08	3389
ENSG00000(	1505.006	1524.628	1542.395	339.3312	265.0844	253.1652	2.4055	1.33E-63	5.06E-62	TXNIP	chr1	+	1.45E+08	1.45E+08	2927
ENSG00000(	1906.893	1971.419	1894.678	2368.577	2943.542	2747.007	-0.48006	5.17E-05	0.000175	ECE1	chr1	-	21543740	21671997	5099
ENSG00000(	708.4817	788.8085	696.6505	336.3349	282.5726	298.3733	1.2529	2.24E-17	2.01E-16	HMGCL	chr1	-	24128375	24165110	2151
ENSG00000(	444.3547	484.1237	329.8534	1091.403	907.5459	1010.195	-1.2519	5.53E-15	4.36E-14	GALE	chr1	-	24122089	24127271	2073
ENSG00000(	4433.189	3978.967	4000.463	6557.407	5302.609	6253.509	-0.54421	3.15E-06	1.24E-05	ID3	chr1	-	23884409	23886285	1251
ENSG00000(	0	0	0	1.498151	1.840864	0	-0.93652	0.47589	NA	CR2	chr1	+	2.08E+08	2.08E+08	4240
ENSG00000(	1578.547	1557.144	1807.597	1609.014	1742.378	1421.999	0.050115	0.6915	0.78954	CD46	chr1	+	2.08E+08	2.08E+08	7826
ENSG00000(	642.191	750.2712	695.3311	937.0935	927.7955	808.8135	-0.35663	0.008247	0.019526	PRPF3	chr1	+	1.5E+08	1.5E+08	2595
ENSG00000(	2383.357	2294.168	2025.3	2516.145	2501.734	3378.276	-0.32381	0.019708	0.04282	APH1A	chr1	-	1.5E+08	1.5E+08	2353
ENSG00000(	6866.265	6226.168	5439.943	1469.686	1207.607	1219.796	2.2443	5.92E-69	2.54E-67	LEPRE1	chr1	-	43212006	43232755	3001
ENSG00000(	2203.129	2101.482	1738.987	8475.041	7052.35	6933.274	-1.8892	3.28E-49	8.91E-48	SLC2A1	chr1	-	43391052	43424530	3318
ENSG00000(	890.781	780.3784	697.9699	3647.249	2537.631	2999.35	-1.9479	7.10E-39	1.42E-37	EBNA1BP2	chr1	-	43629846	43736607	1503
ENSG00000(	554.1487	508.2094	492.1413	5674.247	4130.899	4686.022	-3.2115	1.40E-120	1.47E-118	CDC20	chr1	+	43824626	43828874	1777
ENSG00000(	0	0	1.319414	1.498151	3.681728	4.109825	-1.8025	0.16279	0.2608	MPL	chr1	+	43803478	43818443	1950
ENSG00000(	3.107376	2.408575	1.319414	55.43159	90.20234	86.30632	-4.7425	3.66E-14	2.74E-13	ARTN	chr1	+	44398992	44402913	1943
ENSG00000(	504.4307	531.0909	509.2937	725.8542	700.4487	611.5419	-0.39879	0.004407	0.011036	IPO13	chr1	+	44412611	44433694	3894
ENSG00000(	1208.769	1216.331	1194.069	1409.011	1145.017	1527.211	-0.17338	0.19444	0.30065	ATP6V0B	chr1	+	44440159	44443967	2432

ENSG00000(	1951.432	1835.334	1538.436	1537.852	1365.001	1431.863	0.29669	0.019828	0.043067	B4GALT2	chr1	+	44444615	44456840	2629
ENSG00000(	947.7496	1069.407	806.1618	1331.107	907.5459	968.2747	-0.18343	0.265	0.38493	ERI3	chr1	-	44686742	44820932	1684
ENSG00000(	51.7896	43.35436	59.37362	5.992604	4.60216	9.041614	2.8646	8.37E-09	4.22E-08	PTCH2	chr1	-	45285516	45308735	4298
ENSG00000(	1514.328	1370.479	1277.193	1155.074	1006.032	1089.925	0.3559	0.004513	0.011283	AKR1A1	chr1	+	46016215	46035721	1818
ENSG00000(	5773.504	5870.903	5199.81	11435.39	9986.687	10611.57	-0.92581	5.73E-18	5.28E-17	PRDX1	chr1	-	45976708	45988719	1233
ENSG00000(	1988.72	1846.173	2444.874	494.3899	551.3388	465.2321	2.0499	3.94E-48	1.03E-46	PIK3R3	chr1	-	46505812	46642160	5609
ENSG00000(	23.82321	18.06432	7.916483	12.73428	11.96562	4.93179	0.71157	0.28257	0.40526	TSPAN1	chr1	+	46640745	46651630	1615
ENSG00000(	380.1356	290.2333	410.3377	463.6778	434.4439	337.8276	-0.19326	0.29552	0.41991	BLZF1	chr1	+	1.69E+08	1.69E+08	2749
ENSG00000(	16.57267	1.204288	6.597069	37.45378	15.64734	17.26126	-1.4017	0.044399	0.087597	CCDC181	chr1	-	1.69E+08	1.69E+08	2035
ENSG00000(	116.0087	103.5687	146.4549	394.7628	387.5019	304.127	-1.5639	3.05E-14	2.30E-13	SLC19A2	chr1	-	1.69E+08	1.69E+08	3671
ENSG00000(	19.68005	25.29004	10.55531	44.94453	33.13555	31.23467	-0.94068	0.049106	0.095568	FAAH	chr1	+	46859937	46879520	2094
ENSG00000(	348.0261	291.4376	328.534	439.7073	385.661	383.8576	-0.31971	0.048576	0.09463	NSUN4	chr1	+	46805849	46830824	4344
ENSG00000(	1124.87	1218.739	1395.94	1471.933	1261.912	1082.528	-0.03033	0.83341	0.89318	TMED5	chr1	-	93615299	93646285	6104
ENSG00000(	936.3559	944.1616	1089.836	1026.234	982.1009	914.847	0.022078	0.86313	0.9134	DR1	chr1	+	93811445	93828149	3242
ENSG00000(	3746.459	3618.885	3904.145	5940.918	5323.779	5451.271	-0.56815	4.89E-08	2.31E-07	CNN3	chr1	-	95362507	95392834	2165
ENSG00000(	3404.648	3343.103	4422.675	4053.997	5272.234	3853.372	-0.23804	0.10542	0.18312	PRRC2C	chr1	+	1.71E+08	1.72E+08	10366
ENSG00000(	748.8775	747.8627	626.7215	558.0613	430.7622	470.1639	0.53936	0.000434	0.001286	F3	chr1	-	94994781	95007356	2287
ENSG00000(	544.8265	509.4137	602.9721	1164.812	1256.39	1045.539	-1.0626	7.73E-15	6.04E-14	ABCD3	chr1	+	94883933	94984222	4367
ENSG00000(	274.4849	322.7491	347.0058	107.1178	119.6562	115.0751	1.4575	8.92E-14	6.54E-13	VAMP4	chr1	-	1.72E+08	1.72E+08	5159
ENSG00000(	377.0283	370.9206	390.5465	241.2023	280.7318	277.0022	0.50998	0.001748	0.004707	DPH5	chr1	-	1.01E+08	1.01E+08	2159
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	FASLG	chr1	+	1.73E+08	1.73E+08	1888
ENSG00000(	417.4241	484.1237	505.3355	363.3016	363.5706	343.5813	0.39141	0.011014	0.025372	PTBP2	chr1	+	97187221	97280349	3069
ENSG00000(	31.07376	63.82725	43.54065	23.97042	17.48821	19.72716	1.1388	0.009398	0.021988	TNFSF4	chr1	-	1.73E+08	1.73E+08	3470
ENSG00000(	4590.63	4985.751	4327.677	9279.548	7456.42	8367.603	-0.85085	3.47E-13	2.46E-12	PRDX6	chr1	+	1.73E+08	1.73E+08	1751
ENSG00000(	353.205	415.4793	337.7699	1103.388	890.9782	840.8701	-1.3534	6.46E-18	5.93E-17	DARS2	chr1	+	1.74E+08	1.74E+08	3506
ENSG00000(	8.286335	12.04288	10.55531	2.996302	1.840864	0	2.2798	0.015212	0.033907	HSD11B1	chr1	+	2.1E+08	2.1E+08	1477
ENSG00000(	6.214751	6.021439	3.958241	342.3275	341.4803	316.4565	-5.7856	2.53E-45	6.12E-44	IRF6	chr1	-	2.1E+08	2.1E+08	4306
ENSG00000(	301.4154	301.0719	387.9077	462.9287	330.4351	331.2519	-0.18576	0.32784	0.45556	DIEXF	chr1	+	2.1E+08	2.1E+08	8446
ENSG00000(	0	0	7.916483	6.74168	0.920432	0	0.003778	0.99763	0.99853	LPPR5	chr1	-	99355806	99470588	4134
ENSG00000(	4.143168	4.817151	2.638828	13.48336	21.16994	12.32947	-1.8337	0.015079	0.033648	LPPR4	chr1	+	99729509	99775146	5369
ENSG00000(	0	1.204288	2.638828	0	2.761296	0	0.25736	0.84918	0.90393	SERPINC1	chr1	-	1.74E+08	1.74E+08	1594
ENSG00000(	39.36009	36.12863	35.62417	286.8959	299.1404	198.0935	-2.7881	1.78E-25	2.24E-24	RCAN3	chr1	+	24829387	24863506	2778
ENSG00000(	583.1508	652.7239	610.8886	510.8695	511.7602	551.5385	0.22933	0.095448	0.16874	SYF2	chr1	-	25549170	25558993	1962
ENSG00000(	800.6671	818.9156	633.3186	649.4485	468.4999	618.9396	0.37368	0.022637	0.048424	C1orf63	chr1	-	25568728	25664704	3034
ENSG00000(	279.6638	297.4591	399.7824	356.56	440.8869	418.3801	-0.31631	0.081336	0.14744	SLC35A3	chr1	+	1E+08	1E+08	5533
ENSG00000(	452.6411	509.4137	544.9179	489.8954	555.0205	448.7928	0.011972	0.93783	0.96232	RCOR3	chr1	+	2.11E+08	2.11E+08	4246
ENSG00000(	2727.24	2410.984	2336.682	8473.543	7045.907	7324.529	-1.6083	1.41E-42	3.14E-41	STMN1	chr1	-	26210672	26233482	2947
ENSG00000(	478.5359	550.3595	432.7677	280.1543	214.4607	260.5629	0.94734	4.24E-08	2.02E-07	MTFR1L	chr1	+	26145131	26159432	3262
ENSG00000(	997.4676	899.6029	911.7149	35.95563	34.05598	32.05663	4.7572	2.77E-136	3.57E-134	MAN1C1	chr1	+	25943959	26112698	4641
ENSG00000(	89.0781	109.5902	143.8161	565.552	501.6354	476.7397	-2.1699	4.40E-28	6.18E-27	NEK2	chr1	-	2.12E+08	2.12E+08	2131
ENSG00000(	82.86335	103.5687	76.526	790.2747	791.5715	787.4424	-3.1576	4.43E-73	2.03E-71	RPS6KA1	chr1	+	26856252	26901521	3202
ENSG00000(	701.2311	780.3784	798.2453	796.2673	715.1757	800.5938	-0.02158	0.87021	0.91845	DHDDS	chr1	+	26758773	26797785	3338
ENSG00000(	872.1368	939.3444	672.901	561.8067	554.1001	618.1176	0.51806	0.000685	0.00197	NENF	chr1	+	2.13E+08	2.13E+08	942
ENSG00000(	254.8048	276.9862	224.3003	572.2937	519.1236	480.8495	-1.0515	1.36E-10	7.98E-10	NSL1	chr1	-	2.13E+08	2.13E+08	2317

ENSG0000(	17.60846	13.24716	10.55531	57.67882	145.4283	110.9653	-2.8314	3.29E-11	2.02E-10	PROX1	chr1	+	2.14E+08	2.14E+08	8498
ENSG0000(	1961.79	1905.183	2115.02	2140.858	3193.899	2177.385	-0.32727	0.031174	0.064292	ARID1A	chr1	+	27022524	27108595	8577
ENSG0000(	749.9133	594.9181	766.5794	2208.275	2519.222	2003.129	-1.6678	1.46E-32	2.41E-31	CENPF	chr1	+	2.15E+08	2.15E+08	10307
ENSG0000(	329.3818	364.8992	290.271	1191.779	980.2601	1015.949	-1.6893	1.25E-29	1.87E-28	RPA2	chr1	-	28218035	28241257	1752
ENSG0000(	796.524	833.3671	829.9113	1068.182	961.8514	805.5256	-0.20509	0.14185	0.23337	PPP1R8	chr1	+	28157289	28178187	2651
ENSG0000(	830.7051	826.1414	901.1596	570.0465	454.6934	392.8992	0.84726	7.09E-08	3.30E-07	STX12	chr1	+	28099694	28150963	3079
ENSG0000(	14.50109	27.69862	32.98534	41.19916	36.81728	37.81039	-0.6199	0.16061	0.25797	2-Mar	chr1	+	2.21E+08	2.21E+08	2127
ENSG0000(	11.39371	7.225726	13.19414	2.996302	5.522592	4.109825	1.2133	0.12734	0.21373	SLC5A9	chr1	+	48688357	48714316	3769
ENSG0000(	621.4751	718.9598	744.1494	2602.288	2535.79	2232.457	-1.8195	1.21E-46	3.01E-45	OSBPL9	chr1	+	52042851	52254889	4520
ENSG0000(	894.9242	887.56	767.8988	1605.269	1022.6	1288.841	-0.61691	0.00013	0.000416	TXNDC12	chr1	-	52485803	52521843	2396
ENSG0000(	2055.011	2003.935	2111.062	2585.809	2602.982	2273.555	-0.27394	0.014112	0.031741	ESYT2	chr7	-	1.59E+08	1.59E+08	5960
ENSG0000(	70.43385	90.32158	65.97069	346.822	221.8241	249.0554	-1.8369	6.46E-14	4.77E-13	CD3EAP	chr19	+	45909467	45914024	3286
ENSG0000(	1071.009	1005.58	996.1574	1528.114	1454.283	1620.093	-0.58145	7.42E-07	3.11E-06	MESDC2	chr15	-	81239667	81282219	4257
ENSG0000(	1276.096	1343.985	1397.259	2619.517	2121.596	2068.064	-0.76025	2.73E-09	1.44E-08	RCN2	chr15	+	77223960	77242601	3936
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CHRNB4	chr15	-	78916461	79012628	2623
ENSG0000(	17.60846	12.04288	18.47179	0	9.20432	14.79537	0.91799	0.24565	0.36212	MUC5B	chr11	+	1244296	1283406	17924
ENSG0000(	3043.157	2748.185	2314.252	1585.044	1217.732	1444.192	0.92996	2.49E-11	1.54E-10	CTSD	chr11	-	1773982	1785222	2123
ENSG0000(	2.071584	2.408575	3.958241	6.74168	9.20432	11.50751	-1.5037	0.090559	0.16156	COLEC11	chr2	+	3642426	3692048	1557
ENSG0000(	582.1151	482.9194	785.0512	289.1432	434.4439	309.8808	0.83612	3.23E-05	0.000113	STAG1	chr3	-	1.36E+08	1.36E+08	6053
ENSG0000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	A4GNT	chr3	-	1.38E+08	1.38E+08	1771
ENSG0000(	2030.152	2076.192	1678.294	1476.428	1608.915	1833.804	0.23386	0.076671	0.14018	STK11	chr19	+	1189406	1228428	3553
ENSG0000(	1043.042	959.8173	1411.773	966.3075	1490.179	1053.759	-0.03972	0.82429	0.88656	MLL	chr11	+	1.18E+08	1.18E+08	16594
ENSG0000(	25.8948	27.69862	34.30476	1.498151	2.761296	1.64393	3.6192	2.69E-07	1.19E-06	TREH	chr11	-	1.19E+08	1.19E+08	2770
ENSG0000(	516.8602	519.048	428.8095	386.523	300.9813	315.6345	0.54369	0.001088	0.003035	IFT46	chr11	-	1.18E+08	1.18E+08	1819
ENSG0000(	3.107376	4.817151	3.958241	0	0	0	3.0739	0.018336	0.040125	MMP8	chr11	-	1.03E+08	1.03E+08	3056
ENSG0000(	11.39371	16.86003	0	2.247227	1.840864	11.50751	0.73952	0.43779	0.56742	APOA1	chr11	-	1.17E+08	1.17E+08	1227
ENSG0000(	0	0	0	0	4.60216	1.64393	-1.6592	0.22125	0.33301	ZNF541	chr19	-	48023942	48059113	4632
ENSG0000(	9.322127	14.45145	6.597069	0	0.920432	0	3.8373	0.00055	0.001604	SLC8A2	chr19	-	47931274	47975425	5234
ENSG0000(	187.4783	180.6432	159.6491	166.2948	143.5874	226.0404	-0.02145	0.92403	0.95396	KPTN	chr19	-	47978401	47987525	1691
ENSG0000(	11594.65	12213.89	10088.24	6217.327	6622.508	8334.724	0.67731	2.19E-07	9.75E-07	RPS25	chr11	-	1.19E+08	1.19E+08	1462
ENSG0000(	132.5814	145.7188	154.3714	429.9694	586.3152	452.9027	-1.7564	1.26E-20	1.31E-19	KIF14	chr1	-	2.01E+08	2.01E+08	7274
ENSG0000(	17.60846	8.430014	7.916483	89.88907	83.75931	120.0069	-3.0081	5.08E-13	3.55E-12	TNNT2	chr1	-	2.01E+08	2.01E+08	3014
ENSG0000(	190.5857	187.8689	216.3839	346.822	272.4479	278.6461	-0.59403	0.001628	0.004406	DDX59	chr1	-	2.01E+08	2.01E+08	2900
ENSG0000(	764.4144	793.6256	1141.293	751.3228	976.5783	742.2343	0.12679	0.46319	0.5925	CAMSAP2	chr1	+	2.01E+08	2.01E+08	7352
ENSG0000(	562.435	494.9623	653.1098	904.8833	753.8338	678.1211	-0.44994	0.00464	0.011576	ATF6	chr1	+	1.62E+08	1.62E+08	7496
ENSG0000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	CRYGD	chr2	-	2.09E+08	2.09E+08	619
ENSG0000(	74.57702	63.82725	62.01245	149.066	142.667	170.1467	-1.1906	2.20E-06	8.79E-06	MREG	chr2	-	2.17E+08	2.17E+08	1314
ENSG0000(	367.7061	385.3721	427.4901	898.1416	721.6187	697.0263	-0.97157	3.35E-10	1.91E-09	FASTKD2	chr2	+	2.08E+08	2.08E+08	4999
ENSG0000(	991.2529	1017.623	1165.042	1298.897	2257.82	1615.983	-0.70161	4.91E-05	0.000167	NRP2	chr2	+	2.07E+08	2.07E+08	6662
ENSG0000(	575.9003	673.1968	688.734	522.8547	593.6786	501.3986	0.259	0.075821	0.13894	CREB1	chr2	+	2.08E+08	2.08E+08	7650
ENSG0000(	328.346	338.4048	409.0183	264.4237	411.4331	332.8958	0.092876	0.62712	0.7382	KLF7	chr2	-	2.08E+08	2.08E+08	8362
ENSG0000(	4.143168	1.204288	0	3.745378	2.761296	5.753754	-0.89384	0.4283	0.55848	TTR	chr18	+	29171689	29178974	957
ENSG0000(	93.22127	113.203	106.8725	499.6334	537.5323	406.0507	-2.195	1.27E-29	1.91E-28	B4GALT6	chr18	-	29202210	29265799	4427
ENSG0000(	223.7311	243.2661	170.2044	8.988907	14.72691	14.79537	4.0045	1.36E-35	2.48E-34	C1orf54	chr1	+	1.5E+08	1.5E+08	1251

ENSG00000(	32.10955	28.90291	40.90183	48.68991	49.70333	34.52253	-0.3782	0.33368	0.46178	CA14	chr1	+	1.5E+08	1.5E+08	1788
ENSG00000(	0	0	3.958241	0.749076	0	1.64393	0.36011	0.79032	0.86275	CASC1	chr12	-	25261354	25348096	2445
ENSG00000(	9.322127	7.225726	3.958241	0	0	4.109825	1.834	0.09457	0.16742	LRMP	chr12	+	25173936	25261268	2715
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	ATP10B	chr5	-	1.6E+08	1.6E+08	7566
ENSG00000(	1616.871	1717.314	1649.267	1220.244	1292.287	1391.587	0.35155	0.002333	0.006145	SPCS2	chr11	+	74660292	74690076	2708
ENSG00000(	361.4914	397.4149	374.7135	255.4348	268.7661	307.4149	0.44513	0.006926	0.016695	USP35	chr11	+	77899858	77925757	4216
ENSG00000(	233.0532	213.1589	241.4527	393.2647	417.8761	489.0691	-0.91541	8.03E-08	3.71E-07	ELOVL4	chr6	-	80624529	80657297	3042
ENSG00000(	6.214751	4.817151	0	22.47227	21.16994	13.9734	-2.1388	0.004788	0.011901	FILIP1	chr6	-	76005626	76203496	4580
ENSG00000(	152.2614	161.3746	230.8974	219.4791	308.3447	221.1086	-0.45891	0.04115	0.082055	CASP8AP2	chr6	+	90539613	90584155	7344
ENSG00000(	353.205	387.7806	321.937	1518.376	1156.063	1473.783	-1.9582	1.14E-38	2.28E-37	HMGN3	chr6	-	79910962	79944406	872
ENSG00000(	85.97073	93.93444	105.5531	150.5642	95.72493	129.8705	-0.40001	0.12767	0.2142	UBE3D	chr6	-	83602117	83775560	3255
ENSG00000(	0	0	1.319414	7.490755	4.60216	13.15144	-3.1829	0.005453	0.0134	CNR1	chr6	-	88849583	88876078	8974
ENSG00000(	1097.939	973.0645	1203.305	498.8843	618.5303	489.8911	1.0244	2.59E-12	1.73E-11	ANKRD13C	chr1	-	70726271	70820417	4069
ENSG00000(	126.3666	101.1602	121.3861	23.22134	46.94203	25.48091	1.8506	2.07E-08	1.01E-07	SGIP1	chr1	+	66999066	67213982	7273
ENSG00000(	692.9448	597.3267	721.7193	543.8288	707.8122	524.4136	0.18035	0.25397	0.37203	PHF3	chr6	+	64345725	64489229	8233
ENSG00000(	1355.852	1418.651	1358.996	178.28	193.2907	156.9953	2.9607	2.01E-99	1.52E-97	PLAGL1	chr6	-	1.44E+08	1.44E+08	4430
ENSG00000(	343.8829	335.9963	538.3208	483.1537	563.3044	435.6414	-0.28355	0.14322	0.23492	FBXO30	chr6	-	1.46E+08	1.46E+08	4376
ENSG00000(	307.6302	291.4376	331.1729	704.8801	802.6167	729.9048	-1.2628	5.34E-18	4.93E-17	TNFAIP3	chr6	+	1.38E+08	1.38E+08	4432
ENSG00000(	42.46747	52.98866	55.41538	120.6012	135.3035	111.7872	-1.2758	5.75E-06	2.19E-05	AKAP7	chr6	+	1.31E+08	1.32E+08	2954
ENSG00000(	425.7105	401.0278	422.2124	747.5774	563.3044	697.0263	-0.68366	9.26E-06	3.45E-05	RAB32	chr6	+	1.47E+08	1.47E+08	1217
ENSG00000(	11.39371	1.204288	6.597069	14.23244	11.04518	9.863579	-0.77993	0.317	0.44398	MYB	chr6	+	1.36E+08	1.36E+08	3672
ENSG00000(	20.71584	21.67718	13.19414	1.498151	0	8.219649	2.2579	0.005221	0.012895	ALDH8A1	chr6	-	1.35E+08	1.35E+08	2558
ENSG00000(	1461.502	1412.629	1558.228	661.4337	555.9409	553.1824	1.3197	2.67E-24	3.22E-23	SGK1	chr6	-	1.34E+08	1.35E+08	5474
ENSG00000(	711.589	793.6256	745.4688	518.3603	510.8398	461.9443	0.59202	1.40E-05	5.12E-05	RNF146	chr6	+	1.28E+08	1.28E+08	2369
ENSG00000(	0	6.021439	6.597069	0.749076	0	0	2.436	0.059536	0.11297	ARG1	chr6	+	1.32E+08	1.32E+08	1532
ENSG00000(	555.1845	543.1338	654.4292	2095.164	1259.151	1485.291	-1.4606	4.49E-17	3.96E-16	CTGF	chr6	-	1.32E+08	1.32E+08	2339
ENSG00000(	0	3.612863	1.319414	8.239831	1.840864	6.575719	-1.4084	0.2009	0.30842	TCF21	chr6	+	1.34E+08	1.34E+08	4551
ENSG00000(	10.35792	4.817151	13.19414	11.98521	26.69253	5.753754	-0.59422	0.40603	0.53689	PMFBP1	chr16	-	72146056	72210777	3935
ENSG00000(	872.1368	768.3356	812.7589	1102.639	1100.837	992.1117	-0.37995	0.002667	0.006956	FBXL5	chr4	-	15606162	15683302	3385
ENSG00000(	968.4654	916.463	1014.629	1362.568	1207.607	1391.587	-0.44997	0.000265	0.000812	MED28	chr4	+	17616254	17627477	2394
ENSG00000(	43.50326	22.88147	88.40072	20.97412	24.85166	18.90519	1.2138	0.010776	0.024864	SLC16A7	chr12	+	59989848	60176395	4536
ENSG00000(	249.6258	233.6318	279.7157	367.047	321.2308	287.6877	-0.35548	0.046655	0.09138	TMEM5	chr12	+	64173583	64203338	4531
ENSG00000(	128.4382	166.1917	164.9267	239.7042	209.8585	209.6011	-0.52168	0.011322	0.026002	ZNF430	chr19	+	21203426	21242856	3923
ENSG00000(	7.250543	7.225726	10.55531	591.0206	610.2464	817.0331	-6.2415	1.26E-71	5.65E-70	VAMP8	chr2	+	85788685	85809154	805
ENSG00000(	157.4404	155.3531	183.3985	339.3312	364.4911	344.4033	-1.0761	1.97E-09	1.05E-08	DCLRE1B	chr1	+	1.14E+08	1.14E+08	3940
ENSG00000(	2679.594	2693.992	2578.135	7516.973	5366.119	6251.865	-1.2641	1.99E-22	2.23E-21	MYL12B	chr18	+	3261907	3278282	1249
ENSG00000(	2059.154	1949.742	2250.92	571.5446	831.1501	557.2922	1.671	8.51E-27	1.13E-25	FOXO3	chr6	+	1.09E+08	1.09E+08	7341
ENSG00000(	70.43385	74.66584	79.16483	30.7121	33.13555	29.59074	1.2436	0.000189	0.000593	ARMC2	chr6	+	1.09E+08	1.09E+08	3241
ENSG00000(	6423.981	6479.068	6546.931	6743.178	4375.734	4484.641	0.3167	0.034965	0.07108	RPN2	chr20	+	35806813	35870022	2511
ENSG00000(	420.5315	456.425	378.6718	584.2789	591.8378	522.7697	-0.43396	0.003624	0.009232	TGIF2	chr20	+	35201891	35222560	3613
ENSG00000(	0	0	0	18.72689	17.48821	20.54912	-5.1144	3.44E-06	1.34E-05	CASQ2	chr1	-	1.16E+08	1.16E+08	2674
ENSG00000(	0	0	0	9.737982	4.60216	3.28786	-3.343	0.007553	0.01806	OLFM3	chr1	-	1.02E+08	1.02E+08	3255
ENSG00000(	920.819	915.2587	1121.502	818.7396	973.8171	819.499	0.17846	0.20273	0.31064	PKD2	chr4	+	88928820	88998929	5056
ENSG00000(	26.93059	27.69862	51.45714	1776.058	1927.385	1633.244	-5.6448	1.67E-162	3.17E-160	ABCG2	chr4	-	89011416	89152474	4479

ENSG00000(	3.107376	12.04288	1.319414	10148.48	7165.563	8106.218	-10.189	3.98E-91	2.59E-89	SPP1	chr4	+	88896819	88904562	1664
ENSG00000(	14.50109	26.49433	15.83297	20.97412	13.80648	26.30288	-0.1056	0.84498	0.90101	FAM47E-ST	chr4	+	77172886	77232752	3420
ENSG00000(	6919.09	7324.478	6277.771	5452.521	4371.132	4304.63	0.53732	1.40E-05	5.10E-05	CCNI	chr4	-	77968311	77997158	2772
ENSG00000(	24.85901	22.88147	25.06886	6.74168	18.40864	18.90519	0.70188	0.20317	0.31118	RARRES1	chr3	-	1.58E+08	1.58E+08	1952
ENSG00000(	2063.297	1866.646	2289.183	510.1204	463.8977	406.0507	2.1657	7.07E-57	2.28E-55	MFSD1	chr3	+	1.58E+08	1.59E+08	2423
ENSG00000(	929.1053	887.56	1303.581	640.4596	675.5971	586.061	0.71061	9.30E-06	3.47E-05	RAB3GAP2	chr1	-	2.2E+08	2.2E+08	7257
ENSG00000(	136.7245	140.9017	131.9414	223.2245	215.3811	216.1768	-0.67307	0.000704	0.002025	FAM86A	chr16	-	5134305	5147809	2390
ENSG00000(	71.46964	98.75159	75.20659	1147.584	1514.111	1380.901	-4.026	6.88E-110	6.12E-108	PPL	chr16	-	4932508	5010742	6238
ENSG00000(	1401.426	1275.341	1324.691	1009.754	1584.063	1326.651	0.030392	0.84442	0.9007	UBN1	chr16	+	4896666	4932361	6336
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	BTF3P11	chr13	+	77502200	77502970	477
ENSG00000(	378.064	384.1678	424.8512	163.2985	174.8821	135.6242	1.3193	2.26E-13	1.62E-12	KLF12	chr13	-	74260226	74708394	10637
ENSG00000(	5.17896	4.817151	1.319414	4.494453	6.443024	5.753754	-0.46397	0.62223	0.73429	UCHL3	chr13	+	76123619	76180085	844
ENSG00000(	79.75598	32.51577	84.44248	71.16218	114.1336	58.35951	-0.29967	0.41988	0.55063	PCDH17	chr13	+	58205944	58303445	7523
ENSG00000(	944.6422	906.8287	889.2849	445.7	497.0333	480.0275	0.94479	5.27E-13	3.68E-12	HS1BP3	chr2	-	20760208	20850849	4358
ENSG00000(	357.3482	314.3191	358.8805	692.1458	620.3712	573.7315	-0.86963	1.11E-08	5.55E-08	C2orf43	chr2	-	20883788	21022882	2903
ENSG00000(	265.1627	267.3519	337.7699	226.2208	208.9381	165.2149	0.53038	0.007352	0.017623	WDR35	chr2	-	20110021	20189892	6960
ENSG00000(	2948.9	2984.225	2467.304	5934.926	6363.867	6091.582	-1.128	2.21E-23	2.57E-22	CCND2	chr12	+	4382938	4414516	6480
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	FGF23	chr12	-	4477393	4488894	3018
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	HIN1L	chr12	+	3948625	3951691	3067
ENSG00000(	623.5467	623.821	756.0241	495.1389	395.7858	436.4634	0.58964	0.000124	0.000399	ELL2	chr5	-	95220802	95297775	6046
ENSG00000(	24.85901	20.47289	32.98534	9.737982	6.443024	3.28786	1.8902	0.001947	0.005197	DNAH7	chr2	-	1.97E+08	1.97E+08	12394
ENSG00000(	266.1985	304.6848	250.6886	325.0988	318.4695	306.5929	-0.2087	0.21773	0.32907	CYP20A1	chr2	+	2.04E+08	2.04E+08	2636
ENSG00000(	557.256	580.4667	445.9619	575.29	653.5067	896.7637	-0.42149	0.018798	0.041042	NDUFB3	chr2	+	2.02E+08	2.02E+08	755
ENSG00000(	523.0749	528.6823	609.5692	934.0972	751.9929	771.8251	-0.5653	0.000111	0.000359	GTF3C3	chr2	-	1.98E+08	1.98E+08	4282
ENSG00000(	169.8699	202.3203	236.1751	175.2837	217.222	199.7375	0.036518	0.85929	0.91057	SATB2	chr2	-	2E+08	2E+08	6194
ENSG00000(	521.0033	553.9724	589.778	886.1564	697.6875	901.6955	-0.57823	9.13E-05	0.000299	UBE2B	chr5	+	1.34E+08	1.34E+08	2515
ENSG00000(	0	0	1.319414	8.239831	1.840864	6.575719	-2.5785	0.033831	0.069036	TRPM6	chr9	-	77337411	77503010	8437
ENSG00000(	7.250543	10.83859	1.319414	66.66772	65.35067	56.71558	-3.1329	1.06E-09	5.78E-09	GDA	chr9	+	74729511	74872109	5340
ENSG00000(	542.755	579.2624	672.901	11.98521	23.0108	13.9734	5.1715	7.22E-91	4.64E-89	KLF9	chr9	-	72999503	73029540	5185
ENSG00000(	537.576	520.2523	591.0974	1723.623	2130.8	1583.104	-1.7169	2.60E-33	4.42E-32	TJP2	chr9	+	71736224	71870124	4611
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	C2orf40	chr2	+	1.07E+08	1.07E+08	799
ENSG00000(	1441.822	1362.049	1212.541	695.8912	871.6491	978.1383	0.65703	7.93E-06	2.98E-05	ITGB1BP1	chr2	-	9543604	9563676	4859
ENSG00000(	580.0435	638.2725	601.6527	1503.395	1166.187	1052.937	-1.0299	1.24E-11	7.82E-11	CPSF3	chr2	+	9563697	9613230	3157
ENSG00000(	36.25272	25.29004	34.30476	9.737982	14.72691	16.4393	1.1913	0.017067	0.037665	PIGZ	chr3	-	1.97E+08	1.97E+08	2701
ENSG00000(	577.9719	585.2838	583.1809	874.1712	698.6079	671.5453	-0.36168	0.013717	0.030937	SENP5	chr3	+	1.97E+08	1.97E+08	6308
ENSG00000(	901.139	900.8072	766.5794	688.4004	493.3516	475.0957	0.62951	0.000127	0.000408	CCDC92	chr12	-	1.24E+08	1.24E+08	4883
ENSG00000(	1983.541	1819.679	1990.995	1952.84	2003.78	1771.334	0.016678	0.88331	0.92688	C1orf198	chr1	-	2.31E+08	2.31E+08	3858
ENSG00000(	60.07593	38.53721	77.84541	18.72689	19.32907	11.50751	1.7831	3.77E-05	0.00013	TRIM67	chr1	+	2.31E+08	2.31E+08	9320
ENSG00000(	693.9806	811.6899	1039.698	981.289	1224.175	818.6771	-0.24853	0.1565	0.25256	HEATR1	chr1	-	2.37E+08	2.37E+08	8447
ENSG00000(	663.9426	681.6268	864.216	2233.743	2683.059	1870.792	-1.6148	1.90E-25	2.39E-24	PTBP3	chr9	-	1.15E+08	1.15E+08	7271
ENSG00000(	3891.47	3762.195	4187.819	8513.244	10397.2	10526.9	-1.3114	3.30E-29	4.87E-28	RAD23B	chr9	+	1.1E+08	1.1E+08	4119
ENSG00000(	853.4925	862.27	880.049	555.065	557.7818	558.9361	0.63324	5.25E-07	2.25E-06	FKBP15	chr9	-	1.16E+08	1.16E+08	8807
ENSG00000(	706.4101	753.8841	745.4688	1582.797	1113.723	1015.949	-0.74926	4.50E-06	1.74E-05	CTNNAL1	chr9	-	1.12E+08	1.12E+08	2520
ENSG00000(	288.9859	262.5347	246.7304	437.4601	347.9233	341.9374	-0.49528	0.004907	0.012177	FAM206A	chr9	+	1.12E+08	1.12E+08	2121

ENSG00000(	679.4795	540.7252	591.0974	2181.308	1574.859	1912.712	-1.6404	3.69E-28	5.21E-27	WDR34	chr9	-	1.31E+08	1.31E+08	1755
ENSG00000(	6547.241	6416.445	6859.632	13403.21	12469.09	13446.52	-0.98681	1.43E-23	1.68E-22	SET	chr9	+	1.31E+08	1.31E+08	2915
ENSG00000(	4692.137	4177.674	4008.379	2698.17	2935.258	3800.766	0.44803	0.001133	0.003152	PPP2R4	chr9	+	1.32E+08	1.32E+08	2824
ENSG00000(	500.2875	492.5537	423.5318	603.0058	697.6875	586.061	-0.41045	0.005706	0.013977	GLE1	chr9	+	1.31E+08	1.31E+08	3321
ENSG00000(	1748.417	1743.809	1944.816	1902.652	1773.672	1627.491	0.035207	0.76557	0.84527	RAB14	chr9	-	1.24E+08	1.24E+08	4145
ENSG00000(	179.192	181.8474	170.2044	169.2911	232.8693	157.8173	-0.07262	0.7375	0.82411	CNTRL	chr9	+	1.24E+08	1.24E+08	7660
ENSG00000(	546.8981	564.8109	608.2498	385.0248	420.6374	361.6646	0.55742	0.000141	0.00045	TRIM32	chr9	+	1.19E+08	1.19E+08	3717
ENSG00000(	591.4372	651.5197	696.6505	573.0428	736.3456	678.943	-0.03579	0.80851	0.87565	FBXW2	chr9	-	1.24E+08	1.24E+08	2154
ENSG00000(	633.9046	535.908	515.8908	1067.433	1077.826	1199.247	-0.98406	7.24E-13	5.00E-12	PHF19	chr9	-	1.24E+08	1.24E+08	4241
ENSG00000(	1432.5	1328.329	1661.142	1070.429	881.7739	841.6921	0.65961	2.63E-06	1.04E-05	NEK6	chr9	+	1.27E+08	1.27E+08	3619
ENSG00000(	1.035792	0	1.319414	167.0438	173.0412	221.9305	-7.0758	4.17E-21	4.41E-20	BSPRY	chr9	+	1.16E+08	1.16E+08	2339
ENSG00000(	914.6043	859.8614	771.8571	1408.262	1297.809	1201.713	-0.61566	1.98E-06	7.95E-06	PPP6C	chr9	-	1.28E+08	1.28E+08	4349
ENSG00000(	779.9513	631.0468	612.208	773.046	605.6443	855.6655	-0.14207	0.38176	0.51242	NDUFA8	chr9	-	1.25E+08	1.25E+08	1000
ENSG00000(	114.9729	149.3317	71.24834	291.3904	217.222	322.2102	-1.2936	3.71E-07	1.61E-06	HDHD3	chr9	-	1.16E+08	1.16E+08	1834
ENSG00000(	368.7419	382.9635	399.7824	367.047	267.8457	267.1386	0.34824	0.050332	0.097703	RBM18	chr9	-	1.25E+08	1.25E+08	4974
ENSG00000(	1.035792	3.612863	0	2.247227	0.920432	0	0.33136	0.80263	0.87177	SLC46A2	chr9	-	1.16E+08	1.16E+08	2502
ENSG00000(	749.9133	758.7013	752.0659	807.5034	753.8338	687.1627	0.007476	0.95444	0.97292	HSDL2	chr9	+	1.15E+08	1.15E+08	3350
ENSG00000(	1438.715	1258.481	1467.188	2170.821	1722.128	1772.156	-0.44336	0.000761	0.002178	MAPKAP1	chr9	-	1.28E+08	1.28E+08	3395
ENSG00000(	18.64425	10.83859	18.47179	40.45008	54.30549	41.09825	-1.4548	0.001362	0.003739	NR4A3	chr9	+	1.03E+08	1.03E+08	4982
ENSG00000(	235.1248	245.6747	253.3274	166.2948	208.0176	181.6542	0.4002	0.034889	0.07095	INVS	chr9	+	1.03E+08	1.03E+08	3709
ENSG00000(	13.46529	18.06432	9.235896	25.46857	26.69253	19.72716	-0.77912	0.15178	0.24647	GALNT12	chr9	+	1.02E+08	1.02E+08	2735
ENSG00000(	1082.403	975.4731	829.9113	447.1981	402.2288	452.0807	1.147	3.75E-15	2.99E-14	DENND1A	chr9	-	1.26E+08	1.27E+08	5010
ENSG00000(	599.7235	680.4226	630.6798	749.8246	603.8034	558.9361	-0.00252	0.98678	0.99193	ALG2	chr9	-	1.02E+08	1.02E+08	2966
ENSG00000(	0	0	0	0.749076	10.12475	2.465895	-2.826	0.030277	0.062683	CSF3R	chr1	-	36931644	36948879	6074
ENSG00000(	468.1779	499.7794	472.3501	498.8843	430.7622	455.3686	0.0553	0.70468	0.79966	KDSR	chr18	-	60994959	61034743	5447
ENSG00000(	830.7051	871.9043	887.9655	1014.997	1075.065	910.7371	-0.21179	0.09613	0.16981	VPS4B	chr18	-	61056423	61089716	3324
ENSG00000(	5.17896	6.021439	3.958241	8.988907	9.20432	9.863579	-0.79998	0.31384	0.44033	ONECUT2	chr18	+	55102917	55158530	16122
ENSG00000(	753.0207	676.8097	510.6131	898.8907	795.2532	992.1117	-0.46589	0.003846	0.009749	C19orf25	chr19	-	1461142	1479555	2584
ENSG00000(	526.1823	535.908	414.2959	617.9873	575.27	646.0644	-0.31475	0.038011	0.076583	ZBTB45	chr19	-	59024897	59050278	2541
ENSG00000(	1220.163	1299.426	1529.201	775.2932	1662.3	1073.486	0.20275	0.53457	0.65901	YLPM1	chr14	+	75230069	75304012	7017
ENSG00000(	201.9794	192.686	228.2586	158.0549	172.1208	134.8022	0.41922	0.041039	0.08189	DCAF4	chr14	+	73393040	73426411	2896
ENSG00000(	48.68222	42.15007	40.90183	23.97042	12.88605	18.08323	1.2217	0.005222	0.012895	PROX2	chr14	-	75319736	75330537	3197
ENSG00000(	1049.257	1057.365	988.2409	1291.406	1277.56	1583.104	-0.42277	0.001169	0.003245	FCF1	chr14	+	75179847	75203394	2412
ENSG00000(	142.9393	67.44011	139.8579	68.91495	82.83888	58.35951	0.72981	0.020024	0.043424	PGF	chr14	-	75408537	75422487	3549
ENSG00000(	180.2278	201.116	209.7868	44.19546	48.7829	79.7306	1.7573	3.42E-11	2.09E-10	IFI27L2	chr14	-	94594116	94596590	938
ENSG00000(	23.82321	34.92434	46.17948	16.47966	22.09037	27.94681	0.63268	0.17177	0.27273	CCDC176	chr14	+	74486056	74549566	3106
ENSG00000(	1061.687	1004.376	1204.625	710.1236	870.7287	807.9915	0.45236	0.000908	0.002561	NEK9	chr14	-	75548822	75594047	5544
ENSG00000(	90.1139	87.913	59.37362	100.3761	108.611	166.0369	-0.64723	0.025876	0.054602	ACYP1	chr14	-	75519924	75536186	789
ENSG00000(	424.6747	407.0492	347.0058	185.7707	205.2563	239.1918	0.90143	4.57E-07	1.97E-06	IFT43	chr14	+	76368479	76550928	1765
ENSG00000(	2224.881	2415.801	2091.271	4440.52	3160.763	4072.836	-0.79237	6.19E-09	3.17E-08	NPC2	chr14	-	74942895	74960880	1436
ENSG00000(	130.5098	133.6759	209.7868	62.17327	118.7357	90.41614	0.79688	0.005477	0.013455	DNAL1	chr14	+	74111578	74164463	2312
ENSG00000(	3974.334	3462.327	3421.24	718.3635	942.5224	920.6007	2.0686	1.93E-54	5.90E-53	IRF2BPL	chr14	-	77490888	77495034	4147
ENSG00000(	493.0369	428.7264	376.0329	156.5568	215.3811	172.6126	1.2514	2.74E-11	1.69E-10	ACOT2	chr14	+	74034324	74042357	1774
ENSG00000(	535.5044	427.5221	651.7904	325.0988	302.8221	257.275	0.86211	2.25E-06	8.97E-06	LTBP2	chr14	-	74964873	75079306	8567

ENSG00000(	692.9448	580.4667	845.7442	760.3117	814.5823	729.0829	-0.12099	0.43302	0.56286	AREL1	chr14	-	75119880	75179818	5456
ENSG00000(	269.3059	255.309	311.3817	193.2615	198.8133	172.6126	0.56242	0.002453	0.006434	MLH3	chr14	-	75480467	75518235	7896
ENSG00000(	997.4676	947.7744	1077.961	438.2092	451.0117	373.1721	1.2566	1.70E-19	1.68E-18	TTLL5	chr14	+	76099968	76421421	4683
ENSG00000(	454.7126	469.6722	398.463	85.39461	60.74851	60.00344	2.6615	8.06E-39	1.61E-37	FLVCR2	chr14	+	76044960	76129557	3629
ENSG00000(	579.0077	584.0795	489.5025	538.5853	482.3064	651.8182	-0.01692	0.91532	0.94835	ABCD4	chr14	-	74752126	74769759	3008
ENSG00000(	1638.623	1655.896	1754.82	1800.778	1788.399	1868.326	-0.1123	0.30262	0.42775	DLST	chr14	+	75348594	75370448	2838
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	PPP4R4	chr14	+	94612465	94746072	3868
ENSG00000(	19669.69	19658.79	17536.33	122.0993	224.5854	181.6542	6.7327	0	0	TGFB3	chr14	-	76424442	76449334	2708
ENSG00000(	1.035792	2.408575	9.235896	20.22504	16.56778	16.4393	-1.933	0.011187	0.025732	ZC2HC1C	chr14	+	75530873	75545126	2392
ENSG00000(	524.1107	563.6067	381.3106	928.1046	973.8171	796.484	-0.87209	9.55E-08	4.39E-07	SLIRP	chr14	+	78174414	78227447	865
ENSG00000(	1519.507	1671.551	1684.891	2157.338	2227.445	1787.774	-0.33976	0.006576	0.015904	RBM25	chr14	+	73525144	73588122	6848
ENSG00000(	205.0868	199.9118	193.9538	253.9366	242.0736	240.0138	-0.29556	0.10296	0.17963	ALDH6A1	chr14	-	74523553	74551196	5499
ENSG00000(	18.64425	13.24716	18.47179	14.23244	20.2495	11.50751	0.13012	0.81995	0.88375	GPR68	chr14	-	91698876	91720269	2859
ENSG00000(	0	0	2.638828	2.247227	5.522592	2.465895	-1.3845	0.26617	0.38615	ESRRB	chr14	+	76776957	76968178	2713
ENSG00000(	297.2723	291.4376	304.7846	521.3566	414.1944	460.3004	-0.6427	6.80E-05	0.000227	EIF2B2	chr14	+	75469614	75476292	1537
ENSG00000(	199.9078	220.3847	222.9809	219.4791	342.4007	271.2484	-0.36986	0.069268	0.12861	NRDE2	chr14	-	90742580	90798481	5828
ENSG00000(	49.71801	43.35436	36.94359	40.45008	19.32907	34.52253	0.4491	0.27727	0.39895	COQ6	chr14	+	74416629	74430373	3119
ENSG00000(	31.07376	24.08575	29.0271	12.73428	14.72691	13.15144	1.0173	0.043751	0.086537	ZNF410	chr14	+	74353320	74399214	2601
ENSG00000(	1283.346	1306.652	1535.798	615.7401	532.9301	547.4286	1.2779	1.32E-21	1.44E-20	RHOQ	chr2	+	46768945	46810260	2975
ENSG00000(	30.03797	46.96722	18.47179	79.40201	56.14635	46.03004	-0.904	0.026801	0.056336	GPR75	chr2	-	54080050	54087126	2115
ENSG00000(	493.0369	567.2195	577.9032	720.6107	502.5559	490.7131	-0.06706	0.698	0.79445	SUPT7L	chr2	-	27873679	27886676	4488
ENSG00000(	452.6411	382.9635	514.5714	332.5895	479.5451	397.0091	0.15939	0.3746	0.50514	KLHL29	chr2	+	23608088	23931481	6385
ENSG00000(	804.8103	743.0455	816.7171	561.8067	670.9949	618.1176	0.35331	0.009276	0.021737	DNMT3A	chr2	-	25455845	25565459	4477
ENSG00000(	2289.1	2261.652	2157.242	1682.424	1452.442	1578.173	0.50811	7.30E-06	2.75E-05	TMEM214	chr2	+	27255778	27264563	2990
ENSG00000(	215.4447	196.2989	212.4256	200.0032	260.4823	172.6126	-0.01814	0.93055	0.95822	ATAD2B	chr2	-	23971534	24149984	8103
ENSG00000(	17.60846	15.65574	25.06886	25.46857	21.16994	22.19305	-0.23751	0.63708	0.74574	FKBP1B	chr2	+	24272571	24286551	1601
ENSG00000(	386.3504	373.3292	480.2666	847.9535	772.2424	698.6702	-0.90237	4.91E-09	2.53E-08	ATL2	chr2	-	38522022	38604427	2868
ENSG00000(	1349.637	1424.672	1358.996	296.6339	304.663	253.9872	2.2676	3.28E-64	1.26E-62	YPEL5	chr2	+	30369807	30383399	2560
ENSG00000(	1463.574	1441.532	1787.806	1035.971	1037.327	953.4793	0.6306	1.06E-06	4.40E-06	FAM98A	chr2	-	33808725	33824449	3546
ENSG00000(	521.0033	519.048	605.6109	477.9102	436.2848	531.8113	0.18442	0.22064	0.33241	YIPF4	chr2	+	32502979	32537002	7288
ENSG00000(	232.0174	230.019	222.9809	179.0291	232.8693	233.438	0.087781	0.64917	0.7556	AFTPH	chr2	+	64751465	64820139	4674
ENSG00000(	60.07593	57.80581	80.48424	305.6228	334.1168	308.2368	-2.2482	9.86E-25	1.20E-23	LGALSL	chr2	+	64681103	64688515	3539
ENSG00000(	383.243	334.792	364.1582	241.2023	170.2799	156.9953	0.92165	3.46E-06	1.35E-05	CNRIP1	chr2	-	68511303	68547183	1953
ENSG00000(	179.192	127.6545	104.2337	16.47966	15.64734	12.32947	3.1577	1.70E-19	1.68E-18	BCL11A	chr2	-	60678302	60780702	5942
ENSG00000(	131.5456	195.0946	164.9267	210.4902	147.2691	232.6161	-0.26645	0.25898	0.37775	CRIPT	chr2	+	46843555	46852881	1953
ENSG00000(	5.17896	0	2.638828	4375.35	3733.272	3926.526	-10.136	3.39E-99	2.54E-97	EPCAM	chr2	+	47572297	47614740	1724
ENSG00000(	1893.428	1922.043	2108.423	432.2166	383.8201	431.5316	2.2413	1.41E-72	6.43E-71	SLC17A5	chr6	-	74303102	74363878	3455
ENSG00000(	628.7257	517.8437	701.9281	594.766	472.1816	444.683	0.28776	0.085273	0.15374	OGFRL1	chr6	+	71998506	72011973	1711
ENSG00000(	642.191	634.6596	844.4248	704.8801	844.9566	668.2575	-0.06493	0.68043	0.78111	FAM178A	chr10	+	1.03E+08	1.03E+08	6894
ENSG00000(	267.2343	230.019	332.4923	737.8394	656.268	600.8564	-1.2631	1.42E-13	1.03E-12	IDE	chr10	-	94211441	94333833	5877
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	TECTB	chr10	+	1.14E+08	1.14E+08	2713
ENSG00000(	0	1.204288	1.319414	0.749076	1.840864	0	-0.02598	0.98471	NA	ELOVL3	chr10	+	1.04E+08	1.04E+08	1371
ENSG00000(	97.36444	60.21439	98.95603	15.73059	31.29469	12.32947	2.0769	2.38E-07	1.05E-06	IFIT3	chr10	+	91087651	91100728	2496
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	NKX2-3	chr10	+	1.01E+08	1.01E+08	2094

ENSG00000(	53.86118	49.3758	58.05421	0	0.920432	0	6.2768	4.27E-12	2.80E-11	IFIT2	chr10	+	91061712	91069033	3489
ENSG00000(	245.4827	216.7718	191.315	235.9588	266.9253	187.408	-0.07496	0.71323	0.80626	GPAM	chr10	-	1.14E+08	1.14E+08	6369
ENSG00000(	193.6931	160.1703	186.0373	233.7116	193.2907	154.5294	-0.10691	0.62375	0.73538	CUTC	chr10	+	1.01E+08	1.02E+08	1346
ENSG00000(	336.6324	315.5234	286.3128	5.243529	9.20432	8.219649	5.3073	3.42E-56	1.09E-54	PPP1R3C	chr10	-	93388199	93392811	2524
ENSG00000(	91.14969	115.6116	89.72014	27.7158	51.54419	73.97684	0.93978	0.006639	0.01604	PYROXD2	chr10	-	1E+08	1E+08	2865
ENSG00000(	3.107376	0	1.319414	16.47966	11.96562	18.08323	-2.9105	0.001089	0.003035	CNNM1	chr10	+	1.01E+08	1.01E+08	5959
ENSG00000(	419.4957	427.5221	405.06	202.2504	203.4155	183.2982	1.0845	4.15E-11	2.52E-10	MXI1	chr10	+	1.12E+08	1.12E+08	3470
ENSG00000(	561.3992	615.391	597.6944	913.1231	760.2768	834.2944	-0.49896	0.000254	0.00078	SMNDC1	chr10	-	1.12E+08	1.12E+08	2031
ENSG00000(	169.8699	169.8046	212.4256	190.2652	160.1552	186.586	0.035948	0.86166	0.91221	C10orf88	chr10	-	1.25E+08	1.25E+08	2991
ENSG00000(	280.6996	278.1905	240.1333	1603.022	1613.517	1638.176	-2.5944	2.14E-85	1.25E-83	HELLS	chr10	+	96305547	96373662	4987
ENSG00000(	1281.275	1293.405	1344.483	1406.015	1081.508	974.8504	0.17751	0.22324	0.3354	TCTN3	chr10	-	97423153	97453900	2739
ENSG00000(	381.1714	295.0505	419.5736	518.3603	523.7258	464.4102	-0.45795	0.006256	0.015199	FAM45A	chr10	+	1.21E+08	1.21E+08	2586
ENSG00000(	139.8319	139.6974	88.40072	66.66772	76.39586	60.8254	0.8479	0.002437	0.006392	AVPI1	chr10	-	99437181	99447080	1457
ENSG00000(	923.9264	935.7316	1186.153	808.2525	813.6619	715.1095	0.38006	0.007464	0.017871	WDR11	chr10	+	1.23E+08	1.23E+08	4954
ENSG00000(	616.2962	639.4768	614.8468	543.8288	498.8741	530.9893	0.2482	0.065953	0.1233	C10orf76	chr10	-	1.04E+08	1.04E+08	4119
ENSG00000(	61.11172	39.74149	47.4989	11.98521	16.56778	18.08323	1.6328	0.000183	0.000576	KCNIP2	chr10	-	1.04E+08	1.04E+08	2617
ENSG00000(	19.68005	18.06432	27.70769	9.737982	8.283888	2.465895	1.5694	0.014912	0.033324	CCDC147	chr10	+	1.06E+08	1.06E+08	3313
ENSG00000(	435.0326	441.9736	406.3794	1313.879	967.374	985.5359	-1.3437	3.06E-18	2.85E-17	GOT1	chr10	-	1.01E+08	1.01E+08	1947
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	C10orf95	chr10	-	1.04E+08	1.04E+08	1469
ENSG00000(	1.035792	4.817151	5.277655	0	0	0	2.9213	0.026641	0.056065	SFRP5	chr10	-	99526508	99531709	1836
ENSG00000(	727.1259	659.9497	919.6314	949.8278	1067.701	838.4042	-0.30787	0.047411	0.092684	GNA13	chr17	-	63006833	63052957	4922
ENSG00000(	0	7.225726	10.55531	522.1057	402.2288	433.1755	-5.754	9.04E-15	7.03E-14	HOXB8	chr17	-	46688739	46692478	1823
ENSG00000(	700.1953	708.1212	761.3018	606.7512	844.0361	602.5003	0.080043	0.6122	0.72568	KANSL1	chr17	-	44107282	44302733	9095
ENSG00000(	25.8948	6.021439	15.83297	88.39091	79.15715	91.23811	-2.3599	1.69E-08	8.32E-08	HOXB5	chr17	-	46668619	46671323	2041
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	CRHR1	chr17	+	43699267	43913194	2535
ENSG00000(	206.1226	179.4389	232.2168	170.7892	203.4155	178.3664	0.16034	0.42495	0.55541	HOXB3	chr17	-	46626232	46682274	4208
ENSG00000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	HOXB1	chr17	-	46605888	46608359	2020
ENSG00000(	1610.656	1766.69	1585.935	287.645	236.551	157.8173	2.8499	1.59E-58	5.33E-57	DUSP1	chr5	-	1.72E+08	1.72E+08	2019
ENSG00000(	1314.42	1484.887	1820.791	1777.556	1820.614	1564.199	-0.16062	0.24935	0.36661	PANK3	chr5	-	1.68E+08	1.68E+08	10506
ENSG00000(	156.4046	166.1917	127.9831	5332.669	4883.812	4603.004	-5.0222	1.04E-284	7.01E-282	MSX2	chr5	+	1.74E+08	1.74E+08	2241
ENSG00000(	142.9393	161.3746	241.4527	54.68252	46.0216	44.38611	1.8852	9.26E-12	5.90E-11	TEK	chr9	+	27109139	27230173	4760
ENSG00000(	119.1161	131.2674	114.789	259.9292	233.7897	195.6277	-0.91123	1.91E-05	6.86E-05	RCL1	chr9	+	4792869	4861064	2134
ENSG00000(	126.3666	196.2989	179.4403	423.9768	360.8093	289.3317	-1.0947	3.57E-07	1.55E-06	CAAP1	chr9	-	26840683	26892802	2791
ENSG00000(	3.107376	0	0	5.992604	2.761296	0	-0.93026	0.47272	0.60181	EQTN	chr9	-	27284656	27297137	1031
ENSG00000(	99.43602	109.5902	176.8014	699.6366	621.2916	580.3072	-2.297	1.83E-29	2.72E-28	MOB3B	chr9	-	27325207	27529779	6454
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	INSL4	chr9	+	5231419	5235304	1952
ENSG00000(	22.78742	14.45145	26.38828	2.996302	9.20432	13.15144	1.2554	0.051002	0.098791	MLANA	chr9	+	5890802	5910606	2415
ENSG00000(	8.286335	13.24716	18.47179	49.43899	17.48821	30.4127	-1.2463	0.024316	0.051704	CD274	chr9	+	5450503	5470566	3644
ENSG00000(	0	0	0	5.992604	4.60216	1.64393	-2.7795	0.032401	0.066477	IFNA6	chr9	-	21349834	21351377	1544
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	IFNA8	chr9	+	21409146	21410184	1039
ENSG00000(	95.29286	105.9773	164.9267	0	0	0	8.0134	5.35E-16	4.48E-15	GRIA2	chr4	+	1.58E+08	1.58E+08	5621
ENSG00000(	881.4589	948.9787	827.2724	2388.802	2039.677	2054.09	-1.2836	5.01E-25	6.19E-24	NUP43	chr6	-	1.5E+08	1.5E+08	3874
ENSG00000(	1438.715	1247.642	1253.443	2771.58	2319.489	2379.588	-0.92076	1.15E-13	8.35E-13	MTHFD1L	chr6	+	1.51E+08	1.51E+08	3604
ENSG00000(	321.0955	274.5776	324.5758	379.0322	324.9125	344.4033	-0.18812	0.25916	0.37791	LRP11	chr6	-	1.5E+08	1.5E+08	3260

ENSG00000(	14.50109	22.88147	21.11062	1.498151	0	4.109825	3.0192	0.000173	0.000546	CCDC170	chr6	+	1.52E+08	1.52E+08	5304
ENSG00000(	1166.302	1129.622	1204.625	1888.419	1771.832	1841.201	-0.65145	5.81E-09	2.98E-08	PCMT1	chr6	+	1.5E+08	1.5E+08	1984
ENSG00000(	181.2636	226.4061	241.4527	254.6857	290.8565	212.0669	-0.22374	0.26653	0.38656	PLEKHG1	chr6	+	1.51E+08	1.51E+08	7237
ENSG00000(	331.4534	319.1362	343.0476	403.0026	292.6974	281.112	0.02262	0.9018	0.93906	CYSTM1	chr5	+	1.4E+08	1.4E+08	1334
ENSG00000(	738.5196	758.7013	666.304	576.7882	672.8358	679.765	0.16606	0.23125	0.34466	WDR55	chr5	+	1.4E+08	1.4E+08	4080
ENSG00000(	162.6193	149.3317	138.5384	464.4268	530.1688	402.7628	-1.6223	9.31E-19	8.91E-18	ARAP3	chr5	-	1.41E+08	1.41E+08	5250
ENSG00000(	7.250543	14.45145	7.916483	0	0.920432	0	3.7973	0.000657	0.001894	PCDHB8	chr5	+	1.41E+08	1.41E+08	2711
ENSG00000(	186.4425	209.5461	219.0227	19.47596	48.7829	36.16646	2.5404	4.62E-18	4.28E-17	PCDHB10	chr5	+	1.41E+08	1.41E+08	3274
ENSG00000(	179.192	161.3746	221.6615	53.93344	44.18074	36.16646	2.0413	1.47E-14	1.13E-13	PCDHB14	chr5	+	1.41E+08	1.41E+08	2781
ENSG00000(	25.8948	24.08575	34.30476	4.494453	3.681728	2.465895	2.7987	1.23E-05	4.52E-05	PCDHB12	chr5	+	1.41E+08	1.41E+08	3406
ENSG00000(	0	6.021439	1.319414	0	2.761296	0.821965	0.68802	0.59343	0.70949	SLC25A2	chr5	-	1.41E+08	1.41E+08	1417
ENSG00000(	0	0	0	2.247227	0	6.575719	-2.1455	0.11198	0.1924	TNN	chr1	+	1.75E+08	1.75E+08	5008
ENSG00000(	399.8157	369.7163	374.7135	488.3973	389.3427	453.7246	-0.21839	0.16567	0.26434	MRPS14	chr1	-	1.75E+08	1.75E+08	2115
ENSG00000(	183.3352	222.7932	212.4256	289.8922	282.5726	262.2068	-0.43252	0.017619	0.038744	CENPL	chr1	-	1.74E+08	1.74E+08	2473
ENSG00000(	3.107376	2.408575	1.319414	0.749076	2.761296	0.821965	0.49869	0.68107	0.78162	TNFSF18	chr1	-	1.73E+08	1.73E+08	2008
ENSG00000(	13.46529	8.430014	6.597069	0	0	0	4.4621	0.000172	0.000542	SEC16B	chr1	-	1.78E+08	1.78E+08	3985
ENSG00000(	204.051	239.6533	237.4945	191.0143	203.4155	171.7907	0.26425	0.16942	0.26939	GORAB	chr1	+	1.71E+08	1.71E+08	2467
ENSG00000(	910.4611	902.0115	860.2578	1450.959	1188.278	1129.38	-0.49469	0.00024	0.000741	ACAT2	chr6	+	1.6E+08	1.6E+08	3180
ENSG00000(	3661.524	3745.335	3654.776	6578.381	5544.682	5563.059	-0.67606	9.88E-10	5.42E-09	TCP1	chr6	-	1.6E+08	1.6E+08	2499
ENSG00000(	0	0	0	0	0.920432	4.109825	-1.3831	0.30514	NA	TTLL2	chr6	+	1.68E+08	1.68E+08	2680
ENSG00000(	892.8526	798.4428	1130.738	781.2858	879.0126	685.5187	0.26527	0.091899	0.16355	SNX19	chr11	-	1.31E+08	1.31E+08	6535
ENSG00000(	0	0	0	0.749076	3.681728	4.93179	-2.3524	0.077187	0.14092	KCNJ5	chr11	+	1.29E+08	1.29E+08	5940
ENSG00000(	285.8786	307.0934	224.3003	352.8146	306.5039	308.2368	-0.24119	0.18246	0.28602	MSANTD2	chr11	-	1.25E+08	1.25E+08	3086
ENSG00000(	4.143168	0	1.319414	7.490755	19.32907	9.863579	-2.3109	0.013078	0.0296	TP53AIP1	chr11	-	1.29E+08	1.29E+08	2875
ENSG00000(	27.96638	13.24716	11.87472	11.98521	12.88605	10.68554	0.56053	0.35623	0.48572	ARR3	chrX	+	69488155	69501690	1298
ENSG00000(	794.4524	775.5613	699.2893	650.1976	459.2956	455.3686	0.53341	0.001149	0.003194	PDZD11	chrX	-	69506445	69510364	1043
ENSG00000(	96.32865	110.7945	106.8725	78.65293	66.2711	61.64737	0.59486	0.027696	0.057968	SLC10A7	chr4	-	1.47E+08	1.47E+08	3747
ENSG00000(	232.0174	276.9862	258.6051	1058.444	789.7307	778.4008	-1.7701	5.23E-26	6.73E-25	NUDCD1	chr8	-	1.1E+08	1.1E+08	4217
ENSG00000(	824.4904	918.8715	811.4395	1246.462	1192.88	1375.147	-0.57718	4.97E-06	1.91E-05	ENY2	chr8	+	1.1E+08	1.1E+08	2966
ENSG00000(	150.1898	187.8689	229.578	910.1268	850.4792	762.7834	-2.1499	1.90E-35	3.44E-34	MASTL	chr10	+	27443753	27475853	3623
ENSG00000(	1293.704	1236.803	1318.094	1062.189	1476.373	1101.433	0.080938	0.57345	0.69219	KIAA1217	chr10	+	23983675	24836772	7383
ENSG00000(	0	1.204288	0	0.749076	0.920432	0.821965	-0.45539	0.73631	NA	SEPT7P9	chr10	-	38671997	38691844	743
ENSG00000(	125.3308	96.34302	129.3026	125.0956	150.9508	143.0219	-0.25243	0.28607	0.4094	PLXDC2	chr10	+	20105168	20569286	2969
ENSG00000(	338.704	395.0064	369.4359	319.8553	306.5039	283.5779	0.27559	0.089484	0.16001	EPC1	chr10	-	32556679	32667726	7386
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	IQSEC3	chr12	+	175931	287626	7094
ENSG00000(	120.1519	134.8802	154.3714	315.3608	273.3683	249.0554	-1.0317	3.87E-07	1.67E-06	CCDC77	chr12	+	498439	551811	2371
ENSG00000(	344.9187	414.275	382.63	334.0877	364.4911	390.4333	0.067435	0.67515	0.77702	TAF12	chr1	-	28915835	28969597	1359
ENSG00000(	422.6031	335.9963	368.1164	214.2356	203.4155	147.9537	0.99004	3.44E-07	1.50E-06	ENOX1	chr13	-	43787654	44361044	2982
ENSG00000(	6.214751	15.65574	11.87472	0	0.920432	0	3.9831	0.00028	0.000856	TNFSF11	chr13	+	43136872	43182149	2198
ENSG00000(	180.2278	215.5675	139.8579	205.9958	193.2907	190.6959	-0.13688	0.52001	0.64594	MTRF1	chr13	-	41790505	41837742	2185
ENSG00000(	9.322127	7.225726	5.277655	14.98151	9.20432	13.15144	-0.71143	0.31471	0.44141	SPG20OS	chr13	+	36920568	36943738	566
ENSG00000(	5.17896	3.612863	0	5.992604	7.363456	4.93179	-0.85856	0.38696	0.51775	SOHLH2	chr13	-	36742345	36871979	2193
ENSG00000(	441.2474	419.0921	405.06	1439.723	1196.562	1295.417	-1.631	9.62E-34	1.66E-32	DNAJC15	chr13	+	43597339	43683045	2538
ENSG00000(	456.7842	404.6407	501.3772	1148.333	1187.357	878.6805	-1.2343	2.56E-15	2.06E-14	PROSER1	chr13	-	39584002	39612252	5168

ENSG00000(	1745.309	1941.312	1692.808	1845.722	1797.604	1525.567	0.057498	0.64265	0.7501	UFM1	chr13	+	38923986	38937140	2534
ENSG00000(	305.5586	325.1577	300.8263	487.6482	438.1256	447.1489	-0.55827	0.000289	0.000881	WBP4	chr13	+	41635410	41658137	2618
ENSG00000(	685.6942	659.9497	907.7567	712.3708	792.4919	647.7084	0.064862	0.67881	0.77983	ELF1	chr13	-	41506056	41635576	3566
ENSG00000(	119.1161	167.396	179.4403	114.6086	106.7701	114.2531	0.46473	0.05157	0.099767	SMAD9	chr13	-	37418968	37494902	5592
ENSG00000(	1116.584	1146.482	1468.508	3737.138	3323.68	2975.513	-1.4248	7.80E-25	9.56E-24	HSPH1	chr13	-	31710762	31736525	3612
ENSG00000(	77.68439	89.11729	112.1502	142.3244	165.6778	146.3098	-0.70242	0.004082	0.010295	KBTBD7	chr13	-	41763969	41768702	4734
ENSG00000(	524.1107	593.7138	427.4901	461.4305	338.719	432.3535	0.32449	0.064056	0.12019	ALG5	chr13	-	37523912	37574398	1154
ENSG00000(	378.064	457.6293	278.3963	1371.557	1025.361	1130.202	-1.6543	1.10E-20	1.15E-19	EXOSC8	chr13	+	37572953	37583750	2423
ENSG00000(	1872.712	1893.14	2157.242	3801.558	3677.126	3332.246	-0.86702	4.57E-14	3.41E-13	ETF1	chr5	-	1.38E+08	1.38E+08	3874
ENSG00000(	10929.68	10609.77	10853.5	6459.278	5935.866	5696.217	0.83915	9.64E-17	8.33E-16	TGFBI	chr5	+	1.35E+08	1.35E+08	4661
ENSG00000(	1049.257	1146.482	1343.163	890.6508	1128.45	1022.524	0.21755	0.1249	0.21051	FAM53C	chr5	+	1.38E+08	1.38E+08	4375
ENSG00000(	755.0923	759.9056	699.2893	302.6265	264.164	259.7409	1.4168	3.86E-22	4.27E-21	SIL1	chr5	-	1.38E+08	1.39E+08	1923
ENSG00000(	408.102	349.2434	412.9765	312.3645	480.4655	496.4668	-0.13757	0.46969	0.59888	PAIP2	chr5	+	1.39E+08	1.39E+08	2294
ENSG00000(	0	0	0	2.996302	0.920432	1.64393	-1.649	0.22411	NA	MYOT	chr5	+	1.37E+08	1.37E+08	2337
ENSG00000(	1008.861	1010.397	1157.126	1191.779	1589.586	1198.425	-0.32428	0.024629	0.052266	KDM3B	chr5	+	1.38E+08	1.38E+08	6813
ENSG00000(	663.9426	688.8526	515.8908	37.45378	72.71413	71.51095	3.349	2.71E-50	7.54E-49	EGR1	chr5	+	1.38E+08	1.38E+08	3138
ENSG00000(	3207.848	3365.984	3120.414	2903.417	2971.154	2964.005	0.13322	0.19262	0.29847	SERP1	chr3	-	1.5E+08	1.5E+08	3934
ENSG00000(	5.17896	9.634302	13.19414	330.3423	305.5834	275.3582	-4.9755	1.12E-44	2.65E-43	PLS1	chr3	+	1.42E+08	1.42E+08	3755
ENSG00000(	163.6551	203.5246	183.3985	304.1247	232.8693	230.1502	-0.47893	0.017786	0.039071	ZFP30	chr19	-	38104650	38183238	6090
ENSG00000(	275.5206	268.5562	308.7428	430.7184	367.2524	360.8426	-0.4427	0.008016	0.019043	NR2C1	chr12	-	95415669	95467479	2499
ENSG00000(	460.9274	523.8652	616.1662	1513.882	1233.379	1048.827	-1.2432	2.34E-14	1.77E-13	UTP20	chr12	+	1.02E+08	1.02E+08	9025
ENSG00000(	819.3114	885.1515	1021.226	3189.564	2840.453	2689.469	-1.6753	3.81E-39	7.71E-38	TMPO	chr12	+	98909290	98944157	4242
ENSG00000(	1246.058	1353.619	1490.938	1074.923	991.3053	913.203	0.45526	0.000397	0.001186	ARL1	chr12	-	1.02E+08	1.02E+08	3241
ENSG00000(	1065.83	1059.773	1062.128	87.64184	79.15715	78.08667	3.6878	3.45E-123	3.73E-121	GLT8D2	chr12	-	1.04E+08	1.04E+08	1880
ENSG00000(	177.1204	162.5788	155.6908	77.15478	46.94203	61.64737	1.3973	7.29E-08	3.39E-07	MTERFD3	chr12	-	1.07E+08	1.07E+08	3235
ENSG00000(	103.5792	98.75159	105.5531	356.56	313.8673	286.8658	-1.6284	5.19E-16	4.35E-15	SOCS2	chr12	+	93963590	93977263	3733
ENSG00000(	282.7712	283.0076	323.2564	536.3381	454.6934	492.357	-0.73836	3.20E-06	1.26E-05	NFYB	chr12	-	1.05E+08	1.05E+08	3512
ENSG00000(	240.3037	257.7176	222.9809	160.3022	156.4734	139.734	0.65642	0.000718	0.002061	CCDC53	chr12	-	1.02E+08	1.02E+08	945
ENSG00000(	1002.647	889.9686	1054.212	942.337	971.0558	877.0366	0.078452	0.54005	0.66339	APAF1	chr12	+	99038919	99129204	7055
ENSG00000(	323.1671	314.3191	364.1582	835.2192	728.9821	627.1592	-1.1271	1.29E-12	8.77E-12	DUSP4	chr8	-	29190581	29208185	5537
ENSG00000(	1727.701	1775.12	1489.618	1465.192	1029.043	1085.816	0.47788	0.001392	0.003813	CLU	chr8	-	27454434	27472548	3080
ENSG00000(	4966.622	5000.203	5218.282	3967.104	4074.752	4117.222	0.32014	0.001177	0.003262	TNFRSF10B	chr8	-	22877646	22926692	4146
ENSG00000(	1409.713	1333.147	1030.462	2179.81	1960.52	2269.445	-0.76151	3.25E-08	1.57E-07	SORBS3	chr8	+	22402499	22433301	3459
ENSG00000(	37.28851	56.60152	55.41538	277.158	344.2416	350.1571	-2.6904	2.47E-29	3.65E-28	PTK2B	chr8	+	27168999	27316903	4715
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CHRNA2	chr8	-	27317279	27337400	4066
ENSG00000(	194.7289	180.6432	192.6344	248.6931	177.6434	191.5178	-0.12265	0.55181	0.67278	PPP3CC	chr8	+	22298332	22398652	2189
ENSG00000(	326.2744	339.6091	254.6469	358.8072	302.8221	427.4218	-0.24041	0.19927	0.30689	PDLIM2	chr8	+	22435792	22455538	4592
ENSG00000(	2.071584	0	1.319414	74.90755	58.90765	39.45432	-5.0754	3.28E-11	2.01E-10	EPHX2	chr8	+	27348296	27403081	3140
ENSG00000(	317.9881	348.0392	347.0058	308.6191	296.3791	260.5629	0.22499	0.17584	0.27774	RNF170	chr8	-	42704780	42752433	4116
ENSG00000(	0	0	0	758.0645	508.9989	692.0945	-9.7259	2.42E-26	3.15E-25	NPPB	chr1	-	11917521	11918988	694
ENSG00000(	228.91	197.5032	273.1187	491.3936	451.0117	431.5316	-0.97214	2.26E-08	1.10E-07	UBIAD1	chr1	+	11333263	11356106	3646
ENSG00000(	2106.801	2100.278	2198.143	3973.846	3723.147	3558.286	-0.81227	1.97E-14	1.50E-13	TARDBP	chr1	+	11072414	11085796	2748
ENSG00000(	2.071584	0	3.958241	26.96672	23.93123	18.90519	-3.2095	4.88E-05	0.000166	TNFRSF8	chr1	+	12123434	12204264	3686
ENSG00000(	693.9806	638.2725	585.8197	1695.158	1338.308	1531.321	-1.2469	9.41E-20	9.41E-19	ZNF706	chr8	-	1.02E+08	1.02E+08	3502

ENSG0000(	654.6205	646.7025	787.69	2042.729	1779.195	1726.948	-1.4075	4.52E-26	5.84E-25	LYPLA1	chr8	-	54958938	55014577	2574
ENSG0000(	143.9751	164.9874	200.5509	1062.189	1218.652	1062.801	-2.7104	3.96E-64	1.52E-62	CRISPLD1	chr8	+	75896750	75946793	4287
ENSG0000(	791.345	759.9056	786.3706	642.7068	746.4703	757.0297	0.12366	0.35157	0.48133	COPS5	chr8	-	67955314	67996018	5691
ENSG0000(	206.1226	172.2131	229.578	517.6112	442.7278	407.6946	-1.1666	1.11E-10	6.56E-10	RDH10	chr8	+	74206847	74237516	3949
ENSG0000(	1.035792	3.612863	2.638828	3.745378	0	1.64393	0.29086	0.81057	0.87711	EPX	chr17	+	56270098	56282535	2708
ENSG0000(	284.8428	249.2876	270.4798	632.2198	624.9733	615.6517	-1.2142	3.78E-16	3.19E-15	AKAP1	chr17	+	55162453	55198710	4089
ENSG0000(	372.8851	311.9105	372.0747	570.0465	582.6335	504.6865	-0.64654	2.93E-05	0.000103	COIL	chr17	-	55015548	55038415	2650
ENSG0000(	678.4437	580.4667	720.3999	553.5668	715.1757	577.8413	0.10065	0.51342	0.6404	TRIM25	chr17	-	54965270	54991399	5734
ENSG0000(	678.4437	717.7555	717.7611	149.066	215.3811	179.1884	1.9553	1.43E-31	2.29E-30	SCPEP1	chr17	+	55055466	55084129	1942
ENSG0000(	667.05	655.1325	633.3186	405.9989	387.5019	355.9108	0.76465	6.10E-08	2.86E-07	SPOP	chr17	-	47676246	47755596	3088
ENSG0000(	5049.486	4603.992	4372.537	137.8299	159.2347	170.1467	4.8986	8.55E-301	6.27E-298	TBX2	chr17	+	59477257	59486827	5218
ENSG0000(	779.9513	694.874	654.4292	1117.621	844.0361	893.4759	-0.42165	0.00445	0.011132	SLC35B1	chr17	-	47778305	47786376	2487
ENSG0000(	77.68439	114.4073	84.44248	2.996302	7.363456	3.28786	4.2281	1.31E-18	1.24E-17	TBX4	chr17	+	59529765	59562471	3398
ENSG0000(	1754.631	1706.476	1675.656	2650.229	3829.918	4574.235	-1.1015	1.05E-11	6.65E-11	DYNLL2	chr17	+	56160776	56168592	2500
ENSG0000(	4.143168	0	0	3.745378	0	2.465895	-0.34832	0.79039	0.86277	TEX14	chr17	-	56634039	56769416	4927
ENSG0000(	88.04231	89.11729	91.03955	176.0328	174.8821	153.7074	-0.90586	8.06E-05	0.000266	FAM117A	chr17	-	47787694	47866542	2365
ENSG0000(	223.7311	227.6104	234.8557	945.3333	878.0921	900.8736	-1.9848	6.31E-44	1.46E-42	NCAPH	chr2	+	97001525	97039583	2952
ENSG0000(	0	0	0	107.1178	115.9744	104.3895	-7.4657	8.29E-14	6.09E-13	LRAT	chr4	+	1.56E+08	1.56E+08	5002
ENSG0000(	220.6237	187.8689	249.3692	410.4934	358.048	260.5629	-0.64325	0.001785	0.004801	KIAA0922	chr4	+	1.54E+08	1.55E+08	5017
ENSG0000(	36.25272	46.96722	32.98534	247.1949	177.6434	184.9421	-2.3672	1.01E-17	9.18E-17	MND1	chr4	+	1.54E+08	1.54E+08	968
ENSG0000(	18.64425	16.86003	13.19414	689.1495	499.7946	540.8529	-5.0801	6.27E-72	2.83E-70	TRIM6	chr11	+	5617339	5634188	3403
ENSG0000(	9.322127	2.408575	2.638828	5.243529	2.761296	8.219649	-0.13517	0.88529	0.92836	ABCC11	chr16	-	48200821	48281479	4862
ENSG0000(	371.8493	376.9421	459.156	426.9731	358.9685	310.7027	0.13653	0.43792	0.5675	PAPD5	chr16	+	50186829	50269221	7842
ENSG0000(	63.18331	78.2787	114.789	67.4168	127.94	111.7872	-0.26059	0.40911	0.53984	ADCY7	chr16	+	50280048	50352046	6213
ENSG0000(	739.5554	722.5726	659.7069	900.3888	770.4016	765.2493	-0.19855	0.14336	0.23514	CEP89	chr19	-	33369908	33462897	2903
ENSG0000(	511.6812	476.8979	558.112	25.46857	44.18074	37.81039	3.8342	5.43E-68	2.28E-66	TSHZ3	chr19	-	31765851	31840453	5176
ENSG0000(	15.53688	18.06432	14.51355	496.6371	464.8182	589.3488	-4.9541	3.63E-69	1.56E-67	ECHDC2	chr1	-	53361656	53392884	5817
ENSG0000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	TAS2R8	chr12	-	10958650	10959892	1243
ENSG0000(	13.46529	6.021439	7.916483	67.4168	57.06678	37.81039	-2.4569	8.79E-07	3.67E-06	PLBD1	chr12	-	14656595	14721283	2426
ENSG0000(	3.107376	1.204288	5.277655	0.749076	0	2.465895	1.1169	0.35903	0.48869	TAS2R10	chr12	-	10977916	10978957	1042
ENSG0000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	PRB2	chr12	-	11544476	11653975	1427
ENSG0000(	97.36444	102.3645	97.63662	90.63814	115.054	101.1017	-0.04264	0.8659	0.9154	PYROXD1	chr12	+	21590549	21623300	3639
ENSG0000(	4.143168	1.204288	2.638828	445.7	436.2848	478.3836	-7.0801	4.89E-44	1.14E-42	KCNJ8	chr12	-	21917889	21928515	2389
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	TAS2R7	chr12	-	10954131	10955226	1096
ENSG0000(	4.143168	0	1.319414	2.996302	0	11.50751	-1.0286	0.38396	0.51463	BCL2L14	chr12	+	12202778	12364018	2039
ENSG0000(	588.3298	579.2624	629.3604	956.5695	1027.202	1001.975	-0.73125	7.95E-09	4.02E-08	PSPC1	chr13	-	20248896	20357142	2407
ENSG0000(	170.9057	155.3531	112.1502	162.5494	176.7229	133.1583	-0.102	0.66514	0.76874	ZNF549	chr19	+	58038693	58068910	5505
ENSG0000(	35.21692	27.69862	34.30476	0.749076	0	0.821965	5.0881	4.82E-09	2.49E-08	A1BG	chr19	-	58856544	58864865	2301
ENSG0000(	105.6508	80.68728	118.7472	95.13259	130.7013	124.9387	-0.19836	0.44963	0.57944	ZSCAN18	chr19	-	58595205	58629794	5729
ENSG0000(	174.013	151.7403	176.8014	134.0845	140.8261	121.6508	0.3402	0.11292	0.19377	ZNF211	chr19	+	58141761	58154147	2759
ENSG0000(	5246.286	4867.731	5236.753	170.7892	229.1876	166.8589	4.7517	8.54E-267	4.78E-264	PDZRN3	chr3	-	73431584	73674091	4248
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RGSL1	chr1	+	1.82E+08	1.83E+08	5672
ENSG0000(	59.04014	56.60152	67.2901	46.44268	76.39586	65.75719	-0.04094	0.89983	0.9378	LHX4	chr1	+	1.8E+08	1.8E+08	7083
ENSG0000(	332.4892	320.3405	398.463	632.9688	548.5775	498.1107	-0.67573	3.39E-05	0.000118	RNF2	chr1	+	1.85E+08	1.85E+08	3606

ENSG0000(	313.8449	372.1249	460.4754	449.4453	439.0461	351.801	-0.11578	0.52324	0.64852	TRMT1L	chr1	-	1.85E+08	1.85E+08	4470
ENSG0000(	122.2234	232.4275	175.482	125.0956	118.7357	112.6092	0.56433	0.025506	0.053924	SEC22A	chr3	+	1.23E+08	1.23E+08	4228
ENSG0000(	7.250543	3.612863	0	8.988907	9.20432	8.219649	-1.0825	0.23252	0.34622	CSTA	chr3	+	1.22E+08	1.22E+08	821
ENSG0000(	1.035792	0	1.319414	1465.941	1208.527	1194.315	-9.6934	8.87E-45	2.10E-43	DPPA4	chr3	-	1.09E+08	1.09E+08	3043
ENSG0000(	23.82321	16.86003	26.38828	59.92604	43.2603	42.74218	-1.0976	0.008764	0.020644	POPDC2	chr3	-	1.19E+08	1.19E+08	1958
ENSG0000(	230.9816	211.9546	193.9538	424.7258	334.1168	352.623	-0.79877	9.46E-06	3.52E-05	B4GALT4	chr3	-	1.19E+08	1.19E+08	5794
ENSG0000(	1769.133	1790.776	2177.033	2616.521	2827.567	2693.579	-0.50389	2.93E-05	0.000102	NAA50	chr3	-	1.13E+08	1.13E+08	3601
ENSG0000(	1.035792	0	0	0	0	1.64393	-0.12526	0.92174	NA	CD80	chr3	-	1.19E+08	1.19E+08	2725
ENSG0000(	152.2614	105.9773	196.5927	478.6593	405.9105	371.5281	-1.4595	1.31E-11	8.24E-11	KIF18A	chr11	-	28042167	28129855	3568
ENSG0000(	1040.971	921.2801	1228.374	1443.469	1414.704	1226.372	-0.35608	0.01047	0.024233	DESI2	chr1	+	2.45E+08	2.45E+08	4208
ENSG0000(	845.2062	739.4327	704.567	425.4749	364.4911	340.2935	1.0151	2.00E-11	1.24E-10	MAPK8IP1	chr11	+	45907202	45928016	3180
ENSG0000(	489.9296	457.6293	471.0307	471.1685	469.4203	386.3235	0.096547	0.5261	0.65092	CRY2	chr11	+	45868669	45904798	4203
ENSG0000(	504.4307	464.8551	373.3941	359.5563	306.5039	390.4333	0.34552	0.044913	0.088448	PEX16	chr11	-	45931220	45940363	1639
ENSG0000(	35.21692	38.53721	51.45714	100.3761	60.74851	95.34793	-1.0274	0.00242	0.006355	DEPDC7	chr11	+	33037410	33055128	2012
ENSG0000(	753.0207	717.7555	803.523	168.542	176.7229	189.8739	2.0811	3.68E-43	8.38E-42	CAT	chr11	+	34460472	34493609	2302
ENSG0000(	446.4263	437.1564	332.4923	522.8547	612.0873	877.0366	-0.72086	0.000217	0.000673	PILRB	chr7	+	99933702	99965454	4345
ENSG0000(	831.7409	968.2473	1063.448	794.0201	935.1589	804.7037	0.1753	0.21248	0.32256	ZMYM2	chr13	+	20532810	20665968	10199
ENSG0000(	0	0	0	5.992604	0.920432	0.821965	-2.0618	0.12611	0.21212	GJB6	chr13	-	20796110	20806534	2131
ENSG0000(	29.00217	38.53721	29.0271	7.490755	23.0108	24.65895	0.78537	0.12741	0.21383	GJA3	chr13	-	20712394	20735188	5211
ENSG0000(	292.0933	328.7705	290.271	329.5932	311.106	288.5097	-0.02869	0.86333	0.91356	TBC1D15	chr12	+	72233487	72320629	5785
ENSG0000(	645.2984	632.2511	612.208	182.7744	196.052	161.1051	1.8026	1.98E-30	3.04E-29	BAI2	chr1	-	32192718	32230494	5403
ENSG0000(	3.107376	0	3.958241	2.996302	4.60216	4.109825	-0.57732	0.59856	0.71392	HCRTR1	chr1	+	32083287	32098119	2001
ENSG0000(	381.1714	367.3078	302.1458	773.046	605.6443	693.7384	-0.97536	1.06E-09	5.80E-09	ZCCHC17	chr1	+	31769842	31837783	1730
ENSG0000(	866.9578	840.5928	936.7838	114.6086	129.7809	226.8623	2.4738	1.06E-32	1.76E-31	FABP3	chr1	-	31838472	31849697	725
ENSG0000(	4197.029	4229.458	4197.055	4784.346	5162.703	4669.583	-0.2111	0.037281	0.075287	KHDRBS1	chr1	+	32479430	32526451	2757
ENSG0000(	436.0684	403.4364	378.6718	534.8399	368.1728	363.3085	-0.05624	0.75699	0.83923	TMEM39B	chr1	+	32537632	32568467	2087
ENSG0000(	0	0	0	5.992604	0	0	-1.4779	0.2718	0.39245	CCRL2	chr3	+	46448654	46451014	1796
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CCR2	chr3	+	46395225	46402419	2671
ENSG0000(	816.204	770.7441	738.8717	568.5483	546.7366	487.4252	0.53636	8.48E-05	0.000279	RNF115	chr1	+	1.46E+08	1.46E+08	3560
ENSG0000(	489.9296	456.425	402.4212	110.8632	103.0884	120.0069	2.0051	2.13E-28	3.05E-27	POLR3GL	chr1	-	1.45E+08	1.45E+08	1603
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	GHSR	chr3	-	1.72E+08	1.72E+08	1172
ENSG0000(	1.035792	0	0	1.498151	0	0	-0.08447	0.94679	NA	TNFSF10	chr3	-	1.72E+08	1.72E+08	1953
ENSG0000(	342.8471	396.2107	406.3794	405.9989	363.5706	334.5397	0.050633	0.75578	0.8384	ZNF639	chr3	+	1.79E+08	1.79E+08	3016
ENSG0000(	3.107376	2.408575	3.958241	0	0	3.28786	1.0599	0.39398	0.5248	SLITRK3	chr3	-	1.65E+08	1.65E+08	4555
ENSG0000(	513.7528	523.8652	692.6922	223.2245	278.8909	195.6277	1.3045	1.71E-12	1.15E-11	PIK3CA	chr3	+	1.79E+08	1.79E+08	9093
ENSG0000(	1341.351	1301.835	1794.403	1784.298	1686.231	1374.325	-0.12712	0.40087	0.53214	PDS5A	chr4	-	39824483	39979576	7176
ENSG0000(	0	0	0	0.749076	5.522592	0	-1.6448	0.22514	0.33776	TMEM156	chr4	-	38968365	39034542	1935
ENSG0000(	235.1248	303.4805	261.2439	332.5895	267.8457	344.4033	-0.24169	0.1895	0.29463	LIAS	chr4	+	39460620	39479273	1775
ENSG0000(	0	0	0	241.2023	266.0048	241.6577	-8.5177	8.57E-19	8.22E-18	CPXM2	chr10	-	1.25E+08	1.26E+08	3554
ENSG0000(	80.79177	71.05298	62.01245	686.9023	326.7534	466.8761	-2.7636	1.82E-27	2.50E-26	TMEM54	chr1	-	33360195	33367039	999
ENSG0000(	116.0087	124.0416	143.8161	64.4205	95.72493	111.7872	0.49292	0.068241	0.12695	ZSCAN20	chr1	+	33938246	33962107	4316
ENSG0000(	63.18331	67.44011	73.88717	14.98151	21.16994	16.4393	1.9243	5.05E-07	2.17E-06	CSMD2	chr1	-	33979609	34631443	13684
ENSG0000(	2.071584	1.204288	3.958241	5.992604	5.522592	9.041614	-1.2931	0.18116	0.28427	HPCA	chr1	+	33351595	33364042	1468
ENSG0000(	271.3775	307.0934	325.8952	408.2462	321.2308	307.4149	-0.19941	0.26492	0.38483	LRIF1	chr1	-	1.11E+08	1.12E+08	3475

ENSG00000(	804.8103	750.2712	756.0241	686.9023	704.1305	584.4171	0.22647	0.09676	0.1707	CLCC1	chr1	-	1.09E+08	1.1E+08	4825
ENSG00000(	253.769	260.1261	263.8828	261.4274	277.05	234.26	0.009422	0.95707	0.97462	GPSM2	chr1	+	1.09E+08	1.09E+08	3310
ENSG00000(	329.3818	290.2333	284.9934	191.0143	177.6434	164.393	0.76041	3.05E-05	0.000107	GTDC1	chr2	-	1.45E+08	1.45E+08	2954
ENSG00000(	7.250543	6.021439	1.319414	58.42789	36.81728	40.27628	-3.0205	2.39E-07	1.06E-06	CXCR4	chr2	-	1.37E+08	1.37E+08	1895
ENSG00000(	134.6529	150.536	164.9267	181.2763	212.6198	164.393	-0.31012	0.14666	0.23955	ZRANB3	chr2	-	1.36E+08	1.36E+08	6820
ENSG00000(	215.4447	202.3203	163.6073	152.0623	166.5982	133.1583	0.36509	0.086722	0.15593	ACVR2A	chr2	+	1.49E+08	1.49E+08	5728
ENSG00000(	274.4849	285.4162	315.3399	143.8225	167.5186	144.6658	0.93649	6.10E-07	2.59E-06	POLK	chr5	+	74807581	74896969	5911
ENSG00000(	0	0	0	12.73428	42.33987	22.19305	-5.4921	5.00E-07	2.15E-06	SV2C	chr5	+	75378997	75649764	7158
ENSG00000(	12776.49	13397.7	8851.947	13311.07	9310.17	10683.9	0.07246	0.65019	0.75641	RPL21	chr13	+	27825446	27830828	815
ENSG00000(	353.205	443.1779	287.6322	295.8848	287.1748	235.082	0.40475	0.036313	0.073498	MTIF3	chr13	-	28009776	28024739	1104
ENSG00000(	1313.384	1192.245	1066.086	1330.358	1017.077	1151.573	0.02975	0.83199	0.89247	GTF3A	chr13	+	27998681	28009958	1919
ENSG00000(	339.7397	249.2876	242.7721	99.62705	91.12277	131.5144	1.36	1.70E-09	9.13E-09	RASL11A	chr13	+	27844464	27847827	1543
ENSG00000(	996.4318	1051.343	1170.32	1855.46	1946.714	1626.669	-0.75351	2.55E-09	1.35E-08	UBL3	chr13	-	30338508	30424821	4384
ENSG00000(	1123.834	1175.385	1273.234	850.9498	901.1029	706.8898	0.5373	7.35E-05	0.000244	FYTTD1	chr3	+	1.97E+08	1.98E+08	3654
ENSG00000(	451.6053	498.5751	426.1707	370.7924	348.8437	346.0472	0.36783	0.015652	0.034784	MTERFD2	chr2	-	2.42E+08	2.42E+08	4529
ENSG00000(	7.250543	14.45145	3.958241	0	0	0.821965	3.5846	0.001797	0.004829	XPNPEP2	chrX	+	1.29E+08	1.29E+08	3270
ENSG00000(	1.035792	0	0	0	0	1.64393	-0.12526	0.92174	NA	SASH3	chrX	+	1.29E+08	1.29E+08	2626
ENSG00000(	821.383	817.7114	891.9237	847.2044	1068.622	981.4261	-0.1942	0.15041	0.24452	OCRL	chrX	+	1.29E+08	1.29E+08	5162
ENSG00000(	0	0	0	17.97781	9.20432	18.90519	-4.7979	2.09E-05	7.47E-05	PAEP	chr9	+	1.38E+08	1.38E+08	990
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	OBP2A	chr9	+	1.38E+08	1.38E+08	914
ENSG00000(	534.4686	519.048	452.5589	826.2303	579.8722	698.6702	-0.48119	0.002869	0.007435	MRPS2	chr9	+	1.38E+08	1.38E+08	1640
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	TBX22	chrX	+	79270255	79287268	2351
ENSG00000(	1860.282	1824.496	1806.277	8.239831	2.761296	3.28786	8.3899	1.30E-131	1.59E-129	FMOD	chr1	-	2.03E+08	2.03E+08	3310
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	LAX1	chr1	+	2.04E+08	2.04E+08	3023
ENSG00000(	0	4.817151	0	0	0.920432	3.28786	0.11502	0.93123	0.95867	PLG	chr6	+	1.61E+08	1.61E+08	2741
ENSG00000(	1939.002	1923.247	1971.204	1615.756	1477.293	1465.563	0.35484	0.001341	0.003686	KIAA1191	chr5	-	1.76E+08	1.76E+08	2991
ENSG00000(	7468.06	7447.315	7606.42	3559.607	3634.786	2915.51	1.1535	9.51E-24	1.12E-22	COPA	chr1	-	1.6E+08	1.6E+08	4789
ENSG00000(	0	1.204288	0	4.494453	8.283888	2.465895	-2.482	0.043192	0.085589	HS3ST2	chr16	+	22825498	22927659	2314
ENSG00000(	945.678	906.8287	1046.295	1065.935	1195.641	1000.331	-0.16997	0.19134	0.29698	RBBP6	chr16	+	24549014	24584184	6482
ENSG00000(	1015.076	1148.89	1143.932	991.776	1121.086	926.3545	0.12178	0.34907	0.47869	ZC3H7A	chr16	-	11844442	11891123	3845
ENSG00000(	118.0803	81.89156	129.3026	543.8288	396.7062	414.2703	-2.0298	1.50E-21	1.62E-20	SERAC1	chr6	-	1.59E+08	1.59E+08	4013
ENSG00000(	4534.697	4343.866	3921.298	3922.909	3722.227	3898.58	0.14899	0.16257	0.2605	ANXA11	chr10	-	81910645	81965328	6965
ENSG00000(	7.250543	8.430014	3.958241	11.23613	10.12475	14.79537	-0.80452	0.26897	0.38941	LDB3	chr10	+	88428206	88495825	5436
ENSG00000(	354.2408	387.7806	345.6864	519.8584	439.0461	389.6114	-0.30961	0.060878	0.11506	FAM35A	chr10	+	88854953	88951225	3609
ENSG00000(	1048.221	1134.439	1059.489	1232.978	1249.026	1426.931	-0.26939	0.02819	0.058855	FAM213A	chr10	+	82167585	82192753	2058
ENSG00000(	330.4176	346.8349	245.411	423.9768	412.3535	475.9177	-0.50384	0.003906	0.009893	ZNF205	chr16	+	3162561	3170518	2062
ENSG00000(	156.4046	208.3418	126.6637	240.4533	169.3595	186.586	-0.27784	0.23772	0.35245	NAA60	chr16	+	3493611	3536963	2735
ENSG00000(	23850.14	24872.15	19209.35	19860.99	14910.08	16400.67	0.40772	0.002416	0.006347	RPL5	chr1	+	93297582	93307481	1210
ENSG00000(	740.5912	783.9913	814.0783	718.3635	634.1776	666.6135	0.21016	0.10915	0.18834	ODF2L	chr1	-	86814344	86862023	5723
ENSG00000(	212.3373	257.7176	222.9809	11.98521	16.56778	1.64393	4.2486	5.22E-11	3.16E-10	PTGFR	chr1	+	78769568	79005434	4450
ENSG00000(	50.7538	38.53721	23.74945	3.745378	11.96562	4.93179	2.3651	3.84E-05	0.000132	SPATA1	chr1	+	84971974	85031877	1981
ENSG00000(	153.2972	168.6003	182.0791	206.7449	183.166	175.0785	-0.16703	0.41109	0.54181	TRMT13	chr1	+	1.01E+08	1.01E+08	3129
ENSG00000(	30.03797	10.83859	17.15238	13.48336	16.56778	13.9734	0.39124	0.4982	0.62654	LRRC39	chr1	-	1.01E+08	1.01E+08	1466
ENSG00000(	55.93276	51.78437	76.526	43.44638	39.57858	44.38611	0.51867	0.12847	0.21519	RWDD3	chr1	+	95699711	95712781	1538

ENSG00000(	467.1421	513.0266	604.2915	605.253	705.9713	587.7049	-0.26157	0.088198	0.15806	ZNF644	chr1	-	91380859	91487829	5698
ENSG00000(	94.25706	113.203	125.3443	202.9995	257.721	238.3698	-1.0671	1.02E-06	4.24E-06	CCDC18	chr1	+	93645476	93744287	4867
ENSG00000(	200.9436	213.1589	230.8974	267.42	242.994	244.1236	-0.22768	0.20952	0.31917	RPAP2	chr1	+	92764522	92853730	3110
ENSG00000(	1113.476	1075.429	944.7003	656.1902	647.0637	655.106	0.67743	1.34E-07	6.08E-07	PQLC1	chr18	-	77662420	77711664	2887
ENSG00000(	604.9025	523.8652	733.5941	244.9477	238.3919	198.0935	1.4435	1.17E-16	1.01E-15	NBPF14	chr1	-	1.48E+08	1.48E+08	3689
ENSG00000(	288.9859	311.9105	345.6864	486.8991	439.9665	369.0622	-0.45356	0.007652	0.018271	BBS9	chr7	+	33168856	33645680	4027
ENSG00000(	353.205	311.9105	361.5194	301.1284	332.276	381.3917	0.01706	0.9195	0.95104	PMS2	chr7	-	6012870	6048756	2855
ENSG00000(	1396.247	1378.909	1096.433	1404.517	1465.328	1592.146	-0.20331	0.12355	0.20872	ZMIZ2	chr7	+	44788180	44809477	5141
ENSG00000(	2568.764	2808.399	2980.556	3347.619	3312.635	2987.842	-0.20717	0.065635	0.12277	7-Sep	chr7	+	35840542	35944917	6976
ENSG00000(	201.9794	209.5461	150.4132	75.65663	114.1336	100.2797	0.95202	9.91E-05	0.000324	EEPD1	chr7	+	36192758	36341152	4765
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	KIAA0087	chr7	-	26572740	26578407	4283
ENSG00000(	597.6519	562.4024	614.8468	479.4084	444.5687	394.5432	0.42703	0.003505	0.008951	KLHL7	chr7	+	23145353	23215040	3304
ENSG00000(	356.3124	411.8664	416.9348	558.8104	585.3947	492.357	-0.46546	0.002325	0.006125	HERPUD2	chr7	-	35672269	35735181	3057
ENSG00000(	2495.223	2632.573	2694.243	4307.184	3488.437	4204.351	-0.61667	1.62E-07	7.31E-07	CBX3	chr7	+	26240782	26252976	2128
ENSG00000(	11453.79	11439.53	11472.3	16467.68	19994.54	23024.88	-0.78989	2.84E-10	1.62E-09	HNRNPA2B	chr7	-	26229547	26241149	6284
ENSG00000(	0	3.612863	6.597069	35.95563	31.29469	41.09825	-3.2442	1.41E-06	5.77E-06	WIPF3	chr7	+	29846102	29956682	4002
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	NXPH1	chr7	+	8473585	8792593	2921
ENSG00000(	3.107376	0	0	734.094	723.4595	801.4158	-8.6519	1.70E-41	3.66E-40	NPY	chr7	+	24323782	24331484	705
ENSG00000(	817.2398	806.8728	1157.126	657.6883	775.9242	534.2772	0.49644	0.004706	0.011721	FAM126A	chr7	-	22980878	23053749	6337
ENSG00000(	27.96638	30.10719	26.38828	4.494453	2.761296	9.041614	2.2389	0.000242	0.000745	HOXA7	chr7	-	27193335	27197555	2020
ENSG00000(	1152.836	1136.848	1548.992	358.8072	384.7406	335.3617	1.8247	2.14E-32	3.50E-31	INHBA	chr7	-	41724712	41742706	6064
ENSG00000(	5153.065	5031.514	4421.356	1609.014	1909.896	1680.918	1.4878	1.29E-36	2.41E-35	FKBP9	chr7	+	32997017	33046543	3462
ENSG00000(	288.9859	297.4591	316.6593	498.8843	422.4783	456.1905	-0.60901	0.000113	0.000365	NT5C3A	chr7	-	33053742	33102409	1788
ENSG00000(	559.3276	559.9938	529.0849	343.0766	322.1512	383.8576	0.64983	1.33E-05	4.87E-05	ARL4A	chr7	+	12726481	12730559	3162
ENSG00000(	243.4111	222.7932	201.8703	382.7776	209.8585	240.0138	-0.31641	0.16509	0.26364	CCZ1	chr7	+	5938356	5965605	2867
ENSG00000(	492.0012	527.478	422.2124	216.4828	214.4607	228.5062	1.1251	8.11E-12	5.20E-11	POLM	chr7	-	44111846	44122139	3218
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RAMP3	chr7	+	45197390	45225901	1323
ENSG00000(	486.8222	370.9206	378.6718	970.0528	904.7847	1012.661	-1.2174	3.35E-16	2.83E-15	FTSJ2	chr7	-	2273866	2281840	2511
ENSG00000(	5533.2	5161.577	4796.069	2686.185	3745.238	3367.59	0.65959	6.45E-07	2.73E-06	TWIST1	chr7	-	19060614	19157295	1666
ENSG00000(	1359.995	1377.705	1494.896	1856.209	1850.068	1757.361	-0.36816	0.001038	0.002905	SMU1	chr9	-	33041762	33076665	7122
ENSG00000(	801.7029	816.5071	763.9406	178.28	162.9165	169.3248	2.2146	1.61E-50	4.49E-49	GLIPR2	chr9	+	36136732	36163910	2702
ENSG00000(	302.4512	225.2018	287.6322	232.2134	220.9037	251.5213	0.20989	0.26199	0.38137	SLC25A51	chr9	-	37879400	37904350	1868
ENSG00000(	4965.586	4821.968	4446.424	5101.204	3981.789	4439.433	0.07377	0.53796	0.66184	CLTA	chr9	+	36190853	36304778	1890
ENSG00000(	566.5782	653.9282	734.9135	128.841	147.2691	102.7456	2.3578	3.98E-38	7.81E-37	RECK	chr9	+	36036430	36124448	4888
ENSG00000(	1488.433	1435.511	1641.351	537.8362	497.0333	448.7928	1.617	4.30E-35	7.73E-34	ACO1	chr9	+	32384618	32450834	3601
ENSG00000(	2.071584	0	0	0	0	3.28786	-0.2863	0.83232	NA	KIAA1045	chr9	+	34957484	34982541	5718
ENSG00000(	9.322127	8.430014	0	0.749076	6.443024	4.93179	0.47993	0.63826	0.74653	DNAI1	chr9	+	34457412	34520982	2499
ENSG00000(	508.5738	543.1338	584.5003	385.7739	373.6954	340.2935	0.57019	0.000127	0.000409	DCAF10	chr9	+	37800499	37867663	7801
ENSG00000(	0	0	0	5.243529	5.522592	18.08323	-4.0633	0.000663	0.001913	CNTFR	chr9	-	34551430	34590121	2052
ENSG00000(	357.3482	344.4263	445.9619	393.2647	433.5235	328.786	-0.01083	0.95051	0.97029	KIAA1549	chr7	-	1.39E+08	1.39E+08	12379
ENSG00000(	336.6324	362.4906	469.7113	988.0306	948.9654	800.5938	-1.2264	2.79E-14	2.10E-13	TRIM24	chr7	+	1.38E+08	1.38E+08	8410
ENSG00000(	265.1627	260.1261	329.8534	601.5077	565.1452	559.7581	-1.0129	1.67E-10	9.71E-10	C7orf49	chr7	-	1.35E+08	1.35E+08	2576
ENSG00000(	12723.67	12716.07	16045.39	9884.801	10552.75	8721.048	0.50752	5.04E-05	0.000171	CALD1	chr7	+	1.34E+08	1.35E+08	4544
ENSG00000(	0	1.204288	0	5.992604	0.920432	0.821965	-1.5698	0.23592	0.3503	AKR1D1	chr7	+	1.38E+08	1.38E+08	2347

ENSG00000(	24.85901	25.29004	17.15238	189.5161	200.6542	197.2716	-3.0776	1.45E-25	1.83E-24	NUDT10	chrX	+	51075083	51080377	2001
ENSG00000(	2.071584	0	0	2.247227	0	0	-0.04193	0.97501	NA	SFTPA1	chr10	+	81370695	81375196	2212
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	NEUROG3	chr10	-	71331454	71332994	1376
ENSG00000(	156.4046	160.1703	147.7743	683.906	543.0549	564.6899	-1.9401	2.11E-29	3.13E-28	PLAU	chr10	+	75668935	75677255	2658
ENSG00000(	119.1161	157.7617	139.8579	0	0	0	8.1967	5.82E-17	5.09E-16	SRGN	chr10	+	70847862	70864567	1208
ENSG00000(	751.9849	652.7239	868.1743	1108.632	1566.575	1160.614	-0.75228	2.93E-06	1.16E-05	CHST3	chr10	+	73724123	73773322	6970
ENSG00000(	633.9046	696.0783	668.9428	120.6012	132.5422	100.2797	2.4915	1.56E-49	4.27E-48	BICC1	chr10	+	60272900	60591195	5473
ENSG00000(	373.9209	316.7277	278.3963	773.046	620.3712	590.1708	-1.0272	1.48E-09	8.01E-09	CISD1	chr10	+	60028818	60049346	2479
ENSG00000(	19.68005	19.2686	11.87472	0	2.761296	0	3.6751	7.28E-05	0.000242	EGR2	chr10	-	64571756	64679660	2968
ENSG00000(	658.7637	581.671	583.1809	1069.68	867.0469	741.4124	-0.5523	0.000427	0.001268	ECD	chr10	-	74889913	74927853	3069
ENSG00000(	5841.866	6610.335	6195.967	960.3149	1003.271	907.4493	2.6952	4.81E-134	6.04E-132	P4HA1	chr10	-	74766975	74856732	2937
ENSG00000(	261.0196	284.2119	253.3274	201.5013	195.1316	159.4612	0.51953	0.006078	0.01481	SLC25A16	chr10	-	70242521	70287231	1766
ENSG00000(	363.563	343.222	350.9641	1844.973	1989.054	2195.468	-2.5046	1.24E-82	6.99E-81	ZWINT	chr10	-	58116989	58121036	1961
ENSG00000(	925.998	994.7417	1100.391	1424.742	1556.451	1560.089	-0.58761	1.86E-06	7.51E-06	VPS26A	chr10	+	70883268	70932617	3229
ENSG00000(	757.1639	676.8097	671.5816	1053.2	1069.542	1080.884	-0.6031	1.43E-06	5.83E-06	RBM19	chr12	-	1.14E+08	1.14E+08	4422
ENSG00000(	518.9317	435.9522	581.8615	704.131	851.3996	663.3257	-0.5281	0.000886	0.002505	CIT	chr12	-	1.2E+08	1.2E+08	8708
ENSG00000(	460.9274	380.5549	464.4337	364.0507	361.7298	330.4299	0.30528	0.054443	0.10467	IFT81	chr12	+	1.11E+08	1.11E+08	3108
ENSG00000(	100.4718	114.4073	110.8308	75.65663	83.75931	87.95025	0.39293	0.12438	0.20982	ACADS	chr12	+	1.21E+08	1.21E+08	1950
ENSG00000(	29.00217	18.06432	25.06886	18.72689	13.80648	13.9734	0.6082	0.24337	0.35935	HVCN1	chr12	-	1.11E+08	1.11E+08	2189
ENSG00000(	0	0	0	1.498151	0.920432	3.28786	-1.678	0.21598	NA	NME2P1	chr12	+	1.21E+08	1.21E+08	693
ENSG00000(	1799.171	1695.637	1492.257	1545.343	1880.443	2209.442	-0.17507	0.22419	0.33668	DDX54	chr12	-	1.14E+08	1.14E+08	4380
ENSG00000(	1202.554	1187.428	1723.154	728.8505	1195.641	769.3592	0.60782	0.001409	0.003851	MED13L	chr12	-	1.16E+08	1.17E+08	9530
ENSG00000(	211.3015	171.0089	196.5927	30.7121	29.45382	25.48091	2.7295	3.77E-24	4.51E-23	CDKN2C	chr1	+	51426417	51440305	2904
ENSG00000(	1555.759	1484.887	1744.265	1012.001	940.6815	840.0481	0.77447	1.59E-09	8.55E-09	RNF11	chr1	+	51701943	51739127	3084
ENSG00000(	1550.58	1677.573	2132.173	565.552	568.827	483.3154	1.7226	1.18E-31	1.90E-30	RASSF8	chr12	+	26111962	26232825	5510
ENSG00000(	566.5782	552.7681	554.1538	17.97781	23.0108	8.219649	5.0535	1.82E-86	1.09E-84	BHLHE41	chr12	-	26272959	26278060	3837
ENSG00000(	88.04231	90.32158	98.95603	3.745378	0.920432	8.219649	4.2541	1.77E-18	1.67E-17	SSPN	chr12	+	26274924	26452223	2788
ENSG00000(	981.9307	781.5827	1355.038	356.56	623.1325	366.5964	1.2051	3.00E-08	1.45E-07	ITPR2	chr12	-	26490342	26986131	10511
ENSG00000(	127.4024	156.5574	112.1502	286.1469	226.4263	221.1086	-0.88372	4.60E-05	0.000157	CCDC91	chr12	+	28286182	28732883	2738
ENSG00000(	146.0467	175.826	159.6491	64.4205	63.50981	80.55256	1.1962	1.17E-06	4.81E-06	NECAB1	chr8	+	91803778	91971636	5289
ENSG00000(	413.281	462.4465	596.375	580.5336	612.0873	440.5732	-0.15099	0.39962	0.53074	WWP1	chr8	+	87354967	87490649	4686
ENSG00000(	747.8418	757.497	741.5105	973.7982	834.8318	918.1348	-0.27922	0.029343	0.060987	ACOT9	chrX	-	23720370	23784592	3117
ENSG00000(	3924.616	4266.791	3357.908	2522.137	1727.651	2130.533	0.85331	4.87E-09	2.52E-08	PRDX4	chrX	+	23682379	23704516	1005
ENSG00000(	999.5392	950.183	779.7735	2678.694	1960.52	2445.346	-1.3713	5.98E-21	6.29E-20	DDX39A	chr19	-	14519631	14530192	1903
ENSG00000(	1507.077	1287.384	1095.113	1292.155	1191.039	1348.022	0.022737	0.86991	0.91835	PKN1	chr19	+	14543865	14582679	3518
ENSG00000(	4377.257	4361.93	3755.052	3767.85	3513.289	4335.865	0.10495	0.3847	0.51551	C19orf43	chr19	-	12841454	12845589	988
ENSG00000(	95.29286	108.3859	83.12307	341.5785	392.104	401.1189	-1.971	3.51E-23	4.03E-22	CD97	chr19	+	14491313	14519537	3188
ENSG00000(	69.39806	96.34302	56.73479	69.66403	45.10117	93.704	0.090664	0.78978	0.86243	WDR83	chr19	+	12777614	12786646	1480
ENSG00000(	2397.858	2126.772	2030.578	3236.755	3019.017	3518.01	-0.57476	1.01E-06	4.20E-06	GIPC1	chr19	-	14588572	14606944	2071
ENSG00000(	218.5521	254.1047	248.0498	438.2092	405.9105	423.3119	-0.81372	6.36E-07	2.69E-06	SPRYD7	chr13	-	50486842	50510626	3086
ENSG00000(	1137.3	1113.966	989.5603	706.3782	590.9173	732.3707	0.67319	8.94E-07	3.72E-06	EBPL	chr13	-	50234859	50265611	1026
ENSG00000(	217.5163	237.2447	242.7721	96.63075	150.0304	108.4994	0.97058	1.27E-05	4.66E-05	ATP7B	chr13	-	52506809	52585630	6638
ENSG00000(	1011.969	870.7	997.4768	1128.108	1365.921	1070.198	-0.30593	0.026466	0.055737	ZC3H13	chr13	-	46528600	46626894	8018
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	GUCY1B2	chr13	-	51568647	51654998	2871

ENSG00000(	923.9264	844.2057	948.6585	1438.974	1378.807	1168.834	-0.55212	2.44E-05	8.64E-05	NLN	chr5	+	65018023	65167553	8661
ENSG00000(	96.32865	87.913	122.7055	718.3635	566.0657	570.4437	-2.5876	1.93E-41	4.15E-40	CENPK	chr5	-	64813593	64858998	1734
ENSG00000(	1315.456	1324.716	1242.888	897.3925	759.3564	747.9881	0.68931	6.97E-08	3.25E-07	OPTN	chr10	+	13141449	13180291	3521
ENSG00000(	59.04014	49.3758	76.526	1217.997	1337.388	1418.711	-4.4131	3.44E-130	4.12E-128	ITIH5	chr10	-	7601232	7708961	6945
ENSG00000(	311.7734	245.6747	262.5633	323.6006	311.106	251.5213	-0.10969	0.55253	0.67343	ATF1	chr12	+	51157493	51214905	2181
ENSG00000(	184.371	197.5032	196.5927	397.01	264.164	313.9906	-0.75207	0.000147	0.000467	TSFM	chr12	+	58176372	58201854	2192
ENSG00000(	2.071584	0	6.597069	1.498151	10.12475	2.465895	-0.56197	0.60803	0.72217	ARHGAP9	chr12	-	57866038	57882597	2912
ENSG00000(	0	0	1.319414	0.749076	0.920432	2.465895	-0.8971	0.50767	NA	NCKAP1L	chr12	+	54891495	54937726	4720
ENSG00000(	206.1226	264.9433	174.1626	76.40571	54.30549	50.13986	1.8145	2.61E-12	1.74E-11	MMP19	chr12	-	56229217	56236750	3840
ENSG00000(	3792.034	3946.451	2914.585	2358.09	1969.724	2348.354	0.67253	8.92E-07	3.72E-06	PFDN5	chr12	+	53689075	53693234	1980
ENSG00000(	1104.154	1147.686	1190.111	604.504	478.6246	477.5616	1.1364	4.30E-16	3.62E-15	SPATS2	chr12	+	49760367	49921205	3318
ENSG00000(	90.1139	105.9773	97.63662	146.0697	145.4283	207.1352	-0.75882	0.001967	0.005245	ORMDL2	chr12	+	56211703	56215663	2141
ENSG00000(	97.36444	115.6116	65.97069	74.90755	71.7937	91.23811	0.22945	0.43235	0.5622	NR4A1	chr12	+	52416616	52453291	4837
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	PDE1B	chr12	+	54943134	54973023	4734
ENSG00000(	2.071584	0	5.277655	5.992604	1.840864	2.465895	-0.39901	0.72457	0.81513	HOXC13	chr12	+	54332535	54340328	2437
ENSG00000(	306.5944	367.3078	331.1729	1090.654	917.6707	1069.376	-1.6115	1.51E-28	2.18E-27	CDK2	chr12	+	56360553	56366568	2598
ENSG00000(	33469.54	33588.79	36242.98	2656.222	4101.445	3167.031	3.3709	1.63E-126	1.86E-124	LRP1	chr12	+	57522276	57607134	14897
ENSG00000(	51.7896	85.50443	46.17948	0	0	0	7.1128	4.65E-12	3.04E-11	HOXC11	chr12	+	54366910	54371427	3261
ENSG00000(	460.9274	351.652	374.7135	259.1801	332.276	437.2853	0.20775	0.30152	0.4266	C12orf44	chr12	+	52463030	52471278	1439
ENSG00000(	4.143168	0	0	45.69361	42.33987	53.42772	-4.5118	1.10E-09	6.01E-09	NFE2	chr12	-	54685895	54694905	1833
ENSG00000(	199.9078	174.6217	212.4256	108.616	162.9165	111.7872	0.61348	0.00776	0.018505	IKZF4	chr12	+	56401443	56432219	5229
ENSG00000(	324.2029	368.512	254.6469	353.5637	326.7534	370.7062	-0.14792	0.40724	0.53818	SMUG1	chr12	-	54558529	54582778	2607
ENSG00000(	1636.551	1409.017	1442.119	3121.398	2746.569	2733.855	-0.93643	3.21E-15	2.57E-14	TUBA1B	chr12	-	49521565	49525180	3198
ENSG00000(	248.5901	250.4918	225.6198	68.91495	57.98722	84.66239	1.762	7.15E-15	5.60E-14	METTL21B	chr12	+	58165275	58176324	2762
ENSG00000(	51.7896	83.09585	71.24834	47.19176	49.70333	36.98842	0.60977	0.071527	0.13225	KBTBD4	chr11	-	47593749	47600567	3079
ENSG00000(	2.071584	2.408575	9.235896	2.996302	1.840864	0.821965	0.99947	0.35683	0.48631	SARDH	chr9	-	1.37E+08	1.37E+08	3344
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	DBH	chr9	+	1.37E+08	1.37E+08	2763
ENSG00000(	388.422	363.6949	339.0893	860.6878	659.0293	693.7384	-1.0165	8.53E-11	5.08E-10	ATPAF1	chr1	-	47098409	47139539	4158
ENSG00000(	134.6529	108.3859	113.4696	734.8431	653.5067	568.7997	-2.4421	1.69E-41	3.65E-40	STIL	chr1	-	47715811	47779819	5225
ENSG00000(	277.5922	270.9647	228.2586	1308.635	1083.348	942.7938	-2.0925	6.15E-38	1.20E-36	HJURP	chr2	-	2.35E+08	2.35E+08	3050
ENSG00000(	16.57267	8.430014	22.43003	0	0	0	5.2155	4.02E-06	1.56E-05	IL13RA2	chrX	-	1.14E+08	1.14E+08	1498
ENSG00000(	1.035792	10.83859	14.51355	0	4.60216	3.28786	1.4584	0.14778	0.2409	COL10A1	chr6	-	1.16E+08	1.16E+08	3498
ENSG00000(	1751.524	1631.81	1967.246	2680.941	2480.564	2190.537	-0.45791	0.000261	0.000801	AMD1	chr6	+	1.11E+08	1.11E+08	3438
ENSG00000(	194.7289	189.0732	149.0938	725.1051	427.0804	572.9095	-1.6835	3.04E-16	2.57E-15	NDUFAF4	chr6	-	97337189	97345757	2399
ENSG00000(	204.051	178.2346	278.3963	275.6598	224.5854	178.3664	-0.04174	0.85355	0.9067	USP45	chr6	-	99880190	99969604	6255
ENSG00000(	128.4382	110.7945	163.6073	155.0586	218.1424	230.9721	-0.58133	0.014305	0.032125	PLP1	chrX	+	1.03E+08	1.03E+08	3133
ENSG00000(	0	1.204288	0	0	1.840864	0.821965	-0.461	0.73167	NA	SERPINA7	chrX	-	1.05E+08	1.05E+08	1878
ENSG00000(	7757.046	8004.9	8008.842	5587.355	5140.613	5141.391	0.58204	4.60E-09	2.38E-08	MORF4L2	chrX	-	1.03E+08	1.03E+08	2749
ENSG00000(	35.21692	45.76293	46.17948	26.21764	23.0108	9.863579	1.0686	0.020637	0.044597	RAB9B	chrX	-	1.03E+08	1.03E+08	3748
ENSG00000(	71.46964	55.39724	124.0249	756.5663	846.7974	581.9512	-3.1088	2.10E-40	4.40E-39	NRK	chrX	+	1.05E+08	1.05E+08	8064
ENSG00000(	418.4599	466.0593	687.4146	726.6033	821.9458	581.1292	-0.43793	0.021651	0.046564	FAM199X	chrX	+	1.03E+08	1.03E+08	7457
ENSG00000(	0	2.408575	0	11.98521	10.12475	1.64393	-2.5237	0.025104	0.053168	ESX1	chrX	-	1.03E+08	1.03E+08	1495
ENSG00000(	383.243	398.6192	362.8388	543.8288	421.5579	445.505	-0.30139	0.0604	0.11428	RAB9A	chrX	+	13707244	13728625	2039
ENSG00000(	328.346	317.932	349.6447	296.6339	327.6738	290.1536	0.12286	0.45044	0.58016	METTL8	chr2	-	1.72E+08	1.72E+08	2246

ENSG00000(	212.3373	272.169	300.8263	210.4902	210.7789	206.3132	0.31858	0.09865	0.17343	TTC21B	chr2	-	1.67E+08	1.67E+08	5482
ENSG00000(	188.5141	167.396	217.7033	135.5827	116.8949	119.1849	0.61936	0.004179	0.01052	NMI	chr2	-	1.52E+08	1.52E+08	2094
ENSG00000(	85.97073	90.32158	62.01245	0.749076	0	0	6.8201	9.98E-15	7.75E-14	TNFAIP6	chr2	+	1.52E+08	1.52E+08	1422
ENSG00000(	5.17896	3.612863	1.319414	0.749076	0	0	2.2702	0.079211	0.14412	ACVR1C	chr2	-	1.58E+08	1.58E+08	3385
ENSG00000(	249.6258	201.116	387.9077	232.9625	318.4695	212.8889	0.13172	0.58098	0.69903	BAZ2B	chr2	-	1.6E+08	1.6E+08	8289
ENSG00000(	481.6432	426.3179	550.1955	326.5969	355.2868	286.0438	0.5888	0.000389	0.001163	SLC36A1	chr5	+	1.51E+08	1.51E+08	5781
ENSG00000(	525.1465	593.7138	742.83	629.2235	845.877	674.0112	-0.20725	0.21617	0.327	LPGAT1	chr1	-	2.12E+08	2.12E+08	7782
ENSG00000(	7.250543	12.04288	7.916483	19.47596	15.64734	14.79537	-0.82924	0.19081	0.29628	BATF3	chr1	-	2.13E+08	2.13E+08	2357
ENSG00000(	98.40023	62.62296	77.84541	134.8336	119.6562	118.3629	-0.63236	0.017297	0.038119	G0S2	chr1	+	2.1E+08	2.1E+08	866
ENSG00000(	22.78742	37.33292	44.86007	129.5901	153.7121	111.7872	-1.8986	2.20E-09	1.17E-08	KCNJ2	chr17	+	68164814	68176189	5392
ENSG00000(	471.2853	408.2535	531.7238	666.6772	627.7346	579.4853	-0.40884	0.007012	0.016884	RAP2C	chrX	-	1.31E+08	1.31E+08	3896
ENSG00000(	248.5901	217.9761	248.0498	926.6065	670.0745	666.6135	-1.6569	1.71E-21	1.84E-20	EXOSC9	chr4	+	1.23E+08	1.23E+08	3882
ENSG00000(	538.6118	480.5108	504.0161	528.0983	432.603	457.0125	0.10273	0.49347	0.62242	PLA2G12A	chr4	-	1.11E+08	1.11E+08	5226
ENSG00000(	84.93494	73.46155	92.35896	115.3576	92.96363	96.99186	-0.28394	0.2847	0.40774	B9D2	chr19	-	41860326	41870078	1027
ENSG00000(	651.5131	619.0039	498.7384	543.8288	530.1688	660.0378	0.030298	0.84785	0.90301	ADCK4	chr19	-	41197434	41224112	2443
ENSG00000(	97.36444	119.2245	121.3861	104.1215	158.3143	115.8971	-0.1609	0.52825	0.65296	PFKFB2	chr1	+	2.07E+08	2.07E+08	7094
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	C4BPA	chr1	+	2.07E+08	2.07E+08	2243
ENSG00000(	0	1.204288	0	6.74168	8.283888	4.93179	-2.8822	0.014469	0.032436	C4BPB	chr1	+	2.07E+08	2.07E+08	1992
ENSG00000(	45.57484	40.94578	43.54065	38.20285	57.06678	54.24968	-0.19337	0.59012	0.70687	ZNF137P	chr19	+	53091758	53100660	1920
ENSG00000(	26.93059	20.47289	31.66593	159.5531	137.1444	129.8705	-2.4035	1.04E-14	8.07E-14	RAB38	chr11	-	87846410	87908635	1465
ENSG00000(	0	0	0	6.74168	1.840864	9.863579	-3.3875	0.00681	0.016427	GPR83	chr11	-	94110477	94134585	4282
ENSG00000(	226.8384	208.3418	250.6886	188.018	384.7406	252.3432	-0.26249	0.26826	0.38858	AGO2	chr8	-	1.42E+08	1.42E+08	3572
ENSG00000(	5025.662	4842.441	4354.065	868.9276	907.5459	929.6423	2.3902	9.52E-102	7.38E-100	MXD4	chr4	-	2249159	2264021	4228
ENSG00000(	45.57484	43.35436	43.54065	35.95563	53.38506	36.98842	0.072069	0.84558	0.90136	PMS2P5	chr7	+	74306894	74366314	1220
ENSG00000(	455.7484	375.7378	423.5318	1373.055	1071.383	1412.958	-1.6145	9.93E-27	1.32E-25	CKS2	chr9	+	91926113	91931618	613
ENSG00000(	5.17896	3.612863	1.319414	14.23244	10.12475	13.9734	-1.7057	0.035306	0.071693	DAW1	chr2	+	2.29E+08	2.29E+08	2476
ENSG00000(	1281.275	1215.126	1603.088	1746.844	1709.242	1541.184	-0.28582	0.033599	0.068611	ACSL3	chr2	+	2.24E+08	2.24E+08	5679
ENSG00000(	12623.2	11699.66	10436.56	6448.042	5068.819	5196.462	1.0541	3.91E-17	3.46E-16	CHPF	chr2	-	2.2E+08	2.2E+08	3013
ENSG00000(	744.7344	881.5386	701.9281	552.0687	429.8417	493.179	0.65524	1.86E-05	6.67E-05	DNPEP	chr2	-	2.2E+08	2.2E+08	2425
ENSG00000(	8.286335	7.225726	11.87472	70.4131	59.82808	80.55256	-2.8707	2.58E-10	1.48E-09	INHA	chr2	+	2.2E+08	2.2E+08	1468
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	MOGAT1	chr2	+	2.24E+08	2.24E+08	1048
ENSG00000(	1915.179	1925.656	1609.685	4925.921	5261.189	6071.855	-1.5729	9.23E-37	1.74E-35	OBSL1	chr2	-	2.2E+08	2.2E+08	5841
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	FAM124B	chr2	-	2.25E+08	2.25E+08	2594
ENSG00000(	1857.175	1804.023	1708.641	1200.768	1203.005	1302.814	0.53416	2.58E-06	1.02E-05	SLC12A4	chr16	-	67977377	68003504	4670
ENSG00000(	163.6551	136.0845	102.9143	145.3207	143.5874	185.7641	-0.23064	0.33954	0.46816	ENKD1	chr16	-	67696848	67701168	1579
ENSG00000(	17.60846	20.47289	11.87472	5.243529	14.72691	3.28786	1.0431	0.13329	0.22194	GCNT7	chr20	-	55066548	55100981	2064
ENSG00000(	1530.9	1421.06	1516.006	974.5473	995.9074	863.8851	0.65552	5.94E-08	2.78E-07	FAM210B	chr20	+	54933971	54943719	3046
ENSG00000(	0	1.204288	0	0	0	1.64393	-0.12916	0.91993	NA	FAM209A	chr20	+	55092243	55101198	911
ENSG00000(	537.576	503.3923	364.1582	121.3502	167.5186	156.9953	1.6514	2.04E-16	1.74E-15	SNX21	chr20	+	44462449	44471914	3106
ENSG00000(	2.071584	0	0	0.749076	0	0	0.47431	0.71145	NA	SLPI	chr20	-	43880880	43883205	596
ENSG00000(	4.143168	13.24716	1.319414	0.749076	3.681728	4.93179	0.84426	0.40176	0.53295	WFDC3	chr20	-	44376583	44420571	1000
ENSG00000(	773.7366	733.4112	736.2329	471.9176	491.5107	500.5766	0.61493	3.24E-06	1.27E-05	TTPAL	chr20	+	43104526	43123244	6234
ENSG00000(	948.7854	973.0645	1101.711	288.3941	389.3427	331.2519	1.5799	1.75E-25	2.21E-24	PREX1	chr20	-	47240790	47444420	6737
ENSG00000(	12.4295	13.24716	6.597069	74.90755	94.8045	70.68898	-2.8054	5.99E-11	3.60E-10	KCNS1	chr20	-	43720951	43729753	4538

ENSG00000(	1.035792	9.634302	7.916483	3.745378	6.443024	2.465895	0.46884	0.62	0.73225	SLC12A5	chr20	+	44650329	44688789	6041
ENSG00000(	0	3.612863	5.277655	50.93714	69.95283	60.8254	-4.1746	2.02E-11	1.26E-10	ARHGAP40	chr20	+	37230577	37279678	2841
ENSG00000(	735.4123	641.8854	658.3875	2021.755	2562.483	2748.651	-1.8428	2.71E-39	5.50E-38	SDC4	chr20	-	43953928	43977064	2613
ENSG00000(	583.1508	572.0367	820.6754	478.6593	643.382	376.4599	0.39666	0.045662	0.089719	NCOA3	chr20	+	46130601	46285621	7939
ENSG00000(	2300.494	2260.448	2093.91	1470.435	923.1933	934.5741	0.99523	1.53E-09	8.22E-09	PIGT	chr20	+	44044707	44054884	2235
ENSG00000(	6.214751	2.408575	3.958241	4.494453	1.840864	4.109825	0.22592	0.82083	0.88422	MATN4	chr20	-	43922085	43937169	2282
ENSG00000(	902.1747	782.787	889.2849	1187.285	1198.402	1138.421	-0.45189	0.000259	0.000794	NCOA5	chr20	-	44689624	44718591	3220
ENSG00000(	987.1097	985.1074	988.2409	1705.645	1682.55	1712.975	-0.78372	2.27E-12	1.51E-11	VAPB	chr20	+	56964178	57026157	7936
ENSG00000(	3.107376	4.817151	0	211.2393	197.8929	209.6011	-5.9675	6.02E-29	8.79E-28	PARD6B	chr20	+	49348081	49373332	4615
ENSG00000(	1998.043	2015.978	1694.127	1477.926	1349.353	1832.982	0.29201	0.036376	0.073611	ATP5E	chr20	-	57600522	57607437	3665
ENSG00000(	671.1932	644.2939	866.8549	316.859	420.6374	294.2634	1.0768	1.14E-09	6.22E-09	CHD6	chr20	-	40030741	40247133	10818
ENSG00000(	2244.561	2397.737	2373.625	1529.612	1987.213	1822.296	0.39355	0.001663	0.004489	PLCG1	chr20	+	39765600	39825427	5493
ENSG00000(	6.214751	10.83859	6.597069	50.93714	47.86246	42.74218	-2.4904	1.03E-06	4.27E-06	TOX2	chr20	+	42543492	42698256	2605
ENSG00000(	3410.863	3496.047	3665.331	3805.304	3341.168	3218.815	0.028155	0.80019	0.86983	SRSF6	chr20	+	42086568	42092245	3683
ENSG00000(	1.035792	4.817151	2.638828	6.74168	5.522592	5.753754	-0.9346	0.33646	0.46486	GDAP1L1	chr20	+	42875887	42909013	2265
ENSG00000(	616.2962	614.1867	902.479	448.6963	659.0293	449.6148	0.45141	0.018515	0.040479	ARFGEF2	chr20	+	47538427	47653230	8852
ENSG00000(	656.6921	723.7769	765.26	535.589	490.5903	340.2935	0.64741	0.000189	0.000593	ZNFX1	chr20	-	47854483	47894963	7371
ENSG00000(	0	2.408575	2.638828	0	0	0.821965	1.2658	0.35072	NA	EDN3	chr20	+	57875482	57901047	2655
ENSG00000(	1433.536	1593.273	1575.38	6301.973	4962.969	4644.924	-1.7858	1.36E-41	2.93E-40	CSE1L	chr20	+	47662849	47713489	3553
ENSG00000(	967.4296	773.1527	964.4915	646.4522	565.1452	506.3304	0.65258	1.44E-05	5.24E-05	RAB22A	chr20	+	56884752	56942563	8670
ENSG00000(	1502.934	1463.21	1147.89	12.73428	8.283888	7.397684	7.0808	2.40E-140	3.25E-138	PTGIS	chr20	-	48120411	48184683	5579
ENSG00000(	1995.971	1956.968	1940.858	2745.362	2628.754	2397.672	-0.39834	0.000291	0.000885	STAU1	chr20	-	47729878	47804904	3534
ENSG00000(	9.322127	9.634302	15.83297	2.247227	5.522592	12.32947	0.71973	0.35023	0.47991	CDH26	chr20	+	58533471	58609066	3182
ENSG00000(	632.8689	582.8753	501.3772	243.4496	264.164	290.9756	1.1025	9.42E-12	6.00E-11	SNAI1	chr20	+	48599536	48605423	1686
ENSG00000(	257.9122	190.2775	233.5362	315.3608	287.1748	279.4681	-0.36876	0.046684	0.091423	MOCS3	chr20	+	49575363	49577820	2458
ENSG00000(	1120.727	1014.01	1072.683	864.4332	729.9026	826.8967	0.40433	0.001658	0.004478	STX16	chr20	+	57226328	57254582	4937
ENSG00000(	83.89914	59.0101	117.4278	46.44268	48.7829	63.2913	0.70205	0.033268	0.068001	PPP4R1L	chr20	-	56806188	56884495	3593
ENSG00000(	763.3786	722.5726	711.164	17.22874	8.283888	13.9734	5.7202	1.16E-110	1.04E-108	PMEPA1	chr20	-	56223448	56286592	4845
ENSG00000(	1336.172	1198.266	1223.097	1352.081	1250.867	1442.548	-0.10607	0.38069	0.5114	RNF114	chr20	+	48552948	48570429	2440
ENSG00000(	732.3049	777.9699	744.1494	1065.935	967.374	937.04	-0.39752	0.001677	0.004524	DDX27	chr20	+	47835884	47860614	4929
ENSG00000(	0	1.204288	0	0	0	1.64393	-0.12916	0.91993	NA	RBPJL	chr20	+	43935491	43945803	1830
ENSG00000(	53.86118	51.78437	68.60952	119.103	105.8497	145.4878	-1.0812	0.000118	0.000379	BCAS4	chr20	+	49411431	49493714	1498
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	KCNK15	chr20	+	43374421	43379675	1320
ENSG00000(	19.68005	21.67718	21.11062	3.745378	8.283888	17.26126	1.0333	0.10176	0.17799	TP53TG5	chr20	-	44002526	44036529	1051
ENSG00000(	1.035792	0	0	0	0.920432	0.821965	-0.16752	0.89839	NA	PCK1	chr20	+	56136136	56141513	5074
ENSG00000(	40.39588	45.76293	52.77655	23.97042	20.2495	18.90519	1.1059	0.007152	0.017196	NEURL2	chr20	-	44517264	44519926	1278
ENSG00000(	298.3081	234.8361	321.937	450.1944	385.661	355.9108	-0.47798	0.007914	0.018835	MTRR	chr5	+	7851299	7906138	3274
ENSG00000(	85.97073	77.07441	88.40072	129.5901	106.7701	125.7606	-0.52331	0.038495	0.077422	FASTKD3	chr5	-	7859272	7869150	2402
ENSG00000(	1345.494	1203.083	1066.086	671.1717	542.1344	576.1974	1.0114	1.36E-12	9.22E-12	PEPD	chr19	-	33877856	34012700	1901
ENSG00000(	1.035792	8.430014	3.958241	26.96672	16.56778	12.32947	-1.9047	0.011324	0.026004	CHST8	chr19	+	34112861	34264413	2478
ENSG00000(	211.3015	214.3632	219.0227	17.22874	44.18074	18.90519	2.9844	3.39E-22	3.76E-21	IQSEC2	chrX	-	53262058	53350522	6011
ENSG00000(	559.3276	637.0682	723.0388	618.7364	514.5215	495.6448	0.23369	0.13332	0.22195	VAMP7	chrX	+	1.55E+08	1.55E+08	2646
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	IL9R	chrX	+	1.55E+08	1.55E+08	2278
ENSG00000(	23.82321	42.15007	21.11062	0.749076	11.04518	3.28786	2.3874	0.000517	0.001516	XG	chrX	+	2670091	2734539	2887

ENSG00000(	646.3341	628.6382	696.6505	789.5256	717.937	694.5604	-0.15999	0.231	0.34435	STAMBP	chr2	+	74056086	74100786	6691
ENSG00000(	1804.349	1961.785	1576.699	809.7507	839.434	1013.483	1.0025	2.43E-13	1.74E-12	NAGK	chr2	+	71291474	71306935	4388
ENSG00000(	172.9772	150.536	120.0667	68.16587	68.11197	89.59418	0.96782	0.000191	0.000598	MCEE	chr2	-	71336814	71357369	836
ENSG00000(	7.250543	0	1.319414	24.71949	34.05598	26.30288	-2.9707	5.09E-05	0.000173	PAIP2B	chr2	-	71409869	71454213	6279
ENSG00000(	355.2766	372.1249	353.6029	408.2462	321.2308	351.801	-0.00182	0.99114	0.99478	SNRNP27	chr2	+	70120692	70132707	1802
ENSG00000(	634.9404	720.1641	601.6527	756.5663	636.0185	745.5222	-0.12801	0.36872	0.49901	MPHOSPH1	chr2	+	71357444	71377231	2484
ENSG00000(	2.071584	1.204288	2.638828	0	2.761296	0	0.7081	0.58963	0.70661	IL17C	chr16	+	88704999	88706881	1044
ENSG00000(	87.00652	116.8159	134.5802	53.18436	62.58938	50.96182	1.0072	0.000474	0.001399	ATP8A1	chr4	-	42410390	42659122	8270
ENSG00000(	4088.271	3856.129	3908.104	3099.675	3904.473	3515.544	0.17215	0.13904	0.2295	USP22	chr17	-	20902910	20947073	5216
ENSG00000(	3.107376	0	0	113.1104	165.6778	107.6774	-6.2084	2.13E-18	2.00E-17	POF1B	chrX	-	84532402	84634748	3941
ENSG00000(	709.5175	830.9585	544.9179	14.23244	8.283888	13.15144	5.7873	1.72E-93	1.17E-91	HIF3A	chr19	+	46800303	46846690	5908
ENSG00000(	133.6172	169.8046	112.1502	158.804	171.2004	142.1999	-0.18104	0.43405	0.56385	ZNF576	chr19	+	44100544	44105309	2566
ENSG00000(	292.0933	283.0076	294.2293	188.018	221.8241	184.1201	0.54865	0.002328	0.006133	ZNF45	chr19	-	44416781	44439430	3898
ENSG00000(	2.071584	1.204288	7.916483	50.93714	57.06678	41.09825	-3.5787	5.27E-09	2.71E-08	LYPD3	chr19	-	43964939	43969812	1694
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	PSG8	chr19	-	43256838	43359843	2478
ENSG00000(	0	0	0	1.498151	3.681728	3.28786	-2.2375	0.093716	0.16626	CEACAM8	chr19	-	43084393	43099207	2305
ENSG00000(	0	12.04288	0	0	0.920432	0	2.1276	0.10871	0.1878	NDP	chrX	-	43808022	43832750	1833
ENSG00000(	1247.093	1066.999	1671.697	1237.473	1304.252	1068.554	0.14162	0.37814	0.50885	USP9X	chrX	+	40944888	41093672	10241
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	F13A1	chr6	-	6144318	6321246	3999
ENSG00000(	29.00217	42.15007	43.54065	16.47966	9.20432	14.79537	1.4411	0.002763	0.007184	GRM4	chr6	-	33989628	34123399	3879
ENSG00000(	458.8558	455.2208	469.7113	256.1838	347.0029	270.4265	0.66304	8.07E-05	0.000266	TRERF1	chr6	-	42192669	42419789	7646
ENSG00000(	1.035792	0	3.958241	17.97781	19.32907	13.9734	-2.9938	0.000586	0.001705	PACSIN1	chr6	+	34433916	34503006	4271
ENSG00000(	412.2452	466.0593	390.5465	103.3724	117.8153	142.1999	1.7965	2.76E-21	2.95E-20	BTN2A2	chr6	+	26383324	26395102	3590
ENSG00000(	122.2234	92.73015	101.5949	182.0254	152.7917	146.3098	-0.5973	0.011211	0.025785	SIRT5	chr6	+	13574826	13612524	2339
ENSG00000(	2.071584	2.408575	1.319414	2.996302	3.681728	2.465895	-0.50417	0.654	0.75968	HIST1H4B	chr6	-	26027124	26027480	357
ENSG00000(	199.9078	191.4817	226.9392	1766.32	1767.229	1514.059	-3.0228	1.05E-98	7.83E-97	MRS2	chr6	+	24403153	24425810	3313
ENSG00000(	783.0587	809.2813	709.8446	928.1046	1001.43	927.1764	-0.30974	0.01489	0.033285	WRNIP1	chr6	+	2765648	2787186	3239
ENSG00000(	931.1769	863.4743	874.7713	1715.383	1375.125	1520.635	-0.7869	9.16E-10	5.03E-09	RRP36	chr6	+	42989383	42997335	1159
ENSG00000(	130.5098	148.1274	170.2044	18.72689	34.97642	20.54912	2.5714	2.42E-16	2.05E-15	BTN2A3P	chr6	+	26421619	26432611	2559
ENSG00000(	2.071584	2.408575	0	0	0	0	1.5041	0.26224	NA	BTN1A1	chr6	+	26501449	26510650	2895
ENSG00000(	1461.502	1435.511	1018.587	2641.24	1973.406	2216.017	-0.7995	2.93E-07	1.29E-06	SNRPC	chr6	+	34725183	34741571	1054
ENSG00000(	1314.42	1310.265	1062.128	420.9805	383.8201	400.2969	1.6091	7.10E-31	1.11E-29	SERPINB6	chr6	-	2948393	2972090	3265
ENSG00000(	883.5305	888.7643	928.8673	2089.172	1892.408	1692.426	-1.069	1.08E-17	9.82E-17	XPO5	chr6	-	43490072	43543812	5360
ENSG00000(	812.0609	753.8841	854.9801	563.3048	637.8594	733.1927	0.32298	0.024794	0.052579	ABCC10	chr6	+	43395104	43418168	5088
ENSG00000(	4.143168	1.204288	3.958241	0.749076	7.363456	7.397684	-0.59692	0.56224	0.6822	HIST1H1D	chr6	-	26234440	26235216	777
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	HIST1H4G	chr6	-	26246886	26247259	374
ENSG00000(	734.3765	858.6571	587.1391	409.7443	503.4763	566.3338	0.55836	0.001261	0.00348	PEX6	chr6	-	42931608	42946958	3478
ENSG00000(	330.4176	260.1261	236.1751	141.5753	135.3035	138.0901	0.99138	9.88E-07	4.10E-06	NQO2	chr6	+	2988221	3019996	1515
ENSG00000(	152.2614	156.5574	120.0667	80.90016	82.83888	61.64737	0.92243	0.000322	0.000974	PRICKLE4	chr6	+	41748087	41757879	3947
ENSG00000(	204.051	243.2661	254.6469	388.7702	436.2848	471.8079	-0.88432	3.03E-07	1.33E-06	OARD1	chr6	-	41001366	41065526	3330
ENSG00000(	2.071584	4.817151	1.319414	20.97412	21.16994	25.48091	-2.7848	0.000173	0.000546	UNC5CL	chr6	-	40994772	41006928	2986
ENSG00000(	704.3385	709.3255	595.0556	623.2309	698.6079	749.632	-0.04284	0.76441	0.84443	AARS2	chr6	-	44267391	44281063	3854
ENSG00000(	59.04014	75.87013	63.33186	64.4205	71.7937	59.18147	0.020384	0.94658	0.96771	ZNF391	chr6	+	27342394	27371683	4079
ENSG00000(	31.07376	25.29004	44.86007	77.90386	42.33987	59.18147	-0.81789	0.035892	0.072751	RPS10	chr6	-	34385231	34393902	781

ENSG0000(	193.6931	157.7617	154.3714	174.5346	231.0284	172.6126	-0.18684	0.38734	0.51813	MOCS1	chr6	-	39867354	39902290	4256
ENSG0000(	83.89914	67.44011	79.16483	98.87797	92.96363	97.81383	-0.32545	0.22454	0.33692	HIST1H2BJ	chr6	-	27094058	27100541	718
ENSG0000(	263.0911	329.9748	331.1729	493.6408	423.3987	471.8079	-0.5886	0.000366	0.001099	MED20	chr6	-	41873092	41888877	2602
ENSG0000(	3.107376	2.408575	3.958241	18.72689	7.363456	16.4393	-1.9596	0.015354	0.0342	OR2B6	chr6	+	27925019	27925960	942
ENSG0000(	322.1313	409.4578	321.937	429.9694	337.7985	424.9559	-0.17973	0.30357	0.42865	TBCC	chr6	-	42712219	42714558	2137
ENSG0000(	4.143168	0	5.277655	0.749076	3.681728	4.109825	0.1154	0.91888	0.95073	SPDEF	chr6	-	34505579	34524110	1895
ENSG0000(	1.035792	2.408575	0	0.749076	0.920432	1.64393	0.041603	0.97491	0.98535	TCP11	chr6	-	35085848	35116387	2166
ENSG0000(	278.628	337.2006	245.411	501.8806	370.0137	438.1073	-0.60282	0.000955	0.002685	MAD2L1BP	chr6	+	43597277	43608689	1517
ENSG0000(	12.4295	7.225726	6.597069	4.494453	23.93123	16.4393	-0.69539	0.33401	0.46205	HIST1H3B	chr6	-	26031817	26032288	472
ENSG0000(	0	3.612863	3.958241	0.749076	2.761296	2.465895	0.24048	0.84103	0.89827	APOBEC2	chr6	+	41021043	41032250	1151
ENSG0000(	1751.524	1771.507	1497.535	2138.611	2119.755	2697.689	-0.46889	0.000437	0.001295	KLHDC3	chr6	+	42981951	42989036	1909
ENSG0000(	5.17896	10.83859	7.916483	0	7.363456	9.041614	0.47823	0.60427	0.71923	GNMT	chr6	+	42928496	42931618	1072
ENSG0000(	0	0	0	1.498151	1.840864	2.465895	-1.7134	0.20614	NA	DNAH8	chr6	+	38683117	38998301	14215
ENSG0000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	TREM1	chr6	-	41235664	41254457	2048
ENSG0000(	751.9849	686.444	694.0116	617.2383	841.2748	1136.777	-0.28132	0.12871	0.21551	MEA1	chr6	-	42979832	42981706	1089
ENSG0000(	9.322127	1.204288	17.15238	9.737982	6.443024	1.64393	0.54835	0.53501	0.65921	KLHL31	chr6	-	53512699	53530506	5743
ENSG0000(	622.5109	694.874	699.2893	111.6123	79.15715	110.9653	2.723	9.58E-53	2.82E-51	COL21A1	chr6	-	55921388	56258892	4339
ENSG0000(	19874.78	18711.02	18535.12	7138.69	6748.607	6761.483	1.4661	1.75E-51	5.03E-50	CDKN1A	chr6	+	36644305	36655116	2261
ENSG0000(	4500.516	4339.049	4611.351	734.8431	1169.869	1064.445	2.1739	4.06E-47	1.02E-45	SOX4	chr6	+	21593972	21598847	4876
ENSG0000(	2708.596	2737.346	2884.239	3835.267	3149.718	2975.513	-0.2577	0.035786	0.07256	GLO1	chr6	-	38643701	38670917	2012
ENSG0000(	1.035792	1.204288	0	2.247227	0	0	-0.00597	0.99648	NA	CPNE5	chr6	-	36708552	36807778	3897
ENSG0000(	858.6715	862.27	880.049	915.3703	1259.151	952.6573	-0.26426	0.070429	0.13042	RREB1	chr6	+	7107830	7252213	9067
ENSG0000(	4086.199	4237.888	4558.575	2589.554	2269.785	2216.017	0.86263	2.01E-14	1.53E-13	SSR1	chr6	-	7268539	7347679	9669
ENSG0000(	408.102	302.2762	390.5465	810.4997	613.0077	604.1442	-0.87759	4.36E-07	1.88E-06	RIOK1	chr6	+	7389729	7418270	2810
ENSG0000(	586.2582	500.9837	500.0578	7.490755	11.96562	12.32947	5.5942	8.30E-85	4.82E-83	NRN1	chr6	-	5998232	6007200	1624
ENSG0000(	464.0348	422.705	526.4461	402.2536	380.1384	401.1189	0.25376	0.097894	0.17226	SLC35B3	chr6	-	8413301	8435794	2137
ENSG0000(	163.6551	151.7403	131.9414	168.542	131.6218	126.5826	0.068032	0.76531	0.84506	RPP40	chr6	-	4994966	5004297	1483
ENSG0000(	991.2529	981.4945	1080.6	423.9768	673.7562	488.2472	0.94301	1.54E-08	7.62E-08	ATXN1	chr6	-	16299343	16761722	10602
ENSG0000(	898.0316	942.9573	1025.185	1647.217	2018.507	1602.832	-0.87646	3.93E-11	2.40E-10	NUP153	chr6	-	17615269	17706656	5487
ENSG0000(	1108.297	910.4415	1310.178	3639.009	3489.358	3204.841	-1.6306	3.55E-32	5.76E-31	DEK	chr6	-	18224099	18265054	3427
ENSG0000(	53.86118	61.41867	58.05421	165.5457	92.96363	174.2566	-1.308	1.09E-05	4.01E-05	EEF1E1	chr6	-	8073593	8102811	1077
ENSG0000(	931.1769	1000.763	935.4644	203.7485	233.7897	185.7641	2.1969	4.30E-50	1.19E-48	RUNX2	chr6	+	45295894	45632086	5698
ENSG0000(	0	4.817151	0	2.996302	1.840864	0	-0.00966	0.99417	0.99629	OPN5	chr6	+	47749718	47800516	3500
ENSG0000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	GCM2	chr6	-	10873456	10882174	2441
ENSG0000(	1162.159	1145.278	1147.89	1377.55	1437.715	1332.405	-0.26277	0.021046	0.045426	LRRFIP1	chr2	+	2.39E+08	2.39E+08	4370
ENSG0000(	0	0	2.638828	0	2.761296	0	-0.03456	0.97961	NA	AC105760.	chr2	-	2.38E+08	2.38E+08	2231
ENSG0000(	4.143168	1.204288	0	14.98151	10.12475	14.79537	-2.4591	0.006324	0.015353	RAB17	chr2	-	2.38E+08	2.39E+08	3211
ENSG0000(	101.5076	115.6116	98.95603	8.239831	6.443024	9.041614	3.6461	4.23E-20	4.29E-19	CXCL6	chr4	+	74702214	74714781	1718
ENSG0000(	36.25272	14.45145	29.0271	101.8743	118.7357	87.12828	-1.9045	1.13E-07	5.16E-07	EREG	chr4	+	75230860	75254468	4619
ENSG0000(	0	0	0	4.494453	0	0.821965	-1.4611	0.2797	NA	TRIM51	chr11	+	55650773	55659286	1629
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-467L	chr11	-	61513965	61525127	2466
ENSG0000(	89.0781	104.773	98.95603	37.45378	45.10117	38.63235	1.2585	2.66E-05	9.38E-05	MYRF	chr11	+	61520114	61555990	5927
ENSG0000(	22503.61	21733.78	30102.43	19191.32	30161.64	26064.51	-0.02069	0.89733	0.93631	AHNAK	chr11	-	62201016	62323707	18787
ENSG0000(	1148.693	1079.042	1062.128	952.8241	754.7542	703.602	0.4466	0.001771	0.004763	EMC3	chr3	-	10004221	10052800	2777

ENSG00000(	1.035792	0	0	2.247227	3.681728	5.753754	-2.176	0.086114	0.15498	SSUH2	chr3	-	8661086	8786726	3219
ENSG00000(	9.322127	10.83859	7.916483	20.97412	29.45382	32.8786	-1.494	0.007725	0.018438	SH3TC1	chr4	+	8183799	8242830	5829
ENSG00000(	2324.317	2254.427	2934.376	3161.099	3277.658	2253.828	-0.20999	0.17225	0.27332	CNOT1	chr16	-	58553855	58663790	8471
ENSG00000(	20.71584	42.15007	23.74945	8.988907	4.60216	9.041614	1.8299	0.001717	0.004627	LRRC29	chr16	-	67241042	67260951	1940
ENSG00000(	570.7213	535.908	606.9303	312.3645	395.7858	328.786	0.72357	3.52E-06	1.37E-05	BBS2	chr16	-	56500748	56554195	6073
ENSG00000(	3.107376	4.817151	1.319414	49.43899	38.65814	53.42772	-3.6908	3.64E-09	1.90E-08	MT1G	chr16	-	56700643	56701977	628
ENSG00000(	3305.212	2562.724	2543.83	1001.514	1000.51	1115.406	1.4291	8.83E-27	1.17E-25	MT2A	chr16	+	56642111	56643409	903
ENSG00000(	327.3102	278.1905	350.9641	349.8183	374.6158	335.3617	-0.14747	0.37595	0.50641	C16orf70	chr16	+	67143861	67182442	2865
ENSG00000(	963.2865	951.3873	903.7984	3435.26	2460.315	2468.361	-1.5649	2.25E-27	3.08E-26	GOT2	chr16	-	58741035	58768261	2462
ENSG00000(	477.5001	521.4566	472.3501	4623.294	5075.262	5785.811	-3.3883	1.34E-159	2.37E-157	DOK4	chr16	-	57505863	57521239	2822
ENSG00000(	5.17896	6.021439	3.958241	2.247227	0	8.219649	0.43456	0.6754	0.77716	GPR18	chr13	-	99906968	99913998	1698
ENSG00000(	23.82321	22.88147	35.62417	19.47596	26.69253	18.08323	0.34458	0.472	0.60107	CLYBL	chr13	+	1E+08	1.01E+08	5667
ENSG00000(	213.3731	222.7932	238.8139	597.0132	509.9193	429.8877	-1.184	1.65E-11	1.03E-10	TMTC4	chr13	-	1.01E+08	1.01E+08	3602
ENSG00000(	1693.52	1766.69	2060.924	686.1532	759.3564	593.4587	1.4335	1.52E-25	1.92E-24	RAP2A	chr13	+	98086476	98121382	5487
ENSG00000(	674.3005	668.3797	833.8695	256.9329	240.2328	161.9271	1.7143	2.47E-20	2.54E-19	ABCC4	chr13	-	95672083	95953687	5837
ENSG00000(	1657.267	1590.864	1967.246	2277.19	2841.374	2368.903	-0.52065	8.04E-05	0.000266	EFNB2	chr13	-	1.07E+08	1.07E+08	4461
ENSG00000(	0	1.204288	0	1.498151	0.920432	7.397684	-1.8589	0.15264	0.24765	SOX21	chr13	-	95361886	95364389	2504
ENSG00000(	3107.376	3146.804	3575.611	2694.425	2589.175	2368.081	0.36039	0.001543	0.004192	TM9SF2	chr13	+	1E+08	1E+08	3430
ENSG00000(	54.89697	65.03154	64.65128	303.3756	254.9597	271.2484	-2.1582	9.34E-22	1.02E-20	C17orf53	chr17	+	42219274	42239844	2725
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	KIF25	chr6	+	1.68E+08	1.68E+08	1613
ENSG00000(	234.089	252.9004	257.2857	104.8706	110.4518	83.01846	1.3109	5.07E-10	2.84E-09	IRF1	chr5	-	1.32E+08	1.32E+08	5153
ENSG00000(	351.1335	326.362	352.2835	489.8954	444.5687	410.1605	-0.384	0.013807	0.031132	UPF3B	chrX	-	1.19E+08	1.19E+08	2378
ENSG00000(	179.192	189.0732	153.052	171.5383	101.2475	141.378	0.32694	0.17253	0.27364	RNF113A	chrX	-	1.19E+08	1.19E+08	1295
ENSG00000(	531.3612	475.6936	542.2791	298.1321	304.663	272.0704	0.82208	8.61E-08	3.97E-07	6-Sep	chrX	-	1.19E+08	1.19E+08	4694
ENSG00000(	2.071584	0	2.638828	170.7892	131.6218	140.556	-6.1143	3.07E-21	3.28E-20	TMEM255A	chrX	-	1.19E+08	1.19E+08	3425
ENSG00000(	764.4144	752.6798	695.3311	394.7628	477.7042	861.4192	0.34971	0.10958	0.18892	NDUFA1	chrX	+	1.19E+08	1.19E+08	766
ENSG00000(	2835.998	3050.461	2228.49	0	0	0.821965	11.527	2.10E-54	6.42E-53	AMELX	chrX	+	11311533	11318881	835
ENSG00000(	120.1519	101.1602	130.622	159.5531	115.9744	166.8589	-0.33021	0.17421	0.27583	ATP5S	chr14	+	50779044	50802276	2008
ENSG00000(	1654.16	1675.164	1576.699	1827.744	1580.382	1688.316	-0.05503	0.63244	0.74238	BMP4	chr14	-	54416454	54425479	1917
ENSG00000(	452.6411	534.7037	464.4337	0	0	0	9.7958	7.59E-27	1.01E-25	PTGER2	chr14	+	52781023	52795324	2383
ENSG00000(	991.2529	826.1414	811.4395	689.8986	749.2316	631.2691	0.34516	0.014202	0.031923	FAM193A	chr4	+	2626988	2734292	4846
ENSG00000(	182.2994	211.9546	222.9809	88.39091	84.67974	79.7306	1.2767	8.20E-09	4.14E-08	GRK4	chr4	+	2965335	3042474	2202
ENSG00000(	279.6638	270.9647	308.7428	2033.74	2408.771	2019.568	-2.9044	1.10E-100	8.41E-99	SOX9	chr17	+	70117161	70122561	3935
ENSG00000(	10.35792	9.634302	6.597069	2.996302	0	4.109825	1.6216	0.08398	0.15167	TEKT3	chr17	-	15207128	15244958	1820
ENSG00000(	2.071584	3.612863	0	4.494453	1.840864	2.465895	-0.46854	0.68881	0.78746	MYH2	chr17	-	10424465	10453274	6339
ENSG00000(	1436.643	1499.338	1423.647	101.8743	150.9508	118.3629	3.5485	8.76E-114	8.37E-112	HS3ST3B1	chr17	+	14204400	14252721	5367
ENSG00000(	5.17896	1.204288	22.43003	14.23244	23.93123	18.08323	-0.90893	0.21074	0.32063	SLC25A35	chr17	-	8191081	8198661	2785
ENSG00000(	622.5109	603.3481	496.0996	1379.048	1135.813	1245.277	-1.1225	2.03E-15	1.65E-14	MRPS7	chr17	+	73257755	73262454	1717
ENSG00000(	623.5467	688.8526	651.7904	757.3154	703.21	668.2575	-0.11655	0.38227	0.51301	GGA3	chr17	-	73232694	73258444	5142
ENSG00000(	177.1204	109.5902	126.6637	319.1062	314.7877	271.2484	-1.1181	1.89E-07	8.45E-07	ARMC7	chr17	+	73106047	73126360	2126
ENSG00000(	590.4014	619.0039	457.8366	1382.793	1056.656	1109.653	-1.0854	4.94E-12	3.22E-11	NUP85	chr17	+	73201754	73231853	2233
ENSG00000(	29.00217	34.92434	31.66593	133.3354	138.9852	106.8554	-1.9645	1.33E-10	7.82E-10	SLC25A19	chr17	-	73269073	73285591	2331
ENSG00000(	30.03797	43.35436	15.83297	100.3761	104.9292	108.4994	-1.7758	3.57E-07	1.55E-06	MIF4GD	chr17	-	73262309	73267308	1531
ENSG00000(	573.8287	610.5739	402.4212	574.5409	581.713	672.3673	-0.20206	0.23513	0.34942	NT5C	chr17	-	73126320	73127890	1315

ENSG00000(	286.9144	297.4591	292.9099	370.0433	321.2308	338.6495	-0.23177	0.1547	0.25026	MSTO1	chr1	+	1.56E+08	1.56E+08	2490
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	C1orf61	chr1	-	1.56E+08	1.56E+08	2697
ENSG00000(	277.5922	239.6533	254.6469	373.7887	348.8437	346.8692	-0.46781	0.00481	0.011952	TTF1	chr9	-	1.35E+08	1.35E+08	3052
ENSG00000(	931.1769	912.8501	1104.349	1013.499	1211.289	1064.445	-0.15774	0.24216	0.35783	GTF3C4	chr9	+	1.36E+08	1.36E+08	9043
ENSG00000(	330.4176	345.6306	323.2564	510.1204	407.7514	402.7628	-0.40172	0.014265	0.032051	DDX31	chr9	-	1.35E+08	1.36E+08	4577
ENSG00000(	4.143168	2.408575	5.277655	0	1.840864	0	1.9041	0.12279	0.20782	BARHL1	chr9	+	1.35E+08	1.35E+08	2341
ENSG00000(	2903.325	2660.272	1952.732	1164.063	1160.665	1404.738	1.0084	3.07E-11	1.89E-10	PPP1R12C	chr19	-	55602281	55628927	4141
ENSG00000(	4491.194	4460.682	3604.638	4445.763	4243.192	4467.379	-0.06692	0.56808	0.68723	MBOAT7	chr19	-	54677107	54693733	3039
ENSG00000(	6.214751	2.408575	1.319414	0	6.443024	4.109825	-0.03928	0.97191	0.98371	SRMS	chr20	-	62172163	62178857	1516
ENSG00000(	41.43168	36.12863	39.58241	14.98151	11.96562	4.93179	1.8055	0.000403	0.001203	OPRL1	chr20	+	62711526	62731996	3369
ENSG00000(	1554.724	1412.629	1290.387	1343.842	1165.267	1353.776	0.14046	0.26938	0.38974	SLC2A4RG	chr20	+	62369623	62374858	1731
ENSG00000(	4.143168	7.225726	9.235896	0	2.761296	2.465895	1.6461	0.10888	0.18799	C20orf195	chr20	+	62184373	62188061	1137
ENSG00000(	3415.006	3296.135	2347.237	2627.757	2326.852	2409.179	0.29835	0.036778	0.074348	PPDPF	chr20	+	62152077	62153559	868
ENSG00000(	11.39371	4.817151	1.319414	1.498151	1.840864	4.109825	1.0426	0.30571	0.43121	IL1B	chr2	-	1.14E+08	1.14E+08	1631
ENSG00000(	5.17896	3.612863	7.916483	7.490755	3.681728	0	0.47179	0.64153	0.74914	PLGLB2	chr2	+	88047606	88058312	2077
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	IL37	chr2	+	1.14E+08	1.14E+08	772
ENSG00000(	187.4783	173.4174	176.8014	275.6598	249.4371	264.6727	-0.5518	0.002701	0.007038	CHCHD5	chr2	+	1.13E+08	1.13E+08	3272
ENSG00000(	426.7463	414.275	440.6842	25.46857	58.90765	44.38611	3.3036	4.79E-43	1.09E-41	PAX8	chr2	-	1.14E+08	1.14E+08	4084
ENSG00000(	446.4263	491.3494	372.0747	175.2837	196.052	170.9687	1.2689	8.91E-13	6.12E-12	INSIG2	chr2	+	1.19E+08	1.19E+08	3185
ENSG00000(	251.6974	268.5562	394.5047	621.7327	535.6914	479.2055	-0.83916	1.01E-05	3.73E-05	POLR1B	chr2	+	1.13E+08	1.13E+08	4558
ENSG00000(	6.214751	0	0	0	2.761296	0	0.67679	0.61574	0.72879	HTR5BP	chr2	+	1.19E+08	1.19E+08	1193
ENSG00000(	486.8222	451.6079	634.638	496.6371	575.27	470.1639	0.027655	0.86817	0.91719	CCDC93	chr2	-	1.19E+08	1.19E+08	6899
ENSG00000(	311.7734	239.6533	295.5487	155.8077	170.2799	154.5294	0.81498	2.34E-05	8.29E-05	PSD4	chr2	+	1.14E+08	1.14E+08	5600
ENSG00000(	1657.267	1533.058	1352.399	1032.226	928.7159	960.055	0.63611	4.90E-07	2.10E-06	SLC25A23	chr19	-	6436090	6465214	3425
ENSG00000(	158.4762	185.4603	114.789	189.5161	168.4391	157.8173	-0.16593	0.47001	0.59914	PSPN	chr19	-	6375159	6379069	3911
ENSG00000(	4662.099	4642.529	3186.384	2686.934	2743.808	3525.408	0.47865	0.002158	0.005719	GTF2F1	chr19	-	6379580	6393992	2731
ENSG00000(	685.6942	625.0253	529.0849	522.1057	436.2848	590.9928	0.24763	0.12742	0.21384	ALKBH7	chr19	+	6372444	6375042	1110
ENSG00000(	1161.123	1253.664	862.8966	1800.778	1245.344	1297.883	-0.40454	0.017082	0.037687	CLPP	chr19	+	6361463	6368919	1346
ENSG00000(	381.1714	358.8777	365.4776	44.19546	25.7721	18.90519	3.5912	2.28E-44	5.35E-43	TNFSF9	chr19	+	6531010	6535931	1657
ENSG00000(	23.82321	27.69862	29.0271	3.745378	2.761296	5.753754	2.5497	5.39E-05	0.000182	GRIA3	chrX	+	1.22E+08	1.23E+08	5172
ENSG00000(	1091.725	1138.052	1340.524	963.3112	929.6363	769.3592	0.42137	0.002633	0.006873	THOC2	chrX	-	1.23E+08	1.23E+08	5609
ENSG00000(	1023.362	942.9573	1285.109	603.0058	1202.084	941.9718	0.24239	0.22565	0.33835	MED1	chr17	-	37560538	37607539	5844
ENSG00000(	23141.66	24042.4	16859.47	16162.8	13660.13	15172.65	0.508	0.000204	0.000636	RPL23	chr17	-	37004118	37010096	3081
ENSG00000(	124.295	151.7403	158.3297	198.505	183.166	174.2566	-0.3577	0.090731	0.1618	ATG4C	chr1	+	63249806	63331184	2938
ENSG00000(	544.8265	576.8538	489.5025	9.737982	7.363456	23.01502	5.2626	3.77E-79	2.01E-77	CD70	chr19	-	6583194	6604114	913
ENSG00000(	119.1161	98.75159	97.63662	2.247227	11.04518	19.72716	3.181	8.10E-13	5.57E-12	C3	chr19	-	6677715	6730573	5263
ENSG00000(	13.46529	21.67718	6.597069	474.1648	312.0264	472.6298	-4.8309	5.39E-51	1.52E-49	SH2D3A	chr19	-	6752171	6767599	3493
ENSG00000(	1058.579	977.8816	920.9508	834.4702	857.8426	1038.142	0.11563	0.3971	0.52815	TRIP10	chr19	+	6737936	6751537	2249
ENSG00000(	738.5196	678.014	567.3479	620.9836	520.0441	622.2274	0.17033	0.26253	0.38209	GPR108	chr19	-	6729925	6737614	2057
ENSG00000(	8.286335	8.430014	10.55531	2.247227	4.60216	4.109825	1.1806	0.15883	0.25563	FOSB	chr19	+	45971253	45978437	3775
ENSG00000(	716.768	698.4869	686.0952	862.935	870.7287	920.6007	-0.3359	0.007138	0.017167	OPA3	chr19	-	46030685	46105470	7828
ENSG00000(	2590.516	2544.66	1847.179	3235.257	2490.689	3332.246	-0.37402	0.013958	0.031435	SNRPD2	chr19	-	46190712	46195827	901
ENSG00000(	277.5922	275.7819	221.6615	255.4348	225.5058	263.8507	0.058383	0.75097	0.83476	RTN2	chr19	-	45988547	46000319	2357
ENSG00000(	390.4935	380.5549	424.8512	411.2425	416.9557	709.3557	-0.36105	0.074911	0.13748	EML2	chr19	-	46110252	46148887	2791

ENSG00000(	1832.316	1764.282	1578.019	2450.226	2638.879	3067.573	-0.65457	1.72E-07	7.73E-07	VASP	chr19	+	46009837	46030241	2305
ENSG00000(	1966.969	1852.195	1671.697	2382.06	2149.209	2427.262	-0.34072	0.003696	0.009401	SYMPK	chr19	-	46318668	46366548	6537
ENSG00000(	191.6215	217.9761	183.3985	305.6228	302.8221	255.6311	-0.54029	0.003607	0.009193	GPCPD1	chr20	-	5525085	5591672	6649
ENSG00000(	27.96638	27.69862	22.43003	21.72319	25.7721	27.12484	0.068351	0.88135	0.9258	SDCBP2	chr20	-	1290619	1309883	1519
ENSG00000(	663.9426	676.8097	729.6358	861.4369	856.0018	964.9868	-0.37355	0.004103	0.010347	PANK2	chr20	+	3869486	3907605	4815
ENSG00000(	0	0	2.638828	8.239831	2.761296	0.821965	-1.5381	0.21585	0.32656	TGM3	chr20	+	2276647	2321724	2642
ENSG00000(	2.071584	4.817151	15.83297	5.243529	2.761296	8.219649	0.40237	0.65154	0.75752	GNRH2	chr20	+	3024268	3026393	758
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	FOXA2	chr20	-	22561643	22566093	2422
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	FAM182A	chr20	+	26035291	26073683	5070
ENSG00000(	0	0	0	2.247227	0	0.821965	-0.85594	0.51054	NA	CD93	chr20	-	23059986	23066977	6708
ENSG00000(	332.4892	291.4376	389.2271	382.7776	416.9557	288.5097	-0.10317	0.58228	0.69994	GZF1	chr20	+	23342787	23353700	4835
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	PAX1	chr20	+	21686297	21696620	2838
ENSG00000(	151.2256	192.686	163.6073	209.7412	181.3251	157.8173	-0.11447	0.59255	0.70877	NAPB	chr20	-	23355159	23402125	3837
ENSG00000(	2446.54	2214.685	1973.843	1403.768	1615.358	1676.808	0.49844	8.91E-05	0.000293	CENPB	chr20	-	3764498	3767337	2840
ENSG00000(	1868.569	1897.957	1680.933	2082.43	1717.526	1712.975	-0.01727	0.8901	0.93174	PSMF1	chr20	+	1093906	1149022	4290
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	NKX2-2	chr20	-	21491648	21494664	2092
ENSG00000(	663.9426	735.8198	580.5421	853.9461	729.9026	768.5372	-0.24757	0.083124	0.15029	DTD1	chr20	+	18568537	18744561	2384
ENSG00000(	2033.26	1966.602	1653.225	1089.905	1036.406	1036.498	0.83655	1.36E-11	8.55E-11	RBCK1	chr20	+	388142	411610	2774
ENSG00000(	1032.685	1001.967	1188.792	834.4702	1004.191	817.0331	0.27888	0.042433	0.084257	TMX4	chr20	-	7957995	8000476	6169
ENSG00000(	940.499	880.3343	915.6732	990.2779	1129.37	1075.952	-0.2226	0.071033	0.13145	STK35	chr20	+	2082257	2157684	6685
ENSG00000(	1390.033	1386.135	1190.111	4113.174	2607.584	3387.317	-1.3452	2.58E-18	2.41E-17	SNRPB	chr20	-	2442280	2451499	1450
ENSG00000(	1464.61	1393.361	1369.552	1021.739	896.5008	957.5891	0.55454	3.43E-06	1.34E-05	NRSN2	chr20	+	327527	335512	2088
ENSG00000(	344.9187	245.6747	307.4234	205.2467	152.7917	202.2034	0.67598	0.000878	0.002484	AP5S1	chr20	+	3801178	3805949	1848
ENSG00000(	17388.87	16805.84	16174.69	6621.828	10556.43	11865.06	0.79152	1.41E-06	5.76E-06	RRBP1	chr20	-	17594323	17662940	5041
ENSG00000(	1589.941	1429.49	1473.785	566.3011	583.5539	560.5801	1.3912	1.64E-30	2.53E-29	BMP2	chr20	+	6748311	6760927	3601
ENSG00000(	353.205	385.3721	362.8388	209.7412	191.4499	266.3166	0.71815	7.59E-05	0.000251	ZNF133	chr20	+	18269121	18297640	4060
ENSG00000(	181.2636	161.3746	162.2879	1424.742	1691.754	1311.034	-3.1193	4.36E-90	2.75E-88	FLRT3	chr20	-	14303634	14318262	4776
ENSG00000(	0	0	0	156.5568	124.2583	156.1733	-7.832	2.21E-15	1.78E-14	OVOL2	chr20	-	17937623	18039832	1555
ENSG00000(	0	0	0	400.7554	323.0716	336.1837	-8.9555	2.44E-21	2.61E-20	PCSK2	chr20	+	17206752	17465223	4740
ENSG00000(	553.1129	522.6609	500.0578	728.8505	589.9969	750.454	-0.39188	0.007979	0.018965	MKKS	chr20	-	10385832	10414870	2663
ENSG00000(	153.2972	177.0303	155.6908	79.40201	88.36147	83.84042	0.94376	4.76E-05	0.000162	BFSP1	chr20	-	17474550	17549865	2207
ENSG00000(	7556.102	7727.914	7668.433	15128.33	12866.72	12774.98	-0.82764	1.22E-14	9.40E-14	DSTN	chr20	+	17550508	17588887	1940
ENSG00000(	1.035792	0	0	17.97781	0	3.28786	-2.8005	0.024184	0.051466	LAMP5	chr20	+	9495008	9511171	2039
ENSG00000(	1044.078	1126.009	932.8255	1673.435	1374.205	1586.392	-0.57726	1.08E-05	3.99E-05	SNRPB2	chr20	+	16710606	16722421	1665
ENSG00000(	394.6367	461.2422	439.3648	808.2525	734.5047	704.4239	-0.79424	2.63E-08	1.28E-07	MGME1	chr20	+	17949556	17971765	2336
ENSG00000(	8.286335	0	1.319414	1209.757	1634.687	1480.359	-8.0885	1.02E-31	1.64E-30	LRRN4	chr20	-	6021424	6034695	2692
ENSG00000(	1449.073	1327.125	1355.038	815.7433	871.6491	807.9915	0.72661	1.06E-09	5.80E-09	TBC1D20	chr20	-	416124	443197	5195
ENSG00000(	1426.285	1313.878	1155.806	1032.226	851.3996	984.714	0.44087	0.001052	0.00294	ITPA	chr20	+	3189514	3204516	1185
ENSG00000(	0	0	0	14.23244	10.12475	16.4393	-4.6301	4.66E-05	0.000159	TCF15	chr20	-	584441	591042	1555
ENSG00000(	139.8319	133.6759	133.2608	756.5663	630.4959	618.1176	-2.2919	3.05E-41	6.50E-40	MCM8	chr20	+	5931298	5975852	3715
ENSG00000(	29.00217	9.634302	9.235896	5.992604	2.761296	4.93179	1.656	0.027687	0.057955	TMEM74B	chr20	-	1161205	1166059	1730
ENSG00000(	35.21692	61.41867	31.66593	173.0365	113.2131	124.9387	-1.659	1.92E-07	8.55E-07	FAM110A	chr20	+	814358	826922	1856
ENSG00000(	422.6031	391.3935	365.4776	787.2784	682.9605	899.2296	-1.0023	6.38E-11	3.83E-10	MRPS26	chr20	+	3026591	3028900	1127
ENSG00000(	2.071584	2.408575	1.319414	0	3.681728	0	0.4435	0.73345	0.82174	S1PR4	chr19	+	3172344	3180329	1594

ENSG00000(	3198.525	2845.732	2537.233	4015.794	3543.663	4131.196	-0.44477	0.00028	0.000855	NCLN	chr19	+	3185561	3209573	4005
ENSG00000(	41.43168	42.15007	23.74945	9.737982	4.60216	6.575719	2.2467	4.87E-05	0.000166	CITED1	chrX	-	71521488	71527037	1231
ENSG00000(	2597.766	2554.294	2823.545	3949.875	4730.1	4497.792	-0.72319	2.22E-10	1.28E-09	HNRNPR	chr1	-	23630264	23670829	7646
ENSG00000(	396.7083	411.8664	476.3084	158.804	176.7229	165.2149	1.3538	4.30E-15	3.42E-14	ZNF436	chr1	-	23685941	23695935	4071
ENSG00000(	826.5619	934.5273	804.8424	764.8061	697.6875	866.351	0.13915	0.31546	0.44209	MAX	chr14	-	65472892	65569413	3155
ENSG00000(	214.4089	197.5032	191.315	183.5235	162.9165	185.7641	0.18016	0.35625	0.48572	ARMCX5	chrX	+	1.02E+08	1.02E+08	4640
ENSG00000(	181.2636	192.686	193.9538	2.996302	0.920432	1.64393	6.3343	3.53E-32	5.73E-31	GDF5	chr20	-	34021145	34042568	2572
ENSG00000(	179.192	144.5145	117.4278	56.18067	60.74851	87.95025	1.0986	7.56E-05	0.000251	MMP24	chr20	+	33814457	33864801	4412
ENSG00000(	395.6725	431.135	307.4234	203.7485	177.6434	256.4531	0.8263	3.00E-05	0.000105	NECAB3	chr20	-	32244893	32262269	2142
ENSG00000(	3170.559	2867.409	2582.093	8126.721	6432.899	6846.968	-1.3092	2.24E-25	2.81E-24	ID1	chr20	+	30193086	30194318	1222
ENSG00000(	4101.736	3833.248	3419.921	4637.527	4639.898	4899.733	-0.31937	0.003728	0.009474	RALY	chr20	+	32581452	32696114	1817
ENSG00000(	1640.694	1434.307	1386.704	1838.231	1189.198	1512.415	-0.02518	0.87072	0.91874	DYNLRB1	chr20	+	33104214	33128762	1464
ENSG00000(	2655.77	2826.463	2727.228	4319.919	3374.304	3825.425	-0.48812	4.36E-05	0.00015	EIF2S2	chr20	-	32676104	32700138	2656
ENSG00000(	6414.659	6440.531	5645.772	3522.902	2635.197	2943.456	1.0209	1.03E-15	8.45E-15	ERGIC3	chr20	+	34129770	34145405	2848
ENSG00000(	580.0435	657.5411	571.3062	577.5372	548.5775	711.8216	-0.02322	0.87824	0.92394	ROMO1	chr20	+	34287194	34288906	498
ENSG00000(	2.071584	0	5.277655	2.247227	0	0	1.0099	0.44484	0.57434	BPIFB9P	chr20	+	31935526	31942250	1178
ENSG00000(	1.035792	0	0	2.247227	0	0	-0.31629	0.80869	NA	FAM83C	chr20	-	33873534	33880204	3145
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	BPIFB1	chr20	+	31861286	31897684	1933
ENSG00000(	1520.543	1453.575	1424.967	444.2018	1035.486	819.499	0.92147	0.007042	0.016948	CEP250	chr20	+	34042985	34099804	8398
ENSG00000(	609.0456	563.6067	717.7611	1131.104	1202.084	1020.88	-0.8259	3.85E-09	2.01E-08	PLAGL2	chr20	-	30780306	30795594	5705
ENSG00000(	1254.344	1275.341	986.9215	667.4263	498.8741	512.0841	1.063	1.36E-11	8.58E-11	MMP24-AS	chr20	-	33804634	33865934	1515
ENSG00000(	0	1.204288	0	14.23244	11.96562	18.08323	-4.0275	0.000139	0.000445	GRPR	chrX	+	16141679	16171144	1929
ENSG00000(	2061.226	2233.954	2334.043	1298.148	1947.634	2039.295	0.32606	0.036942	0.074666	KDM5C	chrX	-	53220503	53254604	6096
ENSG00000(	426.7463	491.3494	519.849	3665.976	5883.401	4162.43	-3.2425	5.80E-87	3.49E-85	AMOT	chrX	-	1.12E+08	1.12E+08	6945
ENSG00000(	1252.272	1280.158	1047.615	709.3745	798.0145	827.7187	0.61607	4.77E-06	1.84E-05	TMEM115	chr3	-	50392180	50397041	2197
ENSG00000(	1878.927	1871.463	1654.545	5031.54	3641.229	4041.602	-1.231	6.44E-20	6.50E-19	PSMB2	chr1	-	36067185	36107445	2701
ENSG00000(	172.9772	197.5032	232.2168	221.7264	157.3939	185.7641	0.087738	0.68151	0.78197	AGO3	chr1	+	36396319	36522063	3649
ENSG00000(	1500.862	1623.38	1355.038	1054.698	989.4644	1031.566	0.54134	9.29E-06	3.46E-05	UROD	chr1	+	45477819	45481247	1848
ENSG00000(	315.9165	327.5663	315.3399	170.0401	156.4734	151.2415	0.99975	2.13E-08	1.05E-07	ST3GAL3	chr1	+	44171495	44396831	2449
ENSG00000(	207.1584	130.0631	171.5238	167.7929	95.72493	105.2115	0.45821	0.086739	0.15594	TMEM53	chr1	-	45100910	45140227	2310
ENSG00000(	1045.114	1123.6	957.8944	698.1384	769.4811	670.7234	0.54768	2.95E-05	0.000103	HECTD3	chr1	-	45468212	45477001	3610
ENSG00000(	606.9741	610.5739	484.2249	510.1204	764.879	761.1395	-0.25568	0.14758	0.2407	KLC1	chr14	+	1.04E+08	1.04E+08	3250
ENSG00000(	516.8602	517.8437	354.9223	1077.92	844.9566	1125.27	-1.127	4.77E-11	2.89E-10	XRCC3	chr14	-	1.04E+08	1.04E+08	3668
ENSG00000(	234.089	203.5246	250.6886	613.4929	656.268	600.8564	-1.438	5.66E-20	5.72E-19	TUBGCP3	chr13	-	1.13E+08	1.13E+08	3893
ENSG00000(	6.214751	6.021439	9.235896	17.22874	19.32907	18.90519	-1.2946	0.044117	0.087144	MCF2L	chr13	+	1.14E+08	1.14E+08	6580
ENSG00000(	23.82321	20.47289	15.83297	0.749076	4.60216	9.041614	1.9168	0.008039	0.019088	F10	chr13	+	1.14E+08	1.14E+08	1517
ENSG00000(	495.1085	532.2952	564.7091	874.9202	629.5755	703.602	-0.47227	0.002535	0.006632	PCID2	chr13	-	1.14E+08	1.14E+08	4202
ENSG00000(	9.322127	0	1.319414	20.22504	18.40864	31.23467	-2.4132	0.001714	0.00462	PROZ	chr13	+	1.14E+08	1.14E+08	1551
ENSG00000(	604.9025	529.8866	509.2937	400.0063	264.164	336.1837	0.71254	5.12E-05	0.000174	LRFN3	chr19	+	36426260	36436669	3689
ENSG00000(	1.035792	0	0	4.494453	0.920432	0	-1.1462	0.39775	0.52871	IGFLR1	chr19	-	36230058	36233354	1195
ENSG00000(	7828.515	7322.069	6192.009	7618.098	5782.154	6255.975	0.1185	0.36965	0.50004	CAPNS1	chr19	+	36630477	36641255	1918
ENSG00000(	5.17896	26.49433	14.51355	58.42789	34.97642	43.56414	-1.5257	0.003085	0.007949	PDCD2L	chr19	+	34895289	34917287	1386
ENSG00000(	1912.072	1805.227	1611.004	2399.289	2163.936	2317.119	-0.36768	0.001643	0.004441	RBM42	chr19	+	36119932	36128588	1680
ENSG00000(	0	0	5.277655	0	3.681728	0.821965	0.1308	0.92148	0.95241	KIRREL2	chr19	+	36346763	36358048	2942

ENSG00000(	1153.872	1159.729	1336.566	2931.882	2672.935	2523.432	-1.1536	1.02E-21	1.11E-20	UBA2	chr19	+	34919264	34960853	2802
ENSG00000(	5.17896	10.83859	7.916483	1.498151	4.60216	5.753754	0.89748	0.30588	0.43137	HCST	chr19	+	36393382	36395279	613
ENSG00000(	2914.718	2686.766	2128.214	2025.5	1945.793	2339.312	0.29238	0.033364	0.068191	COX6B1	chr19	+	36139125	36149763	667
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	KRT36	chr17	-	39642388	39648798	1707
ENSG00000(	705.3743	720.1641	672.901	154.3096	127.0196	161.9271	2.2328	8.13E-44	1.88E-42	THRA	chr17	+	38214543	38250120	4895
ENSG00000(	2.071584	4.817151	0	1.498151	3.681728	2.465895	-0.09883	0.93276	0.95977	CCR7	chr17	-	38710021	38721724	2173
ENSG00000(	83.89914	101.1602	75.20659	57.67882	57.98722	49.3179	0.65071	0.028224	0.05891	NR1D1	chr17	-	38249040	38256978	2772
ENSG00000(	1705.949	1564.37	1443.439	764.8061	656.268	820.321	1.0698	9.67E-16	7.97E-15	FRMD8	chr11	+	65154070	65180996	3723
ENSG00000(	5005.982	4948.418	3970.116	1846.471	1862.034	2882.631	1.0752	5.80E-11	3.49E-10	PRDX5	chr11	+	64085560	64089283	893
ENSG00000(	348.0261	296.2548	279.7157	1724.372	1164.346	1753.251	-2.3178	9.69E-42	2.10E-40	BCL2L12	chr19	+	50168823	50177173	1431
ENSG00000(	835.8841	882.7429	794.2871	1173.052	1070.462	1411.314	-0.53907	0.000101	0.000329	IRF3	chr19	-	50162826	50169132	2874
ENSG00000(	3795.142	3518.929	2963.403	8547.701	5830.016	6791.074	-1.0393	9.88E-13	6.77E-12	PRMT1	chr19	+	50179043	50192286	1686
ENSG00000(	845.2062	859.8614	600.3333	572.2937	403.1492	444.683	0.69581	9.27E-05	0.000304	RRAS	chr19	-	50138549	50143458	1044
ENSG00000(	10.35792	2.408575	6.597069	86.89276	90.20234	96.1699	-3.6705	4.79E-15	3.79E-14	PRRG2	chr19	+	50083903	50094272	1583
ENSG00000(	3042.121	2868.613	2359.112	4297.446	4152.989	4621.909	-0.65874	7.14E-08	3.32E-07	SCAF1	chr19	+	50145382	50161899	4306
ENSG00000(	1530.9	1386.135	1277.193	1200.768	1856.511	1889.697	-0.23633	0.14837	0.24167	PRR12	chr19	+	50094900	50129696	6955
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	TSKS	chr19	-	50243010	50266587	1883
ENSG00000(	54.89697	28.90291	29.0271	7.490755	12.88605	12.32947	1.7335	0.000791	0.002256	FLRT1	chr11	+	63870660	63886645	3949
ENSG00000(	244.4469	211.9546	222.9809	247.1949	258.6414	249.0554	-0.14969	0.40185	0.53298	ASL	chr7	+	65540785	65558545	2143
ENSG00000(	625.6183	634.6596	645.1933	1315.377	913.0685	1024.168	-0.77005	4.27E-07	1.84E-06	SBDS	chr7	-	66452664	66460588	1631
ENSG00000(	16.57267	28.90291	29.0271	40.45008	25.7721	28.76877	-0.3521	0.44539	0.57493	STAT5A	chr17	+	40439565	40463961	4301
ENSG00000(	161.5835	119.2245	105.5531	95.88167	114.1336	102.7456	0.30865	0.22307	0.33524	WNK4	chr17	+	40932696	40948954	4001
ENSG00000(	598.6877	479.3065	589.778	468.1722	524.6462	429.0657	0.23032	0.13911	0.22957	BECN1	chr17	-	40962152	40985367	2504
ENSG00000(	0	0	0	2.247227	5.522592	8.219649	-3.1828	0.011907	0.02721	PRKCG	chr19	+	54382444	54410906	3133
ENSG00000(	455.7484	475.6936	461.7948	898.1416	806.2984	735.6586	-0.80687	9.35E-09	4.69E-08	TRAP1	chr16	-	3701640	3767598	2309
ENSG00000(	497.1801	510.618	407.6989	162.5494	190.5294	187.408	1.3859	1.47E-15	1.20E-14	GLIS2	chr16	+	4364762	4389598	4469
ENSG00000(	541.7192	551.5638	547.5567	570.0465	406.8309	476.7397	0.17253	0.27629	0.39784	NSRP1	chr17	+	28442539	28513493	2541
ENSG00000(	1487.397	1429.49	1439.48	2170.072	1931.987	1903.671	-0.46247	5.12E-05	0.000174	DNAJC8	chr1	-	28525967	28559536	1600
ENSG00000(	2129.588	1922.043	1835.305	1706.394	2521.063	2260.404	-0.13902	0.33973	0.46839	AHDC1	chr1	-	27860546	27930942	6438
ENSG00000(	543.7907	485.328	391.8659	128.841	112.2927	148.7757	1.8565	4.27E-22	4.71E-21	IFI6	chr1	-	27992572	27998729	841
ENSG00000(	0	0	0	2.247227	13.80648	6.575719	-3.6757	0.002771	0.007204	DACH2	chrX	+	85403462	86087607	5582
ENSG00000(	749.9133	852.6357	781.093	650.9467	754.7542	739.7684	0.15178	0.25806	0.37673	ZNF384	chr12	-	6775643	6798738	3286
ENSG00000(	27.96638	32.51577	25.06886	51.68621	45.10117	64.93523	-0.89964	0.019311	0.04204	EMG1	chr12	+	7079944	7085781	1575
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	SSX1	chrX	+	48114752	48126879	1298
ENSG00000(	357.3482	351.652	241.4527	315.3608	223.665	263.0288	0.2442	0.22934	0.34277	UXT	chrX	-	47511197	47518560	894
ENSG00000(	15.53688	18.06432	7.916483	13.48336	1.840864	6.575719	0.83504	0.26468	0.38451	CFP	chrX	-	47483612	47489704	4040
ENSG00000(	953.9643	952.5916	1000.116	619.4855	623.1325	572.9095	0.67732	7.67E-08	3.56E-07	ELK1	chrX	-	47494920	47510003	2695
ENSG00000(	525.1465	558.7895	428.8095	1019.492	887.2964	1041.43	-0.95887	5.95E-11	3.58E-10	TIMM17B	chrX	-	48750730	48755426	1528
ENSG00000(	978.8233	1101.923	1207.264	853.9461	857.8426	701.958	0.44392	0.001498	0.004073	PCNXL4	chr14	+	60558629	60635851	4666
ENSG00000(	352.1692	428.7264	485.5443	357.309	380.1384	323.8542	0.25193	0.13829	0.22852	ATG14	chr14	-	55833110	55878576	4742
ENSG00000(	2624.697	2455.543	2886.877	3107.914	3452.54	2864.548	-0.24202	0.042166	0.083815	KTN1	chr14	+	56025790	56168244	6241
ENSG00000(	2552.191	2370.038	2596.606	26.96672	17.48821	20.54912	6.7993	1.92E-250	1.00E-247	SIX1	chr14	-	61110132	61124977	3997
ENSG00000(	259.9838	256.5133	312.7011	127.3428	111.3723	115.8971	1.2157	1.06E-09	5.79E-09	RHOJ	chr14	+	63670832	63759937	3302
ENSG00000(	419.4957	415.4793	477.6278	1689.165	1578.541	1414.602	-1.8318	2.18E-42	4.84E-41	DLGAP5	chr14	-	55614830	55658396	2973

ENSG0000(	328.346	325.1577	300.8263	89.13999	107.6905	93.704	1.7103	2.07E-18	1.95E-17	L3HYPDH	chr14	-	59927081	59951148	1527
ENSG0000(	58.00435	43.35436	63.33186	432.2166	422.4783	404.4067	-2.9177	9.92E-43	2.23E-41	HSPA2	chr14	+	65002623	65009955	2767
ENSG0000(	766.486	805.6685	862.8966	927.3555	977.4988	817.0331	-0.16078	0.22447	0.33686	ZBTB1	chr14	+	64970430	65000408	4119
ENSG0000(	266.1985	301.0719	348.3252	323.6006	277.05	254.8091	0.094254	0.60531	0.72004	TRMT5	chr14	-	61438169	61448076	5573
ENSG0000(	304.5228	316.7277	311.3817	517.6112	517.2828	438.1073	-0.65742	2.53E-05	8.93E-05	SGPP1	chr14	-	64150932	64194757	3312
ENSG0000(	598.6877	544.338	585.8197	1757.331	2483.326	2567.818	-1.9707	2.87E-38	5.66E-37	PLEKHG3	chr14	+	65170820	65213610	6989
ENSG0000(	0	0	0	2.247227	6.443024	10.68554	-3.4617	0.005389	0.013259	PZP	chr12	-	9301436	9360966	4610
ENSG0000(	263.0911	314.3191	317.9787	376.785	300.0608	297.5513	-0.12459	0.48506	0.61422	RHOT1	chr17	+	30469473	30580393	3297
ENSG0000(	8.286335	2.408575	11.87472	3.745378	2.761296	2.465895	1.1443	0.21566	0.32631	EVI2A	chr17	-	29644578	29648902	1860
ENSG0000(	23.82321	33.72006	38.263	11.23613	4.60216	3.28786	2.1853	0.000231	0.000714	OMG	chr17	-	29599031	29624557	2965
ENSG0000(	543.7907	507.0051	515.8908	268.169	314.7877	233.438	0.93878	1.02E-08	5.11E-08	WDR60	chr7	+	1.59E+08	1.59E+08	5410
ENSG0000(	11.39371	4.817151	3.958241	944.5843	1193.8	1274.046	-7.2061	6.45E-90	4.06E-88	AIF1L	chr9	+	1.34E+08	1.34E+08	3515
ENSG0000(	12.4295	7.225726	6.597069	11.23613	20.2495	13.15144	-0.6989	0.29457	0.41896	FAM78A	chr9	-	1.34E+08	1.34E+08	4560
ENSG0000(	880.4231	836.98	989.5603	1301.144	1331.865	1005.263	-0.42578	0.003087	0.007955	NUP214	chr9	+	1.34E+08	1.34E+08	7600
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CTAG2	chrX	-	1.54E+08	1.54E+08	993
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AVPR2	chrX	+	1.53E+08	1.53E+08	1763
ENSG0000(	500.2875	508.2094	435.4065	624.729	505.3172	586.883	-0.24901	0.099186	0.17426	SLC10A3	chrX	-	1.54E+08	1.54E+08	2127
ENSG0000(	5917.479	5493.961	4705.03	4806.069	3491.199	3838.576	0.40817	0.003036	0.007834	MAP2K2	chr19	-	4090319	4124126	2926
ENSG0000(	1232.592	1231.986	1369.552	1243.465	1323.581	1477.071	-0.07711	0.53344	0.658	HNRNPH2	chrX	+	1.01E+08	1.01E+08	2223
ENSG0000(	599.7235	588.8967	566.0285	296.6339	266.0048	300.0172	1.0207	5.69E-12	3.69E-11	ARMCX1	chrX	+	1.01E+08	1.01E+08	2141
ENSG0000(	286.9144	290.2333	294.2293	6.74168	10.12475	10.68554	4.9256	4.23E-54	1.28E-52	TMEM35	chrX	+	1E+08	1E+08	2195
ENSG0000(	176.0846	151.7403	145.1355	259.9292	307.4243	319.7444	-0.89893	3.47E-06	1.35E-05	TIMM8A	chrX	-	1.01E+08	1.01E+08	1664
ENSG0000(	429.8536	401.0278	339.0893	341.5785	304.663	272.0704	0.34918	0.042049	0.08362	ZC4H2	chrX	-	64136250	64254593	4147
ENSG0000(	16728.04	16283.17	18325.34	11439.88	11679.36	9763.299	0.64156	7.65E-09	3.88E-08	CANX	chr5	+	1.79E+08	1.79E+08	4260
ENSG0000(	2097.479	2101.482	1579.338	2343.108	2073.733	2424.797	-0.2426	0.074396	0.13668	CPSF3L	chr1	-	1246965	1260071	3079
ENSG0000(	98.40023	81.89156	91.03955	79.40201	70.87326	55.89361	0.39206	0.16968	0.2697	IPPK	chr9	-	95375466	95432547	4401
ENSG0000(	68.36227	59.0101	101.5949	47.19176	59.82808	62.46933	0.42522	0.18909	0.29417	ZNF484	chr9	-	95607874	95640304	3180
ENSG0000(	3.107376	4.817151	7.916483	0.749076	0.920432	3.28786	1.3465	0.20508	0.31364	OMD	chr9	-	95176527	95186743	2449
ENSG0000(	0	0	0	56.18067	61.66894	49.3179	-6.5902	1.58E-10	9.21E-10	FGD3	chr9	+	95709733	95798518	4697
ENSG0000(	72.50543	73.46155	81.80365	106.3687	155.553	146.3098	-0.83336	0.001559	0.004229	HIVEP3	chr1	-	41972036	42501596	12319
ENSG0000(	474.3927	449.1993	377.3523	561.0576	532.0097	547.4286	-0.33179	0.026674	0.056119	PPCS	chr1	+	42921788	42939056	1617
ENSG0000(	0	0	0	6.74168	0	8.219649	-2.9254	0.025399	0.053725	EDN2	chr1	-	41944446	41950344	1241
ENSG0000(	0	4.817151	6.597069	2.247227	0.920432	12.32947	-0.37642	0.72618	0.81637	BCL11B	chr14	-	99635624	99737861	7603
ENSG0000(	3345.608	3424.994	3028.055	2832.255	2637.038	3791.724	0.081232	0.56333	0.683	COX7C	chr5	+	85913721	85916779	1584
ENSG0000(	201.9794	221.5889	167.5656	773.795	793.4124	845.8019	-2.0199	1.47E-37	2.83E-36	TRAF2	chr9	+	1.4E+08	1.4E+08	2413
ENSG0000(	234.089	172.2131	125.3443	268.9181	280.7318	269.6045	-0.6132	0.005584	0.013707	ABHD8	chr19	-	17402940	17421045	2090
ENSG0000(	24.85901	46.96722	38.263	2.247227	12.88605	9.863579	2.0525	0.000387	0.001157	MASP1	chr3	-	1.87E+08	1.87E+08	5982
ENSG0000(	1.035792	2.408575	0	0	2.761296	0	0.18734	0.89003	0.93174	ATP13A4	chr3	-	1.93E+08	1.93E+08	4208
ENSG0000(	8.286335	4.817151	2.638828	107.1178	47.86246	92.88204	-3.7804	7.88E-13	5.43E-12	HRASLS	chr3	+	1.93E+08	1.93E+08	1066
ENSG0000(	25.8948	54.19295	44.86007	9.737982	24.85166	24.65895	1.044	0.03125	0.064421	HELB	chr12	+	66696325	66737423	3586
ENSG0000(	2371.963	2441.091	2686.326	1859.206	1681.629	1667.767	0.52435	4.19E-06	1.62E-05	RAP1B	chr12	+	69004619	69054372	2129
ENSG0000(	1.035792	2.408575	3.958241	0	0	1.64393	1.3398	0.30558	0.43107	TSPAN8	chr12	-	71518865	71835678	1516
ENSG0000(	0	0	0	5.243529	8.283888	2.465895	-3.1867	0.011736	0.026845	BEST3	chr12	-	70037140	70093256	3532
ENSG0000(	21.75163	21.67718	3.958241	393.2647	385.661	314.8126	-4.4292	2.02E-46	5.01E-45	RAB3IP	chr12	+	70132461	70216984	9646

ENSG00000(	4.143168	0	5.277655	29.96302	31.29469	15.61733	-2.7824	0.000156	0.000496	PTPRB	chr12	-	70910630	71031220	11332
ENSG00000(	548.9697	671.9925	716.4417	531.8436	680.1992	554.8263	0.13195	0.40421	0.53515	DYRK2	chr12	+	68042118	68059186	8912
ENSG00000(	98.40023	90.32158	71.24834	426.224	377.3771	345.2253	-2.1253	6.00E-25	7.39E-24	YEATS4	chr12	+	69753483	69784576	1434
ENSG00000(	3.107376	2.408575	6.597069	1.498151	7.363456	4.93179	-0.15838	0.87218	0.91975	TAS2R3	chr7	+	1.41E+08	1.41E+08	1101
ENSG00000(	2.071584	8.430014	13.19414	2.996302	3.681728	4.93179	0.8867	0.32267	0.44999	TAS2R4	chr7	+	1.41E+08	1.41E+08	994
ENSG00000(	25.8948	2.408575	7.916483	11.98521	22.09037	2.465895	0.007835	0.99223	0.99518	TAS2R5	chr7	+	1.41E+08	1.41E+08	1150
ENSG00000(	0	0	2.638828	6.74168	3.681728	20.54912	-2.8675	0.007773	0.018535	CRYGN	chr7	-	1.51E+08	1.51E+08	2367
ENSG00000(	0	0	0	7.490755	11.96562	9.041614	-4.0932	0.000522	0.00153	LRRC61	chr7	+	1.5E+08	1.5E+08	1877
ENSG00000(	346.9903	325.1577	233.5362	39.701	12.88605	15.61733	3.659	7.62E-31	1.19E-29	IDUA	chr4	+	980785	998316	2251
ENSG00000(	1424.214	1275.341	1159.765	179.0291	209.8585	223.5745	2.6499	1.71E-70	7.47E-69	FGFRL1	chr4	+	1003724	1020685	3639
ENSG00000(	450.5695	404.6407	394.5047	262.9255	226.4263	221.9305	0.80995	1.19E-06	4.91E-06	TMEM175	chr4	+	926175	952444	2236
ENSG00000(	29.00217	33.72006	34.30476	325.8479	301.9017	320.5663	-3.268	2.35E-40	4.90E-39	AUNIP	chr1	-	26158414	26185903	2116
ENSG00000(	1237.771	1132.03	976.3662	1787.294	1715.685	2205.332	-0.76762	4.24E-08	2.02E-07	PIN1	chr19	+	9945933	9960358	4022
ENSG00000(	640.1194	587.6924	534.3626	798.5145	670.9949	688.8066	-0.29105	0.04247	0.084315	FBXL12	chr19	-	9920943	9938492	1920
ENSG00000(	3234.778	2995.064	3216.731	2755.1	2459.394	2401.781	0.31003	0.004988	0.012359	EMC1	chr1	-	19542158	19578046	6664
ENSG00000(	3231.671	3194.975	4239.276	2282.433	2737.365	2165.878	0.56817	5.17E-05	0.000175	UBR4	chr1	-	19401000	19536770	15945
ENSG00000(	2796.638	2675.927	3235.203	1743.848	2263.342	1854.353	0.56986	1.64E-05	5.94E-05	HP1BP3	chr1	-	21069154	21113816	4822
ENSG00000(	0	3.612863	2.638828	87.64184	132.5422	106.0335	-5.4215	6.29E-18	5.78E-17	EMR2	chr19	-	14843205	14889353	6767
ENSG00000(	2022.902	2106.299	1774.612	1853.962	1927.385	2008.06	0.028644	0.80546	0.87389	SIN3B	chr19	+	16940211	16991164	5129
ENSG00000(	1958.682	1769.099	1720.516	902.636	808.1393	832.6505	1.0969	8.83E-20	8.85E-19	SLC35E1	chr19	-	16660642	16683193	5099
ENSG00000(	732.3049	883.9472	697.9699	758.0645	697.6875	663.3257	0.12652	0.37407	0.50455	EPS15L1	chr19	-	16466050	16582896	3915
ENSG00000(	39.36009	62.62296	29.0271	26.21764	11.04518	9.041614	1.436	0.004745	0.01181	KLF2	chr19	+	16435628	16438685	2018
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	OR7C1	chr19	-	14909958	14911023	1066
ENSG00000(	1.035792	3.612863	5.277655	1.498151	0	0	1.7482	0.16991	0.27005	F2RL3	chr19	+	16999671	17003417	3473
ENSG00000(	21.75163	14.45145	13.19414	20.97412	14.72691	32.05663	-0.43077	0.43101	0.56086	UQCR11	chr19	-	1597171	1605480	1315
ENSG00000(	247.5543	291.4376	266.5216	276.4089	250.3575	409.3385	-0.21676	0.29299	0.4173	GFER	chr16	+	2034208	2037750	2345
ENSG00000(	35.21692	18.06432	6.597069	21.72319	8.283888	9.863579	0.55628	0.39247	0.52329	SYNGR3	chr16	+	2039661	2044276	2051
ENSG00000(	111.8655	83.09585	98.95603	1311.631	1105.439	1395.696	-3.6786	7.13E-102	5.59E-100	PKMYT1	chr16	-	3018025	3030540	2308
ENSG00000(	17.60846	8.430014	3.958241	14.98151	23.0108	19.72716	-0.86201	0.1787	0.28134	WFIKKN1	chr16	+	679239	684116	4878
ENSG00000(	248.5901	281.8033	249.3692	351.3164	294.5382	347.6912	-0.34944	0.042833	0.084958	WDR24	chr16	-	734622	740444	3245
ENSG00000(	268.2701	270.9647	233.5362	54.68252	53.38506	49.3179	2.2806	2.92E-24	3.51E-23	FBXL16	chr16	-	742500	755829	3547
ENSG00000(	321.0955	301.0719	266.5216	1058.444	1023.52	1296.239	-1.9183	1.73E-36	3.24E-35	CHTF18	chr16	+	838046	850737	4494
ENSG00000(	2.071584	6.021439	23.74945	1.498151	24.85166	28.76877	-0.72396	0.37812	0.50885	GNG13	chr16	-	848041	850733	984
ENSG00000(	7.250543	12.04288	7.916483	21.72319	5.522592	13.15144	-0.53947	0.44505	0.57458	TUBBP1	chr8	+	30209389	30211034	1646
ENSG00000(	5077.452	4656.981	6750.121	3303.423	4331.553	3208.129	0.60239	9.10E-05	0.000299	MACF1	chr1	+	39546988	39952849	24828
ENSG00000(	4117.273	3747.743	4029.49	4485.464	5352.312	4841.373	-0.30273	0.006479	0.015693	SMARCA4	chr19	+	11071598	11176071	5790
ENSG00000(	2363.677	2627.756	2154.603	911.6249	1267.435	1274.046	1.047	8.84E-13	6.08E-12	KDM4B	chr19	+	4969125	5153606	5593
ENSG00000(	0	0	1.319414	218.7301	173.9616	213.7109	-7.626	8.44E-20	8.46E-19	TICAM1	chr19	-	4815944	4831716	2676
ENSG00000(	40.39588	49.3758	71.24834	110.1141	99.40666	75.62077	-0.82211	0.009733	0.022692	GAN	chr16	+	81348557	81413940	4695
ENSG00000(	50.7538	49.3758	47.4989	80.90016	61.66894	60.8254	-0.45685	0.15727	0.25348	METTL25	chr12	+	82752276	82873015	2093
ENSG00000(	2.071584	1.204288	0	0	0	4.109825	-0.16956	0.89989	0.9378	IL17B	chr5	-	1.49E+08	1.49E+08	696
ENSG00000(	4.143168	0	10.55531	3.745378	4.60216	4.109825	0.18845	0.85223	0.90579	EMC6	chr17	+	3572109	3572962	762
ENSG00000(	466.1064	493.758	469.7113	603.7549	580.7926	599.2124	-0.31888	0.019837	0.043077	METTL16	chr17	-	2319343	2415185	4271
ENSG00000(	63.18331	81.89156	79.16483	65.16957	33.13555	33.70056	0.74219	0.037083	0.074926	TUBA4A	chr2	-	2.2E+08	2.2E+08	2499

ENSG0000(	1.035792	3.612863	1.319414	32.95932	36.81728	27.12484	-3.693	5.35E-07	2.29E-06	VIL1	chr2	+	2.19E+08	2.19E+08	6531
ENSG0000(	2020.83	2002.73	1798.361	2456.968	2178.663	2836.601	-0.35912	0.004785	0.011897	AAMP	chr2	-	2.19E+08	2.19E+08	2270
ENSG0000(	978.8233	836.98	862.8966	802.2599	737.266	875.3926	0.14964	0.26594	0.38596	PNKD	chr2	+	2.19E+08	2.19E+08	3021
ENSG0000(	996.4318	999.5588	990.8798	759.5626	920.432	732.3707	0.30829	0.02158	0.046421	TNFRSF19	chr13	+	24144509	24250232	4151
ENSG0000(	417.4241	404.6407	539.6402	483.1537	601.0421	507.1524	-0.2249	0.17455	0.27628	RNF6	chr13	-	26706253	26796791	3867
ENSG0000(	2056.047	2067.762	1856.415	2316.891	1726.73	1995.731	-0.01439	0.9126	0.94652	ECHS1	chr10	-	1.35E+08	1.35E+08	1617
ENSG0000(	638.0478	573.241	903.7984	465.925	497.0333	386.3235	0.64458	0.000371	0.001113	AKAP9	chr7	+	91570181	91739987	12475
ENSG0000(	669.1216	615.391	649.1516	234.4606	190.5294	298.3733	1.4112	9.00E-16	7.42E-15	GNG11	chr7	+	93551011	93555831	964
ENSG0000(	1114.512	1054.956	982.9633	991.776	1109.121	1669.411	-0.25673	0.13735	0.22723	SHFM1	chr7	-	96110938	96339203	2773
ENSG0000(	305.5586	249.2876	310.0622	530.3455	565.1452	474.2738	-0.85631	1.54E-07	6.95E-07	HIP1	chr7	-	75162621	75368280	8013
ENSG0000(	722.9827	696.0783	946.0197	1336.351	1052.974	1082.528	-0.55377	0.000341	0.001029	PTPN12	chr7	+	77166592	77269388	3406
ENSG0000(	1642.766	1494.521	1352.399	1230.731	862.4448	890.188	0.58745	0.000127	0.000409	POR	chr7	+	75528518	75616173	2532
ENSG0000(	21.75163	34.92434	47.4989	0.749076	0.920432	0.821965	4.7884	3.66E-09	1.91E-08	FGL2	chr7	-	76822688	76829143	4261
ENSG0000(	316.9523	334.792	262.5633	579.0354	335.9577	480.0275	-0.60665	0.002559	0.006688	STYXL1	chr7	-	75625656	75677322	1570
ENSG0000(	29.00217	34.92434	42.22124	2.247227	1.840864	2.465895	3.7438	1.52E-08	7.50E-08	STEAP4	chr7	-	87905744	87936206	4451
ENSG0000(	991.2529	926.0973	1042.337	596.2641	647.0637	548.2506	0.72278	5.09E-08	2.40E-07	GNAI1	chr7	+	79763271	79848718	3347
ENSG0000(	182.2994	168.6003	142.4967	107.1178	146.3487	171.7907	0.21681	0.36282	0.49254	PMS2P3	chr7	-	75132254	75157478	1490
ENSG0000(	192.6573	187.8689	188.6762	182.7744	198.8133	197.2716	-0.02319	0.9036	0.94038	PEX1	chr7	-	92116334	92157845	5333
ENSG0000(	134.6529	145.7188	109.5113	172.2874	115.9744	140.556	-0.13696	0.572	0.69073	MTERF	chr7	-	91500243	91510034	3882
ENSG0000(	753.0207	776.7656	757.3435	673.4189	530.1688	642.7766	0.30684	0.029364	0.061014	SGCE	chr7	-	94214542	94285521	1871
ENSG0000(	215.4447	236.0404	162.2879	296.6339	242.994	234.26	-0.3312	0.10443	0.18171	RBM48	chr7	+	92158087	92167319	4093
ENSG0000(	198.872	225.2018	302.1458	527.3492	435.3643	408.5166	-0.91719	1.64E-06	6.64E-06	CASD1	chr7	+	94138531	94186331	3942
ENSG0000(	341.8113	337.2006	333.8117	208.243	257.721	186.586	0.63347	0.000503	0.001479	ZNF780B	chr19	-	40534167	40562116	8665
ENSG0000(	70.43385	51.78437	51.45714	8.988907	1.840864	1.64393	3.5876	1.36E-10	7.98E-10	LRFN1	chr19	-	39797208	39805976	3381
ENSG0000(	706.4101	658.7454	579.2227	336.3349	388.4223	367.4183	0.83178	2.88E-08	1.39E-07	ZFP36	chr19	+	39897453	39900052	1786
ENSG0000(	338.704	338.4048	328.534	238.206	207.0972	192.3398	0.65368	0.000181	0.000568	SRD5A3	chr4	+	56212276	56239263	4190
ENSG0000(	0	0	0	2.247227	4.60216	3.28786	-2.5096	0.056673	0.10833	SPINK2	chr4	-	57676026	57687908	763
ENSG0000(	51.7896	77.07441	54.09597	161.0512	156.4734	170.9687	-1.4058	6.13E-08	2.87E-07	RASL11B	chr4	+	53728457	53733000	1993
ENSG0000(	5463.802	5512.025	4992.662	12512.56	9416.94	9287.382	-0.96488	1.11E-13	8.12E-13	PAICS	chr4	+	57301907	57327534	3340
ENSG0000(	1945.217	1824.496	2344.598	478.6593	636.9389	490.7131	1.9236	4.04E-38	7.93E-37	KDR	chr4	-	55944644	55991756	5831
ENSG0000(	367.7061	405.845	485.5443	1223.989	986.7031	877.0366	-1.292	3.11E-15	2.49E-14	PPAT	chr4	-	57259528	57301781	4043
ENSG0000(	690.8732	728.5941	701.9281	480.9065	524.6462	612.3639	0.38996	0.006659	0.016085	TUBGCP6	chr22	-	50656118	50683421	6053
ENSG0000(	243.4111	258.9219	167.5656	205.2467	160.1552	175.0785	0.30872	0.15655	0.25258	ADM2	chr22	+	50919985	50924869	4276
ENSG0000(	784.0945	757.497	682.1369	643.4559	449.1708	507.1524	0.47264	0.002965	0.007665	DGCR6L	chr22	-	20301799	20307603	1154
ENSG0000(	533.4328	550.3595	531.7238	741.5848	918.5911	764.4274	-0.58334	3.67E-05	0.000127	DGCR8	chr22	+	20067755	20099400	4695
ENSG0000(	42.46747	31.31148	30.34652	119.8521	96.64536	130.6924	-1.707	4.82E-08	2.28E-07	ASPHD2	chr22	+	26825239	26840981	3357
ENSG0000(	0	2.408575	0	1.498151	3.681728	0.821965	-0.80727	0.53988	0.6633	VPREB3	chr22	-	24094930	24096655	610
ENSG0000(	651.5131	655.1325	525.1267	941.588	768.5607	1009.373	-0.56765	0.000199	0.000621	SDF2L1	chr22	+	21996550	21998587	865
ENSG0000(	0	0	0	13.48336	4.60216	0.821965	-3.356	0.008034	0.019079	GAL3ST1	chr22	-	30950622	30970574	1908
ENSG0000(	967.4296	902.0115	973.7274	4788.091	3793.1	3662.676	-2.1018	1.57E-58	5.25E-57	YWHAH	chr22	+	32340447	32353590	1879
ENSG0000(	4.143168	0	2.638828	2.996302	13.80648	10.68554	-1.6815	0.084703	0.15284	C22orf24	chr22	-	32329507	32341504	1247
ENSG0000(	18.64425	21.67718	15.83297	0	0.920432	0	4.7664	2.74E-06	1.08E-05	POM121L9	chr22	+	24647796	24661493	5018
ENSG0000(	87.00652	115.6116	129.3026	60.67512	69.0324	53.42772	0.84594	0.002889	0.007483	GNAZ	chr22	+	23412540	23467224	3340
ENSG0000(	91.14969	102.3645	118.7472	62.17327	122.4175	119.1849	0.040348	0.8915	0.93263	MGAT3	chr22	+	39853349	39888199	5062

ENSG00000(	12.4295	8.430014	7.916483	0	10.12475	9.041614	0.53293	0.54408	0.66633	ADORA2A	chr22	+	24813847	24838328	2569
ENSG00000(	8022.208	8361.37	6773.87	8027.843	6627.11	7254.662	0.079774	0.50814	0.63563	ATF4	chr22	+	39915700	39918691	2019
ENSG00000(	203.0152	192.686	166.2461	159.5531	114.1336	135.6242	0.45334	0.039608	0.079324	A4GALT	chr22	-	43088127	43117304	2321
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RFPL3	chr22	+	32750872	32757148	1488
ENSG00000(	1918.287	1838.947	1461.91	1890.667	1442.317	1490.222	0.11368	0.43554	0.56513	CDC42EP1	chr22	+	37956454	37965412	2181
ENSG00000(	11.39371	18.06432	21.11062	0	0	1.64393	4.0934	2.36E-05	8.36E-05	APOL3	chr22	-	36536372	36562225	3634
ENSG00000(	32.10955	20.47289	17.15238	99.62705	129.7809	136.4462	-2.334	8.87E-12	5.66E-11	MCHR1	chr22	+	41074754	41078818	2851
ENSG00000(	428.8178	388.9849	426.1707	325.0988	263.2436	233.438	0.5944	0.000671	0.001933	TPST2	chr22	-	26921458	26992681	2188
ENSG00000(	4.143168	9.634302	1.319414	29.21395	16.56778	32.05663	-2.2003	0.001165	0.003233	BAIAP2L2	chr22	-	38480896	38506677	2146
ENSG00000(	1456.323	1431.898	1031.782	2056.212	1636.528	1622.559	-0.43727	0.0044	0.011022	MPST	chr22	+	37415676	37425863	5872
ENSG00000(	0	0	0	2.247227	0.920432	4.93179	-2.1553	0.10814	0.18694	GALR3	chr22	+	38219389	38221502	1157
ENSG00000(	232.0174	211.9546	224.3003	370.0433	257.721	320.5663	-0.50383	0.008004	0.019017	TST	chr22	-	37406900	37415681	1797
ENSG00000(	0	10.83859	1.319414	3.745378	0	0	1.1226	0.37578	0.50624	APOL5	chr22	+	36113919	36125530	1438
ENSG00000(	429.8536	486.5322	395.8241	73.4094	60.74851	68.22309	2.6795	2.72E-42	6.04E-41	APOL2	chr22	-	36622256	36636000	2685
ENSG00000(	122.2234	105.9773	113.4696	1.498151	2.761296	2.465895	5.4392	1.21E-23	1.42E-22	RAC2	chr22	-	37621301	37640488	1482
ENSG00000(	492.0012	521.4566	535.682	125.8447	160.1552	198.0935	1.6714	3.25E-19	3.18E-18	LIF	chr22	-	30636436	30642840	3969
ENSG00000(	375.9925	431.135	341.7282	708.6255	605.6443	775.9349	-0.86048	5.24E-08	2.47E-07	C22orf23	chr22	-	38339528	38349676	1560
ENSG00000(	23.82321	31.31148	32.98534	54.68252	45.10117	55.07165	-0.80452	0.035564	0.072154	APOBEC3F	chr22	+	39436609	39449915	2694
ENSG00000(	1.035792	1.204288	13.19414	13.48336	10.12475	21.37109	-1.4211	0.085044	0.15335	RIBC2	chr22	+	45809572	45828376	1478
ENSG00000(	0	0	0	14.23244	8.283888	8.219649	-4.2056	0.000333	0.001007	KRT17	chr17	-	39775689	39781094	1834
ENSG00000(	1293.704	1330.738	1205.944	1243.465	1132.131	1346.379	0.041315	0.73705	0.82369	EMC4	chr15	+	34517200	34522357	2019
ENSG00000(	54.89697	42.15007	36.94359	2.247227	0	2.465895	4.4377	7.54E-11	4.50E-10	RNF112	chr17	+	19314438	19320589	3212
ENSG00000(	325.2387	320.3405	357.5611	1767.818	1893.329	1762.293	-2.4305	3.31E-81	1.83E-79	SPECC1	chr17	+	19912657	20222339	8133
ENSG00000(	1928.645	2094.256	1997.592	45.69361	45.10117	37.81039	5.5272	2.26E-237	1.02E-234	CPA4	chr7	+	1.3E+08	1.3E+08	2797
ENSG00000(	929.1053	1001.967	1151.848	110.1141	146.3487	129.0485	2.9917	8.42E-75	4.03E-73	DOCK4	chr7	-	1.11E+08	1.12E+08	7997
ENSG00000(	200.9436	223.9975	180.7597	327.346	257.721	238.3698	-0.44111	0.026019	0.054888	POT1	chr7	-	1.24E+08	1.25E+08	4080
ENSG00000(	964.3223	818.9156	667.6234	832.2229	499.7946	457.0125	0.4513	0.028235	0.058929	ATP6V1F	chr7	+	1.29E+08	1.29E+08	711
ENSG00000(	478.5359	486.5322	500.0578	595.5151	712.4144	766.8933	-0.50024	0.000699	0.002011	NAA38	chr7	+	1.18E+08	1.18E+08	4030
ENSG00000(	159.512	140.9017	166.2461	128.841	122.4175	110.1433	0.3656	0.099588	0.17486	CDHR3	chr7	+	1.06E+08	1.06E+08	6500
ENSG00000(	617.332	602.1439	461.7948	481.6556	484.1472	649.3523	0.059019	0.73148	0.82039	PRKRIP1	chr7	+	1.02E+08	1.02E+08	3430
ENSG00000(	153.2972	171.0089	141.1773	4218.044	3201.262	3536.915	-4.5419	2.93E-200	8.72E-198	VGF	chr7	-	1.01E+08	1.01E+08	2575
ENSG00000(	53.86118	25.29004	62.01245	7318.468	10102.66	8402.947	-7.3855	6.14E-97	4.46E-95	PODXL	chr7	-	1.31E+08	1.31E+08	6170
ENSG00000(	176.0846	184.256	221.6615	4.494453	5.522592	14.79537	4.4652	1.31E-33	2.24E-32	FOXP2	chr7	+	1.14E+08	1.14E+08	8301
ENSG00000(	33.14534	55.39724	60.69303	30.7121	33.13555	63.2913	0.21965	0.58895	0.70597	STRIP2	chr7	+	1.29E+08	1.29E+08	5115
ENSG00000(	400.8515	409.4578	402.4212	552.8178	392.104	497.2888	-0.25065	0.12955	0.21662	RABL5	chr7	-	1.01E+08	1.01E+08	1785
ENSG00000(	998.5034	865.8829	1134.696	781.2858	670.0745	629.6251	0.52467	0.000362	0.001088	MKLN1	chr7	+	1.31E+08	1.31E+08	11156
ENSG00000(	272.4133	275.7819	292.9099	368.5452	318.4695	328.786	-0.27297	0.099323	0.17448	DNAJB9	chr7	+	1.08E+08	1.08E+08	2715
ENSG00000(	12073.19	12184.98	12464.5	5687.731	6909.683	7230.825	0.88761	1.12E-14	8.64E-14	FLNC	chr7	+	1.28E+08	1.28E+08	9188
ENSG00000(	846.242	764.7227	839.1472	806.7544	905.7051	936.218	-0.11162	0.39096	0.52178	LRRC4	chr7	-	1.28E+08	1.28E+08	3828
ENSG00000(	12437.79	12317.45	13992.38	6978.388	6801.072	5897.598	0.97586	2.29E-18	2.15E-17	CALU	chr7	+	1.28E+08	1.28E+08	4418
ENSG00000(	193.6931	195.0946	199.2315	29.96302	36.81728	40.27628	2.4386	2.05E-21	2.20E-20	CCDC136	chr7	+	1.28E+08	1.28E+08	4169
ENSG00000(	1076.188	1097.106	961.8526	820.9868	890.0577	796.484	0.3225	0.010899	0.02513	SMO	chr7	+	1.29E+08	1.29E+08	3738
ENSG00000(	0	2.408575	1.319414	4.494453	2.761296	2.465895	-1.033	0.38857	0.5193	IRF5	chr7	+	1.29E+08	1.29E+08	2786
ENSG00000(	1474.968	1531.854	1377.468	29.21395	27.61296	18.90519	5.8216	3.80E-185	9.20E-183	LRRC17	chr7	+	1.03E+08	1.03E+08	2002

ENSG00000(	622.5109	600.9396	861.5772	234.4606	326.7534	240.0138	1.3741	2.00E-13	1.43E-12	KLHDC10	chr7	+	1.3E+08	1.3E+08	4473
ENSG00000(	637.012	756.2927	670.2622	855.4443	733.5843	713.4655	-0.15865	0.2606	0.37968	NDUFA5	chr7	-	1.23E+08	1.23E+08	5608
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	FEZF1	chr7	-	1.22E+08	1.22E+08	2099
ENSG00000(	140.8677	139.6974	110.8308	112.3613	73.63456	78.90863	0.55616	0.035281	0.071653	OPN1SW	chr7	-	1.28E+08	1.28E+08	1096
ENSG00000(	944.6422	958.613	815.3977	1292.904	1048.372	1239.523	-0.39623	0.003366	0.008633	MRPS12	chr19	+	39421188	39423802	1220
ENSG00000(	3278.281	3223.878	3967.477	2311.647	2547.756	1891.341	0.63139	3.83E-06	1.49E-05	MYO1B	chr2	+	1.92E+08	1.92E+08	5082
ENSG00000(	136.7245	113.203	122.7055	2.996302	12.88605	13.9734	3.5855	2.80E-19	2.75E-18	HOXD3	chr2	+	1.77E+08	1.77E+08	4212
ENSG00000(	406.0304	334.792	385.2688	531.8436	406.8309	563.046	-0.41408	0.015245	0.033973	MTX2	chr2	+	1.77E+08	1.77E+08	1592
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	PDE11A	chr2	-	1.78E+08	1.79E+08	4458
ENSG00000(	1022.327	1098.31	968.4497	385.0248	334.1168	326.3201	1.558	4.20E-29	6.15E-28	CHN1	chr2	-	1.76E+08	1.76E+08	2447
ENSG00000(	6.214751	15.65574	5.277655	60.67512	48.7829	36.16646	-2.3322	7.99E-06	3.00E-05	GAD1	chr2	+	1.72E+08	1.72E+08	3988
ENSG00000(	8.286335	7.225726	13.19414	18.72689	17.48821	16.4393	-0.8361	0.17734	0.2795	EIF2S2P4	chr2	+	1.72E+08	1.72E+08	1342
ENSG00000(	99.43602	131.2674	118.7472	143.0734	132.5422	133.9803	-0.23071	0.32176	0.44901	OSGEPL1	chr2	-	1.91E+08	1.91E+08	2216
ENSG00000(	697.088	716.5512	724.3582	806.7544	621.2916	702.78	0.003531	0.98011	0.98845	ORMDL1	chr2	-	1.91E+08	1.91E+08	2692
ENSG00000(	466.1064	509.4137	476.3084	1652.461	1378.807	1375.147	-1.5985	1.31E-32	2.17E-31	HAT1	chr2	+	1.73E+08	1.73E+08	3845
ENSG00000(	407.0662	404.6407	323.2564	0	0	0	9.4804	1.24E-24	1.51E-23	HOXD9	chr2	+	1.77E+08	1.77E+08	2418
ENSG00000(	547.9339	546.7466	554.1538	0	0	0	9.9611	4.55E-28	6.38E-27	HOXD10	chr2	+	1.77E+08	1.77E+08	1989
ENSG00000(	332.4892	321.5448	407.6989	0	0	0	9.3932	4.77E-24	5.69E-23	HOXD11	chr2	+	1.77E+08	1.77E+08	1939
ENSG00000(	36.25272	62.62296	38.263	2.247227	0	0.821965	4.9148	3.84E-11	2.34E-10	HOXD13	chr2	+	1.77E+08	1.77E+08	2240
ENSG00000(	1692.484	1571.595	2116.34	1077.92	1518.713	1288.019	0.46859	0.002232	0.005898	HERC2	chr15	-	28356186	28567298	15337
ENSG00000(	27.96638	22.88147	32.98534	88.39091	94.8045	90.41614	-1.6829	5.11E-07	2.19E-06	SNRPN	chr15	+	25068794	25223870	1904
ENSG00000(	7.250543	8.430014	5.277655	26.96672	12.88605	9.863579	-1.1587	0.095572	0.16892	PSMG2	chr18	+	12702425	12725739	1686
ENSG00000(	1080.331	1164.546	1461.91	1111.628	1021.68	955.1232	0.26124	0.066114	0.12355	TWSG1	chr18	+	9334765	9402418	3756
ENSG00000(	2.071584	14.45145	9.235896	14.23244	1.840864	11.50751	-0.10801	0.89707	0.93616	ARHGAP22	chr10	-	49654077	49864310	2764
ENSG00000(	1337.207	1396.974	1607.046	1828.493	1535.281	1287.197	-0.09998	0.49127	0.62034	EIF2AK4	chr15	+	40226347	40327797	5499
ENSG00000(	3.107376	1.204288	5.277655	304.1247	340.5598	261.3848	-6.3393	9.83E-37	1.85E-35	MYO5C	chr15	-	52484519	52587995	6971
ENSG00000(	13.46529	16.86003	15.83297	304.1247	448.2504	433.1755	-4.6283	6.56E-52	1.90E-50	CGNL1	chr15	+	57668165	57842925	7224
ENSG00000(	290.0217	187.8689	341.7282	131.8373	152.7917	147.1317	0.91828	6.13E-05	0.000205	TMOD2	chr15	+	52043758	52108565	9191
ENSG00000(	161.5835	143.3102	269.1604	68.16587	90.20234	60.00344	1.379	9.40E-07	3.91E-06	TTBK2	chr15	-	43030932	43213007	10905
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	ELL3	chr15	-	44064798	44069741	2352
ENSG00000(	158.4762	118.0202	118.7472	50.18806	49.70333	53.42772	1.3552	7.07E-07	2.98E-06	C15orf57	chr15	-	40820882	40857256	6131
ENSG00000(	490.9654	537.1123	596.375	464.4268	578.9517	619.7615	-0.03436	0.82863	0.88996	INO80	chr15	-	41271078	41408552	6439
ENSG00000(	510.6454	534.7037	592.4168	607.5003	530.1688	486.6032	0.010192	0.94576	0.96733	NARG2	chr15	-	60711808	60771359	7209
ENSG00000(	0	1.204288	2.638828	5.992604	2.761296	3.28786	-1.278	0.27242	0.3932	DLL4	chr15	+	41221538	41231237	3339
ENSG00000(	3.107376	10.83859	10.55531	2.996302	0.920432	0.821965	1.9601	0.047383	0.092645	ALDH1A2	chr15	-	58245622	58790065	4098
ENSG00000(	782.0229	674.4011	957.8944	699.6366	805.378	643.5985	0.16729	0.28863	0.41229	FAM63B	chr15	+	59063391	59154099	9238
ENSG00000(	952.9286	962.2259	915.6732	767.0534	779.6059	824.4308	0.25543	0.037093	0.074938	IVD	chr15	+	40697686	40728146	4665
ENSG00000(	283.807	264.9433	288.9516	1066.684	860.6039	909.9152	-1.7554	5.23E-32	8.46E-31	KNSTRN	chr15	+	40674922	40686446	1899
ENSG00000(	641.1552	594.9181	538.3208	1763.324	1762.627	1962.03	-1.6238	1.56E-37	3.01E-36	DUT	chr15	+	48623208	48635570	2147
ENSG00000(	194.7289	177.0303	158.3297	237.4569	178.5638	172.6126	-0.14975	0.48336	0.61261	CHAC1	chr15	+	41245160	41248710	1842
ENSG00000(	751.9849	757.497	643.8739	1570.811	1445.999	1620.915	-1.1035	3.60E-18	3.35E-17	CLN6	chr15	-	68499330	68549549	2242
ENSG00000(	2791.459	2772.27	3210.134	4104.185	3794.021	3613.358	-0.39153	0.000563	0.00164	ARPP19	chr15	-	52839242	52862080	5362
ENSG00000(	706.4101	699.6912	887.9655	529.5964	761.1973	512.0841	0.34655	0.046503	0.091144	VPS13C	chr15	-	62144588	62352672	13400
ENSG00000(	104.615	87.913	134.5802	173.7855	146.3487	161.1051	-0.55697	0.020044	0.043462	CALML4	chr15	-	68483043	68498417	4155

ENSG0000(	1785.705	1736.583	1453.994	5.992604	5.522592	10.68554	7.7053	7.53E-145	1.09E-142	ISLR	chr15	+	74466012	74469213	2371
ENSG0000(	30.03797	43.35436	43.54065	152.8114	67.19154	91.23811	-1.3968	0.000101	0.000328	THAP10	chr15	-	71173681	71185124	2399
ENSG0000(	2831.855	2732.529	2314.252	89.13999	95.72493	87.95025	4.8395	4.17E-233	1.72E-230	LOXL1	chr15	+	74218330	74244478	2786
ENSG0000(	9.322127	7.225726	10.55531	5.992604	8.283888	0.821965	0.75581	0.37386	0.5044	CCRL1	chr3	+	1.32E+08	1.32E+08	1914
ENSG0000(	629.7615	727.3898	654.4292	1090.654	611.1668	817.8551	-0.3248	0.075841	0.13896	ANAPC13	chr3	-	1.34E+08	1.34E+08	1840
ENSG0000(	344.9187	384.1678	415.6153	537.8362	467.5795	467.698	-0.36521	0.018716	0.040882	MBD4	chr3	-	1.29E+08	1.29E+08	2478
ENSG0000(	2765.564	2807.195	3067.637	2957.35	2223.764	2165.056	0.23299	0.085945	0.15479	COPB1	chr11	-	14464986	14521573	3481
ENSG0000(	68.36227	78.2787	50.13772	101.8743	92.96363	110.9653	-0.62592	0.028219	0.058906	PSMA1	chr11	-	14515329	14665181	1527
ENSG0000(	3634.594	3795.915	2769.45	1612.011	1614.438	1836.27	1.0084	1.19E-13	8.63E-13	SUMF2	chr7	+	56131695	56148363	2052
ENSG0000(	7101.389	7490.67	8251.614	3973.097	4252.396	3308.409	0.98388	8.22E-16	6.80E-15	PALLD	chr4	+	1.69E+08	1.7E+08	6435
ENSG0000(	1550.58	1545.101	1712.599	2274.193	2195.23	2095.189	-0.44892	6.11E-05	0.000205	SPCS3	chr4	+	1.77E+08	1.77E+08	4571
ENSG0000(	15.53688	2.408575	2.638828	4.494453	4.60216	0.821965	0.90715	0.358	0.48751	BBOX1	chr11	+	27062272	27149356	1886
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	MYOD1	chr11	+	17741115	17743678	1801
ENSG0000(	83.89914	109.5902	68.60952	51.68621	30.37426	40.27628	1.0775	0.001316	0.003624	SERGEF	chr11	-	17809595	18034709	1566
ENSG0000(	293.1291	298.6634	306.104	20.22504	18.40864	20.54912	3.8842	3.19E-51	9.08E-50	KCNC1	chr11	+	17756359	17804602	6766
ENSG0000(	1.035792	4.817151	3.958241	5.243529	7.363456	16.4393	-1.3882	0.12086	0.20506	TPH1	chr11	-	18039111	18063973	5325
ENSG0000(	1.035792	2.408575	1.319414	0	0	0	1.6865	0.21314	NA	CSRP3	chr11	-	19203578	19232120	1456
ENSG0000(	15.53688	13.24716	27.70769	135.5827	80.99802	87.12828	-2.3923	7.82E-10	4.32E-09	E2F8	chr11	-	19245610	19263167	3432
ENSG0000(	1902.75	1891.936	1938.219	1590.287	1254.549	1481.181	0.40472	0.001048	0.00293	DCTD	chr4	-	1.84E+08	1.84E+08	1972
ENSG0000(	44.53905	28.90291	32.98534	1226.237	848.6383	1122.804	-4.8624	1.52E-103	1.24E-101	SOX15	chr17	-	7491496	7493488	1396
ENSG0000(	211.3015	183.0517	200.5509	788.7766	634.1776	724.9731	-1.8452	3.49E-30	5.34E-29	FAM64A	chr17	+	6347735	6354789	1948
ENSG0000(	432.961	456.425	376.0329	462.9287	506.2376	568.7997	-0.27911	0.074064	0.13614	RPAIN	chr17	+	5322961	5336196	3817
ENSG0000(	6.214751	1.204288	1.319414	10.48706	6.443024	6.575719	-1.1974	0.2019	0.3096	USP6	chr17	+	5019733	5078329	8464
ENSG0000(	6.214751	3.612863	5.277655	11.98521	12.88605	10.68554	-1.1232	0.13848	0.22876	SHBG	chr17	+	7517382	7536700	1382
ENSG0000(	894.9242	751.4755	786.3706	823.234	847.7179	997.0434	-0.13189	0.3416	0.47048	PLD2	chr17	+	4710391	4726729	3503
ENSG0000(	2.071584	1.204288	0	0	0	0.821965	0.85521	0.52571	NA	CD68	chr17	+	7482785	7485429	1876
ENSG0000(	541.7192	568.4238	620.1245	626.9762	610.2464	911.5591	-0.31219	0.066798	0.12463	TXNDC17	chr17	+	6544078	6547861	2219
ENSG0000(	69.39806	79.48299	52.77655	4.494453	5.522592	3.28786	3.7876	6.40E-14	4.73E-13	ATP1B2	chr17	+	7549945	7561086	3153
ENSG0000(	1124.87	1059.773	1142.612	1325.864	1180.914	1426.931	-0.24144	0.052503	0.10133	FXR2	chr17	-	7494548	7518189	2957
ENSG0000(	4444.583	4175.266	4194.416	4041.263	4434.641	4713.969	-0.04141	0.70029	0.79629	KIF1C	chr17	+	4901243	4931696	7919
ENSG0000(	1175.624	1263.298	976.3662	1436.727	948.9654	1017.593	0.004758	0.97706	0.98664	MPDU1	chr17	+	7486847	7496107	1645
ENSG0000(	10.35792	3.612863	7.916483	14.98151	11.04518	12.32947	-0.74344	0.29642	0.42085	MMP28	chr17	-	34083268	34122711	2459
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CCL4	chr17	+	34430983	34433014	1774
ENSG0000(	116.0087	115.6116	89.72014	235.9588	219.9832	279.4681	-1.1834	5.27E-08	2.48E-07	MRM1	chr17	+	34958001	34965407	1857
ENSG0000(	857.6357	826.1414	1203.305	569.2974	648.9046	468.52	0.77169	8.14E-06	3.05E-05	PHF20L1	chr8	+	1.34E+08	1.34E+08	7809
ENSG0000(	6.214751	9.634302	9.235896	46.44268	54.30549	48.49593	-2.4944	4.77E-07	2.05E-06	LRRC6	chr8	-	1.34E+08	1.34E+08	1734
ENSG0000(	684.6584	670.7883	804.8424	650.1976	643.382	616.4737	0.17607	0.19822	0.30551	CCNT1	chr12	-	49082247	49110681	6973
ENSG0000(	68.36227	87.913	113.4696	126.5938	164.7573	124.9387	-0.6249	0.018947	0.041332	PUS7L	chr12	-	44122410	44152620	4364
ENSG0000(	616.2962	615.391	480.2666	516.8621	559.6227	605.7881	0.026965	0.86032	0.91124	KRI1	chr19	-	10663761	10676713	3744
ENSG0000(	7272.295	7271.489	7310.872	9774.687	11303.83	11724.51	-0.58492	4.89E-08	2.31E-07	ILF3	chr19	+	10764937	10803093	6119
ENSG0000(	1920.358	1913.613	1873.568	3433.762	2852.419	3052.778	-0.70931	5.16E-10	2.89E-09	SLC44A2	chr19	+	10713133	10755235	3784
ENSG0000(	16.57267	12.04288	0	782.0349	776.8446	849.0898	-5.6649	2.00E-11	1.24E-10	AP1M2	chr19	-	10683347	10697991	1757
ENSG0000(	96.32865	121.6331	97.63662	64.4205	45.10117	58.35951	0.89576	0.001881	0.005035	CDKN2D	chr19	-	10677138	10679735	1422
ENSG0000(	163.6551	172.2131	192.6344	117.6049	103.0884	106.8554	0.68252	0.001828	0.004908	MTUS1	chr8	-	17501304	17658426	6256

ENSG0000(	1.035792	3.612863	1.319414	11.98521	13.80648	24.65895	-2.7415	0.001163	0.003229	KLK14	chr19	-	51580752	51587502	1133
ENSG0000(	322.1313	279.3948	271.7992	608.9984	438.1256	511.2622	-0.83147	1.55E-06	6.29E-06	NGDN	chr14	+	23938897	23979071	2763
ENSG0000(	1.035792	0	2.638828	4.494453	1.840864	0	-0.5255	0.6849	0.78429	RIPK3	chr14	-	24805227	24809251	1930
ENSG0000(	8.286335	2.408575	5.277655	0.749076	1.840864	3.28786	1.1938	0.25227	0.37004	ADCY4	chr14	-	24787555	24804299	5276
ENSG0000(	490.9654	511.8223	426.1707	420.2314	322.1512	342.7594	0.39496	0.016846	0.037211	RAB2B	chr14	-	21927179	21945132	2928
ENSG0000(	783.0587	773.1527	811.4395	570.7956	589.9969	732.3707	0.32161	0.024465	0.051961	BCL2L2	chr14	+	23767999	23780968	3605
ENSG0000(	882.4947	794.8299	733.5941	2166.326	1887.806	2096.011	-1.3471	7.85E-27	1.05E-25	AJUBA	chr14	-	23440383	23451851	4262
ENSG0000(	384.2788	403.4364	391.8659	328.0951	221.8241	273.7143	0.51329	0.00429	0.010773	DTD2	chr14	-	31915242	31926716	2717
ENSG0000(	169.8699	213.1589	216.3839	552.8178	389.3427	428.2437	-1.1913	4.53E-10	2.55E-09	PARP2	chr14	+	20811741	20826064	1980
ENSG0000(	244.4469	264.9433	317.9787	266.6709	233.7897	228.5062	0.17841	0.33361	0.46174	HEATR5A	chr14	-	31760994	31889788	7840
ENSG0000(	0	0	1.319414	2.996302	3.681728	3.28786	-1.9089	0.13548	0.22472	FOXA1	chr14	-	38059189	38069245	2862
ENSG0000(	1929.68	1906.387	1992.315	1533.358	1376.046	1161.436	0.51628	5.87E-05	0.000197	SNX6	chr14	-	35030300	35099389	3398
ENSG0000(	331.4534	303.4805	273.1187	313.1136	264.164	306.5929	0.039593	0.81896	0.88301	EAPP	chr14	-	34985135	35008916	1321
ENSG0000(	23.82321	21.67718	27.70769	76.40571	51.54419	21.37109	-1.0004	0.033957	0.069283	EGLN3	chr14	-	34393437	34931980	2849
ENSG0000(	269.3059	217.9761	335.1311	510.8695	557.7818	352.623	-0.78579	0.00014	0.000446	MIS18BP1	chr14	-	45672393	45722743	4777
ENSG0000(	1.035792	13.24716	6.597069	22.47227	9.20432	15.61733	-1.0998	0.14592	0.2386	NRL	chr14	-	24549316	24584223	2103
ENSG0000(	0	0	0	24.71949	14.72691	14.79537	-5.0387	5.62E-06	2.15E-05	RNASE1	chr14	-	21269387	21271437	1348
ENSG0000(	307.6302	309.5019	274.4381	317.608	223.665	340.2935	0.015256	0.93694	0.96179	NEDD8	chr14	-	24686058	24701660	2300
ENSG0000(	3282.425	3074.547	2588.69	2643.488	2291.876	2491.376	0.26815	0.030151	0.062457	DAD1	chr14	-	23033805	23058175	731
ENSG0000(	593.5088	545.5423	643.8739	434.4638	519.1236	521.1258	0.27336	0.066184	0.12366	TEP1	chr14	-	20833826	20881588	10695
ENSG0000(	5.17896	6.021439	2.638828	119.103	181.3251	127.4046	-4.7609	4.66E-23	5.33E-22	EPB41L4A	chr5	-	1.11E+08	1.12E+08	4707
ENSG0000(	94.25706	110.7945	96.31721	117.6049	61.66894	86.30632	0.17511	0.5463	0.66835	CDO1	chr5	-	1.15E+08	1.15E+08	1860
ENSG0000(	1416.963	1358.437	1443.439	1852.464	1499.384	1521.457	-0.20812	0.097831	0.1722	REEP5	chr5	-	1.12E+08	1.12E+08	3318
ENSG0000(	703.3027	573.241	765.26	519.8584	537.5323	489.8911	0.39872	0.007918	0.018843	ITFG1	chr16	-	47188298	47498060	3400
ENSG0000(	95.29286	90.32158	77.84541	134.0845	138.0648	156.1733	-0.69221	0.004265	0.010718	QRICH2	chr17	-	74270130	74303761	5359
ENSG0000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	FOXJ1	chr17	-	74132414	74137380	2641
ENSG0000(	3814.822	3862.151	4398.926	1125.861	1135.813	1156.505	1.8175	8.46E-60	2.93E-58	SEC14L1	chr17	+	75082798	75213179	5437
ENSG0000(	239.2679	219.1804	229.578	488.3973	499.7946	443.8611	-1.0529	5.48E-11	3.31E-10	RHBDF2	chr17	-	74466973	74497872	3599
ENSG0000(	5.17896	1.204288	3.958241	0	7.363456	1.64393	0.17642	0.87666	0.92281	AANAT	chr17	+	74449433	74466199	1913
ENSG0000(	295.2007	262.5347	265.2022	17.97781	17.48821	21.37109	3.8177	3.04E-46	7.50E-45	ARHGEF6	chrX	-	1.36E+08	1.36E+08	6019
ENSG0000(	487.858	457.6293	443.323	327.346	266.0048	225.2184	0.75879	1.53E-05	5.55E-05	MAP7D3	chrX	-	1.35E+08	1.35E+08	4567
ENSG0000(	25.8948	31.31148	42.22124	38.20285	44.18074	36.98842	-0.26405	0.50967	0.63694	FGF13	chrX	-	1.38E+08	1.38E+08	2676
ENSG0000(	789.2734	792.4213	778.4541	782.7839	824.7071	727.439	0.015843	0.90092	0.93847	ASH2L	chr8	+	37962760	38001594	3090
ENSG0000(	134.6529	118.0202	105.5531	240.4533	178.5638	164.393	-0.69681	0.002848	0.007387	TTI2	chr8	-	33330904	33371119	2363
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	ART1	chr11	+	3666358	3685646	1312
ENSG0000(	18.64425	16.86003	17.15238	32.21025	37.73771	27.12484	-0.85142	0.071381	0.132	CHRNA10	chr11	-	3686817	3692614	1945
ENSG0000(	795.4882	827.3457	573.945	289.1432	280.7318	257.275	1.4048	9.71E-17	8.38E-16	CDKN1C	chr11	-	2904443	2907111	2051
ENSG0000(	46.61064	43.35436	35.62417	324.3497	269.6866	263.8507	-2.743	2.53E-29	3.74E-28	SGOL1	chr3	-	20202085	20227784	2587
ENSG0000(	5262.859	5532.498	4021.573	2824.764	2416.134	2723.17	0.89352	2.94E-11	1.81E-10	RPS4Y1	chrY	+	2709527	2734997	998
ENSG0000(	1.035792	0	0	0	1.840864	0	-0.17777	0.89006	NA	CDH15	chr16	+	89238175	89261900	2847
ENSG0000(	864.8862	882.7429	759.9823	801.5108	854.1609	984.714	-0.07342	0.59259	0.70878	KLF16	chr19	-	1852399	1863567	2888
ENSG0000(	1233.628	1171.772	1013.31	1323.616	1028.123	1111.297	-0.01839	0.89503	0.93511	TMEM8A	chr16	-	420773	437113	3691
ENSG0000(	448.4979	446.7907	414.2959	849.4517	752.9134	955.9452	-0.96304	3.21E-11	1.97E-10	DOHH	chr19	-	3490819	3500938	2031
ENSG0000(	1003.682	1099.515	1013.31	739.3376	733.5843	767.7152	0.47486	0.000112	0.000361	MAU2	chr19	+	19431490	19469564	4994

ENSG00000(	352.1692	466.0593	315.3399	384.2758	385.661	384.6796	-0.02602	0.88179	0.92623	SHC2	chr19	-	416583	460996	2650
ENSG00000(	478.5359	367.3078	350.9641	171.5383	190.5294	154.5294	1.2095	1.71E-10	9.97E-10	LPPR3	chr19	-	812518	821978	2357
ENSG00000(	2626.768	2407.371	1840.582	2295.917	1839.023	2294.104	0.096766	0.51063	0.63792	ABHD17A	chr19	-	1876809	1885546	5623
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	LBP	chr20	+	36974759	37005665	1961
ENSG00000(	4.143168	0	2.638828	5.243529	0	0	0.23198	0.85798	0.90972	SYT5	chr19	-	55682567	55691809	3792
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	TNNI3	chr19	-	55663137	55669141	992
ENSG00000(	0	1.204288	1.319414	0.749076	2.761296	8.219649	-1.5834	0.1963	0.30303	CBFA2T3	chr16	-	88941266	89043612	4477
ENSG00000(	756.1281	873.1086	601.6527	585.7771	509.9193	545.7847	0.44141	0.005334	0.013143	GAMT	chr19	-	1397091	1401569	1327
ENSG00000(	212.3373	225.2018	207.148	647.9503	599.2012	525.2356	-1.4539	3.17E-19	3.10E-18	HDHD1	chrX	-	6966961	7066231	2140
ENSG00000(	273.4491	234.8361	295.5487	212.7375	184.0864	187.408	0.45641	0.015216	0.033911	C6orf70	chr6	+	1.7E+08	1.7E+08	2206
ENSG00000(	444.3547	432.3393	477.6278	698.1384	637.8594	614.0078	-0.52552	0.000197	0.000616	PHF10	chr6	-	1.7E+08	1.7E+08	4285
ENSG00000(	0	0	0	2.247227	0	0.821965	-0.85594	0.51054	NA	PRRG3	chrX	+	1.51E+08	1.51E+08	5977
ENSG00000(	0	0	0	3.745378	0	1.64393	-1.4934	0.26982	NA	GALNT8	chr12	+	4829507	4960277	2380
ENSG00000(	13.46529	7.225726	10.55531	8.239831	8.283888	5.753754	0.45522	0.53106	0.65582	EFCAB4B	chr12	-	3715799	3873985	7554
ENSG00000(	12.4295	15.65574	3.958241	8.239831	6.443024	10.68554	0.31653	0.66648	0.76995	NXNL2	chr9	+	91150016	91199189	1457
ENSG00000(	104.615	75.87013	118.7472	212.7375	285.3339	211.245	-1.2354	1.92E-07	8.58E-07	STARD8	chrX	+	67867508	67945684	4864
ENSG00000(	1.035792	0	0	68.91495	55.22592	67.40112	-6.0857	1.83E-11	1.15E-10	FAM155B	chrX	+	68725084	68752351	4013
ENSG00000(	4.143168	4.817151	3.958241	2.247227	9.20432	7.397684	-0.46513	0.61006	0.72378	GDPD2	chrX	+	69642881	69653240	2438
ENSG00000(	1762.918	1908.796	1839.263	693.644	557.7818	647.7084	1.5323	1.88E-33	3.21E-32	SAT1	chrX	+	23801290	23804343	1135
ENSG00000(	573.8287	466.0593	534.3626	756.5663	627.7346	701.1361	-0.40443	0.006057	0.014762	GNL3L	chrX	+	54556644	54587504	2357
ENSG00000(	2169.984	1985.87	2483.137	1467.439	1523.315	1223.906	0.65382	8.21E-07	3.43E-06	SH3BP4	chr2	+	2.36E+08	2.36E+08	5231
ENSG00000(	200.9436	205.9332	263.8828	214.2356	226.4263	178.3664	0.11301	0.5751	0.69347	MOSPD2	chrX	+	14891563	14940449	4163
ENSG00000(	283.807	440.7693	258.6051	161.0512	149.11	192.3398	0.96119	1.63E-05	5.91E-05	DOCK6	chr19	-	11309971	11373157	6358
ENSG00000(	803.7745	771.9484	634.638	676.4152	486.9085	590.9928	0.33206	0.038022	0.076599	ECSIT	chr19	-	11616731	11639989	1700
ENSG00000(	1252.272	1252.459	1203.305	1707.143	1377.887	1325.829	-0.25013	0.056752	0.10845	LDLR	chr19	+	11200038	11244492	5337
ENSG00000(	1108.297	1070.612	844.4248	1042.713	1063.099	1328.295	-0.18222	0.22132	0.33306	ELOF1	chr19	-	11661962	11670051	2154
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	TSPAN16	chr19	+	11406824	11437672	1040
ENSG00000(	4.143168	2.408575	0	1.498151	0.920432	0.821965	0.70181	0.57942	0.69772	C19orf80	chr19	+	11348178	11352619	872
ENSG00000(	15240.64	14562.25	12242.84	7721.471	7176.608	7998.541	0.87532	2.23E-14	1.69E-13	PRKCSH	chr19	+	11546109	11561783	2262
ENSG00000(	135.6887	105.9773	109.5113	916.8685	789.7307	768.5372	-2.8008	1.90E-59	6.56E-58	CNN1	chr19	+	11649532	11661138	1848
ENSG00000(	996.4318	1162.138	1137.335	1459.199	1154.222	1185.273	-0.20551	0.1321	0.2202	CDC16	chr13	+	1.15E+08	1.15E+08	2211
ENSG00000(	205.0868	163.7831	154.3714	478.6593	332.276	370.7062	-1.1665	6.33E-09	3.23E-08	THEM6	chr8	+	1.44E+08	1.44E+08	2279
ENSG00000(	2.071584	6.021439	2.638828	21.72319	18.40864	20.54912	-2.3125	0.001422	0.00388	EXOC3L2	chr19	-	45715879	45737469	1719
ENSG00000(	1517.435	1542.693	1370.871	5029.293	4206.374	4602.182	-1.6396	4.06E-45	9.74E-44	PVRL2	chr19	+	45349432	45392485	2466
ENSG00000(	1280.239	1263.298	897.2014	15515.6	14312.72	18216.39	-3.7916	2.90E-152	4.51E-150	APOE	chr19	+	45409011	45412650	1208
ENSG00000(	1807.457	1769.099	1481.702	5937.173	5065.137	5662.516	-1.7161	7.76E-46	1.90E-44	TOMM40	chr19	+	45393826	45406946	3415
ENSG00000(	37.28851	28.90291	22.43003	45.69361	57.06678	81.37453	-1.0228	0.00911	0.021383	APOC1	chr19	+	45417504	45422606	689
ENSG00000(	38.3243	31.31148	35.62417	225.4717	261.4027	275.3582	-2.8268	2.52E-28	3.59E-27	GADD45G	chr9	+	92219928	92221470	1065
ENSG00000(	126.3666	139.6974	189.9956	41.94823	44.18074	36.98842	1.8662	3.14E-11	1.93E-10	LRCH2	chrX	-	1.14E+08	1.14E+08	4923
ENSG00000(	0	0	0	9.737982	23.0108	14.79537	-4.8315	1.78E-05	6.42E-05	DPP6	chr7	+	1.54E+08	1.55E+08	4798
ENSG00000(	1212.912	1018.827	1296.984	1384.292	1533.44	1297.061	-0.25562	0.055421	0.10626	XPO7	chr8	+	21777180	21864096	4889
ENSG00000(	0	2.408575	0	13.48336	22.09037	6.575719	-3.3775	0.000831	0.00236	ACE2	chrX	-	15579156	15620271	3507
ENSG00000(	216.4805	239.6533	153.052	80.90016	98.48622	96.1699	1.1397	1.97E-06	7.90E-06	FAM98C	chr19	+	38893775	38899728	4133
ENSG00000(	1308.205	1240.416	1203.305	1317.624	1671.505	1777.91	-0.34385	0.011553	0.026476	SAFB2	chr19	-	5587010	5624057	3371

ENSG00000(	10493.61	10871.11	8222.587	4940.153	5595.306	7746.197	0.69231	1.22E-05	4.48E-05	RPL36	chr19	+	5674958	5691887	907
ENSG00000(	59.04014	80.68728	50.13772	31.46117	4.60216	15.61733	1.7968	0.00026	0.000798	ATP8B3	chr19	-	1782074	1812275	5237
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	NCAN	chr19	+	19322838	19363042	6903
ENSG00000(	0	0	2.638828	1385.79	1966.963	1762.293	-10.062	9.64E-49	2.58E-47	KIF1A	chr2	-	2.42E+08	2.42E+08	9162
ENSG00000(	290.0217	332.3834	271.7992	681.6587	560.5431	740.5904	-1.1449	3.15E-12	2.08E-11	GTPBP3	chr19	+	17445729	17453544	2917
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	PLVAP	chr19	-	17462257	17488159	2305
ENSG00000(	2.071584	1.204288	1.319414	0	0	0	1.6469	0.22376	NA	BST2	chr19	-	17513748	17516457	1019
ENSG00000(	790.3092	863.4743	529.0849	144.5716	127.94	152.8855	2.3472	1.18E-33	2.03E-32	SLC27A1	chr19	+	17579578	17616977	4343
ENSG00000(	167.7983	136.0845	116.1084	1072.676	815.5027	883.6123	-2.7044	1.05E-51	3.03E-50	NSUN5	chr7	-	72716514	72722864	2286
ENSG00000(	1.035792	4.817151	7.916483	7.490755	8.283888	15.61733	-1.0874	0.19588	0.30256	USHBP1	chr19	-	17359985	17393595	3598
ENSG00000(	4345.147	4083.74	3356.589	3343.124	2607.584	2888.385	0.41409	0.001936	0.005171	COLGALT1	chr19	+	17666403	17693971	3704
ENSG00000(	1301.99	1305.448	1158.445	1891.416	1683.47	1889.697	-0.53581	6.85E-06	2.59E-05	DDA1	chr19	+	17420327	17434110	4078
ENSG00000(	438.14	451.6079	307.4234	436.711	376.4567	537.5651	-0.17192	0.36357	0.49339	MRPL34	chr19	+	17403418	17417652	968
ENSG00000(	863.8504	927.3015	737.5523	1089.156	606.5647	729.9048	0.059002	0.75379	0.83714	PGLS	chr19	+	17622438	17632097	1601
ENSG00000(	1384.854	1222.352	1054.212	1308.635	1610.756	2054.912	-0.43952	0.007212	0.017319	LSM7	chr19	-	2321520	2328615	710
ENSG00000(	641.1552	622.6168	682.1369	524.3529	694.9262	562.224	0.12788	0.3938	0.52459	TULP4	chr6	+	1.59E+08	1.59E+08	11123
ENSG00000(	1423.178	1324.716	1566.144	865.9313	805.378	856.4874	0.76887	4.67E-10	2.62E-09	SNX9	chr6	+	1.58E+08	1.58E+08	4198
ENSG00000(	67.32647	69.84869	72.56776	122.8484	119.6562	156.9953	-0.92253	0.000407	0.001214	RTN4IP1	chr6	-	1.07E+08	1.07E+08	2266
ENSG00000(	252.7332	273.3733	278.3963	528.0983	455.6138	517.8379	-0.89925	1.28E-08	6.37E-08	QRSL1	chr6	+	1.07E+08	1.07E+08	4106
ENSG00000(	234.089	226.4061	142.4967	208.9921	221.8241	246.5895	-0.16251	0.45528	0.58499	C6orf203	chr6	+	1.07E+08	1.07E+08	1517
ENSG00000(	137.7603	161.3746	158.3297	95.13259	92.96363	80.55256	0.76035	0.001223	0.00338	RSPH3	chr6	-	1.59E+08	1.59E+08	3152
ENSG00000(	6.214751	15.65574	3.958241	4.494453	5.522592	0.821965	1.0962	0.22777	0.34098	ACSBG2	chr19	+	6135258	6193112	2759
ENSG00000(	1114.512	1023.645	969.7691	576.0391	877.1717	902.5175	0.39966	0.016549	0.036612	MLLT1	chr19	-	6212966	6279959	1931
ENSG00000(	741.627	811.6899	910.3955	1818.006	2483.326	1761.471	-1.2956	1.60E-17	1.44E-16	MLLT4	chr6	+	1.68E+08	1.68E+08	7704
ENSG00000(	13711.81	13091.81	12855.05	17338.1	19762.6	21417.94	-0.56027	3.45E-07	1.50E-06	ACTN4	chr19	+	39138289	39222223	4963
ENSG00000(	31.07376	43.35436	36.94359	23.97042	23.0108	18.90519	0.73463	0.090258	0.16116	STK33	chr11	-	8413418	8615836	4677
ENSG00000(	1878.927	1987.075	1771.973	1450.959	1414.704	1394.053	0.40384	0.000308	0.000936	NDUFA10	chr2	-	2.41E+08	2.41E+08	4915
ENSG00000(	0	0	0	23.97042	15.64734	15.61733	-5.0685	4.66E-06	1.80E-05	EPO	chr7	+	1E+08	1E+08	1330
ENSG00000(	426.7463	464.8551	382.63	781.2858	551.3388	595.9246	-0.59607	0.000388	0.00116	ARPC1B	chr7	+	98971872	98992424	1715
ENSG00000(	688.8016	644.2939	777.1347	397.7591	474.0225	343.5813	0.7938	6.87E-07	2.89E-06	ZSWIM6	chr5	+	60628100	60841997	5501
ENSG00000(	8.286335	12.04288	1.319414	14.98151	8.283888	16.4393	-0.79235	0.29185	0.41595	FCHO1	chr19	+	17858527	17899377	3214
ENSG00000(	277.5922	275.7819	271.7992	0.749076	13.80648	9.041614	4.7257	1.24E-10	7.32E-10	UNC13A	chr19	-	17712137	17799401	10101
ENSG00000(	630.7973	546.7466	593.7362	806.7544	805.378	747.9881	-0.41237	0.002027	0.005396	MAP1S	chr19	+	17830051	17845325	3419
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	KLHDC7B	chr22	+	50986462	50989451	2990
ENSG00000(	389.4578	317.932	310.0622	581.2826	416.0353	471.8079	-0.52693	0.002795	0.00726	SCO2	chr22	-	50961997	50964868	1051
ENSG00000(	10374.49	9701.742	11821.95	8015.857	9984.846	8244.308	0.28088	0.022422	0.048042	PXDN	chr2	-	1635659	1748624	6808
ENSG00000(	2862.929	2715.669	2162.519	1385.79	1119.245	1468.029	0.95962	2.08E-11	1.29E-10	SSBP4	chr19	+	18529674	18545372	1694
ENSG00000(	340.7755	293.8462	217.7033	448.6963	322.1512	385.5015	-0.43558	0.028093	0.058657	GDF15	chr19	+	18485541	18499987	1720
ENSG00000(	1307.169	1300.631	1196.708	403.7517	536.6119	549.8945	1.3498	2.69E-20	2.76E-19	PGPEP1	chr19	+	18451397	18480760	7092
ENSG00000(	44.53905	37.33292	39.58241	8.988907	11.96562	11.50751	1.8491	0.000105	0.000342	KIAA1683	chr19	-	18367906	18385319	5521
ENSG00000(	2048.796	1920.839	1583.297	4871.987	4715.373	5597.581	-1.4474	8.57E-30	1.30E-28	LSM4	chr19	-	18417040	18434084	1908
ENSG00000(	2116.123	1871.463	1721.835	2383.558	2181.424	1947.235	-0.18888	0.13789	0.22795	JUND	chr19	-	18390563	18392432	1870
ENSG00000(	3.107376	0	0	0	0	1.64393	0.41335	0.75876	NA	HRC	chr19	-	49654455	49658681	2385
ENSG00000(	419.4957	395.0064	358.8805	184.2726	176.7229	189.0519	1.0896	1.55E-10	9.06E-10	TRPM4	chr19	+	49660998	49715093	4109

ENSG0000(	124.295	132.4716	54.09597	32.95932	33.13555	47.67397	1.4281	7.64E-05	0.000253	SULT4A1	chr22	-	44220389	44258398	2561
ENSG0000(	204.051	152.9445	138.5384	171.5383	150.9508	146.3098	0.083023	0.71197	0.80531	ZNF557	chr19	+	7069455	7087979	5990
ENSG0000(	0	0	2.638828	150.5642	183.166	208.7791	-7.0205	9.54E-21	9.97E-20	CRB3	chr19	+	6463788	6467232	1443
ENSG0000(	4.143168	2.408575	5.277655	26.21764	16.56778	18.90519	-2.2124	0.001799	0.004835	OLFM1	chr9	+	1.38E+08	1.38E+08	2624
ENSG0000(	1190.125	1071.816	1240.249	940.8389	1325.422	1047.183	0.080449	0.58312	0.70069	CAMSAP1	chr9	-	1.39E+08	1.39E+08	7696
ENSG0000(	846.242	845.41	711.164	1159.569	1037.327	1067.732	-0.44046	0.000777	0.002218	UBAC1	chr9	-	1.39E+08	1.39E+08	1867
ENSG0000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	SAG	chr2	+	2.34E+08	2.34E+08	6659
ENSG0000(	190.5857	122.8373	175.482	196.2578	245.7553	224.3964	-0.44106	0.044039	0.087033	ZBTB46	chr20	-	62375019	62462597	5185
ENSG0000(	499.2517	397.4149	445.9619	113.8595	101.2475	122.4728	1.9818	7.31E-27	9.76E-26	HELZ2	chr20	-	62189439	62205592	8064
ENSG0000(	27.96638	32.51577	15.83297	153.5605	114.1336	150.4196	-2.4082	1.92E-13	1.38E-12	SAMD10	chr20	-	62605466	62611361	2181
ENSG0000(	217.5163	214.3632	155.6908	0.749076	5.522592	0.821965	6.1996	1.29E-32	2.13E-31	LSP1	chr11	+	1874200	1913497	2640
ENSG0000(	6.214751	1.204288	1.319414	0	0	0	2.5493	0.057365	0.10947	TNNT3	chr11	+	1940792	1959936	1246
ENSG0000(	3.107376	3.612863	5.277655	0	0	0	3.0852	0.01784	0.039172	TNNI2	chr11	+	1860219	1862910	745
ENSG0000(	1.035792	0	0	2031.493	1805.888	2780.707	-10.782	7.17E-46	1.75E-44	H19	chr11	-	2016406	2022700	2348
ENSG0000(	3.107376	1.204288	2.638828	0	0	0	2.2312	0.098725	0.17353	CYP2G1P	chr19	+	41396731	41406413	2511
ENSG0000(	46509.13	48284.71	43208.16	4576.852	6254.335	5800.606	3.0463	2.31E-130	2.78E-128	COL5A1	chr9	+	1.38E+08	1.38E+08	8468
ENSG0000(	1694.556	1616.154	1674.336	2185.802	1730.412	1777.91	-0.19183	0.12699	0.21329	ATXN10	chr22	+	46067678	46241187	3329
ENSG0000(	1763.954	1646.261	1622.879	1700.401	1443.237	1421.177	0.14053	0.24823	0.36522	TUBGCP2	chr10	-	1.35E+08	1.35E+08	3553
ENSG0000(	4.143168	0	0	0	0	0.821965	0.9919	0.46158	NA	CALY	chr10	-	1.35E+08	1.35E+08	920
ENSG0000(	18.64425	16.86003	9.235896	6.74168	7.363456	5.753754	1.1005	0.10737	0.18598	CYP2E1	chr10	+	1.35E+08	1.35E+08	7918
ENSG0000(	50.7538	66.23582	54.09597	18.72689	35.89685	27.94681	1.0355	0.007873	0.01875	PNPLA7	chr9	-	1.4E+08	1.4E+08	5308
ENSG0000(	1002.647	883.9472	840.4666	1388.786	1353.035	1538.718	-0.64796	3.66E-07	1.59E-06	PAK4	chr19	+	39616410	39673456	5735
ENSG0000(	0	0	0	5.992604	9.20432	2.465895	-3.3334	0.00779	0.018568	MNX1	chr7	-	1.57E+08	1.57E+08	2174
ENSG0000(	31.07376	50.58008	39.58241	10.48706	23.93123	13.9734	1.291	0.006906	0.016649	ZNF337	chr20	-	25654851	25677477	3613
ENSG0000(	182.2994	193.8903	204.5091	601.5077	566.9861	610.7199	-1.6122	1.48E-24	1.80E-23	CEP85	chr1	+	26560691	26605299	3935
ENSG0000(	254.8048	226.4061	287.6322	403.0026	385.661	354.2669	-0.57113	0.000814	0.002317	TAF4	chr20	-	60528525	60640866	4630
ENSG0000(	0	0	0	13.48336	11.96562	6.575719	-4.2615	0.000264	0.00081	GATA5	chr20	-	61038553	61051026	2595
ENSG0000(	0	0	0	120.6012	172.1208	188.23	-7.9435	7.43E-16	6.15E-15	RBBP8NL	chr20	-	60985293	61002589	2793
ENSG0000(	3485.44	3481.596	3211.453	6205.342	9388.406	9155.045	-1.2779	1.93E-18	1.81E-17	LAMA5	chr20	-	60883011	60942368	11426
ENSG0000(	500.2875	515.4351	442.0036	468.1722	530.1688	429.8877	0.031013	0.83937	0.89727	OSBPL2	chr20	+	60813580	60871268	3970
ENSG0000(	454.7126	352.8563	362.8388	674.9171	635.0981	723.3291	-0.79207	2.82E-07	1.24E-06	ADRM1	chr20	+	60877149	60883918	1371
ENSG0000(	2489.008	2205.051	2118.979	249.4422	228.2671	203.8473	3.3125	9.47E-132	1.17E-129	ASS1	chr9	+	1.33E+08	1.33E+08	1973
ENSG0000(	2.071584	0	2.638828	0	0	4.109825	0.11448	0.93155	0.95885	PRDM12	chr9	+	1.34E+08	1.34E+08	2476
ENSG0000(	645.2984	684.0354	592.4168	1286.912	980.2601	1164.724	-0.83448	4.66E-09	2.41E-08	EXOSC2	chr9	+	1.34E+08	1.34E+08	2766
ENSG0000(	432.961	427.5221	341.7282	373.7887	350.6846	391.2553	0.10877	0.50276	0.63072	POMT1	chr9	+	1.34E+08	1.34E+08	3420
ENSG0000(	523.0749	411.8664	407.6989	626.2272	566.0657	663.3257	-0.46343	0.002951	0.007632	UCK1	chr9	-	1.34E+08	1.34E+08	2237
ENSG0000(	17.60846	6.021439	9.235896	10.48706	10.12475	15.61733	-0.11937	0.86021	0.91118	FIBCD1	chr9	-	1.34E+08	1.34E+08	3253
ENSG0000(	6582.458	6204.49	7068.1	3238.254	5215.168	4501.902	0.61428	4.45E-05	0.000152	PRRC2B	chr9	+	1.34E+08	1.34E+08	11042
ENSG0000(	1288.525	1258.481	964.4915	798.5145	704.1305	768.5372	0.62745	1.22E-05	4.48E-05	CHMP2A	chr19	-	59062933	59066491	1178
ENSG0000(	2158.59	1890.732	1810.236	2484.684	2410.611	2605.629	-0.35503	0.002142	0.00568	UBE2M	chr19	-	59067079	59070327	1508
ENSG0000(	8036.709	7170.329	6601.027	18346.36	14716.79	15094.56	-1.1404	1.51E-20	1.56E-19	TRIM28	chr19	+	59055458	59062089	2960
ENSG0000(	837.9557	914.0544	554.1538	901.1379	723.4595	772.647	-0.05486	0.75547	0.83825	C16orf13	chr16	-	684429	686358	1710
ENSG0000(	1290.597	1209.105	1071.364	690.6477	655.3476	800.5938	0.73294	8.08E-08	3.74E-07	YIPF2	chr19	-	11033444	11039357	1550
ENSG0000(	219.5879	185.4603	180.7597	374.5378	294.5382	307.4149	-0.73222	0.0001	0.000328	ATG4D	chr19	+	10654571	10664094	1949

ENSG00000(	3896.649	3931.999	3698.317	3857.739	3694.614	3452.253	0.06686	0.52219	0.64762	EIF2S3	chrX	+	24072833	24096088	2858
ENSG00000(	291.0575	320.3405	253.3274	405.9989	364.4911	540.8529	-0.59739	0.001447	0.003946	TMEM160	chr19	-	47549165	47551888	663
ENSG00000(	1084.474	1135.643	1117.543	1049.455	1597.87	1423.643	-0.28503	0.060931	0.11511	ZC3H4	chr19	-	47567444	47617009	6119
ENSG00000(	97.36444	110.7945	65.97069	135.5827	112.2927	142.1999	-0.50123	0.058882	0.11194	NPAS1	chr19	+	47523077	47549033	2117
ENSG00000(	0	1.204288	0	6.74168	2.761296	9.863579	-2.82	0.017959	0.039389	GMFG	chr19	-	39818993	39833012	1028
ENSG00000(	220.6237	193.8903	225.6198	137.8299	129.7809	166.8589	0.55513	0.007271	0.017446	MAP3K10	chr19	+	40697651	40721482	3436
ENSG00000(	1.035792	0	0	299.6302	281.6522	370.7062	-8.2266	1.00E-23	1.18E-22	ARHGEF16	chr1	+	3370990	3397677	3061
ENSG00000(	1189.089	1142.869	1064.767	1570.811	1460.726	1421.999	-0.38963	0.000977	0.002744	LRRC47	chr1	-	3696784	3713068	2648
ENSG00000(	1467.717	1366.867	1413.092	1351.332	1364.08	1214.864	0.11212	0.33737	0.46591	SESN2	chr1	+	28586038	28609002	3453
ENSG00000(	0	0	0	27.7158	23.93123	26.30288	-5.5619	2.34E-07	1.03E-06	SMPDL3B	chr1	+	28261504	28285668	1913
ENSG00000(	1306.134	1333.147	1319.414	898.1416	997.7483	1626.669	0.16765	0.35728	0.48676	ATPIF1	chr1	+	28562620	28573417	1855
ENSG00000(	331.4534	298.6634	308.7428	488.3973	424.3192	475.9177	-0.56261	0.000311	0.000945	MED18	chr1	+	28655513	28662476	1831
ENSG00000(	37.28851	30.10719	22.43003	20.97412	20.2495	14.79537	0.66527	0.16588	0.26455	THEMIS2	chr1	+	28199055	28213196	2861
ENSG00000(	437.1042	429.9307	631.9992	996.2705	1237.061	946.0816	-1.0822	2.73E-10	1.56E-09	CLIP1	chr12	-	1.23E+08	1.23E+08	5880
ENSG00000(	24.85901	14.45145	17.15238	6.74168	6.443024	9.863579	1.2229	0.052286	0.10098	CCDC62	chr12	+	1.23E+08	1.23E+08	3546
ENSG00000(	275.5206	272.169	286.3128	392.5156	435.3643	534.2772	-0.70499	3.95E-05	0.000136	HIP1R	chr12	+	1.23E+08	1.23E+08	4539
ENSG00000(	543.7907	417.8878	515.8908	489.8954	531.0893	439.7512	0.01758	0.91193	0.94596	ZNF317	chr19	+	9251056	9274100	4186
ENSG00000(	55.93276	62.62296	55.41538	50.18806	41.41944	36.98842	0.42686	0.21036	0.32014	PPAN	chr19	+	10216965	10225414	2412
ENSG00000(	3012.083	2739.755	2590.009	2370.824	2362.749	2638.507	0.17836	0.11771	0.20067	EIF3G	chr19	-	10225693	10230596	1522
ENSG00000(	7.250543	4.817151	3.958241	0	0	0.821965	2.9179	0.016495	0.036501	ANGPTL6	chr19	-	10203014	10213472	1900
ENSG00000(	156.4046	138.4931	133.2608	5.243529	7.363456	6.575719	4.3946	7.42E-29	1.08E-27	C19orf66	chr19	+	10196798	10203928	2140
ENSG00000(	1895.499	1708.884	1989.676	4296.697	4813.859	4300.52	-1.2593	1.31E-28	1.90E-27	DNMT1	chr19	-	10244021	10341962	5408
ENSG00000(	209.23	181.8474	208.4674	145.3207	150.9508	109.3213	0.56102	0.009667	0.022559	ZNF426	chr19	-	9638667	9649303	2402
ENSG00000(	1559.903	1483.682	1422.328	281.6524	243.9145	285.2218	2.4544	4.95E-76	2.44E-74	SLC6A8	chrX	+	1.53E+08	1.53E+08	3763
ENSG00000(	1.035792	6.021439	0	6.74168	0.920432	2.465895	-0.4027	0.72957	0.81879	PNCK	chrX	-	1.53E+08	1.53E+08	2143
ENSG00000(	1078.259	969.4516	1030.462	1909.394	1885.965	1891.341	-0.8836	6.79E-15	5.32E-14	DKC1	chrX	+	1.54E+08	1.54E+08	2577
ENSG00000(	2350.212	2403.758	2104.465	487.6482	637.8594	672.3673	1.9277	1.13E-42	2.54E-41	PLXNA3	chrX	+	1.54E+08	1.54E+08	6752
ENSG00000(	3.107376	6.021439	5.277655	47.19176	59.82808	80.55256	-3.5601	7.70E-11	4.59E-10	DUSP9	chrX	+	1.53E+08	1.53E+08	2433
ENSG00000(	502.3591	517.8437	497.419	319.1062	262.3231	254.8091	0.85538	8.52E-08	3.94E-07	MPP1	chrX	-	1.54E+08	1.54E+08	2378
ENSG00000(	130.5098	193.8903	163.6073	543.8288	523.7258	461.1223	-1.6434	7.43E-19	7.15E-18	ZNF331	chr19	+	54024235	54083523	5042
ENSG00000(	184.371	213.1589	258.6051	165.5457	202.495	149.5976	0.33848	0.11366	0.19485	ZNF236	chr18	+	74534563	74682683	8206
ENSG00000(	4.143168	9.634302	3.958241	12.73428	17.48821	21.37109	-1.431	0.040233	0.08046	SLC7A10	chr19	-	33699571	33716756	1945
ENSG00000(	1201.519	1106.74	909.0761	880.9128	728.0617	734.0147	0.45664	0.001794	0.004822	LRP3	chr19	+	33668509	33698694	3278
ENSG00000(	414.3168	317.932	304.7846	582.7808	451.0117	555.6483	-0.6116	0.000454	0.001343	C12orf65	chr12	+	1.24E+08	1.24E+08	3733
ENSG00000(	616.2962	759.9056	709.8446	1797.781	1325.422	1357.886	-1.101	3.19E-13	2.26E-12	NOL11	chr17	+	65713949	65740647	2947
ENSG00000(	1409.713	1324.716	1628.157	1065.185	1155.142	978.1383	0.44656	0.000616	0.001787	UBE4B	chr1	+	10092890	10241297	5522
ENSG00000(	4.143168	1.204288	10.55531	80.90016	71.7937	97.81383	-3.8643	6.62E-14	4.89E-13	CASZ1	chr1	-	10696661	10856707	7936
ENSG00000(	10.35792	12.04288	10.55531	2.996302	3.681728	2.465895	1.6655	0.041475	0.082606	PKDREJ	chr22	-	46651560	46659219	7660
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	HSD17B3	chr9	-	98997588	99064434	1135
ENSG00000(	5.17896	4.817151	2.638828	3.745378	6.443024	5.753754	-0.27722	0.76381	0.84398	NUTMF	chr9	-	97077605	97090926	4195
ENSG00000(	438.14	385.3721	402.4212	331.8405	389.3427	353.4449	0.19137	0.22305	0.33522	HABP4	chr9	+	99212483	99253618	3150
ENSG00000(	0	0	0	0.749076	0.920432	0.821965	-0.73223	0.57364	NA	FBP2	chr9	-	97321002	97356075	1305
ENSG00000(	270.3417	250.4918	234.8557	595.5151	566.0657	575.3754	-1.195	5.20E-15	4.11E-14	SLC35D2	chr9	-	99082988	99145992	1613
ENSG00000(	535.5044	507.0051	539.6402	362.5526	455.6138	385.5015	0.39464	0.009717	0.02266	PRRG1	chrX	+	37208528	37316548	4600

ENSG00000(	9099.432	9057.448	8804.448	7361.914	7469.306	7218.496	0.28982	0.002333	0.006145	UBA1	chrX	+	47050260	47074527	3559
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	RGN	chrX	+	46937775	46952712	2235
ENSG00000(	70.43385	44.55865	60.69303	11.23613	15.64734	18.08323	1.9237	5.51E-06	2.11E-05	POLN	chr4	-	2073645	2243848	3978
ENSG00000(	671.1932	699.6912	857.619	703.3819	618.5303	565.5119	0.23711	0.11625	0.19866	TXLNG2P	chrY	+	21729199	21768160	7299
ENSG00000(	598.6877	611.7782	635.9574	752.0719	705.0509	640.3107	-0.18416	0.17432	0.27595	PPIL4	chr6	-	1.5E+08	1.5E+08	2232
ENSG00000(	34.18113	25.29004	39.58241	9.737982	7.363456	2.465895	2.2193	0.000139	0.000445	ULBP2	chr6	+	1.5E+08	1.5E+08	1349
ENSG00000(	5495.912	5097.75	6889.979	3381.327	4032.413	2992.774	0.74645	1.56E-07	7.02E-07	AKAP12	chr6	+	1.52E+08	1.52E+08	8432
ENSG00000(	703.3027	633.4553	866.8549	107.8669	105.8497	76.44274	2.9099	3.11E-53	9.24E-52	SYNE1	chr6	-	1.52E+08	1.53E+08	27748
ENSG00000(	48.68222	55.39724	42.22124	25.46857	48.7829	27.12484	0.52589	0.18667	0.29133	ULBP3	chr6	-	1.5E+08	1.5E+08	966
ENSG00000(	559.3276	580.4667	653.1098	511.6186	579.8722	506.3304	0.16529	0.24982	0.36714	LATS1	chr6	-	1.5E+08	1.5E+08	7517
ENSG00000(	24.85901	31.31148	23.74945	180.5272	195.1316	180.8323	-2.7677	4.31E-22	4.75E-21	EPS8L1	chr19	+	55583388	55599291	2536
ENSG00000(	773.7366	800.8513	738.8717	887.6545	727.1413	772.647	-0.04584	0.73391	0.82202	AAR2	chr20	+	34824381	34858840	2689
ENSG00000(	0	1.204288	6.597069	2.247227	6.443024	6.575719	-0.8054	0.45612	0.58585	TTLL9	chr20	+	30458505	30532764	2623
ENSG00000(	3003.797	3013.128	3141.524	3294.434	2801.795	2769.2	0.046493	0.68212	0.78251	RBM39	chr20	-	34291531	34330234	4580
ENSG00000(	0	0	0	1.498151	3.681728	0	-1.4292	0.2903	NA	COX4I2	chr20	+	30225691	30232809	693
ENSG00000(	75.61281	97.54731	56.73479	156.5568	138.0648	139.734	-0.90697	0.000581	0.00169	ZNF341	chr20	+	32319463	32380075	3682
ENSG00000(	1110.369	1186.223	1037.059	300.3793	358.9685	436.4634	1.6008	8.15E-25	9.99E-24	GGT7	chr20	-	33432523	33460663	2642
ENSG00000(	722.9827	734.6155	773.1765	422.4786	406.8309	383.8576	0.87585	1.37E-10	8.01E-10	ACSS2	chr20	+	33459949	33515769	3065
ENSG00000(	763.3786	674.4011	837.8278	477.9102	565.1452	514.55	0.54578	0.000167	0.000528	EDA2R	chrX	-	65815479	65859108	3418
ENSG00000(	298.3081	309.5019	420.893	626.9762	729.9026	597.5685	-0.92476	5.64E-08	2.65E-07	ARHGEF9	chrX	-	62854847	63005426	5413
ENSG00000(	44.53905	75.87013	26.38828	1.498151	1.840864	3.28786	4.1867	1.46E-10	8.56E-10	C1QL1	chr17	-	43037061	43045439	1295
ENSG00000(	12.4295	22.88147	31.66593	0.749076	0.920432	3.28786	3.3784	2.12E-05	7.57E-05	GFAP	chr17	-	42982376	42994305	3086
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	PYY	chr17	-	42030106	42081837	1053
ENSG00000(	2.071584	12.04288	0	5.243529	4.60216	10.68554	-0.45844	0.63737	0.74586	HIGD1B	chr17	+	42923721	42927848	635
ENSG00000(	1664.518	1423.468	1460.591	2813.528	1938.43	1988.333	-0.56566	0.000182	0.000572	ATP6V1E1	chr22	-	18074902	18111584	1402
ENSG00000(	141.9035	143.3102	164.9267	68.91495	94.8045	96.1699	0.78732	0.001423	0.003882	ZNF227	chr19	+	44711700	44741421	3043
ENSG00000(	635.9762	664.7668	567.3479	285.3978	289.9361	420.0241	0.90477	2.90E-07	1.27E-06	ZNF428	chr19	-	44111371	44124026	1412
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	TEX101	chr19	+	43905648	43922763	1446
ENSG00000(	120.1519	108.3859	124.0249	170.7892	161.0756	160.2832	-0.47875	0.028403	0.059246	ZNF141	chr4	+	331603	378653	2970
ENSG00000(	6112.208	5754.087	4561.213	4846.519	4279.088	4852.881	0.23258	0.068766	0.12777	COX4I1	chr16	+	85832239	85840650	3946
ENSG00000(	494.0727	470.8765	416.9348	907.1305	704.1305	787.4424	-0.79259	1.37E-07	6.19E-07	EMC8	chr16	-	85805364	85833214	1962
ENSG00000(	495.1085	551.5638	592.4168	1092.901	1643.892	1214.864	-1.2654	7.54E-15	5.90E-14	GSE1	chr16	+	85645015	85709810	7495
ENSG00000(	124.295	85.50443	118.7472	1167.809	913.989	1094.035	-3.2571	1.15E-74	5.46E-73	GINS2	chr16	-	85709804	85723679	2673
ENSG00000(	1825.065	1689.616	1712.599	2510.152	2308.443	2472.47	-0.47915	1.15E-05	4.23E-05	CHMP1A	chr16	-	89710839	89724253	2483
ENSG00000(	2266.313	2426.64	2344.598	1434.48	941.6019	1026.634	1.0441	4.60E-12	3.00E-11	SH3BGRL	chrX	+	80457442	80554046	1923
ENSG00000(	992.2886	1069.407	745.4688	1103.388	848.6383	843.336	0.006338	0.96895	0.98173	COX7B	chrX	+	77154935	77162870	2471
ENSG00000(	2.071584	0	3.958241	3.745378	3.681728	4.109825	-0.74329	0.50579	0.63344	SLC34A1	chr5	+	1.77E+08	1.77E+08	2916
ENSG00000(	27.96638	27.69862	21.11062	23.97042	27.61296	41.92021	-0.27168	0.55034	0.67158	F12	chr5	-	1.77E+08	1.77E+08	2049
ENSG00000(	650.4773	639.4768	473.6695	344.5748	201.5746	220.2866	1.1936	8.51E-09	4.29E-08	PRR7	chr5	+	1.77E+08	1.77E+08	1476
ENSG00000(	107.7224	114.4073	79.16483	152.0623	117.8153	108.4994	-0.32406	0.21358	0.32387	NFATC1	chr18	+	77155856	77289325	4642
ENSG00000(	3.107376	2.408575	1.319414	1.498151	0	0	1.3156	0.31727	0.4442	IDO1	chr8	+	39759794	39785963	2097
ENSG00000(	1.035792	0	1.319414	3.745378	2.761296	4.109825	-1.5453	0.20385	0.31206	GJA9	chr1	-	39330175	39347289	2377
ENSG00000(	5915.408	5498.778	6305.478	10700.54	10134.88	8929.827	-0.74708	2.85E-11	1.75E-10	CAP1	chr1	+	40505905	40538321	3105
ENSG00000(	874.2084	824.9371	949.9779	1474.181	1300.57	1175.41	-0.57572	1.55E-05	5.61E-05	PPT1	chr1	-	40538379	40563375	2740

ENSG0000(	122.2234	185.4603	178.1209	539.3344	717.0165	750.454	-2.0402	2.10E-25	2.64E-24	RAB11FIP4	chr17	+	29718642	29865236	8629
ENSG0000(	1322.706	1187.428	1542.395	1021.739	1069.542	870.4608	0.45087	0.001285	0.003544	RLIM	chrX	-	73805052	73834452	8317
ENSG0000(	324.2029	332.3834	336.4505	313.8627	341.4803	315.6345	0.032515	0.83781	0.89629	ABCB7	chrX	-	74273115	74376567	2377
ENSG0000(	584.1866	520.2523	599.0139	461.4305	550.4183	548.2506	0.12721	0.38817	0.51894	TRAF3	chr14	+	1.03E+08	1.03E+08	7640
ENSG0000(	91.14969	74.66584	60.69303	432.2166	403.1492	453.7246	-2.485	6.19E-34	1.08E-32	HAUS8	chr19	-	17160539	17186435	3176
ENSG0000(	795.4882	828.55	844.4248	776.7913	797.0941	793.1961	0.060048	0.62648	0.73774	MRPS25	chr3	-	15083967	15106842	4586
ENSG0000(	249.6258	230.019	288.9516	59.17697	106.7701	62.46933	1.7418	3.42E-12	2.26E-11	SH3BP5	chr3	-	15296360	15382875	2822
ENSG0000(	87.00652	78.2787	58.05421	237.4569	208.0176	212.8889	-1.5412	5.76E-11	3.47E-10	HACL1	chr3	-	15602211	15643338	2266
ENSG0000(	511.6812	513.0266	671.5816	322.8516	435.3643	312.3467	0.66136	0.000225	0.000696	TBC1D5	chr3	-	17199899	18486309	6609
ENSG0000(	406.0304	456.425	424.8512	467.4231	467.5795	396.1871	-0.04864	0.7508	0.8347	CAPN7	chr3	+	15247659	15294425	4353
ENSG0000(	1299.919	1375.297	1217.819	492.8917	467.5795	424.1339	1.4879	4.02E-30	6.13E-29	RFTN1	chr3	-	16357352	16555533	2982
ENSG0000(	1.035792	2.408575	7.916483	4.494453	4.60216	2.465895	-0.04338	0.96627	0.98027	C3orf20	chr3	+	14716606	14814541	3326
ENSG0000(	655.6563	798.4428	721.7193	520.6075	587.2356	543.3188	0.39691	0.004869	0.012088	ZFYVE20	chr3	-	15111580	15140670	6678
ENSG0000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	GALNT15	chr3	+	16216156	16273499	4669
ENSG0000(	1384.854	1153.708	1616.282	2459.215	3807.827	3042.092	-1.1597	1.07E-12	7.33E-12	SLC6A6	chr3	+	14444076	14530857	6534
ENSG0000(	25.8948	18.06432	18.47179	17.22874	21.16994	28.76877	-0.09457	0.85183	0.90549	KCNC3	chr19	-	50815194	50836772	5447
ENSG0000(	1.035792	0	0	10.48706	4.60216	7.397684	-3.0821	0.008277	0.01959	NAPSA	chr19	-	50861734	50869087	3288
ENSG0000(	1129.013	1130.826	947.3391	659.9356	570.6678	648.5303	0.76933	1.62E-08	8.02E-08	NR1H2	chr19	+	50832910	50886239	2380
ENSG0000(	0	2.408575	1.319414	8.239831	2.761296	13.9734	-2.2445	0.03324	0.067954	LRRC4B	chr19	-	51020149	51071302	3019
ENSG0000(	2012.544	1760.669	1357.677	145.3207	123.3379	105.2115	3.7616	5.74E-103	4.60E-101	PDLIM4	chr5	+	1.32E+08	1.32E+08	2282
ENSG0000(	366.6703	373.3292	409.0183	422.4786	470.3408	465.2321	-0.2409	0.11041	0.19005	KIF3A	chr5	-	1.32E+08	1.32E+08	6325
ENSG0000(	3520.657	3298.544	2810.351	2492.174	2312.125	2991.13	0.30435	0.021807	0.04687	MGAT1	chr5	-	1.8E+08	1.8E+08	3175
ENSG0000(	3173.666	3506.886	3338.117	70.4131	75.47542	66.57916	5.5453	0	0	GFPT2	chr5	-	1.8E+08	1.8E+08	3093
ENSG0000(	474.3927	433.5436	426.1707	1758.08	1227.856	1249.387	-1.6605	2.27E-25	2.84E-24	TUBG1	chr17	+	40761694	40767252	1611
ENSG0000(	1628.265	1451.167	1716.557	4817.305	3978.107	3835.288	-1.3943	3.21E-28	4.54E-27	PSME3	chr17	+	40976402	40995774	3144
ENSG0000(	14786.97	15219.79	10854.82	10584.44	8943.838	10643.62	0.43647	0.001454	0.003962	RPL27	chr17	+	41150290	41154976	1872
ENSG0000(	64.2191	48.17151	83.12307	201.5013	218.1424	201.3814	-1.6574	2.76E-11	1.70E-10	PSMC3IP	chr17	-	40724333	40729849	1416
ENSG0000(	10.35792	8.430014	5.277655	14.98151	34.05598	36.16646	-1.7107	0.004583	0.011443	AOC3	chr17	+	41003201	41010147	4026
ENSG0000(	6503.737	6156.319	7354.412	5122.179	5446.196	4725.476	0.38735	0.000629	0.001819	ACLY	chr17	-	40023161	40086795	4339
ENSG0000(	535.5044	558.7895	537.0014	1392.531	1117.404	1375.147	-1.2494	5.56E-20	5.62E-19	VPS25	chr17	+	40925454	40931617	1101
ENSG0000(	6.214751	6.021439	15.83297	9.737982	3.681728	9.041614	0.27252	0.72592	0.81625	RAMP2	chr17	+	40910465	40915059	858
ENSG0000(	36.25272	30.10719	30.34652	72.66033	58.90765	57.53754	-0.94819	0.007925	0.018855	AOC2	chr17	+	40996617	41002724	2657
ENSG0000(	0	3.612863	0	0.749076	4.60216	4.109825	-0.95861	0.44273	0.57234	RP11-798G	chr17	+	43580626	43612076	547
ENSG0000(	81.82756	103.5687	60.69303	62.92235	93.88406	78.90863	0.066775	0.82624	0.88808	NDUFA2	chr5	-	1.4E+08	1.4E+08	804
ENSG0000(	37.28851	43.35436	14.51355	22.47227	20.2495	30.4127	0.37313	0.44439	0.57398	ANKHD1	chr5	+	1.4E+08	1.4E+08	8319
ENSG0000(	2013.579	1867.85	2105.784	3325.146	3837.281	3490.885	-0.82984	2.02E-13	1.45E-12	DIAPH1	chr5	-	1.41E+08	1.41E+08	5792
ENSG0000(	1874.783	1855.807	1983.079	1488.413	1589.586	1338.159	0.37097	0.001579	0.004277	NDFIP1	chr5	+	1.41E+08	1.42E+08	4164
ENSG0000(	1679.019	1601.703	1563.505	2716.897	2473.201	2612.205	-0.68635	3.17E-10	1.80E-09	UBE2D2	chr5	+	1.39E+08	1.39E+08	2864
ENSG0000(	1260.559	1198.266	1331.289	696.6403	848.6383	646.8864	0.78856	1.09E-08	5.45E-08	EXOC4	chr7	+	1.33E+08	1.34E+08	4185
ENSG0000(	2148.232	2237.567	1667.739	750.5737	757.5155	995.3995	1.2702	8.70E-17	7.53E-16	ACAP3	chr1	-	1227756	1244989	5319
ENSG0000(	209.23	237.2447	166.2461	552.8178	520.9645	554.0044	-1.4017	3.22E-16	2.72E-15	C1orf159	chr1	-	1017198	1051741	3315
ENSG0000(	21.75163	15.65574	27.70769	0.749076	0	0	4.996	6.54E-07	2.76E-06	ANO1	chr11	+	69924408	70035634	4790
ENSG0000(	517.896	639.4768	766.5794	804.5071	786.9694	739.7684	-0.27843	0.074747	0.13721	PPFIA1	chr11	+	70116806	70230509	5234
ENSG0000(	98.40023	113.203	84.44248	7.490755	9.20432	16.4393	3.0943	4.20E-15	3.33E-14	TMEM204	chr16	+	1578689	1605581	1938

ENSG0000(	4.143168	1.204288	10.55531	99.62705	82.83888	101.1017	-4.0472	6.45E-16	5.37E-15	KREMEN2	chr16	+	3013945	3018384	2339
ENSG0000(	334.5608	375.7378	286.3128	728.8505	525.5667	642.7766	-0.925	6.93E-08	3.23E-07	THOC6	chr16	+	3074028	3077756	1419
ENSG0000(	2511.795	2220.707	2066.202	2141.607	1891.488	2070.53	0.15562	0.19467	0.30092	TRAF7	chr16	+	2205699	2228130	3700
ENSG0000(	6.214751	1.204288	2.638828	0	0	0	2.7795	0.036317	0.073498	BARX1	chr9	-	96713905	96717654	1532
ENSG0000(	220.6237	249.2876	174.1626	199.2541	121.497	180.0103	0.35891	0.12303	0.20813	NINJ1	chr9	-	95883771	95896570	2026
ENSG0000(	767.5218	858.6571	703.2475	167.0438	304.663	239.1918	1.7073	1.10E-18	1.05E-17	NPHP4	chr1	-	5922871	6052533	5548
ENSG0000(	8293.586	8446.874	10539.48	3573.09	3725.909	2884.275	1.4181	2.70E-26	3.51E-25	MAP1B	chr5	+	71403061	71505395	12034
ENSG0000(	972.6086	923.6887	1205.944	604.504	577.1109	563.8679	0.82627	5.69E-09	2.92E-08	IL13RA1	chrX	+	1.18E+08	1.18E+08	4036
ENSG0000(	250.6616	311.9105	352.2835	179.0291	182.2455	158.6392	0.80851	3.35E-05	0.000116	WDR44	chrX	+	1.17E+08	1.18E+08	4111
ENSG0000(	11.39371	22.88147	14.51355	19.47596	57.06678	27.94681	-1.0523	0.049322	0.095932	CKMT2	chr5	+	80529104	80562216	1637
ENSG0000(	147.0825	201.116	159.6491	328.8442	279.8113	277.8241	-0.80177	4.83E-05	0.000164	ZCCHC9	chr5	+	80597409	80609116	4606
ENSG0000(	66.29068	67.44011	88.40072	0	0	0.821965	6.7186	3.06E-14	2.30E-13	KRT34	chr17	-	39533902	39538655	1751
ENSG0000(	0	0	1.319414	2.996302	0	0	-0.52076	0.6968	NA	KRT33B	chr17	-	39519746	39526052	1607
ENSG0000(	23.82321	12.04288	3.958241	26.21764	21.16994	17.26126	-0.64068	0.29709	0.4216	TNS4	chr17	-	38632080	38657849	4067
ENSG0000(	1395.212	1303.039	1774.612	3027.763	3243.602	2894.138	-1.0332	9.05E-15	7.04E-14	TOP2A	chr17	-	38544768	38574202	5758
ENSG0000(	1034.756	975.4731	848.3831	629.9725	613.0077	777.5788	0.49981	0.000603	0.001751	STARD3	chr17	+	37793318	37819737	3451
ENSG0000(	742.6628	776.7656	566.0285	319.1062	297.2995	288.5097	1.201	1.24E-13	9.00E-13	RARA	chr17	+	38465444	38513094	2414
ENSG0000(	1067.901	845.41	821.9948	2.996302	1.840864	3.28786	8.1327	4.31E-76	2.13E-74	PPP1R1B	chr17	+	37782993	37792879	2879
ENSG0000(	54.89697	66.23582	58.05421	310.1173	291.7769	259.7409	-2.2522	1.26E-23	1.48E-22	KHDRBS3	chr8	+	1.36E+08	1.37E+08	5466
ENSG0000(	712.6248	750.2712	738.8717	1048.706	950.8063	985.5359	-0.43886	0.000413	0.001231	CHD1L	chr1	+	1.47E+08	1.47E+08	2967
ENSG0000(	556.2203	516.6394	482.9054	294.3867	205.2563	236.7259	1.0729	7.30E-10	4.04E-09	PEX11B	chr1	+	1.46E+08	1.46E+08	1740
ENSG0000(	38.3243	44.55865	60.69303	6.74168	34.05598	13.9734	1.3515	0.008098	0.019216	FMO5	chr1	-	1.47E+08	1.47E+08	2632
ENSG0000(	1378.639	1427.081	1323.372	364.7998	333.1964	302.4831	2.0396	3.03E-53	9.02E-52	PIAS3	chr1	+	1.46E+08	1.46E+08	2901
ENSG0000(	564.5066	545.5423	620.1245	558.0613	565.1452	484.9593	0.10468	0.46589	0.59507	PRKAB2	chr1	-	1.47E+08	1.47E+08	5417
ENSG0000(	673.2647	690.0569	726.997	785.7803	792.4919	860.5973	-0.22259	0.082963	0.15004	RBM8A	chr1	+	1.46E+08	1.46E+08	2827
ENSG0000(	45.57484	32.51577	44.86007	75.65663	126.0992	83.01846	-1.1888	0.000367	0.001104	CLUHP3	chr16	+	31711911	31721097	1907
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	FSHB	chr11	+	30252563	30256808	1890
ENSG0000(	1464.61	1318.695	1191.431	1518.376	1526.997	1542.828	-0.20566	0.090447	0.1614	PDHA1	chrX	+	19362011	19379823	3484
ENSG0000(	53.86118	92.73015	73.88717	8.239831	6.443024	8.219649	3.1655	1.69E-12	1.14E-11	RAI2	chrX	-	17818169	17879457	2421
ENSG0000(	739.5554	685.2397	753.3853	1540.848	1223.254	1095.679	-0.82346	2.39E-08	1.16E-07	MCCC2	chr5	+	70883115	70954531	3665
ENSG0000(	204.051	216.7718	207.148	220.2282	165.6778	212.0669	0.067919	0.73197	0.82075	ZNF304	chr19	+	57862675	57871266	4313
ENSG0000(	72.50543	89.11729	47.4989	97.37982	114.1336	91.23811	-0.52199	0.078439	0.14293	ZSCAN5A	chr19	-	56732681	56879752	2450
ENSG0000(	38.3243	65.03154	22.43003	12.73428	11.04518	13.9734	1.6742	0.000904	0.002553	ZNF132	chr19	-	58944181	58951589	3031
ENSG0000(	1170.445	1085.063	1027.823	798.5145	670.9949	752.0979	0.56213	1.72E-05	6.20E-05	VIMP	chr15	-	1.02E+08	1.02E+08	2444
ENSG0000(	4875.472	4677.454	5318.557	890.6508	1034.566	844.158	2.4208	7.21E-91	4.64E-89	CHSY1	chr15	-	1.02E+08	1.02E+08	4550
ENSG0000(	409.1378	398.6192	453.8783	1151.329	972.8966	1158.971	-1.3776	7.09E-23	8.04E-22	SNRPA1	chr15	-	1.02E+08	1.02E+08	2440
ENSG0000(	0	0	0	2.996302	0.920432	4.93179	-2.2855	0.086805	0.15605	KRT17P1	chr17	-	16744057	16749197	1546
ENSG0000(	2307.744	2249.609	1899.956	1737.855	1620.881	1786.952	0.32729	0.006607	0.015971	LLGL1	chr17	+	18128901	18148189	6004
ENSG0000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	NR0B2	chr1	-	27237980	27240457	1156
ENSG0000(	0	2.408575	0	14728.32	17102.55	16894.67	-13.123	4.52E-93	3.05E-91	LIN28A	chr1	+	26737269	26756213	4008
ENSG0000(	140.8677	156.5574	147.7743	195.5087	196.9724	143.0219	-0.26517	0.22753	0.3407	THAP1	chr8	-	42691817	42698468	2161
ENSG0000(	90.1139	77.07441	98.95603	545.327	614.8486	557.2922	-2.6788	6.37E-48	1.65E-46	RHPN2	chr19	-	33469499	33555794	3793
ENSG0000(	615.2604	596.1224	579.2227	555.065	469.4203	524.4136	0.20817	0.13951	0.23009	C19orf12	chr19	-	30191721	30206364	2464
ENSG0000(	62.14751	62.62296	56.73479	125.8447	110.4518	128.2265	-0.99559	0.000192	0.000599	C19orf40	chr19	+	33463115	33469128	2298

ENSG00000(	4.143168	2.408575	7.916483	2.247227	0.920432	0.821965	1.4514	0.18551	0.28993	LRRC9	chr14	+	60386431	60530277	4915
ENSG00000(	1030.613	967.043	973.7274	948.3296	942.5224	889.366	0.096146	0.42508	0.55552	ACTR10	chr14	+	58666798	58701750	1815
ENSG00000(	7.250543	6.021439	5.277655	14.98151	12.88605	17.26126	-1.1869	0.086242	0.15517	ABHD12B	chr14	+	51338878	51371688	2863
ENSG00000(	12.4295	19.2686	9.235896	133.3354	123.3379	108.4994	-3.0923	9.08E-17	7.85E-16	GCH1	chr14	-	55308726	55369570	2943
ENSG00000(	3255.494	3050.461	2454.11	397.01	355.2868	417.5582	2.8967	7.14E-97	5.18E-95	LGALS3	chr14	+	55590828	55612126	1729
ENSG00000(	15.53688	26.49433	13.19414	10.48706	4.60216	9.863579	1.0687	0.096485	0.17032	PODNL1	chr19	-	14042000	14064204	2744
ENSG00000(	2493.151	2472.403	2502.928	3306.419	3002.449	3186.758	-0.34611	0.000911	0.002568	DNAJB1	chr19	-	14625582	14640582	2264
ENSG00000(	73.54123	85.50443	68.60952	145.3207	180.4047	152.8855	-1.061	1.68E-05	6.06E-05	ZSWIM4	chr19	+	13906274	13943044	4339
ENSG00000(	283.807	250.4918	220.3421	364.7998	220.9037	228.5062	-0.10922	0.61885	0.73126	FBXW9	chr19	-	12798867	12807457	1803
ENSG00000(	635.9762	549.1552	538.3208	526.6001	485.9881	498.1107	0.19052	0.18417	0.28832	RFX1	chr19	-	14072350	14117851	4332
ENSG00000(	9.322127	0	3.958241	8.239831	0.920432	6.575719	-0.19549	0.84982	0.90441	ZNF20	chr19	-	12203658	12251222	3061
ENSG00000(	17.60846	18.06432	7.916483	20.22504	33.13555	32.05663	-0.91758	0.084435	0.15241	C19orf57	chr19	-	13993161	14017265	2513
ENSG00000(	432.961	402.2321	304.7846	1282.417	1041.929	1262.538	-1.6455	2.81E-25	3.51E-24	DCAF15	chr19	+	14063304	14072254	2271
ENSG00000(	414.3168	440.7693	312.7011	283.8996	310.1856	357.5547	0.29601	0.10281	0.17949	CC2D1A	chr19	+	14017014	14041692	3581
ENSG00000(	3.107376	0	0	2.247227	0	0	0.22117	0.87012	NA	RTBDN	chr19	-	12936292	12946242	2076
ENSG00000(	334.5608	272.169	373.3941	83.14739	82.83888	105.2115	1.8414	3.23E-18	3.00E-17	MATN3	chr2	-	20191872	20212455	2524
ENSG00000(	384.2788	356.4692	350.9641	411.9916	322.1512	314.8126	0.056862	0.7382	0.82474	TRIM21	chr11	-	4406127	4414926	1924
ENSG00000(	54.89697	87.913	83.12307	67.4168	61.66894	53.42772	0.29799	0.34212	0.47102	SPATA6	chr1	-	48761044	48937845	4973
ENSG00000(	2704.453	2575.971	2400.014	1810.516	1513.19	1624.203	0.63304	8.39E-08	3.88E-07	LRRC41	chr1	-	46726868	46769280	4455
ENSG00000(	0	0	0	9.737982	12.88605	1.64393	-3.7704	0.002064	0.005487	LHX1	chr17	+	35294084	35301917	4121
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	GAS2L2	chr17	-	34071530	34079897	3014
ENSG00000(	9.322127	7.225726	11.87472	14.23244	13.80648	15.61733	-0.58637	0.36194	0.4916	CCT6B	chr17	-	33254878	33308097	3353
ENSG00000(	1958.682	1938.903	2458.068	1313.879	1731.333	1373.503	0.52302	0.000269	0.000825	ACACA	chr17	-	35441923	35766909	9962
ENSG00000(	1698.699	1578.821	1560.867	2955.852	2390.362	2513.569	-0.69852	9.24E-09	4.64E-08	DHX30	chr3	+	47844399	47891685	4115
ENSG00000(	1368.281	1271.728	1349.76	1766.32	1366.842	1414.602	-0.18887	0.15258	0.24764	RAF1	chr3	-	12625100	12705725	3300
ENSG00000(	0	0	0	1.498151	4.60216	9.863579	-3.1506	0.01334	0.030147	SLC6A11	chr3	+	10857885	10982419	4296
ENSG00000(	305.5586	322.7491	365.4776	283.8996	226.4263	258.097	0.36626	0.037336	0.07539	PPARG	chr3	+	12328867	12475855	2029
ENSG00000(	81.82756	49.3758	89.72014	1280.919	1628.244	1344.735	-4.2463	9.48E-110	8.37E-108	NUP210	chr3	-	13357737	13461809	7191
ENSG00000(	0	0	0	2.247227	2.761296	6.575719	-2.699	0.038589	0.07756	FCRLA	chr1	+	1.62E+08	1.62E+08	2903
ENSG00000(	166.7625	161.3746	143.8161	459.9324	292.6974	328.786	-1.189	1.40E-08	6.95E-08	HSD17B7	chr1	+	1.63E+08	1.63E+08	2541
ENSG00000(	685.6942	708.1212	480.2666	581.2826	489.6698	536.7431	0.22129	0.18726	0.29194	ENOSF1	chr18	-	672543	712676	4121
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	LINC00470	chr18	-	1254384	1408345	2031
ENSG00000(	1430.429	1465.618	1488.299	1840.479	2005.621	1884.766	-0.38574	0.000473	0.001395	EMILIN2	chr18	+	2847028	2915991	5910
ENSG00000(	1369.317	1247.642	1224.416	1015.746	842.1953	997.8654	0.4266	0.000928	0.002613	ARFIP2	chr11	-	6496910	6502666	2543
ENSG00000(	1000.575	956.2044	959.2138	1108.632	1098.996	921.4227	-0.10122	0.43119	0.56101	TRIM5	chr11	-	5684425	5959849	3399
ENSG00000(	2.071584	2.408575	3.958241	0	0	2.465895	1.1772	0.3551	0.48466	CNGA4	chr11	+	6255995	6265659	1863
ENSG00000(	840.0272	853.84	902.479	170.0401	179.4842	181.6542	2.2829	9.35E-56	2.94E-54	TRIM22	chr11	+	5710919	5758319	2989
ENSG00000(	393.6009	376.9421	341.7282	417.2351	384.7406	400.2969	-0.11098	0.47089	0.5999	RRP8	chr11	-	6616305	6624850	6560
ENSG00000(	537.576	498.5751	455.1978	630.7216	545.8162	482.4934	-0.15255	0.32728	0.45494	TIMM10B	chr11	+	6502677	6505909	2840
ENSG00000(	706.4101	676.8097	959.2138	1132.602	1127.529	909.0932	-0.43597	0.006167	0.015003	EFR3A	chr8	+	1.33E+08	1.33E+08	5438
ENSG00000(	788.2376	909.2372	909.0761	1557.328	1287.684	1246.099	-0.64999	1.77E-06	7.14E-06	PTCD3	chr2	+	86333305	86369280	6734
ENSG00000(	1505.006	1448.758	1513.368	2760.343	1937.509	1794.349	-0.53803	0.000455	0.001346	IMMT	chr2	-	86371055	86422893	3001
ENSG00000(	499.2517	568.4238	527.7655	1014.248	793.4124	812.1013	-0.71465	1.25E-06	5.12E-06	MRPL35	chr2	+	86426478	86440917	3727
ENSG00000(	2.071584	1.204288	0	39.701	58.90765	50.13986	-4.871	2.91E-10	1.66E-09	IQCA1	chr2	-	2.37E+08	2.37E+08	3336

ENSG00000(	369.7777	335.9963	271.7992	798.5145	581.713	654.2841	-1.0513	1.23E-09	6.70E-09	ILKAP	chr2	-	2.39E+08	2.39E+08	2651
ENSG00000(	159.512	149.3317	186.0373	130.3391	127.0196	139.734	0.3136	0.14724	0.24027	PER2	chr2	-	2.39E+08	2.39E+08	6385
ENSG00000(	163.6551	181.8474	112.1502	7.490755	4.60216	7.397684	4.4373	1.87E-28	2.68E-27	RAMP1	chr2	+	2.39E+08	2.39E+08	910
ENSG00000(	60.07593	40.94578	26.38828	80.90016	93.88406	97.81383	-1.066	0.001653	0.004465	SCLY	chr2	+	2.39E+08	2.39E+08	5668
ENSG00000(	0	1.204288	0	42.69731	60.74851	50.96182	-5.7782	3.67E-10	2.08E-09	PTPRE	chr10	+	1.3E+08	1.3E+08	5736
ENSG00000(	6783.401	6974.03	6470.405	14421.95	10313.44	11739.3	-0.84872	3.36E-11	2.06E-10	RAN	chr12	+	1.31E+08	1.31E+08	2661
ENSG00000(	817.2398	868.2914	1076.642	936.3444	879.0126	700.3141	0.13316	0.39106	0.52188	PRKAA1	chr5	-	40759481	40798476	5088
ENSG00000(	45.57484	31.31148	39.58241	18.72689	23.93123	18.08323	0.91995	0.03569	0.072385	CARD6	chr5	+	40841286	40860275	4221
ENSG00000(	6.214751	28.90291	7.916483	77.15478	104.9292	86.30632	-2.5721	1.29E-08	6.41E-08	RAP1GAP2	chr17	+	2680350	2941033	6661
ENSG00000(	1926.573	1844.969	1600.449	2639.742	2940.78	3217.171	-0.70947	1.15E-08	5.76E-08	CLUH	chr17	-	2592680	2615957	5242
ENSG00000(	228.91	177.0303	211.1062	350.5674	268.7661	282.7559	-0.54515	0.004855	0.012058	INPP5K	chr17	-	1397865	1420182	3194
ENSG00000(	1359.995	1274.136	1097.752	2540.115	2939.86	2788.927	-1.1442	3.20E-20	3.27E-19	MYBBP1A	chr17	-	4442192	4458926	4807
ENSG00000(	1283.346	1205.492	1244.207	2823.266	2883.713	2370.547	-1.1111	3.15E-20	3.22E-19	RPA1	chr17	+	1732996	1803376	4340
ENSG00000(	3025.548	3261.211	2727.228	157.3059	137.1444	151.2415	4.325	1.08E-222	3.96E-220	SERPINF1	chr17	+	1665253	1680868	1548
ENSG00000(	920.819	1074.225	1099.072	2076.437	1821.535	1802.569	-0.88091	3.09E-12	2.05E-11	UBE2G1	chr17	-	4172554	4269923	3974
ENSG00000(	256.8764	267.3519	208.4674	377.5341	264.164	259.7409	-0.29743	0.14211	0.23363	EEFSEC	chr3	+	1.28E+08	1.28E+08	2228
ENSG00000(	307.6302	313.1148	370.7553	243.4496	399.4675	253.1652	0.14637	0.48035	0.60954	TBC1D14	chr4	+	6910969	7034845	4925
ENSG00000(	214.4089	195.0946	203.1897	388.7702	325.8329	344.4033	-0.78627	7.03E-06	2.66E-05	TMEM128	chr4	-	4237269	4249950	1737
ENSG00000(	71.46964	120.4288	83.12307	143.0734	116.8949	150.4196	-0.57564	0.030886	0.063758	COQ3	chr6	-	99817276	99842080	1335
ENSG00000(	1447.001	1523.424	1599.13	1263.69	1214.05	1187.739	0.31688	0.00567	0.0139	PNISR	chr6	-	99845927	99873207	5112
ENSG00000(	40.39588	38.53721	29.0271	36.7047	26.69253	17.26126	0.40945	0.3567	0.48622	POPDC3	chr6	-	1.06E+08	1.06E+08	1345
ENSG00000(	4194.957	4177.674	3025.416	2253.219	2333.295	2687.825	0.64653	4.34E-06	1.68E-05	SEC61G	chr7	-	54819943	54827667	1227
ENSG00000(	345.9545	408.2535	406.3794	426.224	387.5019	297.5513	0.060723	0.7322	0.82093	LANCL2	chr7	+	55433141	55501435	4353
ENSG00000(	41.43168	27.69862	51.45714	501.1315	439.9665	353.4449	-3.4011	2.44E-43	5.59E-42	FIGNL1	chr7	-	50511831	50518088	3700
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	DDC	chr7	-	50526134	50633154	2041
ENSG00000(	2816.318	2855.366	2977.917	2818.022	2530.268	2428.906	0.1528	0.16558	0.26426	GRSF1	chr4	-	71681499	71705662	6666
ENSG00000(	0	0	0	1.498151	1.840864	0.821965	-1.2806	0.34348	NA	ENAM	chr4	+	71494461	71552533	5679
ENSG00000(	11.39371	4.817151	3.958241	0	0	0	3.9029	0.001634	0.004421	IGJ	chr4	-	71521258	71547534	1438
ENSG00000(	1999.078	2035.246	2621.675	1690.664	2102.267	1434.329	0.34735	0.025002	0.052972	ANKRD17	chr4	-	73939093	74124515	10784
ENSG00000(	782.0229	790.0127	779.7735	905.6323	960.0106	1018.415	-0.29351	0.018191	0.039839	UTP3	chr4	+	71554196	71556267	2072
ENSG00000(	1892.392	1687.207	1494.896	3874.968	5284.2	4881.65	-1.4636	5.66E-26	7.26E-25	ITGB4	chr17	+	73717408	73753899	5919
ENSG00000(	1507.077	1343.985	1290.387	943.0861	872.5695	885.2562	0.61583	5.65E-07	2.41E-06	WBP2	chr17	-	73841780	73852588	3718
ENSG00000(	6955.343	6710.291	6565.403	10001.66	8922.668	9866.867	-0.50833	5.66E-07	2.41E-06	H3F3B	chr17	-	73772515	73781974	2787
ENSG00000(	664.9784	627.4339	525.1267	352.8146	437.2052	519.4818	0.47296	0.005935	0.014484	UNK	chr17	+	73780681	73821886	4049
ENSG00000(	240.3037	202.3203	154.3714	10.48706	6.443024	11.50751	4.3056	9.48E-35	1.69E-33	TRIM47	chr17	-	73870242	73874656	2266
ENSG00000(	1266.773	1316.286	1637.393	1366.314	1263.753	1125.27	0.16699	0.22765	0.34085	ZRANB2	chr1	-	71528974	71546980	3677
ENSG00000(	0	0	0	0	4.60216	0.821965	-1.4643	0.27877	NA	ANKRD20A	chr9	-	43064966	43133544	3964
ENSG00000(	7713.542	7158.286	6461.169	12343.27	11176.81	14476.45	-0.83094	1.62E-11	1.02E-10	EIF5A	chr17	+	7210318	7215774	1511
ENSG00000(	1836.459	1928.065	1516.006	951.3259	1379.728	1301.992	0.5388	0.000467	0.001377	KDM6B	chr17	+	7743222	7758114	6713
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CLEC10A	chr17	-	6977856	6983626	1800
ENSG00000(	0	1.204288	1.319414	0	0.920432	4.93179	-0.74343	0.57514	0.69349	SLC52A1	chr17	-	4935895	4955304	2989
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	GUCY2D	chr17	+	7905912	7923657	3698
ENSG00000(	5.17896	1.204288	2.638828	1.498151	0.920432	0.821965	1.0858	0.36459	0.4944	GPS2	chr17	-	7214643	7218883	1977
ENSG00000(	2186.557	2267.674	1633.434	385.7739	367.2524	484.9593	2.2903	5.40E-48	1.40E-46	DLG4	chr17	-	7093209	7123021	3975

ENSG00000(	217.5163	244.4704	205.8285	334.8368	219.0628	323.8542	-0.39378	0.053719	0.10342	HRSP12	chr8	-	99114572	99129469	1057
ENSG00000(	765.4502	738.2284	1031.782	258.4311	324.9125	286.8658	1.5372	8.97E-20	8.98E-19	VPS13B	chr8	+	1E+08	1.01E+08	14160
ENSG00000(	0	3.612863	0	0	3.681728	2.465895	-0.46565	0.72438	0.81505	RGS22	chr8	-	1.01E+08	1.01E+08	4296
ENSG00000(	725.0543	652.7239	893.2431	619.4855	634.1776	601.6783	0.28981	0.050689	0.098258	MATN2	chr8	+	98881068	99048944	4109
ENSG00000(	415.3526	481.7151	418.2542	57.67882	55.22592	48.49593	3.0091	1.16E-50	3.25E-49	REEP2	chr5	+	1.38E+08	1.38E+08	2170
ENSG00000(	81.82756	109.5902	88.40072	170.0401	161.996	145.4878	-0.76709	0.001295	0.00357	PCBD2	chr5	+	1.34E+08	1.34E+08	5621
ENSG00000(	808.9535	815.3028	795.6065	754.3191	572.5087	715.1095	0.24326	0.088637	0.15872	SDF2	chr17	-	26975374	26989207	1568
ENSG00000(	1655.195	1472.844	1432.883	2971.583	2511.859	2723.992	-0.84556	1.63E-12	1.10E-11	FLOT2	chr17	-	27206353	27224697	2756
ENSG00000(	571.7571	545.5423	547.5567	1284.665	789.7307	934.5741	-0.85118	6.24E-07	2.64E-06	ERAL1	chr17	+	27181956	27188085	1925
ENSG00000(	604.9025	628.6382	438.0454	1125.111	1064.94	1117.872	-0.97985	8.59E-11	5.11E-10	PRMT7	chr16	+	68344877	68392466	4238
ENSG00000(	519.9675	498.5751	496.0996	1260.694	960.931	1111.297	-1.135	1.46E-15	1.20E-14	NIP7	chr16	+	69373333	69377014	2402
ENSG00000(	416.3883	397.4149	427.4901	507.1241	397.6266	451.2587	-0.12854	0.41105	0.54181	TERF2	chr16	-	69389464	69442474	2983
ENSG00000(	1104.154	985.1074	946.0197	1388.786	1121.086	1325.829	-0.33657	0.011376	0.026106	VPS4A	chr16	+	69333562	69358949	2329
ENSG00000(	1028.541	1036.892	934.145	498.8843	926.875	746.3441	0.46511	0.011418	0.026194	MTSS1L	chr16	-	70695107	70719969	4992
ENSG00000(	44.53905	37.33292	34.30476	5.243529	5.522592	8.219649	2.5103	2.52E-06	1.00E-05	HSPA12B	chr20	+	3713314	3733758	3151
ENSG00000(	18.64425	15.65574	11.87472	131.8373	154.6326	97.81383	-2.9853	3.32E-16	2.80E-15	ANKEF1	chr20	+	10015689	10037410	3762
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	SCP2D1	chr20	+	18794370	18795033	664
ENSG00000(	1094.832	1189.836	969.7691	317.608	262.3231	314.8126	1.8562	1.48E-36	2.77E-35	PCED1A	chr20	-	2815960	2821836	2016
ENSG00000(	64.2191	68.6444	76.526	92.13629	67.19154	55.07165	-0.03852	0.90158	0.93886	SNAP25	chr20	+	10199478	10288066	2256
ENSG00000(	493.0369	476.8979	628.041	1841.228	2151.97	1828.05	-1.8616	2.61E-39	5.30E-38	BTBD3	chr20	+	11871371	11907257	5137
ENSG00000(	1367.245	1245.234	1219.138	4754.383	3736.954	3869.811	-1.6858	1.65E-40	3.47E-39	PCNA	chr20	-	5095599	5107272	1359
ENSG00000(	222.6953	246.879	160.9685	388.7702	297.2995	341.1154	-0.69864	0.000491	0.001445	NXT1	chr20	+	23331373	23335414	1123
ENSG00000(	221.6595	210.7504	205.8285	417.9842	313.8673	372.3501	-0.78781	1.22E-05	4.49E-05	POLR3F	chr20	+	18447771	18465287	2416
ENSG00000(	985.0381	869.4957	1116.224	168.542	209.8585	147.9537	2.4894	9.19E-50	2.51E-48	RIN2	chr20	+	19867165	19983101	4505
ENSG00000(	2474.507	2565.133	2407.93	1206.012	1064.019	990.4677	1.189	2.07E-23	2.40E-22	PTPRA	chr20	+	2844830	3019722	3725
ENSG00000(	1424.214	1351.211	1344.483	1899.656	1514.111	1685.85	-0.30736	0.013428	0.030331	DAP3	chr1	+	1.56E+08	1.56E+08	2089
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RHBG	chr1	+	1.56E+08	1.56E+08	2425
ENSG00000(	692.9448	818.9156	671.5816	788.7766	844.0361	897.5857	-0.21198	0.12252	0.20742	KIAA0907	chr1	-	1.56E+08	1.56E+08	4499
ENSG00000(	0	0	3.958241	2.996302	0	2.465895	-0.31436	0.81223	0.87825	ATP1A4	chr1	+	1.6E+08	1.6E+08	3916
ENSG00000(	263.0911	310.7062	274.4381	5048.769	7966.339	9785.492	-4.7263	1.28E-141	1.78E-139	NES	chr1	-	1.57E+08	1.57E+08	5558
ENSG00000(	5.17896	19.2686	6.597069	17.97781	16.56778	18.08323	-0.7211	0.26617	0.38615	BCAN	chr1	+	1.57E+08	1.57E+08	3461
ENSG00000(	1008.861	816.5071	1004.074	898.8907	1088.871	1087.46	-0.11919	0.39772	0.5287	ARHGEF11	chr1	-	1.57E+08	1.57E+08	6889
ENSG00000(	5.17896	3.612863	2.638828	1380.546	1069.542	1279.799	-8.0759	2.89E-76	1.43E-74	RAB25	chr1	+	1.56E+08	1.56E+08	1100
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	HAPLN2	chr1	+	1.57E+08	1.57E+08	1771
ENSG00000(	524.1107	478.1022	514.5714	515.364	500.715	518.6599	-0.01683	0.90398	0.94066	DCAF8	chr1	-	1.6E+08	1.6E+08	4106
ENSG00000(	656.6921	522.6609	682.1369	138.579	139.9057	96.99186	2.2987	7.11E-34	1.23E-32	SYT11	chr1	+	1.56E+08	1.56E+08	5240
ENSG00000(	350.0977	351.652	279.7157	303.3756	356.2072	418.3801	-0.13239	0.46474	0.59381	IGHMBP2	chr11	+	68671310	68708070	3961
ENSG00000(	0	0	0	53.18436	53.38506	49.3179	-6.5005	3.15E-10	1.80E-09	ALDH3B2	chr11	-	67429633	67448671	2649
ENSG00000(	24.85901	27.69862	3.958241	124.3465	115.054	91.23811	-2.4668	1.81E-09	9.70E-09	MTL5	chr11	-	68474908	68519032	3495
ENSG00000(	124.295	149.3317	125.3443	162.5494	169.3595	189.8739	-0.38499	0.074747	0.13721	MMACHC	chr1	+	45965725	45976739	2981
ENSG00000(	285.8786	329.9748	259.9245	974.5473	919.5116	929.6423	-1.6834	5.28E-31	8.29E-30	DPH2	chr1	+	44435672	44439041	2472
ENSG00000(	142.9393	109.5902	134.5802	341.5785	345.162	417.5582	-1.5028	1.58E-14	1.21E-13	TOE1	chr1	+	45805342	45809647	2389
ENSG00000(	1792.956	1789.572	1731.071	5704.959	6122.714	6128.57	-1.754	1.55E-65	6.14E-64	NASP	chr1	+	46049518	46084566	3659
ENSG00000(	159.512	175.826	116.1084	284.6487	219.9832	282.7559	-0.79554	0.000231	0.000715	MUTYH	chr1	-	45794835	45806142	1929

ENSG00000(	1960.754	1989.483	1708.641	888.4036	848.6383	840.8701	1.1323	3.55E-21	3.77E-20	CTNNBL1	chr20	+	36322408	36500531	2990
ENSG00000(	22.78742	38.53721	26.38828	131.8373	163.8369	191.5178	-2.4453	2.77E-15	2.23E-14	LPIN3	chr20	+	39969560	39989222	4363
ENSG00000(	47.64643	30.10719	59.37362	53.18436	64.43024	59.18147	-0.36135	0.30985	0.43608	ZSWIM3	chr20	+	44486256	44507761	2773
ENSG00000(	288.9859	279.3948	249.3692	1142.34	1148.699	1140.887	-2.0617	2.65E-51	7.57E-50	RBM38	chr20	+	55966463	55984389	2382
ENSG00000(	990.2171	815.3028	703.2475	41.19916	40.49901	30.4127	4.4585	3.68E-101	2.84E-99	VSTM2L	chr20	+	36531499	36573752	1959
ENSG00000(	334.5608	361.2863	286.3128	606.7512	493.3516	523.5917	-0.72221	8.77E-06	3.28E-05	C20orf111	chr20	-	42825136	42839431	1616
ENSG00000(	2249.74	2315.845	2293.141	1013.499	1032.725	996.2215	1.1709	3.89E-27	5.23E-26	SERINC3	chr20	-	43124862	43150750	4445
ENSG00000(	208.1942	203.5246	242.7721	195.5087	173.9616	125.7606	0.39766	0.068568	0.12749	PPP1R3D	chr20	-	58511894	58515352	3459
ENSG00000(	0	0	0	4.494453	0	3.28786	-1.9849	0.14263	0.23417	DMGDH	chr5	-	78293438	78531861	3097
ENSG00000(	1775.347	1810.044	2142.728	1215.001	1186.437	967.4527	0.76338	1.44E-08	7.12E-08	AP3B1	chr5	-	77296349	77590579	5838
ENSG00000(	381.1714	356.4692	376.0329	77.15478	97.56579	64.11326	2.2128	3.86E-27	5.20E-26	ZBED3	chr5	-	76367897	76383148	6172
ENSG00000(	61.11172	84.30014	85.7619	527.3492	615.769	488.2472	-2.8111	2.62E-44	6.13E-43	INADL	chr1	+	62208149	62629592	8505
ENSG00000(	12.4295	8.430014	15.83297	213.4865	292.6974	230.9721	-4.265	5.08E-36	9.39E-35	KANK4	chr1	-	62702651	62785085	4665
ENSG00000(	2.071584	0	2.638828	2.247227	1.840864	0	0.12768	0.92209	0.95285	ANGPTL3	chr1	+	63063158	63071830	2805
ENSG00000(	6.214751	2.408575	3.958241	0	0	0	3.1584	0.015021	0.033529	SLC14A2	chr18	+	42792960	43263072	4167
ENSG00000(	572.7929	581.671	469.7113	181.2763	124.2583	152.8855	1.8137	1.03E-22	1.16E-21	FBXO44	chr1	+	11714432	11723384	3320
ENSG00000(	62.14751	81.89156	55.41538	43.44638	61.66894	64.11326	0.237	0.4706	0.59966	RSG1	chr1	-	16558195	16563657	1545
ENSG00000(	197.8363	148.1274	141.1773	157.3059	153.7121	156.1733	0.063983	0.77066	0.84912	CASP9	chr1	-	15817327	15853029	4463
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	NMUR2	chr5	-	1.52E+08	1.52E+08	2073
ENSG00000(	1272.988	1266.911	1638.712	755.0682	836.6727	702.78	0.86205	1.43E-09	7.71E-09	DCTN4	chr5	-	1.5E+08	1.5E+08	4208
ENSG00000(	0	0	0	0	5.522592	0	-1.3606	0.30939	NA	PDE6A	chr5	-	1.49E+08	1.49E+08	5706
ENSG00000(	4.143168	1.204288	7.916483	8.988907	1.840864	12.32947	-0.71244	0.4408	0.5706	ATP8A2	chr13	+	25946209	26599989	9575
ENSG00000(	19.68005	13.24716	18.47179	13.48336	5.522592	3.28786	1.1118	0.10413	0.1813	MTUS2	chr13	+	29598748	30077892	4747
ENSG00000(	208.1942	187.8689	187.3568	188.767	135.3035	149.5976	0.29737	0.16184	0.25952	ZMYM5	chr13	-	20397622	20437776	3268
ENSG00000(	269.3059	284.2119	325.8952	386.523	353.4459	309.0588	-0.25577	0.13879	0.22918	USPL1	chr13	+	31191830	31233686	3814
ENSG00000(	528.2539	499.7794	687.4146	965.5584	893.7395	741.4124	-0.5999	0.0002	0.000625	XPO4	chr13	-	21351469	21477187	9884
ENSG00000(	1733.916	1843.764	1618.921	2644.237	2115.153	2862.904	-0.55145	3.50E-05	0.000121	POMP	chr13	+	29233241	29253062	1428
ENSG00000(	315.9165	310.7062	304.7846	408.9952	457.4547	344.4033	-0.37599	0.025111	0.053174	CDK8	chr13	+	26828276	26979375	3055
ENSG00000(	0	3.612863	0	10.48706	15.64734	7.397684	-2.6657	0.007952	0.018905	ALOX5AP	chr13	+	31309645	31338556	897
ENSG00000(	79.75598	78.2787	88.40072	134.8336	160.1552	272.0704	-1.1902	2.33E-05	8.25E-05	HMGB1P5	chr3	+	22423310	22424420	985
ENSG00000(	516.8602	572.0367	621.4439	274.1617	301.9017	249.0554	1.0477	3.76E-11	2.29E-10	WASF3	chr13	+	27131840	27263085	4805
ENSG00000(	1.035792	0	0	0	4.60216	1.64393	-1.2925	0.33865	0.46723	RNF17	chr13	+	25338290	25454059	5119
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	GPR12	chr13	-	27329341	27334922	4846
ENSG00000(	0	1.204288	2.638828	54.68252	69.95283	58.35951	-5.1439	6.62E-12	4.27E-11	CHRM3	chr1	+	2.4E+08	2.4E+08	8778
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	MYH8	chr17	-	10293639	10325267	6041
ENSG00000(	3521.692	3488.822	3931.853	3262.224	4717.214	3778.573	-0.1033	0.45281	0.58252	MYH10	chr17	-	8377523	8534079	7762
ENSG00000(	198.872	230.019	197.9121	238.9551	114.1336	147.9537	0.31633	0.21231	0.32242	PEMT	chr17	-	17408877	17495022	1050
ENSG00000(	290.0217	258.9219	228.2586	519.8584	461.1364	437.2853	-0.86211	2.75E-07	1.21E-06	SCO1	chr17	-	10583654	10601692	1749
ENSG00000(	5863.618	5691.464	5848.961	4421.044	5419.504	4833.154	0.24598	0.026335	0.055481	MPRIP	chr17	+	16945859	17120993	10960
ENSG00000(	1.035792	2.408575	1.319414	0	0	0	1.6865	0.21314	NA	CHI3L1	chr1	-	2.03E+08	2.03E+08	1920
ENSG00000(	0	0	0	3.745378	0	2.465895	-1.6796	0.21567	0.32631	MYBPH	chr1	-	2.03E+08	2.03E+08	1805
ENSG00000(	350.0977	384.1678	357.5611	262.9255	396.7062	385.5015	0.064296	0.72887	0.8184	PIK3C2B	chr1	-	2.04E+08	2.04E+08	7686
ENSG00000(	572.7929	500.9837	686.0952	322.1025	346.0824	341.9374	0.79754	6.98E-07	2.94E-06	DSTYK	chr1	-	2.05E+08	2.05E+08	7874
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	CHIT1	chr1	-	2.03E+08	2.03E+08	5607

ENSG00000(	619.4036	662.3582	567.3479	394.0137	530.1688	503.8645	0.37328	0.017896	0.039279	SLC41A1	chr1	-	2.06E+08	2.06E+08	4997
ENSG00000(	1.035792	0	0	1.498151	8.283888	0.821965	-1.9831	0.12645	0.21252	LGR6	chr1	+	2.02E+08	2.02E+08	3567
ENSG00000(	49.71801	65.03154	69.92893	114.6086	102.168	122.4728	-0.87482	0.001678	0.004528	TMCC2	chr1	+	2.05E+08	2.05E+08	3738
ENSG00000(	720.9112	688.8526	924.9091	375.2868	303.7426	230.1502	1.3522	5.01E-13	3.50E-12	DCLK1	chr13	-	36345478	36705443	5703
ENSG00000(	3.107376	4.817151	1.319414	1.498151	0.920432	0.821965	1.1129	0.35004	0.47982	CCNA1	chr13	+	37005967	37017019	1962
ENSG00000(	619.4036	598.531	761.3018	263.6746	280.7318	277.8241	1.2624	6.77E-16	5.64E-15	COG6	chr13	+	40229764	40365802	5257
ENSG00000(	1555.759	1643.853	1636.073	967.8056	1116.484	905.8053	0.69245	2.82E-08	1.36E-07	SPG20	chr13	-	36875775	36944317	4944
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RXFP2	chr13	+	32313674	32377009	2803
ENSG00000(	559.3276	561.1981	451.2395	393.2647	400.3879	414.2703	0.3802	0.012776	0.028968	EPSTI1	chr13	-	43460524	43566407	4603
ENSG00000(	3.107376	6.021439	1.319414	92.13629	58.90765	40.27628	-3.9575	5.39E-11	3.25E-10	TRPC4	chr13	-	38210773	38444562	4059
ENSG00000(	1325.814	1424.672	1434.203	5467.502	5063.296	4415.596	-1.8336	2.53E-54	7.69E-53	POSTN	chr13	-	38136720	38172981	3373
ENSG00000(	100.4718	98.75159	102.9143	132.5864	177.6434	150.4196	-0.60203	0.010774	0.024862	RFXAP	chr13	+	37393361	37403241	2304
ENSG00000(	54265.14	55928.33	45544.84	29143.53	24673.1	25153.77	0.97789	8.89E-17	7.69E-16	TPT1	chr13	-	45911008	45915505	1851
ENSG00000(	484.7506	481.7151	484.2249	405.9989	403.1492	347.6912	0.32561	0.029404	0.061091	KIAA1704	chr13	+	45563687	45607746	4294
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	STOML3	chr13	-	39540062	39565203	2121
ENSG00000(	6.214751	1.204288	0	98.87797	143.5874	124.1167	-5.2256	8.48E-20	8.50E-19	KL	chr13	+	33590207	33640282	5006
ENSG00000(	112.9013	140.9017	143.8161	1345.34	1075.985	1047.183	-3.1181	2.24E-75	1.09E-73	RFC3	chr13	+	34392186	34540695	2402
ENSG00000(	886.6379	961.0216	1192.75	217.2319	263.2436	226.8623	2.0971	2.65E-39	5.39E-38	STARD13	chr13	-	33677272	33924767	5917
ENSG00000(	0	0	5.277655	0.749076	0	1.64393	0.6159	0.64721	0.75384	IRS4	chrX	-	1.08E+08	1.08E+08	3940
ENSG00000(	413.281	457.6293	489.5025	322.1025	314.7877	304.949	0.52714	0.000678	0.001951	MORC4	chrX	-	1.06E+08	1.06E+08	3834
ENSG00000(	0	2.408575	1.319414	74.15848	109.5314	109.3213	-5.8079	7.30E-16	6.05E-15	BEX2	chrX	-	1.03E+08	1.03E+08	1077
ENSG00000(	17.60846	10.83859	22.43003	25.46857	34.97642	31.23467	-0.82145	0.097832	0.1722	RNF128	chrX	+	1.06E+08	1.06E+08	2817
ENSG00000(	487.858	646.7025	657.0681	38.20285	30.37426	26.30288	4.2024	2.30E-78	1.20E-76	TBC1D8B	chrX	+	1.06E+08	1.06E+08	5717
ENSG00000(	2185.521	2179.761	1868.29	528.0983	693.0853	844.158	1.5891	1.69E-23	1.97E-22	TCEAL4	chrX	+	1.03E+08	1.03E+08	1571
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	TEX13A	chrX	-	1.04E+08	1.04E+08	1379
ENSG00000(	3.107376	12.04288	6.597069	68.16587	93.88406	86.30632	-3.4215	7.26E-13	5.01E-12	BEX1	chrX	-	1.02E+08	1.02E+08	864
ENSG00000(	222.6953	198.7075	270.4798	301.1284	324.9125	256.4531	-0.35067	0.066307	0.12387	FAM104A	chr17	-	71203492	71232892	2865
ENSG00000(	250.6616	248.0833	219.0227	141.5753	167.5186	170.9687	0.57994	0.00303	0.007822	SLC39A11	chr17	-	70642088	71088851	2752
ENSG00000(	238.2321	197.5032	269.1604	40.45008	34.05598	37.81039	2.6229	1.22E-25	1.54E-24	EPHB2	chr1	+	23037332	23241818	4641
ENSG00000(	1841.638	1657.1	1851.138	2794.052	3504.085	2740.431	-0.75458	3.85E-09	2.01E-08	SRRM1	chr1	+	24958207	24999758	4011
ENSG00000(	2682.701	2678.336	1994.954	1659.951	1353.955	1325.829	0.75925	1.59E-07	7.14E-07	BTBD2	chr19	-	1985447	2034880	2753
ENSG00000(	5.17896	9.634302	1.319414	5.243529	0	1.64393	0.96515	0.37392	0.50444	PRAM1	chr19	-	8554940	8567996	2667
ENSG00000(	96.32865	101.1602	71.24834	181.2763	179.4842	230.9721	-1.1259	2.53E-06	1.00E-05	SUV420H2	chr19	+	55851221	55859488	2308
ENSG00000(	241.3395	219.1804	189.9956	371.5415	225.5058	255.6311	-0.38804	0.072819	0.13414	ZNF414	chr19	-	8575462	8579048	1400
ENSG00000(	2.071584	1.204288	0	23.22134	33.13555	23.83698	-3.9927	2.10E-06	8.40E-06	PDE6B	chr4	+	619373	664571	3280
ENSG00000(	1119.691	941.753	758.6629	1794.036	1442.317	1657.903	-0.79155	2.06E-07	9.18E-07	HSPBP1	chr19	-	55773599	55791749	1768
ENSG00000(	2583.265	2295.372	2140.089	2313.894	2007.462	2226.703	0.10022	0.40394	0.53494	CSNK1G2	chr19	+	1941188	1981337	2878
ENSG00000(	126.3666	132.4716	112.1502	298.1321	231.9489	204.6693	-0.97924	8.26E-06	3.10E-05	ANKRD32	chr5	+	93954052	94075141	5905
ENSG00000(	1270.917	1328.329	1252.124	3662.979	3376.145	3430.06	-1.4405	9.35E-41	1.98E-39	CNDP2	chr18	+	72163051	72188366	4523
ENSG00000(	129.474	154.1488	126.6637	95.13259	85.60018	95.34793	0.56583	0.018309	0.040079	MACROD1	chr11	-	63766030	63933578	1205
ENSG00000(	369.7777	316.7277	325.8952	470.4194	480.4655	642.7766	-0.65069	0.000153	0.000486	WDR74	chr11	-	62599814	62609281	1736
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	LGALS12	chr11	+	63273556	63284246	1816
ENSG00000(	2211.416	2242.384	2184.949	2285.429	2060.847	2166.7	0.027349	0.79897	0.8689	RTN3	chr11	+	63448918	63527363	4937
ENSG00000(	23.82321	10.83859	11.87472	2.247227	7.363456	4.93179	1.5658	0.034151	0.069642	RARRES3	chr11	+	63304281	63313934	938

ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	HRASLS2	chr11	-	63320242	63330855	742
ENSG00000(	34.18113	20.47289	23.74945	29.21395	20.2495	33.70056	-0.07917	0.86521	0.91494	MYH11	chr16	-	15796992	15950890	6921
ENSG00000(	503.3949	574.4452	523.8073	910.1268	767.6403	693.7384	-0.56549	0.000148	0.000471	FOPNL	chr16	-	15959577	15982482	2275
ENSG00000(	716.768	655.1325	612.208	749.8246	581.713	773.469	-0.08501	0.57508	0.69347	MED10	chr5	-	6371994	6378707	1141
ENSG00000(	42.46747	43.35436	48.81831	32.21025	41.41944	33.70056	0.32173	0.38923	0.51982	PDZD2	chr5	+	31639517	32111037	11704
ENSG00000(	1060.651	1065.795	1042.337	800.0127	1006.032	837.5823	0.26175	0.048202	0.094011	MORC2	chr22	-	31322596	31364284	4469
ENSG00000(	381.1714	449.1993	431.4483	482.4047	607.4851	413.4484	-0.25154	0.14493	0.23727	LARGE	chr22	-	33668847	34318829	4409
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	GSTT2B	chr22	-	24299601	24303373	1099
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	MYO18B	chr22	+	26138111	26427007	8565
ENSG00000(	152.2614	158.966	141.1773	229.2171	219.9832	269.6045	-0.66383	0.000856	0.002426	SLC2A11	chr22	+	24198890	24228496	3219
ENSG00000(	382.2072	441.9736	332.4923	950.5769	824.7071	891.8319	-1.201	1.14E-15	9.33E-15	C1QTNF6	chr22	-	37576207	37595425	5003
ENSG00000(	0	0	0	2.247227	3.681728	2.465895	-2.2336	0.094187	0.16688	GGT2	chr22	-	21562262	21581926	2366
ENSG00000(	0	0	0	89.88907	77.31629	104.3895	-7.2216	7.97E-13	5.49E-12	FAM83F	chr22	+	40390953	40426043	2071
ENSG00000(	0	3.612863	0	459.9324	413.274	445.505	-7.9093	1.09E-33	1.87E-32	ZDHHC8P1	chr22	-	23732793	23744913	2382
ENSG00000(	127.4024	124.0416	127.9831	252.4385	234.7102	231.7941	-0.91756	3.80E-06	1.48E-05	ADCK2	chr7	+	1.4E+08	1.4E+08	2377
ENSG00000(	1261.595	1231.986	1326.011	814.2451	957.2493	1069.376	0.4263	0.00149	0.004051	MKRN1	chr7	-	1.4E+08	1.4E+08	3467
ENSG00000(	1353.78	1390.952	1163.723	1712.387	1633.767	1867.504	-0.41434	0.000806	0.002296	AGAP3	chr7	+	1.51E+08	1.51E+08	3751
ENSG00000(	345.9545	439.565	304.7846	252.4385	231.9489	246.5895	0.57415	0.001715	0.004623	KRBA1	chr7	+	1.49E+08	1.49E+08	4019
ENSG00000(	195.7647	217.9761	221.6615	175.2837	187.7681	174.2566	0.23983	0.21093	0.32081	ZNF767	chr7	-	1.49E+08	1.49E+08	3520
ENSG00000(	190.5857	172.2131	208.4674	244.1986	212.6198	229.3282	-0.26495	0.16618	0.26495	ACTR3B	chr7	+	1.52E+08	1.53E+08	5543
ENSG00000(	0	2.408575	1.319414	417.2351	429.8417	451.2587	-7.8873	1.60E-33	2.74E-32	NTS	chr12	+	86268073	86276770	1237
ENSG00000(	1126.942	1288.588	1034.42	585.7771	520.9645	558.9361	1.0474	1.46E-14	1.12E-13	BTG1	chr12	-	92536286	92539673	2448
ENSG00000(	7.250543	7.225726	11.87472	31.46117	29.45382	24.65895	-1.6344	0.003703	0.009417	LRRIQ1	chr12	+	85430092	85657002	5394
ENSG00000(	247.5543	236.0404	282.3545	313.8627	272.4479	263.8507	-0.15206	0.39411	0.52495	C12orf29	chr12	+	88427623	88443937	3079
ENSG00000(	545.8623	513.0266	759.9823	941.588	1193.8	870.4608	-0.72287	2.95E-05	0.000103	ATP13A3	chr3	-	1.94E+08	1.94E+08	7720
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	SFTPD	chr10	-	81697496	81742927	1281
ENSG00000(	0	0	0	2.996302	0	3.28786	-1.6956	0.21138	0.32124	DYDC2	chr10	+	82104501	82127829	2254
ENSG00000(	255.8406	239.6533	241.4527	452.4416	348.8437	354.2669	-0.64675	0.000246	0.000756	TMEM254	chr10	+	81838402	81852313	2074
ENSG00000(	1158.015	1046.526	1562.186	660.6846	803.5371	580.3072	0.878	2.12E-07	9.41E-07	TMTC1	chr12	-	29653773	29937692	8805
ENSG00000(	815.1682	718.9598	992.1992	1090.654	1289.525	940.3279	-0.3934	0.012741	0.028902	KRAS	chr12	-	25357723	25403870	5765
ENSG00000(	1069.973	973.0645	1440.8	1114.624	1287.684	1052.115	0.011579	0.94101	0.96454	IPO8	chr12	-	30781922	30848920	5325
ENSG00000(	2306.709	2227.932	2323.488	2280.935	2243.093	1757.361	0.12646	0.31878	0.44589	LARS	chr5	-	1.45E+08	1.46E+08	4766
ENSG00000(	61.11172	71.05298	73.88717	57.67882	49.70333	64.11326	0.25713	0.40585	0.5367	SPINK5	chr5	+	1.47E+08	1.48E+08	3656
ENSG00000(	239.2679	231.2232	294.2293	439.7073	383.8201	372.3501	-0.64532	0.000203	0.000634	IMPA1	chr8	-	82570196	82598928	2690
ENSG00000(	40.39588	36.12863	55.41538	293.6376	252.1984	216.1768	-2.5151	1.61E-22	1.80E-21	LRRCC1	chr8	+	86019382	86058311	4493
ENSG00000(	155.3688	139.6974	153.052	796.2673	617.6099	601.6783	-2.1602	2.74E-34	4.80E-33	E2F5	chr8	+	86089460	86129387	5036
ENSG00000(	1.035792	0	2.638828	0	0	0.821965	0.94405	0.48501	NA	CA1	chr8	-	86239837	86291243	2785
ENSG00000(	254.8048	278.1905	226.9392	582.0317	386.5814	488.2472	-0.93503	4.88E-07	2.10E-06	CCDC59	chr12	-	82617460	82752584	2101
ENSG00000(	532.397	500.9837	651.7904	1188.034	1415.624	1219.796	-1.1797	2.72E-16	2.31E-15	SWAP70	chr11	+	9685624	9774538	4882
ENSG00000(	118.0803	97.54731	162.2879	96.63075	114.1336	129.0485	0.14968	0.5665	0.68571	ARNTL	chr11	+	13298199	13408813	3862
ENSG00000(	732.3049	703.304	687.4146	12.73428	35.89685	12.32947	4.9935	2.42E-29	3.59E-28	LYVE1	chr11	-	10578513	10633236	3273
ENSG00000(	150.1898	131.2674	139.8579	41.94823	69.0324	36.98842	1.4999	2.56E-07	1.13E-06	AMPD3	chr11	+	10329860	10529126	3994
ENSG00000(	4.143168	2.408575	5.277655	2.996302	17.48821	14.79537	-1.3971	0.10071	0.17646	MICALCL	chr11	+	12297627	12380691	3044
ENSG00000(	558.2918	655.1325	864.216	363.3016	431.6826	294.2634	0.92636	9.04E-07	3.77E-06	SBF2	chr11	-	9800214	10315754	7439

ENSG00000(	925.998	799.647	1116.224	652.4448	522.8054	472.6298	0.78187	2.25E-06	8.97E-06	MICAL2	chr11	+	12115543	12285334	6307
ENSG00000(	423.6389	482.9194	504.0161	1594.033	1256.39	1428.575	-1.5988	1.17E-29	1.76E-28	RRAS2	chr11	-	14299472	14386052	2358
ENSG00000(	1252.272	1181.406	1410.453	1220.993	1240.742	1212.398	0.064644	0.59352	0.70956	HSD17B4	chr5	+	1.19E+08	1.19E+08	5540
ENSG00000(	672.2289	657.5411	977.6856	506.3751	566.9861	486.6032	0.56148	0.00093	0.002619	ZFC3H1	chr12	-	72003252	72061505	7597
ENSG00000(	23.82321	14.45145	26.38828	51.68621	34.05598	20.54912	-0.69645	0.15509	0.25078	TEX15	chr8	-	30689060	30748122	10187
ENSG00000(	2632.983	2457.951	2715.354	1640.475	1639.289	1436.795	0.72558	2.32E-10	1.34E-09	TMEM66	chr8	-	29920528	29940723	2154
ENSG00000(	282.7712	255.309	232.2168	83.14739	90.20234	85.48435	1.5669	6.86E-14	5.05E-13	RNF122	chr8	-	33405273	33424643	1868
ENSG00000(	0	0	0	2.996302	1.840864	1.64393	-1.8657	0.16751	0.26679	DUSP26	chr8	-	33448856	33457624	1829
ENSG00000(	1531.936	1598.09	1378.787	1161.067	1164.346	1121.16	0.38727	0.001032	0.002888	DPF2	chr11	+	65101225	65120720	4840
ENSG00000(	1020.255	1139.256	919.6314	1339.347	1352.115	1411.314	-0.41274	0.001014	0.00284	MEN1	chr11	-	64570982	64578766	3162
ENSG00000(	1937.967	1962.989	2056.966	1429.985	1022.6	1111.297	0.73845	1.00E-07	4.60E-07	C14orf1	chr14	-	76116134	76127532	2633
ENSG00000(	15.53688	9.634302	7.916483	0	0	0	4.6934	5.89E-05	0.000198	GSC	chr14	-	95234553	95236562	1259
ENSG00000(	67.32647	65.03154	69.92893	65.16957	94.8045	85.48435	-0.27326	0.35296	0.48269	C14orf159	chr14	+	91526677	91691976	3075
ENSG00000(	21.75163	7.225726	6.597069	14.98151	13.80648	14.79537	-0.25609	0.69604	0.79291	UNC79	chr14	+	93799565	94174222	9100
ENSG00000(	775.8081	786.3999	944.7003	850.9498	892.819	771.0031	-0.0054	0.96867	0.98169	NUMB	chr14	-	73741815	73930348	5172
ENSG00000(	5.17896	0	0	0	4.60216	6.575719	-0.73665	0.55448	0.67527	CATSPERB	chr14	-	92047040	92247051	3623
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	VRTN	chr14	+	74769772	74826711	3466
ENSG00000(	105.6508	118.0202	93.67838	122.8484	92.96363	83.01846	0.084718	0.74909	0.83322	COX16	chr14	-	70791798	70826448	1717
ENSG00000(	43.50326	34.92434	35.62417	350.5674	443.6482	410.9825	-3.3676	8.29E-47	2.07E-45	TTC9	chr14	+	71108504	71142077	5217
ENSG00000(	252.7332	195.0946	225.6198	598.5114	444.5687	447.1489	-1.14	6.32E-10	3.52E-09	MED6	chr14	-	71047974	71067384	1995
ENSG00000(	1339.279	1376.501	1574.061	2660.716	2336.056	2315.475	-0.76874	2.26E-10	1.30E-09	EIF2S1	chr14	+	67826714	67853233	4485
ENSG00000(	2.071584	1.204288	0	0	1.840864	0.821965	0.19367	0.88581	0.92875	ADAM20	chr14	-	70989075	71001732	2795
ENSG00000(	12163.3	11799.61	10992.04	3570.843	2733.683	2925.373	1.917	3.86E-56	1.22E-54	LOXL2	chr8	-	23154702	23282841	3549
ENSG00000(	685.6942	663.5625	613.5274	667.4263	692.1649	609.898	-0.00385	0.97728	0.98673	ELP3	chr8	+	27947190	28048673	3452
ENSG00000(	1573.368	1500.542	1485.66	377.5341	420.6374	502.2206	1.806	4.60E-39	9.28E-38	CTIF	chr18	+	46065417	46389588	5750
ENSG00000(	14.50109	16.86003	22.43003	2.996302	0.920432	3.28786	2.6183	0.000629	0.001819	MRO	chr18	-	48324574	48351772	2129
ENSG00000(	664.9784	623.821	589.778	916.8685	644.3024	616.4737	-0.21269	0.20245	0.3103	MBD2	chr18	-	51679079	51751158	4080
ENSG00000(	358.384	380.5549	350.9641	453.1907	346.0824	507.9743	-0.26234	0.13249	0.22074	IER3IP1	chr18	-	44681413	44702745	1481
ENSG00000(	217.5163	260.1261	246.7304	250.1912	240.2328	345.2253	-0.20673	0.29673	0.42119	MRPS36	chr5	+	68513587	68525956	1286
ENSG00000(	999.5392	909.2372	1000.116	5340.16	4157.591	4399.978	-2.2515	1.37E-70	6.01E-69	CCNB1	chr5	+	68462837	68474072	2169
ENSG00000(	493.0369	475.6936	530.4043	799.2636	724.38	827.7187	-0.64875	2.19E-06	8.76E-06	CDK7	chr5	+	68530668	68573250	1455
ENSG00000(	7.250543	0	0	0	0	0.821965	1.5733	0.24536	0.36178	CD180	chr5	-	66478103	66492627	2726
ENSG00000(	74.57702	91.52587	75.20659	31.46117	23.93123	30.4127	1.4637	1.50E-05	5.45E-05	IRAK2	chr3	+	10206549	10285427	3483
ENSG00000(	30.03797	30.10719	38.263	5.992604	8.283888	10.68554	1.9006	0.00038	0.001139	CAMK1	chr3	-	9799026	9811676	1488
ENSG00000(	364.5988	375.7378	407.6989	492.1426	496.1128	436.4634	-0.31156	0.039274	0.078742	THUMPD3	chr3	+	9404526	9428475	3961
ENSG00000(	1319.599	1541.488	1270.595	1734.859	1350.274	1537.896	-0.16217	0.23078	0.34416	VHL	chr3	+	10182692	10193904	3737
ENSG00000(	662.9068	606.961	566.0285	626.2272	648.9046	518.6599	0.034723	0.81444	0.87952	BHLHE40	chr3	+	5020801	5027008	3473
ENSG00000(	1462.538	1412.629	1559.547	1387.288	1253.628	1206.645	0.20395	0.087244	0.15675	ARL8B	chr3	+	5163905	5222596	3005
ENSG00000(	1144.55	1147.686	1271.915	641.2087	800.7758	677.2991	0.74871	2.66E-08	1.29E-07	EDEM1	chr3	+	5229331	5261642	6146
ENSG00000(	0	0	0	19.47596	20.2495	24.65895	-5.2915	1.24E-06	5.08E-06	CNTN6	chr3	+	1134260	1445901	4513
ENSG00000(	0	0	0	3.745378	1.840864	0	-1.5327	0.25777	NA	CHL1	chr3	+	238279	451090	8013
ENSG00000(	1501.898	1469.231	1715.238	970.0528	1034.566	906.6273	0.68518	3.55E-08	1.70E-07	MEIS2	chr15	-	37181409	37393504	4818
ENSG00000(	12.4295	16.86003	32.98534	98.1289	84.67974	77.2647	-2.0412	1.80E-07	8.05E-07	ATPBD4	chr15	-	35509546	35838394	3438
ENSG00000(	450.5695	457.6293	445.9619	588.0243	582.6335	552.3604	-0.34658	0.012384	0.028192	KATNBL1	chr15	-	34432875	34502297	2723

ENSG00000(	850.3852	955.0002	890.6043	900.3888	534.771	790.7303	0.27383	0.11332	0.19441	EMC7	chr15	-	34376218	34394149	1155
ENSG00000(	0	0	1.319414	2.247227	3.681728	0	-1.1774	0.38284	0.51349	TRPM1	chr15	-	31293264	31453476	5715
ENSG00000(	44.53905	38.53721	39.58241	8.239831	13.80648	9.041614	1.9262	7.08E-05	0.000236	GNAT2	chr1	-	1.1E+08	1.1E+08	1339
ENSG00000(	0	0	1.319414	0.749076	5.522592	2.465895	-1.6927	0.19493	0.30126	GSTM1	chr1	+	1.1E+08	1.1E+08	1161
ENSG00000(	820.3472	849.0228	881.3684	1237.473	1362.239	1228.838	-0.58491	1.40E-06	5.72E-06	PRPF38B	chr1	+	1.09E+08	1.09E+08	3728
ENSG00000(	10.35792	12.04288	11.87472	465.1759	481.3859	461.1223	-5.2947	2.69E-65	1.06E-63	TSPAN2	chr1	-	1.16E+08	1.16E+08	3177
ENSG00000(	561.3992	647.9068	554.1538	76.40571	55.22592	79.7306	3.0396	4.85E-57	1.57E-55	GSTM3	chr1	-	1.1E+08	1.1E+08	4128
ENSG00000(	98.40023	144.5145	159.6491	56.92974	72.71413	48.49593	1.1618	5.45E-05	0.000184	SYT6	chr1	-	1.15E+08	1.15E+08	4453
ENSG00000(	24.85901	20.47289	22.43003	42.69731	39.57858	26.30288	-0.65946	0.13889	0.22931	VAV3	chr1	-	1.08E+08	1.09E+08	4990
ENSG00000(	190.5857	202.3203	189.9956	904.1342	849.5587	977.3163	-2.2217	5.44E-50	1.50E-48	PSRC1	chr1	-	1.1E+08	1.1E+08	1870
ENSG00000(	2.071584	0	1.319414	0	0	4.93179	-0.30525	0.81989	0.88374	HMGCS2	chr1	-	1.2E+08	1.2E+08	2428
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	PTPN22	chr1	-	1.14E+08	1.14E+08	3654
ENSG00000(	333.525	256.5133	453.8783	2005.275	2361.829	2137.109	-2.6313	5.04E-54	1.52E-52	SORT1	chr1	-	1.1E+08	1.1E+08	7028
ENSG00000(	204.051	166.1917	257.2857	25.46857	38.65814	10.68554	3.0299	1.18E-19	1.17E-18	WNT2B	chr1	+	1.13E+08	1.13E+08	3818
ENSG00000(	2329.496	2465.177	2708.756	1370.059	1871.238	1450.768	0.67592	9.00E-07	3.75E-06	PTGFRN	chr1	+	1.17E+08	1.18E+08	6178
ENSG00000(	361.4914	332.3834	366.797	634.467	392.104	542.4968	-0.56389	0.00216	0.005723	LAMTOR5	chr1	-	1.11E+08	1.11E+08	1830
ENSG00000(	5336.4	5394.005	7130.112	1442.72	2317.648	1598.722	1.7305	4.51E-25	5.59E-24	NOTCH2	chr1	-	1.2E+08	1.21E+08	11389
ENSG00000(	70.43385	78.2787	72.56776	176.0328	212.6198	225.2184	-1.4609	4.72E-10	2.65E-09	TRIM45	chr1	-	1.18E+08	1.18E+08	3515
ENSG00000(	429.8536	484.1237	455.1978	607.5003	584.4743	560.5801	-0.35604	0.011648	0.026662	CEPT1	chr1	+	1.12E+08	1.12E+08	5300
ENSG00000(	21.75163	7.225726	6.597069	38.20285	19.32907	18.90519	-1.0273	0.090723	0.1618	CD101	chr1	+	1.18E+08	1.18E+08	3547
ENSG00000(	0	0	0	818.7396	787.8898	682.2309	-9.9322	6.81E-28	9.47E-27	VTCN1	chr1	-	1.18E+08	1.18E+08	2612
ENSG00000(	12.4295	27.69862	19.79121	119.8521	82.83888	107.6774	-2.3412	2.94E-10	1.68E-09	NGF	chr1	-	1.16E+08	1.16E+08	1047
ENSG00000(	153.2972	169.8046	191.315	166.2948	150.9508	112.6092	0.25439	0.26525	0.38513	AP4B1	chr1	-	1.14E+08	1.14E+08	2818
ENSG00000(	482.679	539.5209	527.7655	502.6297	497.9537	424.9559	0.11961	0.41927	0.54998	NAPG	chr18	+	10525902	10552758	3860
ENSG00000(	336.6324	262.5347	389.2271	119.103	135.3035	124.9387	1.3742	1.58E-11	9.93E-11	SPIRE1	chr18	-	12446511	12658133	5665
ENSG00000(	776.8439	843.0014	870.8131	936.3444	839.434	860.5973	-0.08308	0.51503	0.6417	PPHLN1	chr12	+	42632249	42853517	5975
ENSG00000(	1468.753	1546.305	1215.18	338.5821	318.4695	299.1952	2.1395	2.04E-51	5.85E-50	FKBP11	chr12	-	49315301	49320257	4957
ENSG00000(	4540.912	4496.81	4190.458	6107.962	5976.365	6919.301	-0.52172	1.33E-06	5.44E-06	ARF3	chr12	-	49297286	49351334	4105
ENSG00000(	292.0933	297.4591	290.271	1035.222	902.0234	962.5209	-1.7165	1.43E-34	2.54E-33	TMEM106C	chr12	+	48357352	48362661	1515
ENSG00000(	5197.604	5086.911	6436.1	3552.116	4349.041	3790.08	0.51502	5.65E-05	0.00019	SLC38A2	chr12	-	46751972	46766650	4888
ENSG00000(	38.3243	55.39724	50.13772	152.8114	117.8153	172.6126	-1.6123	1.74E-08	8.60E-08	PLEKHA8P1	chr12	-	45566847	45609824	1839
ENSG00000(	7701.113	7590.625	7709.335	10439.12	9642.446	9986.874	-0.3861	6.57E-05	0.000219	YWHAQ	chr2	-	9724101	9771143	2216
ENSG00000(	1943.146	2060.536	2571.537	737.8394	900.1825	620.5835	1.5368	5.48E-23	6.26E-22	KIDINS220	chr2	-	8865408	8977760	7361
ENSG00000(	2.071584	0	2.638828	288.3941	235.6306	261.3848	-6.9172	9.37E-29	1.36E-27	GRHL1	chr2	+	10085341	10142411	5400
ENSG00000(	916.6758	903.2158	1332.608	1936.36	2154.731	1617.627	-0.85462	1.60E-07	7.19E-07	ROCK2	chr2	-	11319887	11488456	8292
ENSG00000(	2.071584	1.204288	0	1.498151	0	0	0.53227	0.69456	NA	RSAD2	chr2	+	7005937	7038370	3519
ENSG00000(	13.46529	3.612863	17.15238	346.0729	307.4243	322.2102	-4.7647	1.29E-46	3.21E-45	MYCN	chr2	+	16080686	16087129	2602
ENSG00000(	911.4969	886.3558	1122.821	298.8811	271.5274	267.9606	1.7934	6.15E-33	1.03E-31	LPIN1	chr2	+	11817721	11967535	5432
ENSG00000(	5.17896	9.634302	9.235896	12.73428	19.32907	17.26126	-0.97935	0.13554	0.2248	CMPK2	chr2	-	6980701	7006766	2884
ENSG00000(	330.4176	393.8021	320.6175	262.9255	196.052	215.3548	0.62669	0.000712	0.002045	IAH1	chr2	+	9613787	9636672	2793
ENSG00000(	20548.04	20937.75	18094.44	14032.43	11587.32	11952.19	0.66396	7.30E-09	3.71E-08	LDHA	chr11	+	18415935	18429972	2416
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	SAA2	chr11	-	18260770	18270190	1022
ENSG00000(	0	0	0	0.749076	1.840864	0	-0.68825	0.58858	NA	ANO3	chr11	+	26210829	26684835	6642
ENSG00000(	2078.834	2380.877	3004.305	1002.263	1045.611	730.7268	1.4201	2.47E-18	2.31E-17	IL6ST	chr5	-	55230923	55290821	9057

ENSG00000(	418.4599	444.3822	353.6029	660.6846	559.6227	705.2459	-0.65975	2.80E-05	9.83E-05	FST	chr5	+	52776239	52782964	2538
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CFHR4	chr1	+	1.97E+08	1.97E+08	2178
ENSG00000(	3050.407	3051.665	3745.816	755.0682	1064.019	721.6852	1.949	1.74E-36	3.25E-35	NAV1	chr1	+	2.02E+08	2.02E+08	13091
ENSG00000(	662.9068	671.9925	837.8278	807.5034	818.264	684.6968	-0.08965	0.54238	0.66498	CDC73	chr1	+	1.93E+08	1.93E+08	4969
ENSG00000(	1020.255	1097.106	1091.155	1453.207	1363.16	1450.768	-0.41127	0.000389	0.001162	TIMM17A	chr1	+	2.02E+08	2.02E+08	2523
ENSG00000(	3.107376	1.204288	0	1.498151	0	0	0.77471	0.56777	NA	CRB1	chr1	+	1.97E+08	1.97E+08	9023
ENSG00000(	2.071584	0	0	2.247227	0	1.64393	-0.45565	0.73665	0.82369	ERN2	chr16	-	23701647	23724821	3549
ENSG00000(	544.8265	626.2296	459.156	471.1685	370.0137	432.3535	0.35451	0.032728	0.067031	RPS15A	chr16	-	18792617	18801705	3828
ENSG00000(	1970.076	1999.118	2162.519	3603.802	3007.972	2818.518	-0.62019	5.58E-07	2.38E-06	NARS	chr18	-	55267888	55289445	3099
ENSG00000(	315.9165	296.2548	469.7113	452.4416	454.6934	396.1871	-0.27007	0.15116	0.24562	KIAA1468	chr18	+	59854491	59974355	5579
ENSG00000(	1207.733	1280.158	1307.539	970.8019	1191.959	1157.327	0.19286	0.13089	0.21842	FBXO18	chr10	+	5931535	5979556	3702
ENSG00000(	880.4231	827.3457	886.6461	2080.183	2051.643	2206.154	-1.2864	1.88E-29	2.79E-28	RBM17	chr10	+	6130950	6159420	3751
ENSG00000(	102.5434	131.2674	71.24834	152.8114	79.15715	89.59418	-0.07636	0.80638	0.87431	ANKRD16	chr10	-	5903580	5931869	2738
ENSG00000(	19.68005	30.10719	13.19414	50.18806	23.0108	37.81039	-0.79204	0.10292	0.17959	ECHDC3	chr10	+	11784365	11806069	1767
ENSG00000(	0	1.204288	0	5.243529	2.761296	4.93179	-2.28	0.067462	0.12577	IL15RA	chr10	-	5990855	6020150	1705
ENSG00000(	337.6682	358.8777	407.6989	533.3418	413.274	424.9559	-0.31437	0.05983	0.11344	CCNH	chr5	-	86687311	86708836	2391
ENSG00000(	8.286335	0	0	2.996302	0	0.821965	0.72133	0.57924	0.69757	HRH4	chr18	+	22040593	22059921	3668
ENSG00000(	361.4914	401.0278	401.1018	253.9366	228.2671	256.4531	0.65132	7.13E-05	0.000237	TMEM241	chr18	-	20777108	21017925	2941
ENSG00000(	240.3037	337.2006	296.8681	926.6065	973.8171	891.01	-1.6718	4.45E-27	5.97E-26	KCTD1	chr18	-	24034874	24237365	4590
ENSG00000(	251.6974	230.019	253.3274	211.2393	193.2907	179.1884	0.33037	0.075508	0.13842	CABLES1	chr18	+	20714528	20840431	5002
ENSG00000(	41.43168	30.10719	30.34652	67.4168	43.2603	52.60575	-0.6644	0.078878	0.14357	DOCK2	chr5	+	1.69E+08	1.7E+08	6097
ENSG00000(	5372.653	5568.626	5521.747	2388.053	2382.078	2405.069	1.1965	9.38E-34	1.62E-32	EMP1	chr12	+	13349650	13369708	2756
ENSG00000(	65.25489	67.44011	55.41538	128.0919	137.1444	114.2531	-0.9995	0.000166	0.000524	SOX5	chr12	-	23682440	24103966	6969
ENSG00000(	829.6693	871.9043	877.4102	20.22504	10.12475	18.90519	5.6432	6.91E-126	7.80E-124	RERG	chr12	-	15260717	15501609	2264
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	SLCO1B1	chr12	+	21284136	21392180	2229
ENSG00000(	2.071584	0	0	2.996302	9.20432	1.64393	-1.8663	0.12514	0.2108	KLRC1	chr12	-	10594863	10607284	1598
ENSG00000(	7.250543	1.204288	17.15238	70.4131	34.05598	23.83698	-2.2171	0.000356	0.001072	C12orf39	chr12	+	21679241	21690311	1845
ENSG00000(	5.17896	2.408575	0	2.996302	0	1.64393	0.49511	0.69228	0.79005	PRH2	chr12	+	11081835	11084940	673
ENSG00000(	216.4805	245.6747	262.5633	156.5568	217.222	238.3698	0.24215	0.24587	0.3624	LRP4	chr11	-	46878419	46940193	8076
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	MYBPC3	chr11	-	47352957	47374253	4217
ENSG00000(	650.4773	580.4667	605.6109	620.2346	612.0873	667.4355	-0.0481	0.72183	0.813	DDB2	chr11	+	47236493	47260767	1846
ENSG00000(	417.4241	493.758	350.9641	644.205	520.0441	479.2055	-0.37913	0.029603	0.061429	ACP2	chr11	-	47260853	47270457	2203
ENSG00000(	7380.017	6409.219	5508.553	2612.026	1884.124	1814.899	1.6072	3.63E-26	4.70E-25	FAM127A	chrX	+	1.34E+08	1.34E+08	1236
ENSG00000(	14.50109	9.634302	17.15238	13.48336	22.09037	20.54912	-0.42011	0.46585	0.59506	RAB33A	chrX	+	1.29E+08	1.29E+08	1258
ENSG00000(	0	0	0	34.45748	12.88605	9.041614	-5.041	7.21E-06	2.72E-05	SOX3	chrX	-	1.4E+08	1.4E+08	2074
ENSG00000(	633.9046	645.4982	576.5838	417.9842	416.9557	407.6946	0.57789	3.65E-05	0.000126	RBMX2	chrX	+	1.3E+08	1.3E+08	1528
ENSG00000(	314.8807	298.6634	403.7406	2071.194	1993.656	1627.491	-2.479	2.02E-59	6.95E-58	MST4	chrX	+	1.31E+08	1.31E+08	3288
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	FOLH1B	chr11	+	89371683	89431886	2168
ENSG00000(	6.214751	22.88147	15.83297	40.45008	33.13555	27.94681	-1.1451	0.029493	0.061237	PIWIL4	chr11	+	94277006	94354587	3759
ENSG00000(	1684.198	1581.23	1923.705	1664.446	1894.249	1394.053	0.067037	0.62978	0.73992	PUM1	chr1	-	31404353	31538838	5375
ENSG00000(	387.3862	337.2006	376.0329	450.9435	293.6178	300.0172	0.073419	0.70265	0.79797	SPOCD1	chr1	-	32256023	32281652	3960
ENSG00000(	2591.551	2762.636	2572.857	3256.231	2651.765	2989.486	-0.16661	0.15131	0.24579	YARS	chr1	-	33240840	33283754	3238
ENSG00000(	3511.335	3408.134	3293.257	2596.296	2528.427	2489.732	0.42307	3.60E-05	0.000125	PHC2	chr1	-	33789224	33896653	3870
ENSG00000(	243.4111	267.3519	259.9245	2028.497	1763.548	1767.225	-2.8451	1.87E-98	1.39E-96	CDCA8	chr1	+	38158090	38175391	2469

ENSG00000(	944.6422	948.9787	866.8549	1345.34	1238.901	1260.072	-0.47659	7.16E-05	0.000238	GNL2	chr1	-	38032417	38061536	2409
ENSG00000(	224.7668	237.2447	259.9245	200.7522	242.0736	171.7907	0.23113	0.24355	0.35954	AGO4	chr1	+	36273773	36323491	7116
ENSG00000(	0	0	0	158.0549	246.6758	180.0103	-8.1906	4.92E-17	4.31E-16	HOOK1	chr1	+	60280458	60342050	5857
ENSG00000(	19.68005	10.83859	15.83297	16.47966	2.761296	7.397684	0.72949	0.29918	0.42415	CYP2J2	chr1	-	60358980	60392462	2549
ENSG00000(	793.4166	790.0127	815.3977	1193.277	995.9074	994.5776	-0.40819	0.001821	0.00489	BTF3L4	chr1	+	52521797	52556388	4703
ENSG00000(	765.4502	617.7996	901.1596	659.9356	659.9497	584.4171	0.26102	0.096338	0.17012	ZCCHC11	chr1	-	52873954	53019159	5858
ENSG00000(	467.1421	496.1665	566.0285	1107.134	824.7071	906.6273	-0.89155	5.94E-09	3.05E-08	PRPF38A	chr1	+	52870236	52883992	2755
ENSG00000(	198.872	175.826	225.6198	2406.78	2820.204	2292.46	-3.638	1.01E-137	1.33E-135	DSC2	chr18	-	28645940	28682378	5124
ENSG00000(	0	0	0	38.95193	44.18074	47.67397	-6.2653	1.94E-09	1.04E-08	DSG3	chr18	+	29027758	29058665	5525
ENSG00000(	209.23	168.6003	220.3421	679.4115	594.5991	540.8529	-1.5955	2.25E-20	2.32E-19	RNF138	chr18	+	29671818	29711524	3570
ENSG00000(	1338.243	1313.878	1397.259	997.7686	970.1353	863.8851	0.5147	2.21E-05	7.87E-05	ELP2	chr18	+	33709407	33757909	5849
ENSG00000(	2.071584	0	2.638828	0	1.840864	2.465895	0.08876	0.9457	0.96732	DSG1	chr18	+	28898052	28936992	5045
ENSG00000(	1178.731	1059.773	1397.259	759.5626	983.9418	788.2644	0.52081	0.000499	0.001468	DSC3	chr18	-	28569974	28622781	6978
ENSG00000(	3.107376	2.408575	6.597069	3.745378	2.761296	0.821965	0.5747	0.58925	0.70622	DSC1	chr18	-	28709199	28742819	4271
ENSG00000(	148.1182	116.8159	178.1209	149.066	162.9165	113.4312	0.057344	0.81387	0.87912	DTNA	chr18	+	32073254	32471808	6522
ENSG00000(	430.8894	352.8563	374.7135	294.3867	327.6738	276.1802	0.36789	0.027391	0.057443	FHOD3	chr18	+	33877677	34360018	4967
ENSG00000(	2252.847	2247.201	2231.129	2737.122	2093.983	2067.242	-0.03567	0.78494	0.85858	TPGS2	chr18	-	34359987	34409158	4030
ENSG00000(	132.5814	98.75159	117.4278	75.65663	105.8497	101.1017	0.30516	0.24336	0.35935	DAGLA	chr11	+	61447905	61514473	5757
ENSG00000(	73.54123	28.90291	64.65128	35.20655	34.05598	45.20807	0.53579	0.17897	0.28164	SLC43A3	chr11	-	57174427	57195053	2619
ENSG00000(	458.8558	452.8122	366.797	652.4448	706.8918	921.4227	-0.83026	7.74E-07	3.25E-06	TIMM10	chr11	-	57295936	57298276	680
ENSG00000(	2.071584	0	0	0	4.60216	0	-0.53557	0.69303	0.7906	GIF	chr11	-	59596741	59612974	1623
ENSG00000(	536.5402	599.7353	497.419	874.1712	856.9222	913.203	-0.69265	2.94E-07	1.29E-06	DHX34	chr19	+	47852538	47885961	4372
ENSG00000(	0	4.817151	0	0	0.920432	0	1.0812	0.42455	NA	APLNR	chr11	-	57001051	57004709	1726
ENSG00000(	12717.45	12198.23	11957.85	6457.78	6706.268	7225.072	0.85368	1.97E-17	1.77E-16	FADS2	chr11	+	61560452	61634826	5073
ENSG00000(	27.96638	25.29004	29.0271	8.239831	16.56778	22.19305	0.7817	0.13633	0.22581	TMEM258	chr11	-	61556435	61560274	1692
ENSG00000(	0	0	0	38.95193	16.56778	17.26126	-5.4318	6.64E-07	2.80E-06	TCN1	chr11	-	59620273	59634048	1582
ENSG00000(	1.035792	1.204288	2.638828	0	0	0	1.7123	0.20641	NA	C5AR2	chr19	+	47835404	47846606	2768
ENSG00000(	2076.763	2079.805	2056.966	1441.97	1463.487	1276.512	0.57035	5.07E-07	2.18E-06	TMEM165	chr4	+	56262124	56292339	1928
ENSG00000(	529.2897	473.2851	699.2893	321.3534	396.7062	293.4415	0.74706	4.46E-05	0.000153	CLOCK	chr4	-	56294070	56413305	10304
ENSG00000(	2748.992	2916.785	3435.753	44.94453	69.95283	30.4127	5.9513	1.21E-208	3.89E-206	PDGFRA	chr4	+	55095264	55164414	6576
ENSG00000(	59.04014	55.39724	47.4989	30.7121	42.33987	34.52253	0.58595	0.10417	0.18134	GGACT	chr13	-	1.01E+08	1.01E+08	1431
ENSG00000(	10352.74	10200.32	9788.731	10908.04	14808.83	17029.47	-0.49306	0.000537	0.001569	COL4A2	chr13	+	1.11E+08	1.11E+08	6281
ENSG00000(	3.107376	0	2.638828	38.20285	44.18074	34.52253	-3.975	3.02E-08	1.46E-07	CLDN10	chr13	+	96085858	96232013	2656
ENSG00000(	1271.952	1260.889	1195.389	546.0761	541.214	415.0923	1.308	2.89E-20	2.96E-19	DZIP1	chr13	-	96230457	96296957	7068
ENSG00000(	1189.089	1012.806	961.8526	1050.204	908.4664	947.7256	0.12273	0.35978	0.48943	UBAC2	chr13	+	99853028	1E+08	2525
ENSG00000(	1365.174	1324.716	1574.061	1567.066	1555.53	1597.078	-0.14686	0.21639	0.32731	ARGLU1	chr13	-	1.07E+08	1.07E+08	3390
ENSG00000(	367.7061	393.8021	336.4505	278.6561	207.0972	253.1652	0.56732	0.001435	0.003914	BIVM	chr13	+	1.03E+08	1.03E+08	3857
ENSG00000(	182.2994	210.7504	180.7597	147.5679	126.0992	121.6508	0.53267	0.011913	0.027222	ERCC5	chr13	+	1.03E+08	1.04E+08	5076
ENSG00000(	773.7366	887.56	973.7274	1244.964	1193.8	1026.634	-0.39551	0.004266	0.010718	TPP2	chr13	+	1.03E+08	1.03E+08	4660
ENSG00000(	410.1736	419.0921	419.5736	405.2499	372.775	346.0472	0.15064	0.32407	0.45151	KDELC1	chr13	-	1.03E+08	1.03E+08	2083
ENSG00000(	1135.228	1144.073	1008.032	1652.461	1436.794	1730.236	-0.55053	1.29E-05	4.74E-05	CARS2	chr13	-	1.11E+08	1.11E+08	3516
ENSG00000(	799.6314	668.3797	758.6629	554.3159	721.6187	617.2957	0.23486	0.11395	0.19523	ARHGAP32	chr11	-	1.29E+08	1.29E+08	10111
ENSG00000(	6601.102	6020.234	6339.783	4141.639	4129.058	3660.21	0.66739	3.57E-10	2.02E-09	STT3A	chr11	+	1.25E+08	1.25E+08	4558
ENSG00000(	3.107376	0	5.277655	5.992604	0	5.753754	-0.38627	0.73704	0.82369	ADAMTS8	chr11	-	1.3E+08	1.3E+08	4010

ENSG00000(	8.286335	14.45145	11.87472	16.47966	26.69253	16.4393	-0.7475	0.20569	0.31445	ACRV1	chr11	-	1.26E+08	1.26E+08	2212
ENSG00000(	789.2734	834.5714	982.9633	1692.162	1832.58	1427.753	-0.92437	3.90E-11	2.38E-10	ETS1	chr11	-	1.28E+08	1.28E+08	5123
ENSG00000(	4.143168	1.204288	6.597069	9.737982	1.840864	4.109825	-0.34917	0.72272	0.81363	SLC37A2	chr11	+	1.25E+08	1.25E+08	4654
ENSG00000(	6.214751	4.817151	10.55531	8.239831	19.32907	17.26126	-0.98231	0.1624	0.26029	KLB	chr4	+	39408473	39453156	6082
ENSG00000(	1322.706	1472.844	1509.409	1450.959	1247.185	1182.808	0.14832	0.24589	0.3624	TMED7	chr5	-	1.15E+08	1.15E+08	3757
ENSG00000(	640.1194	645.4982	902.479	340.8294	413.274	304.127	1.0432	4.16E-09	2.16E-08	APC	chr5	+	1.12E+08	1.12E+08	11025
ENSG00000(	2384.393	2702.422	2460.707	931.1009	951.7267	839.2262	1.4685	1.22E-35	2.23E-34	NREP	chr5	-	1.11E+08	1.11E+08	3564
ENSG00000(	481.6432	486.5322	647.8322	755.0682	678.3584	624.6933	-0.34997	0.027652	0.057911	WDR36	chr5	+	1.1E+08	1.1E+08	7048
ENSG00000(	426.7463	399.8235	505.3355	952.075	902.9438	969.0966	-1.0831	1.55E-14	1.19E-13	OSTF1	chr9	+	77703459	77762181	1319
ENSG00000(	211.3015	228.8147	275.7575	510.8695	431.6826	451.2587	-0.96136	2.26E-08	1.10E-07	RFK	chr9	-	79000433	79009433	2684
ENSG00000(	1703.878	1643.853	1837.943	2400.787	2242.172	1987.511	-0.35425	0.003064	0.007901	UBQLN1	chr9	-	86274878	86323118	6055
ENSG00000(	357.3482	385.3721	376.0329	714.6181	633.2572	557.2922	-0.7666	5.59E-07	2.38E-06	NAA35	chr9	+	88556061	88637213	2649
ENSG00000(	189.5499	177.0303	139.8579	600.0095	488.7494	481.6714	-1.6218	6.56E-19	6.33E-18	C9orf40	chr9	-	77561497	77567802	2327
ENSG00000(	3500.977	3589.982	3470.058	16291.64	10515.94	12079.6	-1.8753	7.40E-39	1.48E-37	ANXA1	chr9	+	75766673	75785309	2209
ENSG00000(	2801.817	2796.356	2597.926	752.0719	790.6511	840.0481	1.7796	3.06E-55	9.51E-54	CTSL1	chr9	+	90340434	90346308	2177
ENSG00000(	2454.827	2343.544	3109.858	2930.384	3699.216	3149.77	-0.3058	0.026379	0.055558	TMEM2	chr9	-	74298282	74431606	6523
ENSG00000(	353.205	420.2964	393.1853	451.6926	501.6354	387.9674	-0.2009	0.2176	0.32891	AGTPBP1	chr9	-	88161455	88356944	4393
ENSG00000(	6618.71	6498.337	6367.491	2788.808	2919.61	2850.574	1.1854	2.24E-33	3.80E-32	GOLM1	chr9	-	88641061	88715088	3046
ENSG00000(	0	1.204288	0	102.6234	69.95283	69.04505	-6.3867	7.51E-13	5.18E-12	FAM189A2	chr9	+	71939488	72007371	2423
ENSG00000(	1471.86	1440.328	1304.9	4970.116	4403.347	4114.756	-1.6738	1.24E-45	3.01E-44	PSAT1	chr9	+	80912059	80945009	2188
ENSG00000(	648.4057	697.2826	592.4168	948.3296	787.8898	849.9117	-0.4152	0.002708	0.007055	ISCA1	chr9	-	88879461	88897676	1958
ENSG00000(	1029.577	1138.052	1286.428	1618.752	1848.227	1728.592	-0.5885	3.82E-06	1.49E-05	ADAM19	chr5	-	1.57E+08	1.57E+08	6481
ENSG00000(	3.107376	0	5.277655	6.74168	3.681728	2.465895	-0.51137	0.63391	0.74346	HAVCR2	chr5	-	1.57E+08	1.57E+08	2907
ENSG00000(	169.8699	173.4174	151.7326	384.2758	405.9105	385.5015	-1.2408	9.25E-13	6.34E-12	CCNJL	chr5	-	1.6E+08	1.6E+08	3442
ENSG00000(	416.3883	390.1892	406.3794	167.7929	158.3143	104.3895	1.4862	1.12E-13	8.14E-13	TAOK3	chr12	-	1.19E+08	1.19E+08	4384
ENSG00000(	188.5141	230.019	248.0498	176.7818	115.054	147.9537	0.59035	0.008077	0.019169	USP30	chr12	+	1.09E+08	1.1E+08	3742
ENSG00000(	0	3.612863	2.638828	2.247227	1.840864	2.465895	-0.06872	0.95434	0.97285	SDS	chr12	-	1.14E+08	1.14E+08	1606
ENSG00000(	74.57702	78.2787	69.92893	568.5483	734.5047	744.7002	-3.1819	1.24E-60	4.39E-59	MSI1	chr12	-	1.21E+08	1.21E+08	2975
ENSG00000(	31.07376	22.88147	23.74945	41.19916	47.86246	58.35951	-0.89651	0.025544	0.053994	HNF1A	chr12	+	1.21E+08	1.21E+08	4026
ENSG00000(	584.1866	697.2826	647.8322	538.5853	629.5755	489.0691	0.21871	0.14716	0.24023	FBXO21	chr12	-	1.18E+08	1.18E+08	4687
ENSG00000(	269.3059	240.8575	207.148	2721.391	3458.983	3314.163	-3.7113	3.44E-143	4.87E-141	TBX3	chr12	-	1.15E+08	1.15E+08	4723
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	OASL	chr12	-	1.21E+08	1.21E+08	2085
ENSG00000(	1.035792	6.021439	10.55531	125.8447	135.3035	128.2265	-4.3996	2.17E-21	2.33E-20	HRK	chr12	-	1.17E+08	1.17E+08	5789
ENSG00000(	15.53688	0	13.19414	158.0549	180.4047	122.4728	-3.4919	9.88E-05	0.000323	RNFT2	chr12	+	1.17E+08	1.17E+08	3882
ENSG00000(	165.7267	151.7403	131.9414	223.9736	156.4734	219.4646	-0.41335	0.062923	0.11843	P2RX4	chr12	+	1.22E+08	1.22E+08	4658
ENSG00000(	3.107376	8.430014	3.958241	52.43529	70.87326	91.23811	-3.6481	6.14E-12	3.97E-11	CCDC64	chr12	+	1.2E+08	1.21E+08	3055
ENSG00000(	10.35792	6.021439	1.319414	2.247227	2.761296	7.397684	0.45479	0.63486	0.74397	DTX1	chr12	+	1.13E+08	1.14E+08	3455
ENSG00000(	703.3027	568.4238	664.9845	603.7549	686.6423	632.913	0.011155	0.93769	0.9623	TRAFD1	chr12	+	1.13E+08	1.13E+08	3178
ENSG00000(	806.8819	865.8829	948.6585	727.3524	627.7346	637.0228	0.39346	0.003796	0.009635	DMTF1	chr7	+	86781677	86825653	4460
ENSG00000(	238.2321	231.2232	279.7157	286.1469	237.4715	278.6461	-0.10121	0.57856	0.69696	TMEM243	chr7	-	86825478	86849903	1273
ENSG00000(	51.7896	37.33292	36.94359	14.23244	23.93123	13.15144	1.2712	0.005294	0.013054	CCDC146	chr7	+	76751751	76958850	3333
ENSG00000(	185.4068	223.9975	183.3985	216.4828	161.996	209.6011	0.009307	0.9641	0.97928	TMEM60	chr7	-	77423045	77427897	1023
ENSG00000(	1684.198	1455.984	1715.238	1504.144	1980.77	1476.249	-0.03047	0.82912	0.89032	POM121C	chr7	-	75046066	75115548	5839
ENSG00000(	272.4133	239.6533	354.9223	47.19176	44.18074	39.45432	2.7037	5.28E-29	7.72E-28	CD36	chr7	+	79998891	80308593	6179

ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	UGT2A3	chr4	-	69794181	69817509	2965
ENSG00000(	290.0217	320.3405	407.6989	186.5198	208.0176	156.9953	0.87822	9.04E-06	3.38E-05	PNPLA8	chr7	-	1.08E+08	1.08E+08	4268
ENSG00000(	546.8981	733.4112	411.6571	381.2795	368.1728	399.475	0.55632	0.003459	0.008848	HILPDA	chr7	+	1.28E+08	1.28E+08	1370
ENSG00000(	0	2.408575	3.958241	8.988907	8.283888	4.93179	-1.542	0.12367	0.20884	FAM71F1	chr7	+	1.28E+08	1.28E+08	1818
ENSG00000(	277.5922	327.5663	391.8659	276.4089	272.4479	226.0404	0.35917	0.054668	0.10506	RINT1	chr7	+	1.05E+08	1.05E+08	2976
ENSG00000(	618.3678	682.8311	833.8695	462.9287	505.3172	409.3385	0.62895	7.16E-05	0.000238	SRPK2	chr7	-	1.05E+08	1.05E+08	3700
ENSG00000(	10.35792	1.204288	3.958241	0.749076	5.522592	12.32947	-0.20203	0.83642	0.89542	KCP	chr7	-	1.29E+08	1.29E+08	5108
ENSG00000(	1040.971	1058.569	965.8109	3498.183	3111.06	2806.188	-1.6154	1.89E-39	3.86E-38	TES	chr7	+	1.16E+08	1.16E+08	2782
ENSG00000(	1520.543	1519.811	1674.336	478.6593	469.4203	424.1339	1.7764	3.73E-45	8.96E-44	MDFIC	chr7	+	1.15E+08	1.15E+08	4598
ENSG00000(	247.5543	220.3847	286.3128	311.6154	323.9921	304.949	-0.31835	0.069818	0.12948	MTO1	chr6	+	74171301	74218959	10857
ENSG00000(	9.322127	9.634302	7.916483	6.74168	11.96562	0.821965	0.42088	0.6158	0.72883	BAI3	chr6	+	69345259	70099403	6010
ENSG00000(	46.61064	57.80581	58.05421	156.5568	179.4842	159.4612	-1.5982	5.27E-10	2.95E-09	ANKRD6	chr6	+	90142889	90343553	5258
ENSG00000(	2.071584	3.612863	2.638828	22.47227	20.2495	13.15144	-2.507	0.001116	0.003106	HTR1B	chr6	-	78171948	78173490	1543
ENSG00000(	40.39588	85.50443	50.13772	44.19546	28.53339	25.48091	0.816	0.043586	0.086247	KHDC1	chr6	-	73951037	74020088	2053
ENSG00000(	137.7603	154.1488	163.6073	138.579	124.2583	139.734	0.17391	0.42534	0.5557	KIAA1009	chr6	-	84833960	84937353	5156
ENSG00000(	4180.456	4175.266	4579.685	5383.606	5828.175	5278.659	-0.34987	0.000845	0.002397	SYNCRIP	chr6	-	86267696	86353510	6443
ENSG00000(	538.6118	569.6281	628.041	925.1083	701.3692	659.2159	-0.39703	0.01268	0.028789	SNX14	chr6	-	86215214	86303874	3615
ENSG00000(	2099.55	1991.892	2477.859	609.7475	453.773	392.8992	2.1641	2.35E-41	5.03E-40	NT5E	chr6	+	86159809	86205500	3548
ENSG00000(	32.10955	34.92434	36.94359	13.48336	2.761296	4.93179	2.1581	0.000208	0.000647	MRAP2	chr6	+	84743475	84800600	2153
ENSG00000(	564.5066	533.4995	641.2351	11.98521	4.60216	7.397684	6.061	6.45E-86	3.83E-84	EPHA7	chr6	-	93949738	94129265	6588
ENSG00000(	514.7886	490.1451	478.9472	940.0898	700.4487	685.5187	-0.64666	4.09E-05	0.000141	AKIRIN2	chr6	-	88384790	88411927	1662
ENSG00000(	352.1692	303.4805	360.2	686.9023	462.0569	530.1674	-0.72326	4.48E-05	0.000154	ORC3	chr6	+	88299839	88377169	2512
ENSG00000(	158.4762	166.1917	192.6344	93.63444	95.72493	72.33291	0.97421	3.82E-05	0.000132	LCA5	chr6	-	80194708	80247147	4719
ENSG00000(	1183.91	1085.063	1366.913	1026.234	963.6923	897.5857	0.33092	0.012649	0.028729	MAP3K7	chr6	-	91223292	91296764	4911
ENSG00000(	0	7.225726	0	17.22874	12.88605	19.72716	-2.4547	0.005342	0.013158	CGA	chr6	-	87795216	87804824	710
ENSG00000(	196.8005	191.4817	180.7597	307.8701	265.0844	253.1652	-0.53509	0.003991	0.01009	PRR5L	chr11	+	36317838	36486754	3930
ENSG00000(	62.14751	34.92434	59.37362	21.72319	44.18074	27.94681	0.72834	0.07673	0.14022	LMO2	chr11	-	33880122	33913836	2294
ENSG00000(	1558.867	1623.38	1467.188	528.0983	550.4183	528.5234	1.5301	1.01E-36	1.90E-35	PHF21A	chr11	-	45950871	46142985	8954
ENSG00000(	1079.295	1081.45	1019.907	1612.76	1523.315	1376.791	-0.50354	3.03E-05	0.000106	NAT10	chr11	+	34127149	34169217	4002
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	EHF	chr11	+	34642640	34682604	3150
ENSG00000(	0	6.021439	0	0.749076	0	0	1.3768	0.31019	0.43627	ELF5	chr11	-	34500340	34535352	2450
ENSG00000(	1.035792	4.817151	2.638828	196.2578	170.2799	198.9155	-5.8304	2.32E-27	3.16E-26	PRRG4	chr11	+	32851489	32879669	5530
ENSG00000(	5021.519	4666.615	5850.281	7404.612	7076.281	5704.437	-0.37675	0.003918	0.00992	CAPRIN1	chr11	+	34073230	34122703	4108
ENSG00000(	3496.833	3512.907	2530.636	2526.632	1991.815	2103.408	0.52539	0.000327	0.00099	ATP5G2	chr12	-	54026510	54071192	1976
ENSG00000(	291.0575	285.4162	299.5069	142.3244	251.2779	205.4912	0.54787	0.010267	0.023806	DNAJC14	chr12	-	56214744	56224608	3416
ENSG00000(	23461.72	23382.45	19328.09	6359.651	7182.131	9062.985	1.5457	3.63E-29	5.34E-28	CD63	chr12	-	56119107	56123491	1233
ENSG00000(	122.2234	128.8588	96.31721	29.21395	38.65814	48.49593	1.5622	3.58E-07	1.56E-06	AVIL	chr12	-	58191159	58212487	2939
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AMHR2	chr12	+	53817639	53825318	2162
ENSG00000(	1039.935	1082.655	1079.28	405.9989	487.829	505.5084	1.192	3.02E-18	2.81E-17	GDF11	chr12	+	56137064	56150911	3731
ENSG00000(	51.7896	66.23582	62.01245	79.40201	93.88406	77.2647	-0.47272	0.10957	0.18892	GLS2	chr12	-	56864736	56882198	2694
ENSG00000(	15.53688	16.86003	18.47179	58.42789	48.7829	42.74218	-1.5246	0.000393	0.001173	ITGA7	chr12	-	56078352	56109827	4348
ENSG00000(	0	0	0	0.749076	1.840864	0.821965	-1.0455	0.43461	NA	TESPA1	chr12	-	55341802	55378530	4188
ENSG00000(	19.68005	21.67718	22.43003	0.749076	4.60216	11.50751	1.7822	0.012488	0.028411	FAM186B	chr12	-	49976668	49999422	3088
ENSG00000(	14.50109	8.430014	13.19414	0.749076	10.12475	10.68554	0.68763	0.38546	0.51632	RDH5	chr12	+	56114151	56118489	1419

ENSG00000(	25.8948	13.24716	27.70769	0.749076	0	0	5.0263	5.59E-07	2.38E-06	AGAP2	chr12	-	58118980	58135940	4464
ENSG00000(	5.17896	8.430014	7.916483	13.48336	11.04518	4.93179	-0.42195	0.57955	0.6978	BLOC1S1	chr12	+	56109820	56113871	1229
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	KRT85	chr12	-	52753790	52761265	2447
ENSG00000(	1764.989	1775.12	1798.361	2195.54	2197.992	2242.32	-0.31347	0.002858	0.007409	CDK4	chr12	-	58141510	58149796	2076
ENSG00000(	0	0	0	5.243529	0	0.821965	-1.6239	0.23093	0.34427	PPP1R1A	chr12	-	54969171	54982443	2491
ENSG00000(	242.3753	246.879	175.482	942.337	799.8554	946.9036	-2.0053	1.21E-33	2.07E-32	TROAP	chr12	+	49717019	49725514	2771
ENSG00000(	414.3168	387.7806	308.7428	266.6709	224.5854	199.7375	0.68247	0.000277	0.000848	TSPAN31	chr12	+	58131796	58143994	3434
ENSG00000(	50.7538	28.90291	32.98534	10.48706	11.04518	3.28786	2.0943	0.000146	0.000465	B4GALNT1	chr12	-	58017193	58027138	5580
ENSG00000(	617.332	575.6495	591.0974	803.7581	679.2788	687.1627	-0.28221	0.041049	0.081895	TFCP2	chr12	-	51487446	51566926	3562
ENSG00000(	65.25489	87.913	40.90183	89.88907	71.7937	55.89361	-0.1603	0.63905	0.74712	COQ10A	chr12	+	56660642	56664750	1652
ENSG00000(	15.53688	32.51577	22.43003	0	0	0	5.8006	1.09E-07	4.97E-07	FAIM2	chr12	-	50260679	50298000	4654
ENSG00000(	270.3417	308.2977	277.0769	211.9884	223.665	191.5178	0.44646	0.012836	0.029093	PAN2	chr12	-	56710007	56727837	5372
ENSG00000(	269.3059	295.0505	255.9663	1158.071	1313.456	1234.591	-2.1691	6.35E-55	1.96E-53	ESPL1	chr12	+	53662083	53687427	6662
ENSG00000(	0	0	0	0	4.60216	1.64393	-1.6592	0.22125	0.33301	KRT121P	chr12	-	52644250	52652651	1769
ENSG00000(	13.46529	7.225726	7.916483	3272.711	3209.546	3358.549	-8.2851	6.81E-169	1.39E-166	KRT7	chr12	+	52626304	52645970	1754
ENSG00000(	50.7538	74.66584	80.48424	53.18436	49.70333	64.93523	0.28434	0.38121	0.51193	ZC3H10	chr12	+	56511943	56516278	2208
ENSG00000(	35969.95	35972.07	31824.26	28268.61	35485.41	38601.94	0.019739	0.87584	0.9222	HNRNPA1	chr12	+	54673977	54680872	4121
ENSG00000(	14.50109	9.634302	9.235896	0	0	0.821965	4.0103	0.000252	0.000774	SLC26A10	chr12	+	58013310	58019934	2515
ENSG00000(	521.0033	551.5638	604.2915	453.9398	649.825	579.4853	-0.00505	0.97522	0.98554	ACVR1B	chr12	+	52345451	52390862	4563
ENSG00000(	6938.77	6267.113	5625.98	1443.469	1654.937	1643.93	1.9862	2.99E-62	1.10E-60	OS9	chr12	+	58087738	58115340	3870
ENSG00000(	2.071584	0	0	3.745378	0	4.109825	-1.139	0.38703	0.51778	MIP	chr12	-	56843286	56862950	2599
ENSG00000(	33.14534	31.31148	17.15238	2.996302	3.681728	9.863579	2.1723	0.000652	0.001882	KCNH3	chr12	+	49932940	49952091	3867
ENSG00000(	342.8471	337.2006	319.2981	835.2192	572.5087	635.3789	-1.0282	1.35E-09	7.33E-09	LTV1	chr6	+	1.44E+08	1.44E+08	1847
ENSG00000(	3.107376	1.204288	0	381.2795	428.0009	405.2287	-7.5277	3.43E-35	6.19E-34	MAP7	chr6	-	1.37E+08	1.37E+08	3841
ENSG00000(	3686.383	3624.906	4402.884	3784.33	3351.293	3102.918	0.19345	0.11815	0.20131	CD164	chr6	-	1.1E+08	1.1E+08	4963
ENSG00000(	83.89914	62.62296	77.84541	104.1215	117.8153	101.9236	-0.5214	0.051711	0.1	LACE1	chr6	+	1.09E+08	1.09E+08	4755
ENSG00000(	775.8081	710.5298	919.6314	676.4152	1155.142	774.291	-0.11404	0.5365	0.6605	NHSL1	chr6	-	1.39E+08	1.39E+08	7500
ENSG00000(	418.4599	388.9849	393.1853	199.2541	180.4047	193.1618	1.0632	1.67E-10	9.72E-10	AHI1	chr6	-	1.36E+08	1.36E+08	5921
ENSG00000(	0	3.612863	1.319414	108.616	101.2475	109.3213	-5.6474	1.38E-17	1.25E-16	HEY2	chr6	+	1.26E+08	1.26E+08	2678
ENSG00000(	68.36227	68.6444	62.01245	435.2129	326.7534	337.8276	-2.4492	3.67E-29	5.39E-28	PKIB	chr6	+	1.23E+08	1.23E+08	1875
ENSG00000(	0	4.817151	0	1.498151	2.761296	0	0.10859	0.93488	0.96073	NMBR	chr6	-	1.42E+08	1.42E+08	1354
ENSG00000(	81.82756	89.11729	73.88717	101.1252	69.95283	93.704	-0.11373	0.68532	0.78465	SMPD2	chr6	+	1.1E+08	1.1E+08	1645
ENSG00000(	1792.956	1801.614	1662.461	989.5288	882.6943	1181.986	0.78135	5.13E-09	2.65E-08	MICAL1	chr6	-	1.1E+08	1.1E+08	4381
ENSG00000(	573.8287	500.9837	525.1267	1394.03	1182.755	1115.406	-1.2028	5.92E-18	5.45E-17	REPS1	chr6	-	1.39E+08	1.39E+08	6069
ENSG00000(	0	0	0	2.247227	4.60216	0.821965	-2.0706	0.12372	0.20888	STX11	chr6	+	1.44E+08	1.45E+08	1926
ENSG00000(	17.60846	22.88147	25.06886	8.239831	23.93123	5.753754	0.75656	0.21722	0.3284	TEC	chr4	-	48137800	48271881	3687
ENSG00000(	301.4154	283.0076	246.7304	247.944	218.1424	216.1768	0.28452	0.11615	0.19851	PRADC1	chr2	-	73455134	73460366	1083
ENSG00000(	153.2972	174.6217	159.6491	46.44268	66.2711	75.62077	1.3626	1.73E-07	7.75E-07	SEMA4F	chr2	+	74881355	74909186	4312
ENSG00000(	6564.849	6240.619	5656.327	8788.154	8171.595	8156.358	-0.44324	2.73E-05	9.60E-05	CCT7	chr2	+	73460548	73480149	2031
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	EGR4	chr2	-	73518058	73520833	2372
ENSG00000(	1727.701	1788.367	1645.309	263.6746	333.1964	230.9721	2.635	2.44E-71	1.09E-69	RAB11FIP5	chr2	-	73300510	73383849	4342
ENSG00000(	443.3189	449.1993	373.3941	683.1569	587.2356	709.3557	-0.64232	2.22E-05	7.87E-05	SMYD5	chr2	+	73441350	73454365	2593
ENSG00000(	17.60846	12.04288	25.06886	803.009	934.2385	858.1314	-5.5304	5.75E-102	4.52E-100	DYSF	chr2	+	71680852	71913898	6796
ENSG00000(	241.3395	177.0303	191.315	123.5975	146.3487	173.4346	0.45992	0.038627	0.077625	CCDC142	chr2	-	74699113	74710535	3406

ENSG00000(	1.035792	0	3.958241	0	1.840864	0	0.78419	0.5618	0.68181	EMX1	chr2	+	73143389	73162020	2188
ENSG00000(	93.22127	111.9988	83.12307	304.8737	275.2092	293.4415	-1.5889	2.00E-14	1.52E-13	KCNMB4	chr12	+	70760056	70828072	4731
ENSG00000(	417.4241	469.6722	556.7926	741.5848	623.1325	530.9893	-0.39367	0.019747	0.042902	USP15	chr12	+	62654119	62811211	4748
ENSG00000(	4466.335	4140.341	5285.572	2188.799	2117.914	1823.94	1.1773	2.18E-20	2.25E-19	GNS	chr12	-	65107225	65153227	5122
ENSG00000(	40.39588	45.76293	50.13772	26.21764	32.21512	43.56414	0.40814	0.29347	0.41775	CPM	chr12	-	69235977	69365350	6655
ENSG00000(	2413.395	2583.197	2662.577	2928.885	3084.368	2811.942	-0.20433	0.057289	0.10936	MDM2	chr12	+	69201956	69239214	7381
ENSG00000(	655.6563	611.7782	837.8278	617.2383	810.9006	738.1245	-0.04144	0.79671	0.86741	KLHL36	chr16	+	84682131	84701292	6488
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	BCMO1	chr16	+	81272053	81324747	2670
ENSG00000(	497.1801	492.5537	430.1289	592.5188	396.7062	529.3454	-0.09721	0.57158	0.69037	MPHOSPH6	chr16	-	82181403	82203831	1103
ENSG00000(	0	1.204288	0	0.749076	0	0.821965	-0.12128	0.92635	NA	CHST5	chr16	-	75562433	75569145	3245
ENSG00000(	550.0055	444.3822	529.0849	143.0734	139.9057	158.6392	1.7793	7.37E-25	9.05E-24	KIAA0513	chr16	+	85061375	85127836	7772
ENSG00000(	1670.732	1689.616	2248.281	847.2044	1434.953	1121.16	0.71801	4.68E-05	0.00016	DYNC1LI2	chr16	-	66754796	66785701	4515
ENSG00000(	52.82539	51.78437	43.54065	14.98151	12.88605	21.37109	1.5479	0.000301	0.000915	FBXL8	chr16	+	67193834	67198473	1658
ENSG00000(	890.781	811.6899	794.2871	740.0866	637.8594	633.735	0.31095	0.021403	0.046102	FHOD1	chr16	-	67263290	67281561	4321
ENSG00000(	541.7192	510.618	422.2124	289.8922	358.048	332.8958	0.58893	0.000374	0.001123	CCDC102A	chr16	-	57546090	57570511	2463
ENSG00000(	218.5521	227.6104	143.8161	8.988907	10.12475	14.79537	4.058	1.92E-32	3.14E-31	SLC9A5	chr16	+	67271586	67306093	4617
ENSG00000(	53.86118	43.35436	40.90183	0	6.443024	4.109825	3.5564	6.10E-09	3.12E-08	AGT	chr1	-	2.31E+08	2.31E+08	2291
ENSG00000(	71.46964	60.21439	80.48424	161.0512	168.4391	141.378	-1.1416	5.13E-06	1.97E-05	ZNF670	chr1	-	2.47E+08	2.47E+08	2751
ENSG00000(	641.1552	497.3708	651.7904	426.224	420.6374	349.3351	0.57977	0.000368	0.001105	PCNXL2	chr1	-	2.33E+08	2.33E+08	6817
ENSG00000(	65.25489	66.23582	60.69303	316.1099	295.4587	263.0288	-2.1704	5.60E-23	6.39E-22	KCNK1	chr1	+	2.34E+08	2.34E+08	2161
ENSG00000(	223.7311	245.6747	226.9392	656.9393	811.821	712.6436	-1.6415	1.08E-25	1.37E-24	URB2	chr1	+	2.3E+08	2.3E+08	5613
ENSG00000(	1526.757	1554.735	1568.783	1502.646	1495.702	1444.192	0.065681	0.54866	0.67019	EGLN1	chr1	-	2.31E+08	2.32E+08	7097
ENSG00000(	5.17896	0	1.319414	0	4.60216	3.28786	-0.17032	0.89007	0.93174	CAPN9	chr1	+	2.31E+08	2.31E+08	2484
ENSG00000(	250.6616	295.0505	274.4381	481.6556	418.7966	425.7778	-0.69284	2.07E-05	7.37E-05	COG2	chr1	+	2.31E+08	2.31E+08	7836
ENSG00000(	184.371	150.536	219.0227	393.2647	442.7278	396.1871	-1.1495	5.13E-10	2.88E-09	ABCB10	chr1	-	2.3E+08	2.3E+08	3857
ENSG00000(	275.5206	276.9862	274.4381	411.9916	376.4567	470.1639	-0.60423	0.000241	0.000744	NTPCR	chr1	+	2.33E+08	2.33E+08	8705
ENSG00000(	350.0977	316.7277	360.2	582.0317	612.0873	535.9211	-0.74991	5.40E-07	2.31E-06	TAF5L	chr1	-	2.3E+08	2.3E+08	4062
ENSG00000(	3347.679	3399.704	3409.365	4850.264	5101.955	4582.454	-0.51631	4.57E-07	1.97E-06	GLUL	chr1	-	1.82E+08	1.82E+08	6132
ENSG00000(	692.9448	722.5726	741.5105	491.3936	555.9409	570.4437	0.41413	0.002408	0.006326	STX6	chr1	-	1.81E+08	1.81E+08	4851
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RGS8	chr1	-	1.83E+08	1.83E+08	1432
ENSG00000(	228.91	174.6217	226.9392	57.67882	66.2711	79.7306	1.6189	1.79E-11	1.12E-10	RNASEL	chr1	-	1.83E+08	1.83E+08	4238
ENSG00000(	3080.445	2884.269	3590.125	5180.606	5358.755	4861.922	-0.68774	3.60E-09	1.88E-08	DHX9	chr1	+	1.83E+08	1.83E+08	4240
ENSG00000(	224.7668	244.4704	164.9267	29.21395	46.94203	29.59074	2.5673	3.53E-20	3.60E-19	KIAA1614	chr1	+	1.81E+08	1.81E+08	9654
ENSG00000(	432.961	440.7693	654.4292	381.2795	466.659	327.964	0.37503	0.052615	0.10151	CEP350	chr1	+	1.8E+08	1.8E+08	13491
ENSG00000(	46.61064	49.3758	81.80365	31.46117	26.69253	23.01502	1.0995	0.004862	0.012073	NPL	chr1	+	1.83E+08	1.83E+08	2418
ENSG00000(	174.013	208.3418	233.5362	763.308	755.6747	652.6401	-1.8157	3.96E-28	5.58E-27	FAM129A	chr1	-	1.85E+08	1.85E+08	6928
ENSG00000(	395.6725	426.3179	410.3377	838.2155	681.1197	675.6552	-0.83148	2.43E-08	1.18E-07	PIGC	chr1	-	1.72E+08	1.72E+08	2630
ENSG00000(	965.3581	1041.709	886.6461	862.935	867.0469	815.3892	0.18508	0.14432	0.23642	ACBD6	chr1	-	1.8E+08	1.8E+08	1670
ENSG00000(	11314.99	10577.26	13104.42	13830.18	16030.24	12555.51	-0.27683	0.026545	0.055878	LAMC1	chr1	+	1.83E+08	1.83E+08	7889
ENSG00000(	552.0771	588.8967	592.4168	674.9171	737.266	625.5153	-0.23289	0.090525	0.16151	RC3H1	chr1	-	1.74E+08	1.74E+08	11261
ENSG00000(	4.143168	3.612863	1.319414	4.494453	9.20432	15.61733	-1.4596	0.1021	0.17844	GPR55	chr2	-	2.32E+08	2.32E+08	3828
ENSG00000(	346.9903	272.169	290.271	33.7084	34.05598	24.65895	3.2733	2.66E-40	5.54E-39	SP110	chr2	-	2.31E+08	2.31E+08	2725
ENSG00000(	564.5066	603.3481	554.1538	713.869	642.4615	642.7766	-0.21515	0.11285	0.19368	MRPL44	chr2	+	2.25E+08	2.25E+08	1748
ENSG00000(	7.250543	0	1.319414	0	0	0	2.3814	0.078455	0.14295	CHRND	chr2	+	2.33E+08	2.33E+08	3022

ENSG0000(	10.35792	4.817151	21.11062	508.6223	515.4419	380.5698	-5.2281	5.81E-58	1.93E-56	PAX3	chr2	-	2.23E+08	2.23E+08	3610
ENSG0000(	253.769	231.2232	281.0351	140.8262	181.3251	129.0485	0.7609	0.00023	0.000712	DOCK10	chr2	-	2.26E+08	2.26E+08	7288
ENSG0000(	394.6367	343.222	397.1435	1582.048	1226.015	1154.861	-1.7984	2.87E-31	4.55E-30	TTLL4	chr2	+	2.2E+08	2.2E+08	4967
ENSG0000(	87.00652	66.23582	120.0667	102.6234	186.8477	101.1017	-0.50824	0.0988	0.17361	USP37	chr2	-	2.19E+08	2.19E+08	8032
ENSG0000(	11.39371	16.86003	5.277655	2.996302	4.60216	8.219649	0.99026	0.20957	0.31919	HTR2B	chr2	-	2.32E+08	2.32E+08	2246
ENSG0000(	18516.85	17954.73	17692.02	4904.947	5359.676	6018.427	1.7312	6.73E-57	2.18E-55	ITM2C	chr2	+	2.32E+08	2.32E+08	2078
ENSG0000(	7.250543	6.021439	6.597069	44.19546	62.58938	42.74218	-2.791	1.00E-07	4.60E-07	SLC19A3	chr2	-	2.29E+08	2.29E+08	3517
ENSG0000(	6341.118	6049.137	6260.618	7612.106	5550.205	5638.679	-0.01169	0.92904	0.95729	SERPINE2	chr2	-	2.25E+08	2.25E+08	5989
ENSG0000(	1028.541	1069.407	914.3538	701.1347	814.5823	993.7556	0.26341	0.079724	0.14496	DNAJB2	chr2	+	2.2E+08	2.2E+08	4487
ENSG0000(	0	0	0	10.48706	24.85166	9.041614	-4.7142	3.46E-05	0.00012	WNT10A	chr2	+	2.2E+08	2.2E+08	2547
ENSG0000(	721.947	682.8311	692.6922	1016.496	974.7375	1036.498	-0.52827	1.81E-05	6.50E-05	TMBIM1	chr2	-	2.19E+08	2.19E+08	2936
ENSG0000(	67.32647	46.96722	54.09597	104.8706	80.99802	72.33291	-0.60613	0.050991	0.098778	CYP27A1	chr2	+	2.2E+08	2.2E+08	2566
ENSG0000(	1569.225	1649.874	1455.313	1449.461	1399.057	1566.665	0.082302	0.48285	0.61209	EIF4E2	chr2	+	2.33E+08	2.33E+08	3525
ENSG0000(	1233.628	1311.469	1390.662	552.0687	653.5067	589.3488	1.1306	2.18E-18	2.05E-17	ARMC9	chr2	+	2.32E+08	2.32E+08	5758
ENSG0000(	814.1324	757.497	947.3391	1112.377	1140.415	1024.168	-0.37936	0.004377	0.010966	CAB39	chr2	+	2.32E+08	2.32E+08	3826
ENSG0000(	1748.417	1692.024	1361.635	1289.908	1309.775	1909.425	0.090963	0.57493	0.69339	COX5B	chr2	+	98262503	98264846	738
ENSG0000(	395.6725	415.4793	430.1289	507.1241	476.7838	452.9027	-0.2116	0.14952	0.24336	REV1	chr2	-	1E+08	1E+08	4751
ENSG0000(	72.50543	81.89156	62.01245	95.13259	86.52061	95.34793	-0.3514	0.20363	0.31176	TSGA10	chr2	-	99613724	99771427	3878
ENSG0000(	126.3666	109.5902	121.3861	198.505	210.7789	208.7791	-0.78438	0.000165	0.000522	MFSD9	chr2	-	1.03E+08	1.03E+08	4049
ENSG0000(	1227.413	1178.998	1275.873	962.5621	985.7827	941.9718	0.34866	0.002905	0.00752	TMEM127	chr2	-	96916312	96931732	4208
ENSG0000(	5.17896	3.612863	0	1.498151	0	3.28786	0.62929	0.60891	0.72296	EDAR	chr2	-	1.1E+08	1.1E+08	4323
ENSG0000(	284.8428	340.8134	303.4652	661.4337	636.9389	523.5917	-0.96909	1.79E-09	9.61E-09	TGFBRAP1	chr2	-	1.06E+08	1.06E+08	5979
ENSG0000(	443.3189	511.8223	560.7509	303.3756	347.9233	254.8091	0.73898	1.74E-05	6.26E-05	GCC2	chr2	+	1.09E+08	1.09E+08	6772
ENSG0000(	250.6616	197.5032	259.9245	522.1057	380.1384	441.3952	-0.92113	6.23E-07	2.64E-06	MRPS9	chr2	+	1.06E+08	1.06E+08	1500
ENSG0000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	GPR45	chr2	+	1.06E+08	1.06E+08	1725
ENSG0000(	448.4979	473.2851	469.7113	392.5156	345.162	330.4299	0.37909	0.013244	0.029936	C2orf49	chr2	+	1.06E+08	1.06E+08	4768
ENSG0000(	90.1139	98.75159	157.0102	40.45008	87.44104	76.44274	0.7489	0.022539	0.048246	ANKRD36	chr2	+	97779233	97930258	6269
ENSG0000(	484.7506	454.0165	589.778	416.486	511.7602	453.7246	0.14463	0.36713	0.49712	EPC2	chr2	+	1.49E+08	1.5E+08	3642
ENSG0000(	225.8026	196.2989	179.4403	47.94084	83.75931	71.51095	1.5597	9.97E-10	5.47E-09	ARHGEF4	chr2	+	1.32E+08	1.32E+08	4788
ENSG0000(	1380.711	1309.061	1417.05	1657.704	1252.708	1412.136	-0.07439	0.57349	0.69221	ISCU	chr12	+	1.09E+08	1.09E+08	3685
ENSG0000(	1452.18	1480.07	1725.793	289.1432	244.8349	179.1884	2.6956	6.46E-59	2.19E-57	ALDH1L2	chr12	-	1.05E+08	1.05E+08	7547
ENSG0000(	13.46529	14.45145	18.47179	9.737982	14.72691	8.219649	0.4786	0.44039	0.5701	STAB2	chr12	+	1.04E+08	1.04E+08	8251
ENSG0000(	0	4.817151	5.277655	12.73428	7.363456	3.28786	-1.0589	0.27418	0.39528	USP44	chr12	-	95910336	95945266	4022
ENSG0000(	720.9112	771.9484	1006.713	1110.879	1159.744	933.7521	-0.35859	0.019841	0.043082	SCYL2	chr12	+	1.01E+08	1.01E+08	5779
ENSG0000(	10439.75	9899.245	9770.259	3753.618	3713.943	3645.414	1.4362	4.19E-49	1.13E-47	CKAP4	chr12	-	1.07E+08	1.07E+08	3093
ENSG0000(	87.00652	83.09585	105.5531	28.46487	26.69253	22.19305	1.8027	5.77E-08	2.71E-07	PLXNC1	chr12	+	94542499	94701451	7346
ENSG0000(	1263.666	1235.599	1450.036	395.5119	323.0716	374.816	1.8458	5.48E-40	1.13E-38	APPL2	chr12	-	1.06E+08	1.06E+08	3239
ENSG0000(	1248.129	1177.793	1165.042	1452.457	1201.164	1153.217	-0.08419	0.5177	0.64399	PWP1	chr12	+	1.08E+08	1.08E+08	2621
ENSG0000(	453.6769	427.5221	431.4483	805.2562	784.2081	744.7002	-0.82784	8.18E-10	4.51E-09	DRAM1	chr12	+	1.02E+08	1.02E+08	3519
ENSG0000(	865.922	818.9156	1095.113	737.8394	828.3888	625.5153	0.34137	0.028771	0.059936	KIAA1033	chr12	+	1.06E+08	1.06E+08	5819
ENSG0000(	55.93276	49.3758	34.30476	63.67142	49.70333	55.07165	-0.26163	0.4539	0.58363	SLC41A2	chr12	-	1.05E+08	1.05E+08	4449
ENSG0000(	192.6573	154.1488	141.1773	84.64554	80.99802	110.9653	0.81465	0.000951	0.002674	VILL	chr3	+	38029550	38048679	4439
ENSG0000(	1085.51	1085.063	1146.571	6675.012	9183.15	7896.617	-2.8338	3.64E-106	3.06E-104	FLNB	chr3	+	57994127	58157982	9537
ENSG0000(	191.6215	189.0732	157.0102	179.7781	156.4734	120.0069	0.23623	0.29427	0.41871	NEK3	chr13	-	52706775	52733996	3255

ENSG00000(	0	0	0	24.71949	22.09037	32.05663	-5.573	2.26E-07	1.00E-06	PCDH8	chr13	-	53418109	53422775	4003
ENSG00000(	594.5446	608.1653	758.6629	653.943	713.3348	578.6633	0.010317	0.94586	0.96733	VPS36	chr13	-	52986737	53024763	4417
ENSG00000(	284.8428	284.2119	314.0205	379.7813	323.0716	328.786	-0.22548	0.17541	0.27716	RNASEH2B	chr13	+	51483814	51544592	1629
ENSG00000(	779.9513	764.7227	976.3662	1933.364	1877.681	1606.941	-1.1021	1.59E-15	1.30E-14	CKAP2	chr13	+	53029564	53050763	3629
ENSG00000(	2.071584	4.817151	0	17.22874	11.96562	5.753754	-2.0157	0.027748	0.058062	LECT1	chr13	-	53277399	53313947	1444
ENSG00000(	881.4589	973.0645	1155.806	470.4194	535.6914	439.7512	1.0544	1.63E-12	1.10E-11	TBC1D4	chr13	-	75858808	76056250	6364
ENSG00000(	91.14969	67.44011	80.48424	8.988907	8.283888	9.041614	3.1052	9.55E-14	6.98E-13	THSD1	chr13	-	52951305	52980629	3186
ENSG00000(	82.86335	97.54731	87.08131	319.8553	368.1728	271.2484	-1.8316	8.69E-18	7.93E-17	BORA	chr13	+	73302061	73330336	2759
ENSG00000(	500.2875	475.6936	507.9743	476.412	533.8506	478.3836	-0.00392	0.97812	0.98728	LRCH1	chr13	+	47127303	47327175	4710
ENSG00000(	663.9426	625.0253	651.7904	806.7544	699.5283	797.306	-0.24708	0.063486	0.11931	SUCLA2	chr13	-	48510622	48612125	2164
ENSG00000(	262.0554	291.4376	364.1582	309.3682	304.663	295.0854	0.010287	0.95392	0.97255	RCBTB1	chr13	-	50106082	50159719	4025
ENSG00000(	336.6324	320.3405	358.8805	285.3978	381.9793	389.6114	-0.05612	0.74966	0.83377	MED4	chr13	-	48627459	48669267	2022
ENSG00000(	133.6172	155.3531	162.2879	152.0623	115.054	129.8705	0.17892	0.43091	0.56079	PHF11	chr13	+	50069746	50103123	1626
ENSG00000(	38.3243	39.74149	52.77655	33.7084	16.56778	20.54912	0.85072	0.04987	0.096871	RPL13AP25	chr13	-	55014839	55015450	612
ENSG00000(	470.2495	528.6823	612.208	289.1432	291.7769	240.0138	0.96755	7.53E-09	3.82E-08	COG3	chr13	+	46039060	46110765	4498
ENSG00000(	1011.969	840.5928	1254.763	1092.152	1125.688	909.9152	-0.01003	0.94924	0.96942	LMO7	chr13	+	76194570	76434004	8128
ENSG00000(	6.214751	0	0	0	0	2.465895	0.74299	0.58201	0.69965	SCEL	chr13	+	78109809	78219398	3096
ENSG00000(	5943.374	5874.515	5290.849	6583.625	5181.112	4994.259	0.029695	0.81453	0.87956	ITM2B	chr13	+	48807294	48837063	1876
ENSG00000(	271.3775	261.3304	299.5069	976.7945	986.7031	858.9533	-1.7581	8.76E-34	1.52E-32	SPRY2	chr13	-	80910111	80915086	2708
ENSG00000(	394.6367	331.1791	325.8952	1396.277	1068.622	1209.11	-1.7973	1.68E-32	2.76E-31	NUDT15	chr13	+	48611703	48621358	2098
ENSG00000(	3.107376	0	0	350.5674	363.5706	395.3651	-7.6764	2.77E-31	4.39E-30	EDNRB	chr13	-	78469616	78493903	4471
ENSG00000(	396.7083	488.9408	473.6695	168.542	185.0068	101.9236	1.5679	2.02E-13	1.45E-12	RCBTB2	chr13	-	49063095	49107369	3232
ENSG00000(	9.322127	14.45145	25.06886	3700.433	3568.515	3116.891	-7.7091	3.42E-200	9.91E-198	LCP1	chr13	-	46700055	46786006	3944
ENSG00000(	84.93494	97.54731	142.4967	98.1289	100.3271	78.08667	0.22518	0.41807	0.54874	SETDB2	chr13	+	50018429	50069138	6183
ENSG00000(	2545.977	2384.49	2997.708	2832.255	3117.503	2551.379	-0.10063	0.42953	0.55968	SCRN1	chr7	-	29959719	30029905	5275
ENSG00000(	3.107376	2.408575	14.51355	2.996302	11.04518	8.219649	-0.14591	0.86774	0.91692	C7orf25	chr7	-	42948325	42951904	2451
ENSG00000(	424.6747	338.4048	506.6549	2227.751	2904.883	2374.657	-2.5561	2.94E-59	1.00E-57	TNS3	chr7	-	47314752	47622156	7625
ENSG00000(	20.71584	39.74149	25.06886	11.23613	15.64734	20.54912	0.81849	0.11334	0.19444	SPDYE1	chr7	+	44040488	44049721	2649
ENSG00000(	364.5988	355.2649	270.4798	370.7924	233.7897	299.1952	0.13097	0.51647	0.64297	CHST12	chr7	+	2443223	2474242	2103
ENSG00000(	667.05	717.7555	988.2409	770.7987	1487.418	851.5557	-0.38776	0.069449	0.12886	IGF2BP3	chr7	-	23349828	23510086	4250
ENSG00000(	662.9068	659.9497	746.7882	22.47227	21.16994	13.9734	5.1257	1.48E-106	1.26E-104	GPNMB	chr7	+	23275586	23314727	2862
ENSG00000(	21.75163	24.08575	29.0271	74.90755	53.38506	52.60575	-1.2544	0.001223	0.00338	RAPGEF5	chr7	-	22157856	22396763	6621
ENSG00000(	5626.422	5389.188	5549.454	7702.744	6276.426	5655.941	-0.24486	0.050309	0.097666	RAC1	chr7	+	6414154	6443608	2323
ENSG00000(	7138.678	7336.521	7185.527	3993.322	3438.734	3509.79	0.98351	1.70E-20	1.76E-19	KDELR2	chr7	-	6485584	6523873	2884
ENSG00000(	239.2679	279.3948	295.5487	536.3381	488.7494	541.6749	-0.94417	3.36E-09	1.76E-08	NUPL2	chr7	+	23221446	23240630	2529
ENSG00000(	2.071584	6.021439	3.958241	1.498151	3.681728	0	0.94793	0.405	0.5359	IL6	chr7	+	22765503	22771621	1527
ENSG00000(	290.0217	303.4805	261.2439	349.0692	304.663	269.6045	-0.11077	0.53114	0.65585	ZDHHC4	chr7	+	6617065	6629005	1942
ENSG00000(	101.5076	90.32158	83.12307	4.494453	7.363456	6.575719	3.8097	2.42E-18	2.26E-17	AOAH	chr7	-	36552456	36764154	2396
ENSG00000(	1340.315	1284.975	1339.205	2395.544	2232.048	1925.042	-0.72354	3.10E-09	1.63E-08	BZW2	chr7	+	16685756	16746148	2101
ENSG00000(	1.035792	6.021439	3.958241	0	0	0	2.9047	0.02768	0.05795	DGKB	chr7	-	14184674	15014402	6917
ENSG00000(	1123.834	921.2801	819.356	2263.706	1897.931	1924.22	-1.0829	2.21E-14	1.68E-13	TBRG4	chr7	-	45139699	45151646	3409
ENSG00000(	1370.353	1506.564	1143.932	2474.946	1848.227	1903.671	-0.62904	2.02E-05	7.21E-05	DDX56	chr7	-	44605016	44614650	3028
ENSG00000(	230.9816	254.1047	237.4945	388.0211	345.162	307.4149	-0.52507	0.002649	0.00691	HUS1	chr7	-	47735328	48019178	2935
ENSG00000(	399.8157	443.1779	308.7428	119.8521	117.8153	110.1433	1.7195	3.02E-18	2.81E-17	NACAD	chr7	-	45120037	45128513	4780

ENSG00000(	2645.413	2702.422	2268.072	1678.678	1673.345	2004.772	0.50683	5.46E-05	0.000184	DBNL	chr7	+	44084239	44109055	9618
ENSG00000(	972.6086	951.3873	839.1472	1173.052	923.1933	1035.676	-0.18024	0.1881	0.29299	CCM2	chr7	+	45039074	45116068	5304
ENSG00000(	2.071584	3.612863	6.597069	2.247227	0	2.465895	1.0406	0.35923	0.48876	MYO1G	chr7	-	45002261	45018697	5672
ENSG00000(	17091.6	16290.4	15656.16	5313.193	6619.747	6358.721	1.4204	8.14E-36	1.50E-34	TTYH3	chr7	+	2671585	2704436	4840
ENSG00000(	292.0933	331.1791	320.6175	298.1321	258.6414	261.3848	0.20338	0.23064	0.34404	TTC5	chr14	-	20724717	20774153	5014
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	NKX2-8	chr14	-	37049784	37051812	1261
ENSG00000(	46.61064	50.58008	54.09597	122.0993	206.1768	172.6126	-1.7087	1.52E-09	8.20E-09	ZFHX2	chr14	-	23990125	24025401	8855
ENSG00000(	3.107376	3.612863	2.638828	3.745378	0	1.64393	0.58333	0.61716	0.7297	MTHFS	chr15	-	80125927	80189721	907
ENSG00000(	865.922	774.357	723.0388	343.8257	408.6718	467.698	0.95222	1.10E-09	6.01E-09	ADAMTS7	chr15	-	79051545	79103773	5490
ENSG00000(	235.1248	174.6217	204.5091	420.9805	393.0245	295.0854	-0.84614	1.88E-05	6.74E-05	ABHD17C	chr15	+	80972025	81047962	2435
ENSG00000(	1440.787	1458.392	1618.921	1250.207	1524.235	1203.357	0.18346	0.16127	0.25883	IREB2	chr15	+	78729773	78793798	6354
ENSG00000(	26.93059	7.225726	9.235896	5.243529	9.20432	18.08323	0.401	0.57139	0.69031	ALPK3	chr15	+	85359911	85416713	10917
ENSG00000(	34.18113	31.31148	40.90183	81.64923	51.54419	46.852	-0.75005	0.04598	0.090285	TM6SF1	chr15	+	83776159	83813606	2074
ENSG00000(	59.04014	55.39724	59.37362	140.8262	127.94	135.6242	-1.2074	3.73E-06	1.45E-05	CIB2	chr15	-	78396948	78423886	1598
ENSG00000(	1230.521	1283.771	1162.404	433.7147	366.3319	300.8392	1.7334	2.61E-30	4.00E-29	CALCOCO2	chr17	+	46908350	46943884	3682
ENSG00000(	535.5044	562.4024	460.4754	410.4934	329.5147	404.4067	0.4435	0.005622	0.013793	RSAD1	chr17	+	48556161	48563336	2528
ENSG00000(	1942.11	1829.313	1868.29	2976.077	2721.717	2701.799	-0.57375	1.18E-07	5.35E-07	NMT1	chr17	+	43128978	43186384	4999
ENSG00000(	4.143168	2.408575	7.916483	0	0.920432	1.64393	1.8874	0.10302	0.17971	MYCBPAP	chr17	+	48585745	48608862	3186
ENSG00000(	2769.708	2836.098	3103.261	4448.011	4906.823	4774.794	-0.69725	7.50E-11	4.49E-10	SRSF1	chr17	-	56080854	56084707	2983
ENSG00000(	714.6964	749.067	818.0365	895.8944	868.8878	823.6088	-0.18255	0.15565	0.25151	VEZF1	chr17	-	56048910	56065620	3946
ENSG00000(	14.50109	20.47289	10.55531	5.243529	23.0108	23.01502	-0.15179	0.8118	0.87799	CHAD	chr17	-	48541857	48546327	1789
ENSG00000(	290.0217	342.0177	269.1604	503.3788	479.5451	478.3836	-0.69469	1.32E-05	4.82E-05	TACO1	chr17	+	61678231	61685725	2304
ENSG00000(	445.3905	460.0379	496.0996	495.1389	592.7582	457.0125	-0.13996	0.36717	0.49712	TEX2	chr17	-	62224587	62340661	5232
ENSG00000(	1529.865	1541.488	1647.948	1661.45	2010.223	1695.714	-0.18512	0.12893	0.21583	DCAF7	chr17	+	61627822	61671639	6351
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	GH2	chr17	-	61957578	61959295	1138
ENSG00000(	584.1866	481.7151	443.323	963.3112	981.1805	1050.471	-0.98344	7.55E-12	4.85E-11	LIMD2	chr17	-	61773262	61778532	3193
ENSG00000(	109.7939	157.7617	126.6637	600.7586	691.2444	567.9778	-2.2306	4.20E-34	7.34E-33	BRIP1	chr17	-	59758627	59940882	6048
ENSG00000(	423.6389	472.0808	509.2937	951.3259	841.2748	761.9615	-0.86195	4.69E-09	2.43E-08	KAT7	chr17	+	47865917	47906458	3996
ENSG00000(	427.7821	451.6079	476.3084	1212.753	1041.009	1226.372	-1.3583	1.43E-23	1.67E-22	ACTL6A	chr3	+	1.79E+08	1.79E+08	1901
ENSG00000(	836.9199	855.0443	769.2182	928.1046	785.1285	951.8354	-0.1147	0.39229	0.52313	NDUFB5	chr3	+	1.79E+08	1.79E+08	4046
ENSG00000(	543.7907	575.6495	407.6989	798.5145	699.5283	741.4124	-0.54914	0.000466	0.001375	MRPL47	chr3	-	1.79E+08	1.79E+08	1370
ENSG00000(	1965.933	1981.053	2190.227	3751.37	3515.13	3599.384	-0.82335	1.88E-14	1.43E-13	TRA2B	chr3	-	1.86E+08	1.86E+08	4485
ENSG00000(	220.6237	243.2661	263.8828	0.749076	9.20432	13.9734	4.5193	1.49E-09	8.03E-09	SCN2A	chr2	+	1.66E+08	1.66E+08	8792
ENSG00000(	1078.259	1178.998	1364.274	1310.882	1267.435	1086.638	-0.01817	0.89359	0.93415	7-Mar	chr2	+	1.61E+08	1.61E+08	3743
ENSG00000(	657.7279	652.7239	1001.435	1.498151	7.363456	4.109825	7.3642	3.49E-77	1.77E-75	GALNT5	chr2	+	1.58E+08	1.58E+08	6171
ENSG00000(	482.679	467.2636	546.2373	322.8516	273.3683	255.6311	0.80765	7.93E-07	3.32E-06	TANK	chr2	+	1.62E+08	1.62E+08	2171
ENSG00000(	0	4.817151	0	1.498151	5.522592	1.64393	-0.59062	0.634	0.7435	BLK	chr8	+	11351510	11422113	2606
ENSG00000(	49.71801	90.32158	83.12307	5.992604	5.522592	8.219649	3.3849	4.06E-13	2.86E-12	GATA4	chr8	+	11534468	11617511	3414
ENSG00000(	186.4425	211.9546	236.1751	349.8183	370.0137	318.9224	-0.71059	6.93E-05	0.000231	SKIL	chr3	+	1.7E+08	1.7E+08	7182
ENSG00000(	2603.981	2365.221	2760.214	2939.372	2834.931	2442.88	-0.08826	0.46143	0.59073	EPRS	chr1	-	2.2E+08	2.2E+08	5014
ENSG00000(	512.717	497.3708	337.7699	0.749076	2.761296	1.64393	7.7159	2.79E-46	6.89E-45	HLX	chr1	+	2.21E+08	2.21E+08	3323
ENSG00000(	478.5359	464.8551	531.7238	554.3159	495.1924	530.9893	-0.10075	0.4841	0.61324	VPS45	chr1	+	1.5E+08	1.5E+08	2790
ENSG00000(	15.53688	14.45145	19.79121	14.23244	1.840864	7.397684	0.98674	0.16041	0.25776	IL10	chr1	-	2.07E+08	2.07E+08	1630
ENSG00000(	641.1552	785.1956	756.0241	780.5367	782.3672	630.4471	-0.00815	0.95588	0.97381	KCTD3	chr1	+	2.16E+08	2.16E+08	3931

ENSG00000(	452.6411	455.2208	563.3897	301.1284	263.2436	235.082	0.87414	3.22E-07	1.41E-06	RPS6KC1	chr1	+	2.13E+08	2.13E+08	5490
ENSG00000(	61.11172	33.72006	58.05421	12.73428	11.96562	9.041614	2.1143	5.23E-06	2.01E-05	RASSF5	chr1	+	2.07E+08	2.07E+08	4499
ENSG00000(	267.2343	335.9963	319.2981	371.5415	372.775	410.9825	-0.32542	0.049875	0.096871	CBWD2	chr2	+	1.14E+08	1.14E+08	3305
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	IL36G	chr2	+	1.14E+08	1.14E+08	1195
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	IL1RN	chr2	+	1.14E+08	1.14E+08	1922
ENSG00000(	0	0	0	26.96672	14.72691	12.32947	-5.0216	6.54E-06	2.48E-05	IL36RN	chr2	+	1.14E+08	1.14E+08	2700
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	IL36B	chr2	-	1.14E+08	1.14E+08	1186
ENSG00000(	0	0	0	0	1.840864	2.465895	-1.2108	0.36631	NA	IL1F10	chr2	+	1.14E+08	1.14E+08	1366
ENSG00000(	1652.088	1500.542	1413.092	2671.203	2467.678	2427.262	-0.7268	3.28E-10	1.87E-09	SMPD4	chr2	-	1.31E+08	1.31E+08	4896
ENSG00000(	1075.152	1058.569	1108.308	1406.015	1538.962	1618.449	-0.49223	3.25E-05	0.000113	WDR33	chr2	-	1.28E+08	1.29E+08	9471
ENSG00000(	509.6096	482.9194	411.6571	195.5087	194.2112	212.8889	1.2171	3.77E-13	2.66E-12	CCDC115	chr2	-	1.31E+08	1.31E+08	3562
ENSG00000(	511.6812	440.7693	613.5274	995.5214	993.1461	763.6054	-0.81164	6.20E-07	2.63E-06	SAP130	chr2	-	1.29E+08	1.29E+08	4173
ENSG00000(	1673.84	1536.671	1315.456	541.5816	530.1688	590.1708	1.4425	1.06E-26	1.40E-25	BIN1	chr2	-	1.28E+08	1.28E+08	5141
ENSG00000(	1149.729	1168.159	1116.224	1561.073	1329.104	1231.303	-0.2629	0.041059	0.081899	IMP4	chr2	+	1.31E+08	1.31E+08	2379
ENSG00000(	1907.929	2042.472	1768.014	1062.189	1307.934	1371.859	0.61101	3.57E-06	1.40E-05	HS6ST1	chr2	-	1.29E+08	1.29E+08	3932
ENSG00000(	3542.408	3463.531	3836.855	3318.405	3194.819	3227.034	0.15424	0.13721	0.22712	UGGT1	chr2	+	1.29E+08	1.29E+08	10930
ENSG00000(	1548.509	1578.821	1237.61	1226.986	1133.052	1209.932	0.28989	0.026522	0.055839	GYPC	chr2	+	1.27E+08	1.27E+08	1805
ENSG00000(	349.0619	364.8992	463.1142	724.3561	589.9969	540.8529	-0.65663	0.000115	0.000371	STAM	chr10	+	17686124	17757913	2972
ENSG00000(	783.0587	798.4428	942.0614	1137.846	1185.516	1143.353	-0.45815	0.000339	0.001022	ABI1	chr10	-	27035522	27150016	3728
ENSG00000(	3010.011	2751.797	2902.71	3112.409	3108.299	2654.125	-0.0344	0.76225	0.84295	YME1L1	chr10	-	27399383	27444195	3994
ENSG00000(	846.242	821.3242	786.3706	773.795	658.1089	606.6101	0.26662	0.056461	0.10796	DNAJC1	chr10	-	22045466	22292698	2106
ENSG00000(	304.5228	309.5019	337.7699	292.8885	312.0264	393.7212	-0.06976	0.69176	0.78968	NIPSNAP3A	chr9	+	1.08E+08	1.08E+08	1633
ENSG00000(	903.2105	711.734	703.2475	1775.309	1798.524	1732.702	-1.1901	2.50E-19	2.46E-18	LRRC8A	chr9	+	1.32E+08	1.32E+08	4619
ENSG00000(	8.286335	6.021439	7.916483	0	0.920432	0	3.3797	0.003504	0.00895	FRRS1L	chr9	-	1.12E+08	1.12E+08	1603
ENSG00000(	1093.796	962.2259	1034.42	1148.333	1089.791	1144.175	-0.12969	0.28225	0.4049	CDK9	chr9	+	1.31E+08	1.31E+08	2700
ENSG00000(	4618.596	4759.345	3786.718	4720.674	3685.41	4244.627	0.057342	0.65942	0.7639	TXN	chr9	-	1.13E+08	1.13E+08	869
ENSG00000(	1269.881	1241.621	1166.362	977.5436	1057.576	897.5857	0.32672	0.008381	0.019818	ODF2	chr9	+	1.31E+08	1.31E+08	3707
ENSG00000(	2032.224	2076.192	2390.778	1961.08	1827.058	1586.392	0.27298	0.030391	0.062881	KIAA0368	chr9	-	1.14E+08	1.14E+08	7391
ENSG00000(	898.0316	791.217	902.479	535.589	555.0205	480.8495	0.72032	1.37E-07	6.19E-07	TOR1B	chr9	+	1.33E+08	1.33E+08	2769
ENSG00000(	600.7593	581.671	498.7384	1034.473	775.9242	932.1082	-0.70341	3.15E-06	1.24E-05	C9orf78	chr9	-	1.33E+08	1.33E+08	2390
ENSG00000(	388.422	331.1791	460.4754	970.0528	956.3288	751.2759	-1.179	6.70E-13	4.64E-12	SMC2	chr9	+	1.07E+08	1.07E+08	5976
ENSG00000(	995.396	1035.687	857.619	214.9847	193.2907	184.1201	2.2781	1.37E-51	3.94E-50	KLF4	chr9	-	1.1E+08	1.1E+08	2813
ENSG00000(	653.5847	749.067	687.4146	1255.451	893.7395	969.0966	-0.57656	0.000153	0.000487	TOR1A	chr9	-	1.33E+08	1.33E+08	2076
ENSG00000(	17.60846	24.08575	17.15238	106.3687	104.9292	102.7456	-2.3765	8.09E-12	5.18E-11	RALGPS1	chr9	+	1.3E+08	1.3E+08	6336
ENSG00000(	12145.7	11249.25	10353.44	10530.5	10005.1	12262.07	0.041223	0.72272	0.81363	FAM129B	chr9	-	1.3E+08	1.3E+08	3957
ENSG00000(	1030.613	957.4087	778.4541	27.7158	34.05598	39.45432	4.7504	1.85E-117	1.89E-115	ST6GALNA(	chr9	-	1.31E+08	1.31E+08	1691
ENSG00000(	1.035792	0	5.277655	29.21395	22.09037	16.4393	-3.128	0.000111	0.000359	TMOD1	chr9	+	1E+08	1E+08	3259
ENSG00000(	1481.182	1407.812	1465.869	988.7797	1383.409	1360.352	0.22258	0.11964	0.20322	DAB2IP	chr9	+	1.24E+08	1.25E+08	6784
ENSG00000(	859.7073	753.8841	835.1889	352.0655	333.1964	283.5779	1.3337	1.92E-19	1.89E-18	STXBP1	chr9	+	1.3E+08	1.3E+08	3909
ENSG00000(	167.7983	139.6974	154.3714	1236.724	1240.742	1243.633	-2.9988	5.49E-93	3.68E-91	SLC2A8	chr9	+	1.3E+08	1.3E+08	2172
ENSG00000(	471.2853	479.3065	383.9494	182.7744	183.166	187.408	1.2664	1.34E-13	9.72E-13	ANGPTL2	chr9	-	1.3E+08	1.3E+08	3707
ENSG00000(	729.1975	667.1754	667.6234	1067.433	1225.095	1193.493	-0.75328	3.85E-09	2.01E-08	CDK5RAP2	chr9	-	1.23E+08	1.23E+08	6235
ENSG00000(	138.7961	130.0631	130.622	20.22504	32.21512	39.45432	2.0988	9.82E-12	6.25E-11	ZFP37	chr9	-	1.16E+08	1.16E+08	6266
ENSG00000(	0	0	2.638828	0	2.761296	0	-0.03456	0.97961	NA	SLC31A2	chr9	+	1.16E+08	1.16E+08	1785

ENSG0000(	1106.226	1015.215	1109.627	941.588	902.0234	966.6307	0.20077	0.096211	0.16993	SLC31A1	chr9	+	1.16E+08	1.16E+08	4744
ENSG0000(	179.192	151.7403	237.4945	107.8669	116.8949	104.3895	0.7807	0.00084	0.002384	TLR4	chr9	+	1.2E+08	1.2E+08	4844
ENSG0000(	445.3905	447.995	469.7113	270.4163	294.5382	233.438	0.7694	2.10E-06	8.43E-06	ZNF189	chr9	+	1.04E+08	1.04E+08	3134
ENSG0000(	13.46529	9.634302	3.958241	1.498151	0	0	3.1875	0.003494	0.008927	ALDOB	chr9	-	1.04E+08	1.04E+08	2451
ENSG0000(	147.0825	115.6116	141.1773	144.5716	188.6886	152.0635	-0.26025	0.25123	0.36885	STX17	chr9	+	1.03E+08	1.03E+08	2708
ENSG0000(	751.9849	747.8627	724.3582	1394.03	1328.183	1311.034	-0.85684	5.17E-13	3.61E-12	PRPF4	chr9	+	1.16E+08	1.16E+08	3212
ENSG0000(	1205.662	1203.083	938.1032	1244.214	985.7827	1035.676	0.035631	0.80676	0.87467	FPGS	chr9	+	1.31E+08	1.31E+08	2339
ENSG0000(	468.1779	449.1993	492.1413	271.1653	308.3447	303.3051	0.67344	1.33E-05	4.87E-05	USP20	chr9	+	1.33E+08	1.33E+08	4458
ENSG0000(	9.322127	2.408575	3.958241	18.72689	0.920432	4.109825	-0.51238	0.58846	0.7056	BAAT	chr9	-	1.04E+08	1.04E+08	3377
ENSG0000(	1301.99	1222.352	1229.694	1627.741	1697.277	1920.932	-0.48144	5.66E-05	0.000191	ATP6V1G1	chr9	+	1.17E+08	1.17E+08	1080
ENSG0000(	587.294	599.7353	638.5963	1137.097	1128.45	1001.975	-0.83861	8.23E-11	4.90E-10	TEX10	chr9	-	1.03E+08	1.03E+08	4457
ENSG0000(	36.25272	59.0101	62.01245	51.68621	87.44104	74.79881	-0.44017	0.2034	0.31149	GARNL3	chr9	+	1.3E+08	1.3E+08	4816
ENSG0000(	294.1649	367.3078	304.7846	591.0206	483.2268	555.6483	-0.75307	3.62E-06	1.41E-05	MRPL50	chr9	-	1.04E+08	1.04E+08	3332
ENSG0000(	1112.441	1164.546	939.4226	930.3518	815.5027	1043.073	0.20537	0.14703	0.24006	DPM2	chr9	-	1.31E+08	1.31E+08	1662
ENSG0000(	1.035792	2.408575	1.319414	3.745378	0	3.28786	-0.41166	0.73853	0.82488	WDR38	chr9	+	1.28E+08	1.28E+08	1252
ENSG0000(	120.1519	113.203	232.2168	61.42419	140.8261	80.55256	0.70933	0.031625	0.065091	TSTD2	chr9	-	1E+08	1E+08	4320
ENSG0000(	4.143168	3.612863	1.319414	4.494453	3.681728	1.64393	-0.08159	0.93883	0.9628	GABBR2	chr9	-	1.01E+08	1.01E+08	5761
ENSG0000(	2425.825	2259.244	2192.866	2586.558	2256.899	2666.454	-0.12651	0.27367	0.39476	PSMB7	chr9	-	1.27E+08	1.27E+08	988
ENSG0000(	0	0	0	3.745378	2.761296	7.397684	-2.9832	0.019899	0.04318	NR5A1	chr9	-	1.27E+08	1.27E+08	3104
ENSG0000(	108.7581	133.6759	116.1084	144.5716	123.3379	124.9387	-0.13332	0.56753	0.68671	C9orf156	chr9	-	1.01E+08	1.01E+08	2971
ENSG0000(	823.4546	746.6584	683.4563	782.7839	713.3348	772.647	-0.0088	0.94782	0.9686	RABEPK	chr9	+	1.28E+08	1.28E+08	2450
ENSG0000(	273.4491	276.9862	274.4381	253.9366	276.1296	218.6427	0.13988	0.43147	0.56126	GOLGA1	chr9	-	1.28E+08	1.28E+08	4801
ENSG0000(	218.5521	257.7176	228.2586	114.6086	99.40666	113.4312	1.0967	1.09E-07	5.00E-07	XPA	chr9	-	1E+08	1E+08	1584
ENSG0000(	944.6422	971.8602	1108.308	1660.7	1565.655	1477.071	-0.6366	2.57E-07	1.13E-06	NCBP1	chr9	+	1E+08	1E+08	5178
ENSG0000(	2923.005	2897.516	2527.997	4904.947	4776.122	5083.853	-0.82092	3.87E-14	2.90E-13	ANP32B	chr9	+	1.01E+08	1.01E+08	1463
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	OR1L4	chr9	+	1.25E+08	1.25E+08	936
ENSG0000(	476.4643	427.5221	522.4879	367.7961	458.3751	395.3651	0.22365	0.16051	0.25789	PDCL	chr9	-	1.26E+08	1.26E+08	2813
ENSG0000(	15252.04	15465.46	10933.98	11330.52	10225.08	14104.92	0.22341	0.13684	0.22654	RPL35	chr9	-	1.28E+08	1.28E+08	785
ENSG0000(	16.57267	15.65574	10.55531	1988.047	1938.43	2305.612	-7.0964	1.16E-157	1.95E-155	CTSL2	chr9	-	99794940	99801925	1546
ENSG0000(	0	0	1.319414	133.3354	218.1424	207.9571	-7.5032	6.68E-19	6.44E-18	LMX1B	chr9	+	1.29E+08	1.29E+08	5809
ENSG0000(	943.6064	823.7328	753.3853	1716.881	1480.055	1729.414	-0.96325	4.53E-13	3.17E-12	ARPC5L	chr9	+	1.28E+08	1.28E+08	2498
ENSG0000(	1202.554	1334.351	1265.318	232.2134	172.1208	152.0635	2.7593	2.54E-64	9.81E-63	ENPP2	chr8	-	1.21E+08	1.21E+08	3647
ENSG0000(	81.82756	79.48299	73.88717	608.9984	510.8398	466.0541	-2.737	5.84E-44	1.35E-42	DSCC1	chr8	-	1.21E+08	1.21E+08	2314
ENSG0000(	1151.801	1174.181	1250.804	955.8204	905.7051	935.3961	0.35346	0.002823	0.007326	DERL1	chr8	-	1.24E+08	1.24E+08	5513
ENSG0000(	1961.79	1887.119	1721.835	940.8389	711.4939	640.3107	1.2763	1.39E-17	1.25E-16	MYC	chr8	+	1.29E+08	1.29E+08	2345
ENSG0000(	101.5076	101.1602	85.7619	25.46857	18.40864	8.219649	2.413	3.87E-10	2.19E-09	NOV	chr8	+	1.2E+08	1.2E+08	2522
ENSG0000(	1.035792	4.817151	3.958241	0	0	0	2.7313	0.039906	0.079846	IL33	chr9	+	6215805	6257983	2641
ENSG0000(	571.7571	688.8526	550.1955	817.9905	631.4163	834.2944	-0.33437	0.03311	0.067702	C9orf123	chr9	-	7796490	7888380	2755
ENSG0000(	367.7061	435.9522	506.6549	477.1611	525.5667	421.668	-0.12185	0.46663	0.59592	RANBP6	chr9	-	6011043	6015618	4576
ENSG0000(	1578.547	1517.403	1269.276	1120.617	906.6255	1077.596	0.49037	0.000334	0.001009	POLR1E	chr9	+	37485932	37503694	2229
ENSG0000(	499.2517	516.6394	599.0139	1003.761	867.0469	699.4921	-0.66967	2.86E-05	0.0001	PLAA	chr9	-	26904081	26947461	4234
ENSG0000(	147.0825	150.536	135.8996	46.44268	34.05598	46.03004	1.7544	1.15E-10	6.81E-10	IL11RA	chr9	+	34650699	34661889	3008
ENSG0000(	1135.228	1106.74	1136.015	2453.222	2287.274	1875.724	-0.96772	6.66E-14	4.91E-13	UBAP2	chr9	-	33921691	34048947	4572
ENSG0000(	545.8623	612.9824	472.3501	739.3376	601.9625	737.3025	-0.34852	0.023617	0.050351	APTX	chr9	-	32972604	33025166	2106

ENSG00000(	464.0348	410.6621	521.1684	906.3814	1012.475	853.1996	-0.98745	1.16E-11	7.36E-11	RNF38	chr9	-	36336393	36487545	5254
ENSG00000(	12417.07	11529.85	13037.13	8218.108	10782.86	9792.068	0.36055	0.002832	0.007347	TLN1	chr9	-	35696945	35732392	8823
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	CCL21	chr9	-	34709002	34710121	852
ENSG00000(	0	0	0	0	0.920432	3.28786	-1.1769	0.37857	NA	SIT1	chr9	-	35649292	35650937	1231
ENSG00000(	0	0	0	3.745378	7.363456	8.219649	-3.4916	0.0047	0.011706	DMRT1	chr9	+	841690	969090	2222
ENSG00000(	207.1584	193.8903	228.2586	128.0919	151.8713	156.9953	0.52376	0.010522	0.024338	DNAJB5	chr9	+	34989638	34998897	5228
ENSG00000(	2.071584	20.47289	9.235896	5.992604	3.681728	8.219649	0.72959	0.37855	0.50927	SPAG8	chr9	-	35808042	35812269	2481
ENSG00000(	1394.176	1377.705	1187.472	669.6735	656.268	653.4621	0.99861	2.27E-15	1.83E-14	DCTN3	chr9	-	34613548	34620515	3877
ENSG00000(	7.250543	7.225726	6.597069	1.498151	2.761296	0.821965	1.7414	0.076851	0.14042	CD72	chr9	-	35609530	35646807	2035
ENSG00000(	651.5131	575.6495	500.0578	110.1141	65.35067	101.1017	2.6224	7.59E-38	1.48E-36	TMEM8B	chr9	+	35814448	35854844	3713
ENSG00000(	1576.475	1221.148	1300.942	1097.396	1044.69	1155.683	0.31358	0.018258	0.039973	GRHPR	chr9	+	37422663	37436987	4762
ENSG00000(	774.7723	662.3582	609.5692	800.7618	694.0057	621.4055	-0.04703	0.75705	0.83925	ALDH1B1	chr9	+	38392661	38398658	3066
ENSG00000(	95.29286	108.3859	83.12307	217.2319	148.1896	185.7641	-0.93559	0.000111	0.000359	HINT2	chr9	-	35812957	35815351	2167
ENSG00000(	26.93059	39.74149	30.34652	331.8405	289.9361	304.949	-3.2334	1.09E-37	2.11E-36	ARHGEF39	chr9	-	35658872	35675863	4498
ENSG00000(	22.78742	19.2686	36.94359	93.63444	139.9057	97.81383	-2.0419	6.05E-09	3.10E-08	IGFBPL1	chr9	-	38408991	38424444	1093
ENSG00000(	660.8352	671.9925	868.1743	349.0692	372.775	314.8126	1.0816	1.12E-11	7.10E-11	DENND4C	chr9	+	19230433	19374139	7161
ENSG00000(	33412.58	34442.63	24680.95	26449.86	20858.83	22165.11	0.41246	0.003117	0.008028	RPS6	chr9	-	19375713	19380252	1387
ENSG00000(	922.8906	938.1401	738.8717	1065.935	958.1697	1305.28	-0.35505	0.019649	0.042704	CNPY3	chr6	+	42896938	42907025	1704
ENSG00000(	426.7463	376.9421	373.3941	1215.75	1035.486	1140.887	-1.5218	3.59E-28	5.08E-27	FOXP4	chr6	+	41514164	41570122	5948
ENSG00000(	305.5586	248.0833	339.0893	1397.026	918.5911	1091.569	-1.9255	1.23E-27	1.70E-26	PPIL1	chr6	-	36822603	36842800	1739
ENSG00000(	189.5499	231.2232	216.3839	128.841	116.8949	120.8288	0.79038	0.000137	0.000438	KLC4	chr6	+	43008515	43042837	3604
ENSG00000(	886.6379	881.5386	1254.763	476.412	575.27	480.0275	0.97683	2.80E-09	1.48E-08	KIF13A	chr6	-	17759414	17987854	6924
ENSG00000(	290.0217	261.3304	234.8557	229.2171	240.2328	245.7675	0.13854	0.43938	0.56914	ZSCAN9	chr6	+	28192664	28201260	2062
ENSG00000(	208.1942	161.3746	153.052	366.2979	404.0696	398.653	-1.1509	4.39E-10	2.47E-09	PIM1	chr6	+	37137979	37143202	2650
ENSG00000(	21.75163	18.06432	21.11062	397.7591	468.4999	518.6599	-4.4589	3.71E-62	1.36E-60	GMPR	chr6	+	16238811	16295780	1515
ENSG00000(	662.9068	626.2296	679.4981	573.7919	584.4743	634.5569	0.13456	0.31555	0.44219	FTSJD2	chr6	+	37400995	37450603	4033
ENSG00000(	37.28851	24.08575	17.15238	5045.773	5737.053	4773.15	-7.5465	1.35E-274	8.32E-272	TFAP2A	chr6	-	10393419	10419892	3317
ENSG00000(	2843.249	2873.43	2570.218	1584.295	1119.245	1232.947	1.0705	1.54E-14	1.18E-13	YIPF3	chr6	-	43479565	43484728	1674
ENSG00000(	304.5228	313.1148	286.3128	773.046	458.3751	573.7315	-0.99388	1.64E-07	7.35E-07	TMEM14B	chr6	+	10747992	10930656	1589
ENSG00000(	1188.053	1135.643	1136.015	849.4517	764.879	802.2378	0.51643	2.01E-05	7.18E-05	TMEM63B	chr6	+	44094651	44123256	3318
ENSG00000(	62.14751	74.66584	60.69303	77.90386	64.43024	49.3179	0.041129	0.89692	0.93605	FRS3	chr6	-	41737914	41754280	2174
ENSG00000(	835.8841	752.6798	634.638	722.1088	737.266	727.439	0.025506	0.85665	0.90907	TJAP1	chr6	+	43445261	43474294	3468
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CAPN11	chr6	+	44126548	44152139	2728
ENSG00000(	3.107376	3.612863	2.638828	0	0	0	2.6995	0.042216	0.083876	TINAG	chr6	+	54172657	54254950	1754
ENSG00000(	5.17896	3.612863	2.638828	7.490755	3.681728	4.109825	-0.35466	0.70868	0.80314	HCRTR2	chr6	+	55039050	55147418	1837
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	HIST1H2AB	chr6	-	26033320	26033796	477
ENSG00000(	0	4.817151	0	4.494453	3.681728	3.28786	-0.93266	0.43148	0.56126	KIAA0319	chr6	-	24544332	24646383	6896
ENSG00000(	3.107376	0	0	7.490755	11.04518	11.50751	-2.5906	0.01142	0.026196	IRF4	chr6	+	391739	411447	5331
ENSG00000(	681.5511	759.9056	857.619	253.9366	397.6266	280.29	1.2988	5.30E-13	3.70E-12	SLC22A23	chr6	-	3269196	3457256	6641
ENSG00000(	830.7051	693.6697	750.7464	2818.771	2864.384	3284.572	-1.9737	2.44E-56	7.81E-55	TUBB2A	chr6	-	3153903	3157760	1595
ENSG00000(	135.6887	122.8373	126.6637	220.2282	231.9489	266.3166	-0.89284	1.13E-05	4.16E-05	LRRC1	chr6	+	53659295	53788919	3180
ENSG00000(	0	1.204288	0	9.737982	8.283888	7.397684	-3.2333	0.00452	0.011299	GCM1	chr6	-	52991762	53013627	2765
ENSG00000(	16.57267	16.86003	2.638828	205.2467	148.1896	180.0103	-3.7745	7.34E-24	8.70E-23	FOXF2	chr6	+	1390069	1395832	2187
ENSG00000(	240.3037	184.256	233.5362	194.0106	202.495	265.4947	-0.0078	0.96988	0.98229	BPHL	chr6	+	3118608	3153812	3723

ENSG00000(	624.5825	550.3595	625.4021	594.0169	602.883	508.7963	0.077955	0.58818	0.70538	RIPK1	chr6	+	3064225	3115421	4160
ENSG00000(	2232.132	2229.137	1976.482	9621.126	10071.37	11443.4	-2.2696	8.94E-89	5.50E-87	TUBB2B	chr6	-	3224495	3231964	2020
ENSG00000(	313.8449	298.6634	250.6886	223.2245	289.9361	441.3952	-0.14228	0.53099	0.65577	MNF1	chr6	-	33665345	33679504	507
ENSG00000(	12828.28	11352.82	10933.98	26384.69	24701.63	24754.3	-1.1091	4.29E-26	5.55E-25	HMGA1	chr6	+	34204650	34214008	2159
ENSG00000(	76.6486	101.1602	77.84541	142.3244	196.052	146.3098	-0.91356	0.000305	0.000927	TCF19	chr6	+	31126319	31134936	3290
ENSG00000(	3357.002	3270.845	3042.568	2038.235	1781.956	2163.412	0.69119	3.12E-09	1.64E-08	FLOT1	chr6	-	30695486	30710510	1912
ENSG00000(	698.1237	625.0253	550.1955	1157.322	693.0853	843.336	-0.52162	0.003696	0.009402	IER3	chr6	-	30710976	30712331	1350
ENSG00000(	507.538	533.4995	559.4314	1018.743	1409.181	1037.32	-1.1108	5.26E-13	3.67E-12	MDC1	chr6	-	30667584	30685666	7576
ENSG00000(	204.051	166.1917	189.9956	235.9588	219.9832	213.7109	-0.25527	0.18487	0.28936	PGBD1	chr6	+	28249314	28270326	3114
ENSG00000(	530.3255	631.0468	505.3355	486.8991	386.5814	447.1489	0.33356	0.035042	0.071225	ATAT1	chr6	+	30594619	30614600	2646
ENSG00000(	576.9361	535.908	478.9472	439.7073	349.7642	413.4484	0.40274	0.010452	0.024194	TPMT	chr6	-	18128542	18155305	3181
ENSG00000(	3.107376	9.634302	17.15238	45.69361	57.06678	50.96182	-2.3086	7.25E-06	2.73E-05	RNF144B	chr6	+	18368779	18469105	5036
ENSG00000(	471.2853	402.2321	361.5194	740.8357	577.1109	519.4818	-0.56959	0.001022	0.002864	NRM	chr6	-	30655824	30659197	1755
ENSG00000(	5502.127	5294.049	5058.632	5652.524	4898.539	5616.486	-0.02814	0.79395	0.86525	MTCH1	chr6	-	36935917	36954074	2057
ENSG00000(	498.2159	594.9181	422.2124	549.0724	535.6914	721.6852	-0.25194	0.14543	0.238	VARS2	chr6	+	30876019	30894236	6054
ENSG00000(	452.6411	490.1451	395.8241	529.5964	462.0569	537.5651	-0.19119	0.21279	0.32296	TAF8	chr6	+	42018251	42055199	6680
ENSG00000(	584.1866	570.8324	635.9574	313.1136	292.6974	195.6277	1.1542	2.75E-10	1.57E-09	FAM8A1	chr6	+	17600586	17611950	4677
ENSG00000(	7.250543	4.817151	19.79121	48.68991	19.32907	25.48091	-1.4955	0.01327	0.029993	C6orf52	chr6	-	10671651	10695030	682
ENSG00000(	0	0	0	828.4776	552.2592	613.1858	-9.7471	1.74E-26	2.28E-25	FGFBP1	chr4	-	15937192	15940363	1359
ENSG00000(	2.071584	10.83859	3.958241	11.98521	15.64734	18.90519	-1.3539	0.067852	0.1264	FGFBP2	chr4	-	15961866	15970932	1168
ENSG00000(	1172.516	1188.632	1554.269	134.0845	271.5274	176.7225	2.7376	1.62E-40	3.40E-39	CPEB2	chr4	+	15004298	15071777	6878
ENSG00000(	17.60846	22.88147	19.79121	194.7596	232.8693	208.7791	-3.3624	2.52E-29	3.73E-28	FHDC1	chr4	+	1.54E+08	1.54E+08	6583
ENSG00000(	19.68005	13.24716	11.87472	17.97781	9.20432	5.753754	0.41562	0.52609	0.65092	TLR2	chr4	+	1.55E+08	1.55E+08	4200
ENSG00000(	6.214751	9.634302	11.87472	0	0	0.821965	3.7217	0.000956	0.002687	MGARP	chr4	-	1.4E+08	1.4E+08	1339
ENSG00000(	30.03797	8.430014	25.06886	11.98521	25.7721	11.50751	0.35969	0.5462	0.66826	TTC29	chr4	-	1.48E+08	1.48E+08	2226
ENSG00000(	0	1.204288	3.958241	9.737982	5.522592	4.93179	-1.6468	0.11666	0.19929	MYO7A	chr11	+	76839310	76926284	7462
ENSG00000(	307.6302	314.3191	379.9912	270.4163	331.3555	213.7109	0.29542	0.13072	0.21824	FCHSD2	chr11	-	72547790	72853306	4509
ENSG00000(	158.4762	196.2989	228.2586	423.9768	646.1433	530.1674	-1.4517	3.00E-13	2.14E-12	ARRB1	chr11	-	74975226	75062873	3336
ENSG00000(	1.035792	4.817151	3.958241	2.996302	0	0	1.1468	0.35911	0.48869	SLCO2B1	chr11	+	74811608	74917594	5875
ENSG00000(	457.82	464.8551	533.0432	887.6545	934.2385	809.6354	-0.85309	8.70E-10	4.79E-09	PRKRIR	chr11	-	76061000	76092015	6795
ENSG00000(	257.9122	220.3847	203.1897	141.5753	138.9852	124.9387	0.74708	0.000259	0.000794	ANKRD42	chr11	+	82904781	82971736	4066
ENSG00000(	82.86335	127.6545	93.67838	68.16587	127.94	90.41614	0.087915	0.76826	0.8474	IL18BP	chr11	+	71709587	71716761	4080
ENSG00000(	3949.475	3650.196	3637.624	1730.365	2157.493	1999.019	0.93154	3.52E-15	2.81E-14	NUMA1	chr11	-	71713910	71791739	7343
ENSG00000(	736.448	824.9371	694.0116	961.813	761.1973	808.8135	-0.16689	0.24276	0.3586	CCDC90B	chr11	-	82970139	82997450	4014
ENSG00000(	251.6974	302.2762	303.4652	283.8996	341.4803	264.6727	-0.05425	0.76427	0.84435	SYTL2	chr11	-	85405267	85522184	6314
ENSG00000(	379.0998	392.5978	464.4337	108.616	138.9852	75.62077	1.925	9.44E-19	9.03E-18	RAB30	chr11	-	82684175	82782965	9929
ENSG00000(	850.3852	935.7316	1077.961	704.8801	793.4124	709.3557	0.37389	0.006799	0.016404	CREBZF	chr11	-	85370752	85393951	4329
ENSG00000(	846.242	782.787	814.0783	77.15478	92.0432	64.93523	3.3739	9.96E-85	5.75E-83	LRRC32	chr11	-	76368568	76381791	4311
ENSG00000(	1858.211	1987.075	1832.666	1050.953	989.4644	917.3128	0.93891	1.29E-15	1.05E-14	PRCP	chr11	-	82534544	82681626	7072
ENSG00000(	167.7983	186.6646	188.6762	494.3899	358.048	466.8761	-1.2774	5.70E-12	3.70E-11	NARS2	chr11	-	78147007	78285919	2519
ENSG00000(	425.7105	385.3721	428.8095	383.5267	336.8781	433.9975	0.10196	0.52739	0.65215	RNF121	chr11	+	71639747	71708643	2625
ENSG00000(	691.909	741.8412	647.8322	1477.177	1055.736	1324.185	-0.88759	1.81E-09	9.68E-09	MRPL15	chr8	+	55047770	55060461	1147
ENSG00000(	128.4382	98.75159	234.8557	72.66033	96.64536	55.07165	1.0261	0.001398	0.003827	PI15	chr8	+	75736772	75767264	6732
ENSG00000(	0	0	0	58.42789	45.10117	47.67397	-6.4579	4.53E-10	2.55E-09	TTPA	chr8	-	63961112	63998612	2338

ENSG00000(	664.9784	785.1956	649.1516	1838.231	1665.061	1651.328	-1.2932	8.44E-24	9.99E-23	GGH	chr8	-	63927638	63951730	1607
ENSG00000(	10.35792	15.65574	14.51355	0.749076	3.681728	0.821965	2.6282	0.002532	0.006626	SLCO5A1	chr8	-	70584568	70747299	3790
ENSG00000(	1850.96	1985.87	1935.58	617.2383	662.711	531.8113	1.6685	1.36E-39	2.78E-38	SULF1	chr8	+	70378859	70573150	5710
ENSG00000(	332.4892	333.5877	416.9348	677.9134	628.6551	524.4136	-0.757	4.15E-06	1.61E-05	TGS1	chr8	+	56685701	56738007	3782
ENSG00000(	4395.901	4504.036	5066.549	3498.932	3150.639	3136.618	0.51192	4.00E-06	1.55E-05	SDCBP	chr8	+	59465483	59495419	3589
ENSG00000(	381.1714	373.3292	448.6007	223.2245	226.4263	178.3664	0.93295	1.61E-07	7.26E-07	NEK1	chr4	-	1.7E+08	1.71E+08	5653
ENSG00000(	59.04014	68.6444	104.2337	20.97412	41.41944	10.68554	1.6283	0.000176	0.000555	DDX60	chr4	-	1.69E+08	1.69E+08	6071
ENSG00000(	0	2.408575	0	1.498151	0	0	0.25968	0.84497	NA	NXPE4	chr11	-	1.14E+08	1.14E+08	1822
ENSG00000(	5.17896	4.817151	7.916483	362.5526	536.6119	340.2935	-5.9831	2.52E-48	6.64E-47	SORL1	chr11	+	1.21E+08	1.22E+08	10904
ENSG00000(	0	0	0	4.494453	3.681728	1.64393	-2.458	0.06291	0.11842	TMPRSS4	chr11	+	1.18E+08	1.18E+08	5550
ENSG00000(	195.7647	140.9017	170.2044	438.9583	477.7042	395.3651	-1.3625	1.69E-13	1.22E-12	BUD13	chr11	-	1.17E+08	1.17E+08	2196
ENSG00000(	18.64425	18.06432	9.235896	8.988907	9.20432	5.753754	0.88752	0.18152	0.2847	TRPC6	chr11	-	1.01E+08	1.02E+08	4612
ENSG00000(	2.071584	8.430014	5.277655	1.498151	3.681728	0.821965	1.1446	0.27513	0.39651	MMP7	chr11	-	1.02E+08	1.02E+08	1323
ENSG00000(	0	0	0	17.97781	10.12475	5.753754	-4.3257	0.000212	0.00066	MMP20	chr11	-	1.02E+08	1.02E+08	1956
ENSG00000(	70.43385	72.25726	117.4278	23.22134	22.09037	18.08323	1.9935	5.77E-08	2.71E-07	C11orf70	chr11	+	1.02E+08	1.02E+08	2193
ENSG00000(	770.6292	684.0354	678.1787	1471.933	1149.62	1373.503	-0.90275	5.59E-11	3.37E-10	DCUN1D5	chr11	-	1.03E+08	1.03E+08	1535
ENSG00000(	2318.102	2396.533	2801.115	3033.756	3814.27	3197.444	-0.41779	0.001088	0.003035	YAP1	chr11	+	1.02E+08	1.02E+08	5386
ENSG00000(	11.39371	7.225726	7.916483	43.44638	46.0216	48.49593	-2.2818	4.47E-06	1.73E-05	TRIM29	chr11	-	1.2E+08	1.2E+08	3328
ENSG00000(	210.2658	146.9231	176.8014	362.5526	394.8653	344.4033	-1.0364	3.99E-08	1.91E-07	SLC37A4	chr11	-	1.19E+08	1.19E+08	5862
ENSG00000(	1.035792	1.204288	0	0	2.761296	4.109825	-0.98084	0.45443	0.58415	BTG4	chr11	-	1.11E+08	1.11E+08	1394
ENSG00000(	23.82321	14.45145	5.277655	2.996302	0	3.28786	2.4388	0.005414	0.013316	POU2F3	chr11	+	1.2E+08	1.2E+08	3013
ENSG00000(	1817.815	1660.713	2213.976	2331.123	2877.27	2401.781	-0.418	0.00238	0.006259	RDX	chr11	-	1.1E+08	1.1E+08	4491
ENSG00000(	582.1151	596.1224	724.3582	1143.838	1178.153	1008.551	-0.80707	7.71E-09	3.91E-08	PPP2R1B	chr11	-	1.12E+08	1.12E+08	5587
ENSG00000(	286.9144	337.2006	295.5487	536.3381	464.8182	461.1223	-0.66795	2.84E-05	9.97E-05	FDX1	chr11	+	1.1E+08	1.1E+08	3206
ENSG00000(	97.36444	98.75159	96.31721	179.7781	133.4626	200.5594	-0.80827	0.000823	0.00234	C11orf1	chr11	+	1.12E+08	1.12E+08	2885
ENSG00000(	54.89697	59.0101	44.86007	64.4205	47.86246	47.67397	-0.01098	0.97416	0.98485	FXYD6	chr11	-	1.18E+08	1.18E+08	2171
ENSG00000(	102.5434	85.50443	97.63662	0	3.681728	0.821965	5.712	1.62E-19	1.61E-18	ARHGAP20	chr11	-	1.1E+08	1.11E+08	6189
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	FXYD2	chr11	-	1.18E+08	1.18E+08	1567
ENSG00000(	299.3439	344.4263	306.104	0	0	0.821965	8.6836	5.63E-27	7.54E-26	MMP13	chr11	-	1.03E+08	1.03E+08	2716
ENSG00000(	3.107376	0	0	36.7047	25.7721	35.34449	-4.2825	2.13E-07	9.48E-07	TMPRSS13	chr11	-	1.18E+08	1.18E+08	3269
ENSG00000(	8.286335	2.408575	7.916483	0	0	0	3.7637	0.002628	0.006859	CASP1	chr11	-	1.05E+08	1.05E+08	2001
ENSG00000(	78.72018	78.2787	118.7472	158.0549	177.6434	133.9803	-0.7663	0.002792	0.007253	ALKBH8	chr11	-	1.07E+08	1.07E+08	4079
ENSG00000(	366.6703	393.8021	347.0058	180.5272	202.495	207.9571	0.9038	1.40E-07	6.33E-07	MAP2K5	chr15	+	67835047	68099461	2347
ENSG00000(	0	0	0	2.247227	2.761296	4.109825	-2.3558	0.075912	0.13903	UNC13C	chr15	+	54305101	54920806	8140
ENSG00000(	21.75163	33.72006	21.11062	45.69361	32.21512	24.65895	-0.41274	0.3655	0.49535	SQRDL	chr15	+	45923346	45983492	2003
ENSG00000(	422.6031	522.6609	555.4732	720.6107	765.7994	558.9361	-0.44652	0.007201	0.0173	CTDSPL2	chr15	+	44719432	44821236	6828
ENSG00000(	1245.022	1163.342	1227.055	1220.993	1478.214	1254.318	-0.12009	0.33782	0.46645	SLTM	chr15	-	59171244	59225852	4147
ENSG00000(	9007.246	8430.014	11283.63	9028.608	9920.416	8068.408	0.087923	0.50235	0.63035	THBS1	chr15	+	39873280	39891667	7775
ENSG00000(	1067.901	962.2259	1027.823	316.1099	523.7258	489.8911	1.1985	6.22E-12	4.02E-11	MAPKBP1	chr15	+	42066632	42120053	7232
ENSG00000(	490.9654	496.1665	480.2666	1744.597	1497.543	1509.95	-1.6916	1.19E-39	2.44E-38	NUSAP1	chr15	+	41624892	41673248	2409
ENSG00000(	264.1269	332.3834	232.2168	253.9366	253.1188	313.9906	0.013885	0.94276	0.96545	NDUFAF1	chr15	-	41679551	41694717	1585
ENSG00000(	292.0933	249.2876	354.9223	1961.08	1544.485	1485.291	-2.4707	1.10E-52	3.23E-51	KIF23	chr15	+	69706585	69740764	3610
ENSG00000(	1381.746	1446.35	1493.576	2.247227	9.20432	2.465895	8.1914	1.93E-113	1.81E-111	ITGA11	chr15	-	68594050	68724501	5013
ENSG00000(	218.5521	151.7403	279.7157	656.1902	645.2228	489.8911	-1.456	1.80E-12	1.21E-11	CASC5	chr15	+	40886218	40956540	9573

ENSG0000(	389.4578	399.8235	369.4359	1005.259	840.3544	932.9302	-1.2585	2.80E-19	2.75E-18	HAUS2	chr15	+	42841008	42862192	3949
ENSG0000(	1471.86	1358.437	1546.353	1638.977	1636.528	1657.903	-0.17265	0.12811	0.21482	RTF1	chr15	+	41700606	41775761	5021
ENSG0000(	416.3883	402.2321	391.8659	486.8991	375.5363	427.4218	-0.09214	0.56226	0.6822	PARP6	chr15	-	72533522	72565340	3657
ENSG0000(	22434.22	23386.06	19544.48	22121.7	15429.2	24290.71	0.079672	0.59354	0.70956	RPLP1	chr15	+	69745123	69748255	1962
ENSG0000(	33.14534	37.33292	58.05421	62.17327	56.14635	55.89361	-0.44045	0.21591	0.32662	PAQR5	chr15	+	69591286	69700119	5480
ENSG0000(	138.7961	137.2888	127.9831	136.3317	127.94	107.6774	0.11916	0.60307	0.71816	LRRC49	chr15	+	71145578	71342414	3061
ENSG0000(	482.679	451.6079	324.5758	490.6445	482.3064	497.2888	-0.2204	0.19319	0.29904	TUBGCP4	chr15	+	43661419	43699293	4379
ENSG0000(	480.6074	492.5537	488.1831	625.4781	606.5647	633.735	-0.35196	0.009182	0.021538	RMDN3	chr15	-	41028082	41048049	3138
ENSG0000(	71.46964	60.21439	59.37362	73.4094	60.74851	68.22309	-0.08077	0.78966	0.86243	ITPKA	chr15	+	41785591	41795747	1822
ENSG0000(	835.8841	696.0783	840.4666	547.5742	512.6806	483.3154	0.61818	1.30E-05	4.75E-05	UACA	chr15	-	70946893	71055932	6939
ENSG0000(	417.4241	401.0278	377.3523	834.4702	726.2208	731.5488	-0.93564	4.45E-11	2.70E-10	SMAD6	chr15	+	66994566	67074338	2987
ENSG0000(	68.36227	84.30014	48.81831	115.3576	115.054	105.2115	-0.72441	0.010374	0.024034	PLCB2	chr15	-	40570377	40600136	4643
ENSG0000(	30.03797	4.817151	5.277655	158.804	185.0068	186.586	-3.4194	2.10E-06	8.40E-06	TMEM62	chr15	+	43415477	43477344	2771
ENSG0000(	7.250543	10.83859	1.319414	172.2874	130.7013	118.3629	-4.2862	5.63E-22	6.17E-21	PAK6	chr15	+	40509629	40569688	4215
ENSG0000(	2588.444	2536.23	3422.559	2051.718	2625.072	1902.849	0.37619	0.013089	0.029619	ADAM10	chr15	-	58887403	59042177	5034
ENSG0000(	35.21692	26.49433	31.66593	20.22504	26.69253	28.76877	0.29938	0.49895	0.62725	DUOX1	chr15	+	45422131	45457774	5738
ENSG0000(	7.250543	9.634302	6.597069	3.745378	8.283888	0.821965	0.77451	0.3864	0.51729	SLC28A2	chr15	+	45544428	45568149	2464
ENSG0000(	149.154	157.7617	109.5113	510.1204	532.0097	480.0275	-1.8568	3.30E-24	3.96E-23	STRA6	chr15	-	74471807	74504608	2887
ENSG0000(	33.14534	12.04288	14.51355	14.98151	16.56778	13.9734	0.38615	0.50351	0.63139	CYP19A1	chr15	-	51500254	51630807	4417
ENSG0000(	416.3883	366.1035	423.5318	206.7449	191.4499	158.6392	1.1095	5.07E-10	2.84E-09	ZNF280D	chr15	-	56922379	57210769	4902
ENSG0000(	7.250543	4.817151	10.55531	31.46117	41.41944	27.94681	-2.0647	0.000257	0.000788	SEMA6D	chr15	+	47476298	48066420	6099
ENSG0000(	4.143168	6.021439	0	2.996302	1.840864	0	0.77988	0.51956	0.64559	BCL2L10	chr15	-	52401460	52404972	1249
ENSG0000(	1496.719	1653.487	1390.662	1916.884	1445.999	1612.695	-0.13192	0.33105	0.45896	RSL24D1	chr15	-	55473004	55489265	2015
ENSG0000(	16.57267	45.76293	11.87472	56.92974	97.56579	143.8439	-1.9502	1.23E-05	4.51E-05	SPTBN5	chr15	-	42140345	42186275	11722
ENSG0000(	8.286335	0	2.638828	0	0	0	2.7634	0.039058	0.078375	GCOM1	chr15	+	57884106	58006943	3156
ENSG0000(	43.50326	72.25726	62.01245	76.40571	96.64536	115.8971	-0.69564	0.025049	0.053062	GCHFR	chr15	+	41056218	41059906	785
ENSG0000(	566.5782	481.7151	579.2227	480.9065	467.5795	446.327	0.22181	0.12999	0.21722	BCAR3	chr1	-	94027347	94312706	3217
ENSG0000(	456.7842	550.3595	616.1662	436.711	471.2612	380.5698	0.33054	0.04304	0.085314	TTLL7	chr1	-	84330711	84464833	8452
ENSG0000(	1387.961	1360.845	1686.211	1700.401	1923.703	1513.237	-0.21191	0.11916	0.20261	FNBP1L	chr1	+	93913688	94020218	5341
ENSG0000(	230.9816	256.5133	237.4945	489.8954	301.9017	349.3351	-0.65309	0.0011	0.003064	CCBL2	chr1	-	89401456	89458636	2070
ENSG0000(	300.3797	279.3948	283.674	455.4379	306.5039	352.623	-0.36782	0.046184	0.090601	GTF2B	chr1	-	89318615	89357627	1351
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	BRDT	chr1	+	92414928	92479983	3696
ENSG0000(	1049.257	1079.042	1029.143	1586.542	1463.487	1535.43	-0.53749	2.75E-06	1.09E-05	RABGGTB	chr1	+	76251879	76260764	3863
ENSG0000(	142.9393	208.3418	204.5091	0	0	0	8.5592	6.91E-19	6.66E-18	IFI44L	chr1	+	79085607	79108484	5152
ENSG0000(	6.214751	9.634302	30.34652	9.737982	19.32907	17.26126	-0.01674	0.97963	0.98809	GIPC2	chr1	+	78445226	78604133	3847
ENSG0000(	2328.46	2261.652	3005.625	2528.879	3017.176	2391.918	-0.06366	0.64932	0.75574	ARHGAP29	chr1	-	94614544	94740624	8480
ENSG0000(	184.371	185.4603	203.1897	0	0	0	8.6096	3.21E-19	3.14E-18	IFI44	chr1	+	79115481	79129763	1687
ENSG0000(	37.28851	34.92434	19.79121	83.14739	49.70333	38.63235	-0.87158	0.036964	0.074704	SLC44A5	chr1	-	75667816	76076801	4406
ENSG0000(	153.2972	164.9874	141.1773	129.5901	100.3271	148.7757	0.27543	0.23902	0.35399	RP11-122C	chr1	-	97144430	97145176	747
ENSG0000(	43.50326	73.46155	40.90183	226.9699	248.5166	180.0103	-2.0333	7.59E-14	5.58E-13	CLCA2	chr1	+	86889769	86922241	4025
ENSG0000(	378.064	327.5663	315.3399	307.8701	312.0264	326.3201	0.11129	0.49648	0.62507	DBT	chr1	-	1.01E+08	1.01E+08	3538
ENSG0000(	975.716	1024.849	984.2827	1145.337	1112.802	1201.713	-0.21287	0.070971	0.13134	RTCA	chr1	+	1.01E+08	1.01E+08	2535
ENSG0000(	540.6834	556.3809	546.2373	227.719	295.4587	253.9872	1.0787	1.38E-11	8.72E-11	IFT172	chr2	-	27667238	27712656	5565
ENSG0000(	655.6563	573.241	864.216	1311.631	1389.852	1176.232	-0.88785	1.44E-08	7.14E-08	EPT1	chr2	+	26531415	26618759	8101

ENSG00000(	48.68222	33.72006	36.94359	0.749076	2.761296	2.465895	4.0614	1.18E-09	6.44E-09	CGREF1	chr2	-	27321757	27341995	1902
ENSG00000(	2139.946	2250.814	2037.175	1298.897	1224.175	1174.588	0.79629	2.19E-12	1.47E-11	HADHB	chr2	+	26466038	26513336	2883
ENSG00000(	4.143168	9.634302	5.277655	61.42419	63.50981	73.97684	-3.2742	5.56E-11	3.35E-10	KHK	chr2	+	27309615	27323640	2411
ENSG00000(	599.7235	590.101	651.7904	343.8257	460.216	439.7512	0.56535	0.000316	0.000959	ADCY3	chr2	-	25042038	25142708	5050
ENSG00000(	345.9545	382.9635	397.1435	568.5483	611.1668	609.076	-0.66703	4.48E-06	1.73E-05	PPM1B	chr2	+	44395108	44471523	3877
ENSG00000(	323.1671	307.0934	372.0747	1197.023	966.4536	962.5209	-1.6378	3.83E-27	5.17E-26	PNPT1	chr2	-	55861400	55921045	4411
ENSG00000(	277.5922	302.2762	242.7721	161.0512	110.4518	171.7907	0.88427	3.69E-05	0.000127	DYNC2LI1	chr2	+	44001178	44037149	2903
ENSG00000(	0	0	0	8.988907	13.80648	9.041614	-4.2587	0.00026	0.000798	LHCGR	chr2	-	48859428	48982880	3044
ENSG00000(	971.5728	939.3444	1074.003	1064.436	1098.996	889.366	-0.03267	0.80726	0.87485	SMEK2	chr2	-	55774428	55846015	5242
ENSG00000(	142.9393	167.396	139.8579	207.4939	145.4283	141.378	-0.13623	0.55677	0.67732	THUMPD2	chr2	-	39963200	40006407	3148
ENSG00000(	4866.15	4750.915	5946.598	5104.201	5480.252	4284.903	0.065548	0.61463	0.72785	CYP1B1	chr2	-	38294116	38337044	5247
ENSG00000(	3948.439	3847.699	4062.475	4019.539	3609.014	4194.487	0.004136	0.96928	0.98193	RAB1A	chr2	-	65297835	65357240	2447
ENSG00000(	7539.529	7723.097	9253.049	5379.861	7071.679	5923.901	0.41499	0.001402	0.003837	ACTR2	chr2	+	65454887	65498387	3861
ENSG00000(	928.0695	851.4314	869.4937	1173.801	979.3396	995.3995	-0.24879	0.056565	0.10813	PREB	chr2	-	27353624	27357543	3057
ENSG00000(	680.5153	605.7567	527.7655	3756.614	3312.635	3418.552	-2.5237	1.01E-86	6.05E-85	SLC5A6	chr2	-	27422455	27435826	3231
ENSG00000(	0	0	0	1.498151	2.761296	0.821965	-1.5229	0.26162	NA	ABCG5	chr2	-	44039611	44066004	3033
ENSG00000(	711.589	686.444	876.0908	581.2826	468.4999	385.5015	0.65964	0.000122	0.000393	PREPL	chr2	-	44543420	44589001	6273
ENSG00000(	1.035792	2.408575	5.277655	0	0	4.93179	0.55895	0.65437	0.75992	SLC3A1	chr2	+	44502599	44548633	2989
ENSG00000(	8415.809	8458.917	6750.121	95.13259	132.5422	207.1352	5.6759	5.45E-65	2.13E-63	EMILIN1	chr2	+	27301435	27309271	3938
ENSG00000(	934.2843	926.0973	1120.182	885.4073	1101.757	822.7869	0.084737	0.56665	0.68585	FBXO11	chr2	-	48016455	48132932	4055
ENSG00000(	560.3634	676.8097	534.3626	597.0132	395.7858	486.6032	0.25745	0.13903	0.2295	ATRAID	chr2	+	27434895	27440046	1240
ENSG00000(	218.5521	209.5461	253.3274	593.2678	617.6099	591.8147	-1.4007	3.49E-19	3.40E-18	CENPO	chr2	+	25016005	25045245	4386
ENSG00000(	2728.276	2732.529	3303.812	4266.734	3738.795	3476.09	-0.38922	0.001917	0.005123	LRPPRC	chr2	-	44113647	44223144	6335
ENSG00000(	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	TRIM54	chr2	+	27505260	27530307	2027
ENSG00000(	84.93494	84.30014	84.44248	120.6012	116.8949	83.01846	-0.334	0.21395	0.32429	DTNB	chr2	-	25600067	25896503	2474
ENSG00000(	3090.803	2880.656	2946.251	3360.353	3110.14	3147.304	-0.10884	0.29697	0.42151	ACTR1A	chr10	-	1.04E+08	1.04E+08	3519
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	CYP2C9	chr10	+	96698415	96749147	1847
ENSG00000(	17.60846	22.88147	13.19414	64.4205	50.62376	50.13986	-1.5786	0.000183	0.000574	TMEM180	chr10	+	1.04E+08	1.04E+08	2834
ENSG00000(	0	0	0	11.98521	20.2495	9.863579	-4.661	4.15E-05	0.000142	CYP2C8	chr10	-	96796530	96829254	2117
ENSG00000(	5925.765	5599.938	7465.243	4731.161	5164.544	3965.159	0.45302	0.000991	0.002781	MYOF	chr10	-	95066186	95242074	6842
ENSG00000(	153.2972	158.966	113.4696	10.48706	11.96562	4.109825	3.9282	1.15E-24	1.40E-23	LOXL4	chr10	-	1E+08	1E+08	3653
ENSG00000(	118.0803	116.8159	100.2754	70.4131	60.74851	64.93523	0.7659	0.003964	0.010027	STAMBPL1	chr10	+	90639491	90734910	4184
ENSG00000(	81.82756	115.6116	63.33186	14.98151	2.761296	4.109825	3.4215	2.32E-12	1.55E-11	CH25H	chr10	-	90965694	90967071	1378
ENSG00000(	0	0	0	3.745378	1.840864	0	-1.5327	0.25777	NA	LBX1	chr10	-	1.03E+08	1.03E+08	2119
ENSG00000(	733.3407	738.2284	781.093	1000.765	885.4556	781.6886	-0.24422	0.076258	0.13962	ATAD1	chr10	-	89511269	89601100	4640
ENSG00000(	0	1.204288	2.638828	0	0	0	1.2853	0.33195	NA	BTBD16	chr10	+	1.24E+08	1.24E+08	1851
ENSG00000(	482.679	476.8979	602.9721	1589.538	1645.732	1449.946	-1.582	9.98E-31	1.55E-29	KIF11	chr10	+	94353043	94415150	4858
ENSG00000(	15.53688	15.65574	30.34652	16.47966	14.72691	12.32947	0.46718	0.40408	0.53503	CUZD1	chr10	-	1.25E+08	1.25E+08	2903
ENSG00000(	436.0684	349.2434	427.4901	440.4564	605.6443	532.6333	-0.37734	0.025636	0.054148	TACC2	chr10	+	1.24E+08	1.24E+08	9673
ENSG00000(	909.4253	974.2688	1050.253	515.364	360.8093	389.6114	1.2063	2.24E-14	1.70E-13	DUSP5	chr10	+	1.12E+08	1.12E+08	2557
ENSG00000(	84.93494	54.19295	69.92893	65.91865	85.60018	78.90863	-0.13299	0.66053	0.76496	CALHM2	chr10	-	1.05E+08	1.05E+08	2026
ENSG00000(	710.5532	829.7542	674.2204	583.5299	527.4075	692.9164	0.29465	0.053291	0.10271	ARL3	chr10	-	1.04E+08	1.04E+08	1017
ENSG00000(	214.4089	269.7604	270.4798	1170.805	1053.895	956.7672	-2.0726	6.09E-41	1.29E-39	CEP55	chr10	+	95256389	95288849	2638
ENSG00000(	192.6573	177.0303	215.0644	751.3228	825.6275	732.3707	-1.9763	8.16E-37	1.54E-35	KIF20B	chr10	+	91461367	91534700	6520

ENSG00000(	199.9078	210.7504	275.7575	274.1617	348.8437	292.6195	-0.41554	0.03211	0.065966	ENTPD1	chr10	+	97471536	97637023	12589
ENSG00000(	19.68005	12.04288	17.15238	211.2393	166.5982	209.6011	-3.5279	1.39E-27	1.91E-26	EXOC6	chr10	+	94590935	94819250	3567
ENSG00000(	445.3905	408.2535	531.7238	56.92974	76.39586	30.4127	3.0598	1.15E-34	2.03E-33	PLCE1	chr10	+	95753746	96088149	7992
ENSG00000(	22.78742	20.47289	7.916483	18.72689	5.522592	9.041614	0.57885	0.38124	0.51193	RBP4	chr10	-	95351444	95361501	1314
ENSG00000(	323.1671	303.4805	255.9663	518.3603	457.4547	506.3304	-0.74322	4.18E-06	1.62E-05	DBR1	chr3	-	1.38E+08	1.38E+08	2666
ENSG00000(	1451.144	1246.438	1744.265	834.4702	961.8514	726.617	0.81348	1.10E-07	5.03E-07	DNAJC13	chr3	+	1.32E+08	1.32E+08	7730
ENSG00000(	1.035792	0	0	350.5674	242.994	286.8658	-8.1209	6.04E-23	6.88E-22	GPR87	chr3	-	1.51E+08	1.51E+08	1608
ENSG00000(	659.7994	650.3154	792.9677	1113.126	984.8622	899.2296	-0.51116	0.000332	0.001002	ANXA7	chr10	-	75135203	75173834	2174
ENSG00000(	313.8449	372.1249	348.3252	400.0063	347.9233	285.2218	-6.44E-05	0.99971	0.99974	FAM149B1	chr10	+	74927924	75004262	5408
ENSG00000(	2587.408	2488.058	2934.376	3082.446	2851.498	2336.846	-0.04646	0.72179	0.813	NCOA4	chr10	+	51565108	51590734	3735
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	MSMB	chr10	+	51549498	51562517	751
ENSG00000(	496.1443	550.3595	382.63	1335.602	946.2041	1076.774	-1.2272	4.01E-13	2.83E-12	TIMM23	chr10	-	51592080	51623365	1682
ENSG00000(	504.4307	537.1123	507.9743	640.4596	496.1128	530.1674	-0.10616	0.48246	0.61165	ASCC1	chr10	-	73856278	73976892	2422
ENSG00000(	0	2.408575	0	0	1.840864	0	0.16879	0.89944	NA	PLA2G12B	chr10	-	74694928	74714536	1128
ENSG00000(	60.07593	52.98866	50.13772	32.21025	19.32907	23.01502	1.1017	0.004855	0.012059	ZNF365	chr10	+	64133951	64431771	4173
ENSG00000(	0	0	3.958241	0	0	3.28786	0.12119	0.92879	0.95719	OIT3	chr10	+	74653339	74692791	2365
ENSG00000(	3174.702	3033.601	2979.236	3.745378	4.60216	4.109825	9.3522	4.07E-146	5.90E-144	ADAMTS14	chr10	+	72432559	72522197	5269
ENSG00000(	19778.45	21143.68	14987.22	14041.42	11678.44	14126.29	0.48742	0.000371	0.001114	RPS24	chr10	+	79793518	79816570	2814
ENSG00000(	76.6486	77.07441	80.48424	204.4976	277.9705	196.4496	-1.5228	1.26E-10	7.39E-10	TET1	chr10	+	70320413	70454239	9288
ENSG00000(	134.6529	109.5902	135.8996	567.7993	470.3408	378.9258	-1.888	9.75E-21	1.02E-19	DNA2	chr10	-	70173821	70231879	4416
ENSG00000(	13.46529	2.408575	11.87472	1.498151	0.920432	4.109825	1.7841	0.059873	0.11351	MYPN	chr10	+	69865912	69971774	6013
ENSG00000(	71.46964	57.80581	104.2337	12.73428	10.12475	4.93179	2.977	2.44E-11	1.51E-10	AOX1	chr2	+	2.01E+08	2.02E+08	5070
ENSG00000(	1105.19	1115.17	1087.197	3040.498	2335.136	2328.627	-1.2172	4.89E-20	4.96E-19	ATIC	chr2	+	2.16E+08	2.16E+08	2275
ENSG00000(	484.7506	425.1136	405.06	632.9688	582.6335	526.0575	-0.40285	0.007774	0.018536	SMARCAL1	chr2	+	2.17E+08	2.17E+08	3271
ENSG00000(	73.54123	77.07441	92.35896	385.0248	419.717	383.0357	-2.2819	1.51E-30	2.34E-29	BARD1	chr2	-	2.16E+08	2.16E+08	5499
ENSG00000(	13.46529	13.24716	21.11062	3.745378	6.443024	0	2.0198	0.012381	0.028189	STAT4	chr2	-	1.92E+08	1.92E+08	2822
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	MSTN	chr2	-	1.91E+08	1.91E+08	2822
ENSG00000(	85.97073	119.2245	106.8725	45.69361	34.05598	42.74218	1.3257	1.29E-05	4.72E-05	ALS2CR8	chr2	+	2.04E+08	2.04E+08	5934
ENSG00000(	708.4817	674.4011	756.0241	1015.746	877.1717	826.0747	-0.34619	0.011239	0.025844	ASNSD1	chr2	+	1.91E+08	1.91E+08	2450
ENSG00000(	299.3439	339.6091	281.0351	613.4929	454.6934	459.4784	-0.72938	2.93E-05	0.000103	METTL5	chr2	-	1.71E+08	1.71E+08	1370
ENSG00000(	1466.681	1440.328	1476.424	1821.752	1793.002	1664.479	-0.26786	0.015887	0.035286	SSB	chr2	+	1.71E+08	1.71E+08	2463
ENSG00000(	177.1204	230.019	240.1333	643.4559	675.5971	567.9778	-1.5416	1.23E-19	1.23E-18	NAB1	chr2	+	1.92E+08	1.92E+08	4358
ENSG00000(	35.21692	28.90291	46.17948	0.749076	0	4.109825	4.1229	1.03E-08	5.15E-08	CDK15	chr2	+	2.03E+08	2.03E+08	3659
ENSG00000(	769.5934	699.6912	771.8571	1219.495	1171.71	1023.346	-0.60607	3.40E-06	1.33E-05	PPIG	chr2	+	1.7E+08	1.7E+08	6368
ENSG00000(	160.5477	248.0833	180.7597	414.9879	425.2396	323.8542	-0.97789	1.46E-06	5.96E-06	FASTKD1	chr2	-	1.7E+08	1.7E+08	2967
ENSG00000(	18.64425	22.88147	27.70769	30.7121	23.0108	23.83698	-0.16764	0.72309	0.8139	MDH1B	chr2	-	2.08E+08	2.08E+08	2553
ENSG00000(	309.7018	286.6205	414.2959	74.15848	105.8497	65.75719	2.028	2.62E-18	2.44E-17	HECW2	chr2	-	1.97E+08	1.97E+08	6926
ENSG00000(	1839.566	1920.839	2074.118	2553.599	2221.002	2086.147	-0.2339	0.053414	0.10293	IDH1	chr2	-	2.09E+08	2.09E+08	2441
ENSG00000(	2160.662	2177.352	1884.123	2756.598	2265.183	2186.427	-0.2117	0.0976	0.1719	OLA1	chr2	-	1.75E+08	1.75E+08	4417
ENSG00000(	499.2517	451.6079	405.06	346.0729	334.1168	338.6495	0.41251	0.008127	0.019276	CIR1	chr2	-	1.75E+08	1.75E+08	1921
ENSG00000(	1163.194	1150.095	1460.591	5640.539	6362.026	5046.865	-2.1712	5.88E-60	2.05E-58	SSFA2	chr2	+	1.83E+08	1.83E+08	6473
ENSG00000(	26.93059	18.06432	34.30476	0	0	0.821965	5.2659	7.79E-08	3.61E-07	CHRNA1	chr2	-	1.76E+08	1.76E+08	1984
ENSG00000(	54.89697	60.21439	106.8725	139.3281	140.8261	139.734	-0.91886	0.001177	0.003262	FAM117B	chr2	+	2.03E+08	2.04E+08	5772
ENSG00000(	551.0413	479.3065	456.5172	891.3999	722.5391	771.0031	-0.67872	4.28E-06	1.66E-05	WDR12	chr2	-	2.04E+08	2.04E+08	2282

ENSG00000(	953.9643	912.8501	1142.612	841.2118	833.9114	741.4124	0.3149	0.021575	0.046413	ABI2	chr2	+	2.04E+08	2.04E+08	6659
ENSG00000(	2741.741	2696.4	4394.967	5008.319	6570.964	4778.904	-0.73155	3.01E-05	0.000105	ITGAV	chr2	+	1.87E+08	1.88E+08	7030
ENSG00000(	99.43602	142.106	178.1209	182.0254	242.0736	227.6843	-0.63513	0.007936	0.018872	SLC40A1	chr2	-	1.9E+08	1.9E+08	3442
ENSG00000(	507.538	599.7353	595.0556	522.8547	471.2612	428.2437	0.25672	0.089478	0.16001	SLC35A5	chr3	+	1.12E+08	1.12E+08	4399
ENSG00000(	121.1877	116.8159	117.4278	197.7559	150.0304	138.0901	-0.44902	0.054706	0.10513	DIRC2	chr3	+	1.23E+08	1.23E+08	3596
ENSG00000(	362.5272	307.0934	515.8908	213.4865	255.8801	231.7941	0.7525	0.000207	0.000645	SENP7	chr3	-	1.01E+08	1.01E+08	4945
ENSG00000(	0	0	0	4.494453	0	3.28786	-1.9849	0.14263	0.23417	CCDC54	chr3	+	1.07E+08	1.07E+08	1294
ENSG00000(	188.5141	178.2346	192.6344	334.0877	299.1404	441.3952	-0.93771	1.71E-06	6.90E-06	COX17	chr3	-	1.19E+08	1.19E+08	684
ENSG00000(	83.89914	72.25726	97.63662	30.7121	32.21512	33.70056	1.3719	2.55E-05	8.99E-05	PARP9	chr3	-	1.22E+08	1.22E+08	6769
ENSG00000(	68.36227	63.82725	100.2754	107.8669	89.2819	82.19649	-0.26835	0.35507	0.48466	MNS1	chr15	-	56713742	56757335	2023
ENSG00000(	653.5847	661.154	818.0365	510.8695	611.1668	503.0425	0.39063	0.010263	0.023802	USP8	chr15	+	50716577	50793280	5848
ENSG00000(	735.4123	735.8198	1033.101	781.2858	1001.43	714.2875	0.003614	0.98316	0.99033	SECISBP2L	chr15	-	49280673	49338760	7176
ENSG00000(	2368.856	2343.544	2735.145	1273.428	1350.274	1171.3	0.97061	7.31E-16	6.06E-15	TMOD3	chr15	+	52121825	52239492	4668
ENSG00000(	414.3168	348.0392	432.7677	447.1981	444.5687	411.8044	-0.12508	0.42304	0.55356	SPPL2A	chr15	-	50999506	51058005	2329
ENSG00000(	365.6345	355.2649	471.0307	702.6329	720.6983	615.6517	-0.77395	1.04E-06	4.32E-06	GLCE	chr15	+	69452923	69564556	5037
ENSG00000(	219.5879	191.4817	186.0373	303.3756	303.7426	350.979	-0.67684	0.00018	0.000567	SHF	chr15	-	45459412	45493373	2500
ENSG00000(	419.4957	409.4578	422.2124	137.0808	140.8261	152.8855	1.5323	3.25E-19	3.17E-18	APH1B	chr15	+	63568217	63601325	4189
ENSG00000(	396.7083	363.6949	397.1435	887.6545	799.8554	678.943	-1.0286	1.16E-11	7.34E-11	VWA9	chr15	-	65871091	65903627	2615
ENSG00000(	726.0901	699.6912	770.5376	0.749076	0.920432	0	9.4045	1.31E-41	2.83E-40	CILP	chr15	-	65488337	65503826	4454
ENSG00000(	169.8699	162.5788	146.4549	71.16218	40.49901	66.57916	1.4065	1.90E-07	8.47E-07	PARP16	chr15	-	65526798	65592956	2731
ENSG00000(	118.0803	134.8802	112.1502	210.4902	173.9616	229.3282	-0.74534	0.000647	0.001868	PPCDC	chr15	+	75315896	75409803	2250
ENSG00000(	0	0	0	38.95193	79.15715	58.35951	-6.6381	1.31E-10	7.69E-10	HCN4	chr15	-	73612200	73661605	7228
ENSG00000(	346.9903	317.932	328.534	197.0069	235.6306	299.1952	0.44005	0.021117	0.045567	SEMA7A	chr15	-	74701630	74726808	3885
ENSG00000(	554.1487	567.2195	502.6967	1098.145	706.8918	822.7869	-0.69212	3.74E-05	0.000129	UBL7	chr15	-	74738318	74753523	1720
ENSG00000(	642.191	617.7996	732.2746	29.21395	33.13555	31.23467	4.389	2.36E-99	1.78E-97	ARHGAP24	chr4	+	86396267	86923823	4661
ENSG00000(	359.4198	391.3935	390.5465	202.2504	225.5058	189.0519	0.88474	1.94E-07	8.66E-07	FAM13A	chr4	-	89647106	90032549	5858
ENSG00000(	196.8005	232.4275	273.1187	59.92604	61.66894	59.18147	1.9412	8.07E-17	7.01E-16	HERC3	chr4	+	89442199	89629693	4974
ENSG00000(	13.46529	8.430014	11.87472	75.65663	133.4626	101.9236	-3.1169	5.08E-14	3.79E-13	HERC6	chr4	+	89299891	89364263	3781
ENSG00000(	1.035792	7.225726	3.958241	95.13259	92.96363	83.84042	-4.3309	3.70E-16	3.13E-15	HERC5	chr4	+	89378268	89427314	3513
ENSG00000(	198.872	157.7617	232.2168	330.3423	465.7386	348.5131	-0.95342	2.84E-06	1.12E-05	PCDH10	chr4	+	1.34E+08	1.34E+08	5366
ENSG00000(	4.143168	3.612863	6.597069	2.247227	0	0.821965	1.674	0.14094	0.23208	NDST4	chr4	-	1.16E+08	1.16E+08	3351
ENSG00000(	81.82756	66.23582	92.35896	259.1801	260.4823	233.438	-1.638	1.59E-13	1.15E-12	C4orf21	chr4	-	1.13E+08	1.14E+08	6652
ENSG00000(	267.2343	373.3292	299.5069	564.0539	580.7926	511.2622	-0.81515	1.03E-06	4.28E-06	AP1AR	chr4	+	1.13E+08	1.13E+08	2902
ENSG00000(	581.0793	546.7466	664.9845	865.1823	751.9929	708.5338	-0.37575	0.009523	0.022257	COPS4	chr4	+	83955600	83996971	2273
ENSG00000(	4667.278	4818.355	4511.076	7820.349	8634.573	11122.83	-0.97603	1.67E-13	1.21E-12	HNRNPD	chr4	-	83273651	83295656	4597
ENSG00000(	0	0	2.638828	7.490755	8.283888	9.041614	-2.6112	0.01592	0.035347	PRKG2	chr4	-	82009837	82136218	3431
ENSG00000(	0	0	0	171.5383	201.5746	166.0369	-8.099	1.21E-16	1.04E-15	RASGEF1B	chr4	-	82347547	82393082	6323
ENSG00000(	7249.508	7259.446	7987.731	3528.895	3126.707	2682.072	1.2658	3.26E-25	4.05E-24	SEC31A	chr4	-	83739814	83822319	4278
ENSG00000(	186.4425	201.116	302.1458	0	0	1.64393	7.809	4.45E-26	5.75E-25	FGF5	chr4	+	81187753	81257834	5234
ENSG00000(	30.03797	9.634302	19.79121	871.9239	803.5371	738.9465	-5.2667	1.14E-92	7.58E-91	AGPAT9	chr4	+	84457067	84527028	2631
ENSG00000(	138.7961	107.1816	151.7326	177.5309	274.2887	170.1467	-0.63809	0.009334	0.021853	FGF2	chr4	+	1.24E+08	1.24E+08	6775
ENSG00000(	321.0955	404.6407	364.1582	399.2573	411.4331	330.4299	-0.06699	0.69183	0.78972	BBS7	chr4	-	1.23E+08	1.23E+08	3752
ENSG00000(	673.2647	726.1855	1117.543	391.7665	428.0009	363.3085	1.0828	4.92E-09	2.54E-08	KIAA1109	chr4	+	1.23E+08	1.23E+08	15896
ENSG00000(	78.72018	52.98866	92.35896	24.71949	20.2495	11.50751	1.9393	1.47E-06	5.99E-06	BMPR1B	chr4	+	95679119	96079599	5567

ENSG00000(	855.5641	781.5827	906.4373	1303.391	883.6147	949.3695	-0.30225	0.05619	0.10752	RAP1GDS1	chr4	+	99182535	99365012	3681
ENSG00000(	185.4068	150.536	212.4256	334.0877	267.8457	313.1686	-0.73737	0.000178	0.000561	LARP1B	chr4	+	1.29E+08	1.29E+08	4891
ENSG00000(	0	0	1.319414	8.239831	7.363456	13.9734	-3.4236	0.002165	0.005732	MMRN1	chr4	+	90800683	90875780	5217
ENSG00000(	62.14751	74.66584	121.3861	197.0069	284.4135	189.8739	-1.3717	4.45E-07	1.92E-06	PDE5A	chr4	-	1.2E+08	1.21E+08	7154
ENSG00000(	56.96855	65.03154	110.8308	155.0586	190.5294	175.0785	-1.1579	2.15E-05	7.65E-05	PRDM5	chr4	-	1.22E+08	1.22E+08	5330
ENSG00000(	10.35792	1.204288	17.15238	2.996302	9.20432	4.109825	0.72665	0.40391	0.53493	TRPC3	chr4	-	1.23E+08	1.23E+08	3675
ENSG00000(	203.0152	197.5032	208.4674	61.42419	52.46462	50.96182	1.8683	1.94E-15	1.57E-14	NAAA	chr4	-	76831809	76862204	1897
ENSG00000(	557.256	447.995	498.7384	1012.75	832.0705	728.2609	-0.77155	1.27E-06	5.23E-06	NUP54	chr4	-	77035812	77069668	2367
ENSG00000(	181.2636	161.3746	286.3128	149.066	194.2112	161.1051	0.31405	0.18979	0.295	BMP2K	chr4	+	79697496	79837526	6902
ENSG00000(	2623.661	2513.348	3409.365	2963.343	3234.398	2785.639	-0.07212	0.59165	0.70798	G3BP2	chr4	-	76567966	76649709	4883
ENSG00000(	7737.366	7739.957	9536.723	5620.314	6108.907	5177.557	0.56392	3.17E-06	1.25E-05	11-Sep	chr4	+	77870856	77961537	5593
ENSG00000(	764.4144	771.9484	951.2973	718.3635	1078.746	657.5719	0.019443	0.9141	0.94754	FRAS1	chr4	+	78978724	79465423	12479
ENSG00000(	3775.461	3877.806	4030.809	1089.156	1212.209	989.6458	1.8249	1.74E-55	5.45E-54	SCARB2	chr4	-	77079890	77135046	4763
ENSG00000(	1079.295	1127.213	1125.46	298.1321	306.5039	281.934	1.9057	1.94E-47	4.94E-46	CCNG2	chr4	+	78078304	78354542	5526
ENSG00000(	269.3059	242.0618	290.271	277.907	326.7534	257.275	-0.10363	0.5654	0.68477	CNOT6L	chr4	-	78634541	78740769	8843
ENSG00000(	2176.199	2353.178	2667.855	1287.661	1260.071	977.3163	1.0267	1.15E-13	8.36E-13	USO1	chr4	+	76649777	76735382	3589
ENSG00000(	4.143168	1.204288	1.319414	19.47596	34.97642	21.37109	-3.1453	3.45E-05	0.00012	CDKL2	chr4	-	76503215	76555900	3383
ENSG00000(	169.8699	145.7188	221.6615	1486.166	2101.346	1794.349	-3.314	8.31E-81	4.53E-79	SHROOM3	chr4	+	77356253	77704406	11020
ENSG00000(	15.53688	18.06432	14.51355	5361.883	3964.301	4230.653	-8.0614	4.96E-214	1.69E-211	ANXA3	chr4	+	79472673	79531597	2924
ENSG00000(	736.448	751.4755	766.5794	722.8579	686.6423	745.5222	0.06438	0.61215	0.72568	PPA2	chr4	-	1.06E+08	1.06E+08	1684
ENSG00000(	322.1313	370.9206	445.9619	871.1749	745.5499	751.2759	-1.0557	2.62E-11	1.62E-10	CENPE	chr4	-	1.04E+08	1.04E+08	8612
ENSG00000(	133.6172	133.6759	145.1355	567.7993	649.825	567.9778	-2.107	9.07E-36	1.66E-34	GSTCD	chr4	+	1.07E+08	1.07E+08	4273
ENSG00000(	91.14969	133.6759	117.4278	126.5938	99.40666	87.12828	0.12223	0.64502	0.75219	INTS12	chr4	-	1.07E+08	1.07E+08	1975
ENSG00000(	36.25272	38.53721	36.94359	134.8336	153.7121	129.0485	-1.8805	4.19E-11	2.54E-10	ENPEP	chr4	+	1.11E+08	1.11E+08	6943
ENSG00000(	192.6573	177.0303	137.219	642.7068	610.2464	652.6401	-1.8978	5.54E-29	8.10E-28	CASP6	chr4	-	1.11E+08	1.11E+08	1548
ENSG00000(	381.1714	362.4906	320.6175	1728.117	1634.687	1357.886	-2.1412	4.96E-50	1.37E-48	LEF1	chr4	-	1.09E+08	1.09E+08	3477
ENSG00000(	499.2517	447.995	440.6842	1059.193	742.7886	823.6088	-0.91642	1.01E-08	5.07E-08	HADH	chr4	+	1.09E+08	1.09E+08	2044
ENSG00000(	14.50109	3.612863	7.916483	112.3613	74.55499	69.86702	-3.1737	1.03E-11	6.57E-11	EGF	chr4	+	1.11E+08	1.11E+08	4880
ENSG00000(	1925.537	1782.346	2115.02	1911.641	1886.886	1909.425	0.028382	0.80362	0.87261	PAPSS1	chr4	-	1.09E+08	1.09E+08	2731
ENSG00000(	707.4459	668.3797	866.8549	760.3117	797.0941	690.4505	-0.00423	0.97668	0.98648	SEC24B	chr4	+	1.1E+08	1.1E+08	5083
ENSG00000(	1903.786	1958.172	2244.323	816.4923	821.0253	731.5488	1.3627	3.79E-28	5.36E-27	PPP3CA	chr4	-	1.02E+08	1.02E+08	4685
ENSG00000(	87.00652	109.5902	102.9143	1197.023	1168.028	1007.729	-3.4847	3.45E-96	2.49E-94	SLC39A8	chr4	-	1.03E+08	1.03E+08	4032
ENSG00000(	7.250543	1.204288	0	1.498151	2.761296	0	0.70664	0.5742	0.69285	MTTP	chr4	+	1E+08	1.01E+08	4092
ENSG00000(	9919.779	9763.161	13323.44	5982.117	8736.741	6134.324	0.66025	3.00E-05	0.000105	FBN2	chr5	-	1.28E+08	1.28E+08	11132
ENSG00000(	4147.311	4383.607	3270.827	846.4554	1104.518	1346.379	1.8336	1.10E-29	1.65E-28	MAPK8IP3	chr16	+	1756184	1820318	5661
ENSG00000(	1693.52	1548.714	1570.102	817.9905	775.9242	813.7453	0.99733	1.56E-17	1.40E-16	RGS3	chr9	+	1.16E+08	1.16E+08	4591
ENSG00000(	1742.202	1831.722	1500.173	1409.76	1620.881	1566.665	0.14283	0.25271	0.37048	GUCD1	chr22	-	24936406	24951903	3613
ENSG00000(	625.6183	570.8324	666.304	559.5594	456.5343	371.5281	0.42208	0.012276	0.027971	RNF185	chr22	+	31556168	31602999	3165
ENSG00000(	19.68005	15.65574	17.15238	24.71949	51.54419	38.63235	-1.0861	0.022752	0.04864	KIAA1644	chr22	-	44639547	44708731	6751
ENSG00000(	5.17896	6.021439	0	0	0	0	2.825	0.034246	0.069818	PARVG	chr22	+	44568836	44615413	5069
ENSG00000(	4.143168	2.408575	2.638828	35.95563	40.49901	53.42772	-3.5693	1.90E-08	9.33E-08	B4GALNT3	chr12	+	569530	672675	5068
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	PDE6H	chr12	+	15125956	15134799	747
ENSG00000(	4.143168	1.204288	0	314.6117	176.7229	210.423	-6.5176	2.37E-27	3.23E-26	ERP27	chr12	-	15066969	15092016	2096
ENSG00000(	123.2592	111.9988	133.2608	146.8188	139.9057	133.1583	-0.18819	0.40283	0.53396	ETV6	chr12	+	11802788	12044558	2211

ENSG00000(	393.6009	381.7592	496.0996	546.8252	547.657	558.1142	-0.37902	0.013938	0.031392	GABARAPL1	chr12	+	10365057	10375727	3214
ENSG00000(	51.7896	54.19295	73.88717	343.0766	388.4223	303.3051	-2.5145	1.27E-28	1.83E-27	KIF21A	chr12	-	39687030	39837192	6643
ENSG00000(	117.0445	134.8802	137.219	298.1321	284.4135	230.1502	-1.059	2.42E-07	1.07E-06	CPNE8	chr12	-	39040624	39301232	3489
ENSG00000(	414.3168	432.3393	440.6842	770.7987	593.6786	594.2806	-0.60505	0.000103	0.000336	YARS2	chr12	-	32880424	32908836	2122
ENSG00000(	116.0087	66.23582	135.8996	177.5309	181.3251	148.7757	-0.66868	0.011599	0.026558	FGD4	chr12	+	32552463	32798984	8242
ENSG00000(	18.64425	22.88147	17.15238	78.65293	58.90765	77.2647	-1.8345	1.99E-06	7.98E-06	ALG10	chr12	+	34175216	34182629	2393
ENSG00000(	0	0	0	36.7047	27.61296	22.19305	-5.697	1.06E-07	4.84E-07	PIK3C2G	chr12	+	18400548	18801348	4840
ENSG00000(	477.5001	551.5638	530.4043	3894.444	4030.572	3890.36	-2.9176	5.13E-141	7.01E-139	FAM60A	chr12	-	31433518	31479992	3163
ENSG00000(	740.5912	780.3784	820.6754	437.4601	634.1776	632.913	0.45727	0.004785	0.011897	AEBP2	chr12	+	19556979	19873735	3620
ENSG00000(	0	0	2.638828	1.498151	0	0.821965	0.061979	0.96354	NA	SLCO1C1	chr12	+	20848289	20906320	3466
ENSG00000(	72.50543	48.17151	59.37362	20.22504	33.13555	35.34449	1.0082	0.008461	0.019993	METTL20	chr12	+	31800094	31826048	6128
ENSG00000(	783.0587	929.7101	1059.489	829.9757	823.7866	798.9499	0.17466	0.21466	0.32521	ETNK1	chr12	+	22778009	22843599	7159
ENSG00000(	840.0272	1026.053	774.4959	576.7882	466.659	530.1674	0.74362	1.09E-06	4.49E-06	ZCRB1	chr12	-	42705880	42719920	1827
ENSG00000(	76.6486	63.82725	96.31721	110.1141	109.5314	86.30632	-0.36858	0.18571	0.29018	TMEM117	chr12	+	44229770	44783545	2758
ENSG00000(	111.8655	101.1602	116.1084	85.39461	143.5874	87.95025	0.057811	0.8331	0.89318	PRICKLE1	chr12	-	42852140	42984157	4253
ENSG00000(	506.5022	534.7037	464.4337	243.4496	275.2092	249.0554	0.97012	6.75E-10	3.75E-09	C1RL	chr12	-	7242183	7261869	3394
ENSG00000(	163.6551	155.3531	171.5238	200.0032	209.8585	180.0103	-0.26465	0.18482	0.28931	NDUFA9	chr12	+	4714110	4798454	3334
ENSG00000(	523.0749	562.4024	463.1142	588.7734	603.8034	741.4124	-0.31885	0.037465	0.075613	CLSTN3	chr12	+	7282294	7311541	4296
ENSG00000(	35.21692	27.69862	32.98534	18.72689	20.2495	31.23467	0.43844	0.334	0.46205	KLRG1	chr12	+	9102640	9163356	1335
ENSG00000(	204.051	164.9874	159.6491	152.0623	126.0992	129.0485	0.37546	0.086556	0.15565	VAMP1	chr12	-	6571403	6580153	3449
ENSG00000(	41.43168	66.23582	39.58241	18.72689	23.93123	14.79537	1.3261	0.002159	0.00572	TAPBPL	chr12	+	6560856	6575683	2344
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	CD27	chr12	+	6554033	6560884	1338
ENSG00000(	34.18113	54.19295	39.58241	7.490755	44.18074	31.23467	0.61091	0.23165	0.34518	RBP5	chr12	-	7276280	7281538	1012
ENSG00000(	889.7452	965.8388	762.6212	443.4527	441.8074	433.9975	0.98682	3.10E-12	2.05E-11	PEX5	chr12	+	7341281	7371170	3252
ENSG00000(	274.4849	269.7604	233.5362	3.745378	10.12475	15.61733	4.6671	9.54E-44	2.20E-42	PIANP	chr12	-	6802958	6809966	2695
ENSG00000(	15.53688	28.90291	15.83297	163.2985	231.0284	206.3132	-3.2725	1.54E-24	1.87E-23	SLC38A4	chr12	-	47158546	47226191	3789
ENSG00000(	95.29286	62.62296	96.31721	225.4717	249.4371	204.6693	-1.4063	2.52E-09	1.34E-08	AMIGO2	chr12	-	47469490	47473734	3763
ENSG00000(	758.1997	816.5071	1113.585	990.2779	1266.514	881.1464	-0.22302	0.19514	0.30153	SCAF11	chr12	-	46312914	46385903	5296
ENSG00000(	2.071584	13.24716	14.51355	1307.137	1427.59	1470.495	-7.1105	1.21E-113	1.15E-111	COL2A1	chr12	-	48366748	48398269	5071
ENSG00000(	3.107376	6.021439	7.916483	5.243529	11.04518	4.93179	-0.28714	0.73504	0.82278	PPFIA2	chr12	-	81652045	82153332	5405
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	ANP32D	chr12	+	48866448	48866843	396
ENSG00000(	127.4024	160.1703	102.9143	332.5895	270.607	366.5964	-1.303	1.40E-09	7.56E-09	LLPH	chr12	-	66516842	66524548	1239
ENSG00000(	73.54123	71.05298	71.24834	38.20285	45.10117	90.41614	0.30835	0.38787	0.51868	RPL14P1	chr12	+	63359095	63359764	670
ENSG00000(	527.2181	584.0795	645.1933	480.1574	381.9793	396.1871	0.47703	0.002391	0.006284	LRIG3	chr12	-	59265931	59314303	4070
ENSG00000(	184.371	190.2775	125.3443	141.5753	104.0088	145.4878	0.35241	0.14776	0.24089	9-Mar	chr12	+	58148881	58154190	2982
ENSG00000(	100.4718	110.7945	68.60952	10.48706	3.681728	10.68554	3.3834	3.60E-15	2.87E-14	INHBE	chr12	+	57846106	57853063	2429
ENSG00000(	10922.43	10714.55	12387.98	362.5526	262.3231	225.2184	5.3036	5.56E-270	3.27E-267	GLIPR1	chr12	+	75874460	75897633	5877
ENSG00000(	0	0	0	0.749076	2.761296	4.93179	-2.204	0.099832	0.17524	TPH2	chr12	+	72332626	72580398	2992
ENSG00000(	10609.62	10747.06	11952.57	2425.507	2245.854	2024.5	2.3104	4.50E-94	3.08E-92	PHLDA1	chr12	-	76419227	76427712	8069
ENSG00000(	210.2658	217.9761	197.9121	359.5563	352.5255	374.816	-0.79196	2.63E-06	1.04E-05	TMEM19	chr12	+	72079867	72097836	4666
ENSG00000(	41.43168	40.94578	40.90183	1.498151	4.60216	0	4.0878	1.30E-09	7.04E-09	LGR5	chr12	+	71833550	71980090	4611
ENSG00000(	13.46529	10.83859	21.11062	0	1.840864	0	3.8971	7.54E-05	0.00025	PTPRQ	chr12	+	80799774	81074013	7201
ENSG00000(	535.5044	590.101	573.945	856.1934	741.8682	788.2644	-0.48967	0.000288	0.000877	DUSP6	chr12	-	89741009	89747048	4400
ENSG00000(	103.5792	139.6974	149.0938	224.7227	206.1768	181.6542	-0.64362	0.003805	0.009656	POC1B	chr12	-	89813495	89919801	5840

ENSG00000(	669.1216	741.8412	1063.448	588.7734	739.1069	656.75	0.31583	0.07082	0.1311	TMTC3	chr12	+	88536073	88593664	7203
ENSG00000(	2003.222	2389.307	1812.875	3946.13	3011.653	3355.261	-0.73105	1.33E-07	6.01E-07	LUM	chr12	-	91496406	91505608	3008
ENSG00000(	0	4.817151	0	5.243529	0.920432	1.64393	-0.49058	0.69655	0.79334	KERA	chr12	-	91444268	91451760	2162
ENSG00000(	875.2442	927.3015	782.4124	1804.523	1812.331	2343.422	-1.2016	9.37E-18	8.52E-17	SNRPF	chr12	+	96252706	96297606	1389
ENSG00000(	3.107376	1.204288	2.638828	10.48706	10.12475	11.50751	-1.9292	0.028731	0.059862	AMDHD1	chr12	+	96337071	96362370	2136
ENSG00000(	174.013	183.0517	209.7868	622.4818	570.6678	587.7049	-1.6491	1.64E-24	1.99E-23	NEDD1	chr12	+	97301001	97347129	3620
ENSG00000(	14.50109	12.04288	10.55531	15.73059	14.72691	8.219649	-0.05199	0.93469	0.9607	SYCP3	chr12	-	1.02E+08	1.02E+08	3690
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	ASCL1	chr12	+	1.03E+08	1.03E+08	2472
ENSG00000(	162.6193	121.6331	212.4256	319.1062	405.9105	295.0854	-1.0331	2.81E-06	1.11E-05	GAS2L3	chr12	+	1.01E+08	1.01E+08	3948
ENSG00000(	1320.635	1445.145	1680.933	103.3724	128.8605	113.4312	3.6758	1.18E-120	1.25E-118	TMEM132B	chr12	+	1.26E+08	1.26E+08	10906
ENSG00000(	387.3862	444.3822	394.5047	398.5082	317.549	381.3917	0.1579	0.33156	0.4595	SLC15A4	chr12	-	1.29E+08	1.29E+08	2776
ENSG00000(	508.5738	568.4238	724.3582	1247.211	1361.319	1079.24	-1.0322	3.65E-11	2.23E-10	TDG	chr12	+	1.04E+08	1.04E+08	3251
ENSG00000(	407.0662	408.2535	376.0329	492.1426	386.5814	416.7362	-0.12107	0.44678	0.57647	C12orf52	chr12	+	1.14E+08	1.14E+08	2053
ENSG00000(	6.214751	24.08575	10.55531	80.90016	56.14635	72.33291	-2.3016	5.25E-07	2.25E-06	SDSL	chr12	+	1.14E+08	1.14E+08	1449
ENSG00000(	362.5272	416.6836	465.7531	442.7036	414.1944	383.8576	0.002396	0.98808	0.99282	MMAB	chr12	-	1.1E+08	1.1E+08	2725
ENSG00000(	935.3201	793.6256	736.2329	442.7036	368.1728	309.0588	1.1341	7.91E-12	5.08E-11	GLTP	chr12	-	1.1E+08	1.1E+08	2356
ENSG00000(	407.0662	417.8878	493.4608	155.8077	149.11	123.2947	1.6135	7.34E-19	7.07E-18	GIT2	chr12	-	1.1E+08	1.1E+08	5471
ENSG00000(	261.0196	283.0076	261.2439	325.0988	370.0137	333.7178	-0.35143	0.03417	0.069674	TCHP	chr12	+	1.1E+08	1.1E+08	3428
ENSG00000(	84.93494	90.32158	75.20659	95.13259	87.44104	108.4994	-0.21403	0.42082	0.55152	FAM222A	chr12	+	1.1E+08	1.1E+08	3294
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	FOXN4	chr12	-	1.1E+08	1.1E+08	3350
ENSG00000(	923.9264	902.0115	1050.253	1301.893	1258.231	1157.327	-0.37016	0.003244	0.008337	NUPL1	chr13	+	25875662	25923938	6360
ENSG00000(	530.3255	616.5953	816.7171	439.7073	423.3987	439.7512	0.58722	0.000521	0.001527	MTMR6	chr13	-	25802307	25862147	5659
ENSG00000(	297.2723	249.2876	411.6571	16.47966	18.40864	11.50751	4.317	1.85E-47	4.73E-46	SLC46A3	chr13	-	29274201	29293107	3178
ENSG00000(	1631.372	1548.714	1863.012	2763.34	3082.527	2426.44	-0.7126	3.17E-08	1.53E-07	SLC7A1	chr13	-	30083547	30169825	7347
ENSG00000(	0	0	0	2.247227	2.761296	8.219649	-2.8878	0.025375	0.053681	PDX1	chr13	+	28494157	28500368	2501
ENSG00000(	89.0781	142.106	167.5656	228.468	314.7877	215.3548	-0.92507	0.000198	0.00062	LNX2	chr13	-	28120050	28194541	4625
ENSG00000(	266.1985	284.2119	221.6615	310.8664	277.05	267.9606	-0.14707	0.41456	0.54502	SUOX	chr12	+	56390964	56400425	2860
ENSG00000(	109.7939	142.106	93.67838	119.103	77.31629	104.3895	0.1959	0.47085	0.59989	CCDC65	chr12	+	49297893	49325623	2084
ENSG00000(	2.071584	4.817151	6.597069	2.247227	8.283888	7.397684	-0.36296	0.69489	0.79211	SLC39A5	chr12	+	56623833	56631630	2031
ENSG00000(	500.2875	498.5751	460.4754	1155.074	980.2601	1169.656	-1.1761	5.74E-18	5.29E-17	TARBP2	chr12	+	53894705	53900215	1867
ENSG00000(	3.107376	4.817151	3.958241	2.247227	5.522592	6.575719	-0.23043	0.80984	0.87669	RDH16	chr12	-	57345219	57353158	3198
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	DHH	chr12	-	49483204	49488602	1936
ENSG00000(	1.035792	0	3.958241	8.988907	9.20432	11.50751	-2.2088	0.022761	0.048649	ACVRL1	chr12	+	52300692	52317145	4121
ENSG00000(	2.071584	0	0	5.243529	0	0.821965	-0.85519	0.52385	0.64906	GPR84	chr12	-	54756229	54758271	2041
ENSG00000(	20.71584	20.47289	22.43003	17.22874	12.88605	20.54912	0.31157	0.55192	0.67288	NPFF	chr12	-	53900472	53902004	1406
ENSG00000(	876.28	880.3343	726.997	919.1157	693.0853	804.7037	0.039108	0.79214	0.8642	NABP2	chr12	+	56615799	56623638	1775
ENSG00000(	8.286335	8.430014	9.235896	11.98521	2.761296	6.575719	0.24334	0.7578	0.83977	N4BP2L1	chr13	-	32974861	33002315	3046
ENSG00000(	1913.108	2002.73	2060.924	823.9831	970.1353	945.2597	1.1237	7.14E-21	7.49E-20	SMARCC2	chr12	-	56556767	56583351	4271
ENSG00000(	90.1139	60.21439	96.31721	421.7295	384.7406	302.4831	-2.154	1.74E-21	1.87E-20	BRCA2	chr13	+	32889611	32973805	10984
ENSG00000(	359.4198	392.5978	442.0036	586.5262	463.8977	489.8911	-0.36891	0.022125	0.047475	KANSL2	chr12	-	49047184	49076021	2714
ENSG00000(	1222.234	1154.912	1075.322	1250.207	985.7827	931.2863	0.12393	0.38157	0.51225	CERS5	chr12	-	50523575	50561288	2998
ENSG00000(	591.4372	669.584	589.778	235.2097	227.3467	268.7825	1.3346	8.79E-18	8.02E-17	MAP3K12	chr12	-	53874274	53893847	5627
ENSG00000(	6.214751	0	11.87472	27.7158	11.96562	17.26126	-1.5293	0.043243	0.085662	ITGB7	chr12	-	53585102	53601091	2867
ENSG00000(	4.143168	2.408575	6.597069	829.9757	885.4556	841.6921	-7.4253	5.10E-69	2.19E-67	GALNT6	chr12	-	51745031	51786651	5207

ENSG00000(	572.7929	591.3053	489.5025	237.4569	222.7445	275.3582	1.1647	1.10E-12	7.52E-12	CSAD	chr12	-	53551447	53575135	2645
ENSG00000(	579.0077	608.1653	566.0285	200.7522	277.9705	261.3848	1.242	8.39E-14	6.15E-13	LMBR1L	chr12	-	49490919	49504683	2800
ENSG00000(	604.9025	608.1653	453.8783	513.1168	371.8545	485.7813	0.28116	0.10639	0.18455	C12orf10	chr12	+	53693470	53700961	1369
ENSG00000(	3921.508	3574.326	3543.945	3802.307	3393.633	3242.652	0.080725	0.471	0.59994	ESYT1	chr12	+	56512034	56538455	4388
ENSG00000(	9423.635	9431.981	9428.531	12322.29	11567.99	11156.53	-0.30892	0.001558	0.004227	TMBIM6	chr12	+	50101508	50158717	3254
ENSG00000(	4026.123	3965.719	4516.353	2680.192	5043.967	4727.942	0.006615	0.97046	0.98271	ANKRD52	chr12	-	56631591	56652175	8688
ENSG00000(	523.0749	521.4566	613.5274	341.5785	514.5215	493.179	0.29674	0.091615	0.16319	ZNF740	chr12	+	53574484	53584596	4249
ENSG00000(	184.371	198.7075	315.3399	324.3497	357.1276	340.2935	-0.55	0.008297	0.019632	WDFY2	chr13	+	52158644	52336171	3649
ENSG00000(	141.9035	127.6545	108.1919	105.6197	116.8949	133.9803	0.086819	0.71773	0.80996	HNRNPA1L	chr13	+	53191605	53217919	2365
ENSG00000(	237.1963	230.019	265.2022	120.6012	108.611	90.41614	1.187	1.81E-08	8.93E-08	LPAR6	chr13	-	48963707	49018840	3004
ENSG00000(	2243.525	2317.05	2031.897	1746.095	1393.534	1527.211	0.49703	6.91E-05	0.00023	ESD	chr13	-	47345391	47371367	1192
ENSG00000(	456.7842	391.3935	687.4146	823.9831	809.9802	715.1095	-0.61254	0.000933	0.002625	RB1	chr13	+	48877887	49056122	4840
ENSG00000(	1056.508	951.3873	1278.512	876.4184	970.1353	747.9881	0.33968	0.023844	0.050793	SBNO1	chr12	-	1.24E+08	1.24E+08	10981
ENSG00000(	13.46529	6.021439	5.277655	29.21395	17.48821	48.49593	-1.8204	0.002576	0.006731	MORN3	chr12	-	1.22E+08	1.22E+08	1427
ENSG00000(	855.5641	883.9472	804.8424	573.0428	995.9074	794.0181	0.10769	0.53963	0.66319	SETD1B	chr12	+	1.22E+08	1.22E+08	8195
ENSG00000(	224.7668	208.3418	222.9809	423.9768	404.0696	383.0357	-0.88101	9.57E-08	4.40E-07	VPS33A	chr12	-	1.23E+08	1.23E+08	4586
ENSG00000(	624.5825	616.5953	569.9868	841.9609	799.8554	859.7753	-0.46433	0.000341	0.001028	VPS37B	chr12	-	1.23E+08	1.23E+08	3021
ENSG00000(	7.250543	3.612863	1.319414	3.745378	10.12475	1.64393	-0.26469	0.78921	0.86218	RHOF	chr12	-	1.22E+08	1.22E+08	3005
ENSG00000(	1729.772	1891.936	1749.543	2412.023	2181.424	2184.783	-0.33537	0.002756	0.007167	DENR	chr12	+	1.23E+08	1.23E+08	2769
ENSG00000(	132.5814	204.7289	209.7868	1282.417	1399.057	1159.793	-2.8069	2.49E-59	8.53E-58	DIAPH3	chr13	-	60239717	60738121	4804
ENSG00000(	3.107376	1.204288	0	101.1252	115.9744	82.19649	-5.5679	1.13E-16	9.76E-16	SLAIN1	chr13	+	78272023	78338377	2637
ENSG00000(	987.1097	998.3545	1120.182	1163.314	1283.082	1125.27	-0.20163	0.10615	0.1842	RBM26	chr13	-	79885962	79980612	4132
ENSG00000(	0	0	0	23.22134	26.69253	18.90519	-5.3826	7.24E-07	3.05E-06	SRRM4	chr12	+	1.19E+08	1.2E+08	8477
ENSG00000(	0	3.612863	2.638828	0	0.920432	0.821965	1.1047	0.40473	0.53556	METTL21C	chr13	-	1.03E+08	1.03E+08	1088
ENSG00000(	610.0814	708.1212	852.3413	401.5045	437.2052	371.5281	0.83867	1.58E-07	7.12E-07	MBNL2	chr13	+	97873688	98046374	4669
ENSG00000(	0	4.817151	3.958241	0.749076	3.681728	0	0.68718	0.58264	0.70026	RNF113B	chr13	-	98828039	98829519	1376
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	ZIC5	chr13	-	1.01E+08	1.01E+08	4639
ENSG00000(	161.5835	146.9231	220.3421	339.3312	323.0716	293.4415	-0.8532	1.85E-05	6.65E-05	ABHD13	chr13	+	1.09E+08	1.09E+08	5338
ENSG00000(	156.4046	144.5145	145.1355	312.3645	289.0156	435.6414	-1.2094	5.28E-09	2.72E-08	RAB20	chr13	-	1.11E+08	1.11E+08	1514
ENSG00000(	20.71584	18.06432	36.94359	140.8262	100.3271	159.4612	-2.3794	5.32E-12	3.46E-11	GRTP1	chr13	-	1.14E+08	1.14E+08	1446
ENSG00000(	1609.621	1492.112	1727.113	1888.419	1677.027	1562.555	-0.08701	0.48151	0.61065	CUL4A	chr13	+	1.14E+08	1.14E+08	3724
ENSG00000(	4.143168	13.24716	5.277655	0	0	0	4.0704	0.000891	0.002518	TTC6	chr14	+	38065052	38510647	5833
ENSG00000(	6.214751	1.204288	9.235896	0	0	0	3.5466	0.005371	0.01322	SSTR1	chr14	+	38677204	38682272	4295
ENSG00000(	419.4957	441.9736	386.5882	895.1453	878.0921	1008.551	-1.1527	1.07E-16	9.25E-16	CDH24	chr14	-	23516271	23526747	3552
ENSG00000(	1.035792	1.204288	0	5.992604	4.60216	3.28786	-1.91	0.10413	0.1813	REM2	chr14	+	23352374	23356895	1923
ENSG00000(	66.29068	96.34302	67.2901	2.247227	0.920432	1.64393	5.2127	6.17E-17	5.38E-16	CBLN3	chr14	-	24895738	24900160	2346
ENSG00000(	63.18331	78.2787	75.20659	30.7121	39.57858	41.92021	0.93534	0.005053	0.01251	TSSK4	chr14	+	24674903	24677568	1394
ENSG00000(	1.035792	1.204288	1.319414	11.98521	9.20432	10.68554	-2.666	0.005983	0.014595	NOVA1	chr14	-	26912299	27066960	6575
ENSG00000(	0	0	0	2.996302	1.840864	6.575719	-2.6739	0.04084	0.081526	FITM1	chr14	+	24600484	24602058	1194
ENSG00000(	2.071584	0	0	15.73059	25.7721	11.50751	-3.7698	0.000101	0.000329	MDGA2	chr14	-	47308826	48144157	5239
ENSG00000(	614.2246	732.2069	833.8695	1098.894	1077.826	992.9336	-0.54023	0.000148	0.00047	TMX1	chr14	+	51706880	51722759	2490
ENSG00000(	1589.941	1569.187	2199.463	1099.643	1359.478	1089.925	0.59227	0.000117	0.000378	FRMD6	chr14	+	51955818	52197445	5123
ENSG00000(	129.474	140.9017	116.1084	26.21764	39.57858	29.59074	2.0019	2.01E-11	1.25E-10	PELI2	chr14	+	56584532	56768244	5909
ENSG00000(	1.035792	1.204288	3.958241	34.45748	13.80648	16.4393	-3.0758	0.000158	0.000502	RTN1	chr14	-	60062694	60337684	3435

ENSG00000(	421.5673	481.7151	569.9868	25.46857	40.49901	27.12484	3.9654	1.27E-64	4.94E-63	C14orf37	chr14	-	58466453	58764857	6495
ENSG00000(	0	4.817151	1.319414	5.992604	8.283888	15.61733	-1.9533	0.043653	0.086371	SYT16	chr14	+	62453803	62568431	3219
ENSG00000(	232.0174	274.5776	255.9663	101.1252	92.0432	50.13986	1.6324	1.01E-10	5.97E-10	SLC38A6	chr14	+	61447832	61550451	2787
ENSG00000(	509.6096	500.9837	560.7509	761.0608	773.1629	759.4956	-0.54517	4.06E-05	0.00014	NAA30	chr14	+	57857262	57882635	7644
ENSG00000(	8.286335	2.408575	10.55531	11.23613	13.80648	10.68554	-0.69016	0.35027	0.47991	ADAM21	chr14	+	70918874	70926622	2658
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RDH12	chr14	+	68168603	68201169	1879
ENSG00000(	1134.192	1016.419	1262.679	564.0539	676.5175	581.1292	0.90398	9.94E-11	5.89E-10	DCAF5	chr14	-	69517598	69619867	5953
ENSG00000(	656.6921	599.7353	645.1933	610.4966	693.0853	603.3223	-0.0031	0.98193	0.98977	RAB15	chr14	-	65412532	65439494	3515
ENSG00000(	126.3666	122.8373	124.0249	194.0106	219.9832	206.3132	-0.72744	0.000414	0.001233	WDR89	chr14	-	64063757	64108579	2993
ENSG00000(	2.071584	1.204288	2.638828	10.48706	10.12475	15.61733	-2.293	0.0096	0.022422	ESR2	chr14	-	64550950	64804830	5458
ENSG00000(	1.035792	0	0	1.498151	0.920432	0.821965	-0.68763	0.61221	NA	KCNH5	chr14	-	63173287	63568755	4175
ENSG00000(	286.9144	357.6735	265.2022	674.168	791.5715	649.3523	-1.2117	1.49E-13	1.08E-12	STON2	chr14	-	81727000	81902809	4302
ENSG00000(	32.10955	34.92434	21.11062	119.103	95.72493	111.7872	-1.8553	1.30E-08	6.46E-08	EFCAB11	chr14	-	90261013	90421121	3095
ENSG00000(	0	0	0	3.745378	0	0.821965	-1.2809	0.34031	NA	GPR65	chr14	+	88471468	88478419	1786
ENSG00000(	97.36444	99.95588	67.2901	80.15108	95.72493	97.81383	-0.04277	0.87734	0.92329	PTGR2	chr14	+	74318547	74353530	4859
ENSG00000(	315.9165	391.3935	315.3399	494.3899	472.1816	598.3905	-0.61202	0.000245	0.000753	JDP2	chr14	+	75894419	75940814	5401
ENSG00000(	18.64425	22.88147	22.43003	26.96672	31.29469	20.54912	-0.29302	0.54074	0.66379	AK7	chr14	+	96858448	96955764	3300
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	SLC24A4	chr14	+	92788925	92962596	4747
ENSG00000(	928.0695	973.0645	906.4373	47.19176	29.45382	35.34449	4.6108	4.40E-126	4.99E-124	FBLN5	chr14	-	92335756	92414331	2423
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	SERPINA10	chr14	-	94749650	94759608	2526
ENSG00000(	293.1291	276.9862	267.841	182.7744	173.0412	187.408	0.62298	0.000531	0.001554	C14orf79	chr14	+	1.05E+08	1.05E+08	2503
ENSG00000(	1916.215	1975.032	1898.636	4063.735	3030.062	2880.987	-0.78297	1.38E-08	6.87E-08	WARS	chr14	-	1.01E+08	1.01E+08	3092
ENSG00000(	2.071584	1.204288	0	0	0.920432	1.64393	0.21609	0.87277	NA	SLC25A47	chr14	+	1.01E+08	1.01E+08	1738
ENSG00000(	406.0304	378.1463	488.1831	403.7517	496.1128	508.7963	-0.14678	0.37574	0.50624	WDR20	chr14	+	1.03E+08	1.03E+08	3060
ENSG00000(	751.9849	751.4755	814.0783	957.3186	990.3848	882.7903	-0.28821	0.022773	0.048666	NIPA2	chr15	-	23004684	23034427	3233
ENSG00000(	1164.23	1281.362	1215.18	652.4448	611.1668	633.735	0.94557	1.32E-14	1.01E-13	HERC2P2	chr15	-	23282281	23378228	5970
ENSG00000(	117.0445	96.34302	150.4132	76.40571	99.40666	73.15488	0.54187	0.046511	0.091152	SLC12A6	chr15	-	34525460	34630261	5407
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	DUOXA1	chr15	-	45409569	45422136	2684
ENSG00000(	710.5532	631.0468	588.4585	816.4923	863.3652	752.9199	-0.33139	0.016206	0.035909	MFAP1	chr15	-	44096690	44117000	2155
ENSG00000(	2694.095	2616.917	3311.729	1343.092	1434.953	1176.232	1.1219	2.01E-17	1.80E-16	TCF12	chr15	+	57210821	57591479	6061
ENSG00000(	770.6292	781.5827	852.3413	408.2462	351.605	363.3085	1.0936	7.56E-15	5.91E-14	SORD	chr15	+	45315302	45369383	4909
ENSG00000(	11792.49	11360.05	8807.087	6009.084	5573.216	7236.579	0.76219	2.86E-08	1.38E-07	SERF2	chr15	+	44069285	44094787	2792
ENSG00000(	348.0261	340.8134	358.8805	454.6889	589.9969	526.8795	-0.58205	0.000237	0.000733	ZSCAN29	chr15	-	43650370	43663223	5595
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	DUOX2	chr15	-	45384848	45406542	6641
ENSG00000(	48.68222	34.92434	59.37362	52.43529	59.82808	40.27628	-0.0925	0.79857	0.86876	LYSMD2	chr15	-	52015208	52043782	1759
ENSG00000(	0	0	0	287.645	216.3015	249.0554	-8.5214	8.59E-19	8.24E-18	SLC27A2	chr15	+	50474393	50528592	2394
ENSG00000(	1.035792	0	5.277655	2.996302	0	0	0.61494	0.64367	0.75095	FGF7	chr15	+	49715293	49780972	5467
ENSG00000(	4.143168	1.204288	2.638828	2.996302	1.840864	3.28786	-0.01435	0.98964	0.99397	GCNT3	chr15	+	59887074	59932438	3034
ENSG00000(	1021.291	1029.666	1101.711	817.9905	718.8574	616.4737	0.54774	8.78E-05	0.000288	BNIP2	chr15	-	59951345	59981733	6325
ENSG00000(	685.6942	621.4125	671.5816	1252.454	1016.157	1343.913	-0.86639	8.97E-10	4.94E-09	GTF2A2	chr15	-	59930261	59949740	1582
ENSG00000(	4649.67	4717.195	3733.941	4234.524	3304.351	3702.952	0.22028	0.094544	0.16739	SRP14	chr15	-	40327940	40331389	1077
ENSG00000(	910.4611	788.8085	903.7984	531.0946	757.5155	783.3326	0.32913	0.041867	0.083308	BAHD1	chr15	+	40731920	40760441	4698
ENSG00000(	52.82539	49.3758	26.38828	8.988907	22.09037	22.19305	1.243	0.010266	0.023805	DISP2	chr15	+	40650436	40663257	5031
ENSG00000(	349.0619	368.512	302.1458	416.486	435.3643	436.4634	-0.33465	0.032765	0.067101	CDAN1	chr15	-	43015757	43029324	4637

ENSG0000(	729.1975	620.2082	661.0263	880.9128	1341.069	1223.084	-0.77289	1.84E-06	7.41E-06	TLE3	chr15	-	70340129	70390515	7809
ENSG0000(	2551.155	2742.163	2393.417	4137.144	4548.775	4956.448	-0.82595	8.05E-13	5.54E-12	ANP32A	chr15	-	69070874	69113236	3711
ENSG0000(	740.5912	569.6281	649.1516	1395.528	1087.03	1325.829	-0.95541	1.04E-10	6.12E-10	COMMD4	chr15	+	75628232	75634268	4204
ENSG0000(	843.1346	758.7013	938.1032	729.5996	786.9694	659.2159	0.22252	0.11163	0.19185	UBE2Q2	chr15	+	76135622	76193419	3130
ENSG0000(	10.35792	8.430014	5.277655	0	5.522592	7.397684	0.79007	0.39845	0.52949	PSTPIP1	chr15	+	77285700	77329673	1962
ENSG0000(	1821.958	1735.379	1658.503	2125.127	1797.604	2040.939	-0.19293	0.10042	0.17608	ETFA	chr15	-	76507696	76603813	2287
ENSG0000(	771.665	750.2712	774.4959	611.2456	678.3584	577.0194	0.29885	0.024859	0.052706	HMG20A	chr15	+	77712754	77777949	4112
ENSG0000(	110.8297	118.0202	92.35896	124.3465	109.5314	97.81383	-0.04493	0.85736	0.90935	SCAPER	chr15	-	76640526	77197785	5438
ENSG0000(	3374.61	3107.062	3141.524	1979.058	1602.472	1755.717	0.8485	6.69E-13	4.64E-12	TSPAN3	chr15	-	77336359	77376326	3854
ENSG0000(	460.9274	426.3179	472.3501	615.7401	446.4095	482.4934	-0.18488	0.25703	0.3755	WDR61	chr15	-	78570177	78592136	3629
ENSG0000(	370.8135	333.5877	575.2644	344.5748	555.9409	309.0588	0.080368	0.73053	0.8196	NCOA2	chr8	-	71021997	71316040	8447
ENSG0000(	84.93494	121.6331	67.2901	86.14369	74.55499	119.1849	-0.03077	0.91884	0.95073	NEIL1	chr15	+	75639296	75647592	3271
ENSG0000(	896.9958	958.613	732.2746	723.607	619.4507	741.4124	0.31142	0.034076	0.069502	MAN2C1	chr15	-	75648133	75660971	4820
ENSG0000(	7.250543	15.65574	3.958241	38.95193	27.61296	48.49593	-2.0026	0.000328	0.000991	DNAJA4	chr15	+	78556428	78574538	3245
ENSG0000(	720.9112	669.584	612.208	1602.273	1616.279	1496.798	-1.2314	4.41E-23	5.05E-22	MESDC1	chr15	+	81293295	81296342	3048
ENSG0000(	2302.565	2280.921	2330.085	16368.05	15707.17	15037.85	-2.765	1.92E-172	3.99E-170	TPM1	chr15	+	63334831	63364114	2855
ENSG0000(	1090.689	1014.01	1196.708	1319.122	1846.387	1393.231	-0.46386	0.00165	0.004459	IGF1R	chr15	+	99192200	99507759	11803
ENSG0000(	383.243	319.1362	379.9912	144.5716	176.7229	158.6392	1.1702	1.72E-10	1.00E-09	ARRDC4	chr15	+	98462784	98517068	4072
ENSG0000(	149.154	122.8373	138.5384	377.5341	372.775	455.3686	-1.5452	1.89E-16	1.61E-15	PIF1	chr15	-	65107831	65117867	2687
ENSG0000(	404.9946	438.3607	395.8241	181.2763	210.7789	190.6959	1.0859	9.76E-11	5.79E-10	USP3	chr15	+	63796793	63886839	5499
ENSG0000(	1.035792	3.612863	0	16.47966	10.12475	8.219649	-2.466	0.009352	0.021892	CYP11A1	chr15	-	74630100	74660081	2001
ENSG0000(	384.2788	325.1577	447.2813	125.8447	121.497	148.7757	1.5367	2.48E-15	2.00E-14	BBS4	chr15	+	72978527	73030817	2490
ENSG0000(	2791.459	2535.026	2388.139	692.1458	722.5391	677.2991	1.8799	4.11E-57	1.34E-55	PML	chr15	+	74287014	74340153	5393
ENSG0000(	1.035792	1.204288	0	520.6075	599.2012	485.7813	-8.5054	7.92E-33	1.32E-31	CYP1A1	chr15	-	75011883	75017951	2685
ENSG0000(	30.03797	21.67718	22.43003	40.45008	57.06678	41.92021	-0.88054	0.0327	0.066989	ADAMTS17	chr15	-	1.01E+08	1.01E+08	6207
ENSG0000(	141.9035	162.5788	141.1773	185.0217	180.4047	181.6542	-0.29453	0.15017	0.24427	LINS	chr15	-	1.01E+08	1.01E+08	4821
ENSG0000(	223.7311	196.2989	208.4674	337.084	343.3211	383.0357	-0.75443	1.29E-05	4.71E-05	ULK3	chr15	-	75128457	75135687	2951
ENSG0000(	5.17896	10.83859	5.277655	84.64554	86.52061	62.46933	-3.3491	2.04E-12	1.37E-11	PCSK6	chr15	-	1.02E+08	1.02E+08	4407
ENSG0000(	1434.572	1492.112	1381.426	1688.416	1588.666	1594.612	-0.17708	0.11358	0.19474	SCAMP2	chr15	-	75136071	75165706	3162
ENSG0000(	0	0	0	1.498151	6.443024	3.28786	-2.637	0.044147	0.087167	CYP1A2	chr15	+	75041185	75048543	2728
ENSG0000(	152.2614	157.7617	110.8308	1540.099	1589.586	2107.518	-3.6174	8.27E-96	5.94E-94	HAPLN3	chr15	-	89420519	89438857	3071
ENSG0000(	0	0	0	5.243529	4.60216	0.821965	-2.5476	0.053447	0.10297	RHCG	chr15	-	89998680	90039844	1982
ENSG0000(	1031.649	991.1288	1014.629	820.9868	1126.609	1060.335	0.014964	0.91624	0.94889	POLG	chr15	-	89859534	89878092	4502
ENSG0000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	RLBP1	chr15	-	89753100	89764982	1810
ENSG0000(	246.5185	215.5675	281.0351	1204.513	1308.854	1049.649	-2.2555	1.75E-48	4.64E-47	FANCI	chr15	+	89787180	89860492	4743
ENSG0000(	1174.588	1122.396	1443.439	521.3566	1055.736	833.4724	0.63121	0.001476	0.004018	ABHD2	chr15	+	89630690	89745591	8735
ENSG0000(	1.035792	4.817151	9.235896	1.498151	13.80648	1.64393	-0.14322	0.8865	0.92922	WDR93	chr15	+	90234028	90286869	2409
ENSG0000(	207.1584	168.6003	151.7326	536.3381	561.4635	440.5732	-1.5322	6.90E-17	6.01E-16	TICRR	chr15	+	90118713	90174287	6771
ENSG0000(	11.39371	2.408575	0	156.5568	167.5186	129.8705	-4.461	7.00E-08	3.26E-07	NTRK3	chr15	-	88402982	88799999	19984
ENSG0000(	135.6887	134.8802	143.8161	120.6012	95.72493	98.63579	0.38994	0.096966	0.17096	DET1	chr15	-	89054790	89089906	2315
ENSG0000(	4450.798	4325.801	3773.523	10448.11	9530.153	10742.26	-1.2891	2.39E-31	3.79E-30	MFGE8	chr15	-	89441916	89456642	1987
ENSG0000(	323.1671	319.1362	300.8263	363.3016	511.7602	433.9975	-0.46888	0.006565	0.015879	ZNF710	chr15	+	90544624	90625438	4617
ENSG0000(	1687.305	1605.316	1447.397	1301.893	1206.686	1434.329	0.2654	0.03271	0.066999	UNC45A	chr15	+	91473410	91497323	4002
ENSG0000(	172.9772	143.3102	171.5238	185.7707	182.2455	137.2681	-0.05002	0.81966	0.88364	ST8SIA2	chr15	+	92937058	93011958	5708

ENSG00000(	16.57267	33.72006	27.70769	29.96302	28.53339	16.4393	0.0492	0.92015	0.95145	MCTP2	chr15	+	94774767	95023632	4493
ENSG00000(	1300.955	1294.609	1224.416	2671.952	2991.404	3441.567	-1.2501	1.23E-23	1.45E-22	FURIN	chr15	+	91411822	91426688	4244
ENSG00000(	2800.781	2733.733	3931.853	4647.265	5273.155	3942.966	-0.54899	0.000324	0.000981	IQGAP1	chr15	+	90931450	91045475	7233
ENSG00000(	527.2181	427.5221	585.8197	304.8737	309.2652	298.3733	0.75232	4.74E-06	1.83E-05	CRTC3	chr15	+	91073157	91188577	5209
ENSG00000(	89.0781	93.93444	112.1502	459.1833	505.3172	397.0091	-2.1984	2.24E-29	3.32E-28	EFTUD1	chr15	-	82422571	82555104	3675
ENSG00000(	2.071584	1.204288	0	55.43159	36.81728	39.45432	-4.701	2.18E-09	1.16E-08	SH3GL3	chr15	+	84115980	84287495	2012
ENSG00000(	3736.101	3747.743	3331.52	3181.324	2927.894	3205.663	0.21522	0.047636	0.093061	SEC11A	chr15	-	85212775	85259947	3626
ENSG00000(	1061.687	1044.117	1067.406	1901.903	1763.548	1645.574	-0.74184	2.47E-10	1.42E-09	GLYR1	chr16	-	4853204	4897343	3772
ENSG00000(	308.666	356.4692	299.5069	240.4533	260.4823	221.9305	0.41532	0.017316	0.038153	PMM2	chr16	+	8882680	8943188	5409
ENSG00000(	4.143168	3.612863	2.638828	0.749076	1.840864	1.64393	1.013	0.37325	0.50375	SLC5A2	chr16	+	31494323	31502181	2467
ENSG00000(	2695.131	2596.444	2022.661	1107.883	859.6835	923.8886	1.3349	2.45E-20	2.52E-19	TGFB1I1	chr16	+	31482906	31489281	4973
ENSG00000(	805.8461	753.8841	675.5399	273.4126	359.8889	323.8542	1.2224	5.40E-15	4.26E-14	C16orf58	chr16	-	31500792	31520630	2793
ENSG00000(	370.8135	349.2434	295.5487	322.1025	254.0392	300.8392	0.21123	0.23092	0.34427	ARMC5	chr16	+	31469401	31478487	4844
ENSG00000(	350.0977	340.8134	419.5736	643.4559	606.5647	562.224	-0.70632	3.80E-06	1.48E-05	PARN	chr16	-	14529558	14726585	3078
ENSG00000(	558.2918	460.0379	538.3208	241.2023	386.5814	249.0554	0.82671	2.06E-05	7.36E-05	FTO	chr16	+	53737875	54155853	11766
ENSG00000(	2541.833	2473.607	2210.018	2698.17	2347.102	2150.26	0.006107	0.96064	0.97719	UQCRC2	chr16	+	21963981	21994981	2615
ENSG00000(	416.3883	407.0492	493.4608	536.3381	555.9409	500.5766	-0.27489	0.066675	0.12446	CDR2	chr16	-	22357257	22448486	2702
ENSG00000(	11.39371	6.021439	1.319414	4.494453	9.20432	8.219649	-0.17444	0.83899	0.89715	IGSF6	chr16	-	21652609	21663981	1184
ENSG00000(	872.1368	721.3683	853.6607	626.2272	669.1541	584.4171	0.38017	0.006201	0.01508	ARHGAP17	chr16	-	24930706	25026987	4966
ENSG00000(	4.143168	7.225726	1.319414	8.988907	4.60216	8.219649	-0.68064	0.44666	0.57634	MYLK3	chr16	-	46740891	46824319	3301
ENSG00000(	959.1433	912.8501	1128.099	205.2467	321.2308	304.949	1.8457	5.57E-26	7.15E-25	NKD1	chr16	+	50582241	50670647	4592
ENSG00000(	1237.771	1180.202	1306.22	1132.602	1404.579	1066.088	0.047942	0.7245	0.8151	DHX38	chr16	+	72127461	72146811	4608
ENSG00000(	293.1291	275.7819	310.0622	261.4274	210.7789	175.9005	0.43549	0.025576	0.054047	TXNL4B	chr16	-	72078188	72128330	2556
ENSG00000(	46.61064	42.15007	63.33186	452.4416	422.4783	521.1258	-3.1859	1.19E-47	3.06E-46	MARVELD3	chr16	+	71660064	71676017	2912
ENSG00000(	0	0	0	4.494453	2.761296	1.64393	-2.3139	0.082115	0.14869	CHST4	chr16	+	71559136	71572649	2412
ENSG00000(	1490.505	1575.208	1971.204	853.9461	2030.473	1302.814	0.26168	0.47719	0.60634	ZFHX3	chr16	-	72816784	73093597	16064
ENSG00000(	6.214751	16.86003	1.319414	17.22874	2.761296	9.863579	-0.26433	0.75418	0.83746	CLEC18B	chr16	-	74442529	74455368	1865
ENSG00000(	565.5424	487.7365	485.5443	1756.582	1424.829	1400.628	-1.5688	1.34E-28	1.93E-27	CPNE2	chr16	+	57126449	57181878	3446
ENSG00000(	124.295	118.0202	106.8725	2.996302	1.840864	0.821965	5.638	1.53E-23	1.79E-22	NLRC5	chr16	+	57023397	57117443	6886
ENSG00000(	311.7734	311.9105	200.5509	595.5151	426.16	498.1107	-0.87591	9.01E-06	3.37E-05	KATNB1	chr16	+	57769642	57791162	3854
ENSG00000(	885.6021	816.5071	795.6065	981.289	836.6727	1073.486	-0.21051	0.12568	0.21154	KIFC3	chr16	-	57792129	57896957	3427
ENSG00000(	0	3.612863	0	458.4342	626.8142	484.9593	-8.1407	1.04E-35	1.90E-34	ADAMTS18	chr16	-	77281710	77469011	5913
ENSG00000(	6.214751	3.612863	6.597069	1.498151	1.840864	5.753754	0.72126	0.46198	0.59121	NUDT7	chr16	+	77756411	77776157	1096
ENSG00000(	265.1627	161.3746	153.052	247.944	300.9813	289.3317	-0.52234	0.019938	0.043249	GCSH	chr16	-	81115566	81130008	1552
ENSG00000(	780.9871	839.3885	682.1369	2106.4	1670.584	1869.148	-1.2905	2.20E-21	2.36E-20	CMTM3	chr16	+	66637777	66647795	2330
ENSG00000(	0	0	0	1.498151	4.60216	2.465895	-2.2479	0.092142	0.1639	CMTM2	chr16	+	66613351	66622178	1054
ENSG00000(	9843.13	10205.13	10730.79	2468.204	2942.621	2206.976	2.0106	1.27E-60	4.48E-59	CDH11	chr16	-	64977656	65160015	6874
ENSG00000(	254.8048	208.3418	176.8014	120.6012	72.71413	136.4462	0.94695	0.000211	0.000656	NOL3	chr16	+	67204057	67209643	1885
ENSG00000(	1770.168	1853.399	1906.553	1908.644	1290.446	1417.889	0.25875	0.077684	0.14172	MAP1LC3B	chr16	+	87417601	87438385	3085
ENSG00000(	1805.385	1848.582	1769.334	1346.838	1259.151	1168.834	0.52168	5.94E-06	2.26E-05	MBTPS1	chr16	-	84087368	84150511	4338
ENSG00000(	2058.119	2056.923	2522.719	567.7993	563.3044	452.0807	2.062	4.68E-49	1.26E-47	CDH13	chr16	+	82660408	83830204	4001
ENSG00000(	1104.154	1020.032	1244.207	706.3782	836.6727	612.3639	0.64249	1.41E-05	5.14E-05	ZCCHC14	chr16	-	87439852	87525651	7102
ENSG00000(	493.0369	476.8979	493.4608	460.6815	438.1256	499.7547	0.064876	0.65188	0.75778	TLDC1	chr16	-	84511681	84587639	3392
ENSG00000(	62.14751	43.35436	50.13772	222.4754	152.7917	197.2716	-1.8569	4.10E-12	2.69E-11	OSGIN1	chr16	+	83981887	83999937	2391

ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	IRF8	chr16	+	85932409	85956215	3030
ENSG00000(	1877.891	1842.56	1500.173	2069.696	1894.249	2368.903	-0.27749	0.037407	0.075509	RHOT2	chr16	+	718086	724174	4361
ENSG00000(	3.107376	0	7.916483	1.498151	0	0	1.8009	0.16248	0.26039	RPL3L	chr16	-	1993975	2007607	2182
ENSG00000(	210.2658	168.6003	189.9956	200.7522	188.6886	143.8439	0.093654	0.66155	0.76595	ZSCAN32	chr16	-	3432085	3451065	3169
ENSG00000(	73157.98	73174.93	55476.07	44152.76	40147.4	50212.19	0.58388	9.17E-06	3.42E-05	RPS2	chr16	-	2012053	2014861	1548
ENSG00000(	1196.34	1242.825	1083.239	1331.107	1174.471	1230.481	-0.08472	0.48952	0.61854	NDUFB10	chr16	+	2009509	2011976	958
ENSG00000(	634.9404	621.4125	740.1911	620.2346	643.382	611.5419	0.089388	0.51534	0.64201	PDPK1	chr16	+	2587965	2653189	7241
ENSG00000(	12.4295	10.83859	36.94359	9.737982	11.04518	9.041614	0.94397	0.13886	0.22927	TIGD7	chr16	-	3348832	3355729	3612
ENSG00000(	910.4611	704.5083	696.6505	1165.562	1077.826	1142.531	-0.5476	9.77E-05	0.000319	DEF8	chr16	+	90014333	90034468	4450
ENSG00000(	3003.797	2865	2674.452	1468.188	1304.252	1389.943	1.0355	4.64E-20	4.71E-19	TCF25	chr16	+	89940000	89977792	2233
ENSG00000(	988.1455	924.893	667.6234	499.6334	452.8525	543.3188	0.78493	1.78E-06	7.20E-06	GALNS	chr16	-	88880142	88923378	5682
ENSG00000(	6.214751	3.612863	7.916483	32.95932	37.73771	38.63235	-2.5039	1.25E-05	4.59E-05	GAS8	chr16	+	90086037	90111383	3856
ENSG00000(	244.4469	231.2232	255.9663	321.3534	274.2887	263.8507	-0.23278	0.19049	0.29589	MED9	chr17	+	17380300	17396540	3351
ENSG00000(	1483.254	1398.178	1760.098	1952.84	2096.744	1550.226	-0.27034	0.058262	0.11095	NCOR1	chr17	-	15932471	16121499	10720
ENSG00000(	11.39371	19.2686	18.47179	11.98521	15.64734	13.9734	0.22428	0.70039	0.79636	CDRT15P1	chr17	+	13927802	13928991	768
ENSG00000(	913.5685	857.4529	872.1325	2174.566	1550.007	1620.093	-1.0132	3.21E-12	2.12E-11	COPS3	chr17	-	17150141	17184607	1692
ENSG00000(	277.5922	255.309	331.1729	185.7707	235.6306	211.245	0.44783	0.018479	0.040408	GID4	chr17	+	17942606	17971718	4237
ENSG00000(	83.89914	125.2459	137.219	53.93344	33.13555	21.37109	1.6375	3.36E-06	1.31E-05	ZNF287	chr17	-	16454701	16472520	3373
ENSG00000(	0	1.204288	6.597069	8.239831	34.05598	22.19305	-2.7668	0.000991	0.002781	MYOCD	chr17	+	12569207	12672266	8466
ENSG00000(	641.1552	626.2296	626.7215	298.8811	374.6158	262.2068	1.0156	4.95E-10	2.77E-09	KSR1	chr17	+	25783670	25953461	7234
ENSG00000(	759.2355	803.2599	720.3999	1579.051	1227.856	1214.042	-0.81477	7.57E-09	3.84E-08	CIRH1A	chr16	+	69165194	69202941	4183
ENSG00000(	564.5066	603.3481	562.0703	475.663	559.6227	531.8113	0.14305	0.3125	0.43892	RANBP10	chr16	-	67757005	67840555	5305
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	DPEP3	chr16	-	68009566	68014732	2018
ENSG00000(	750.9491	765.927	676.8593	673.4189	680.1992	722.5072	0.080001	0.54203	0.66469	GFOD2	chr16	-	67708434	67753324	2951
ENSG00000(	832.7767	900.8072	922.2702	647.9503	541.214	488.2472	0.65968	5.87E-06	2.24E-05	NOB1	chr16	-	69775770	69788843	1734
ENSG00000(	298.3081	319.1362	358.8805	623.9799	560.5431	601.6783	-0.87137	8.71E-09	4.38E-08	PRPSAP2	chr17	+	18743398	18834581	1910
ENSG00000(	674.3005	664.7668	585.8197	1350.583	1391.693	1334.049	-1.079	4.12E-18	3.82E-17	MYO19	chr17	-	34851477	34899284	5763
ENSG00000(	523.0749	529.8866	511.9325	1283.166	956.3288	904.9834	-1.004	1.08E-10	6.39E-10	DDX52	chr17	-	35969787	36003493	6359
ENSG00000(	1476.003	1336.759	1431.564	381.2795	441.8074	413.4484	1.7765	3.06E-43	6.98E-42	RASL10B	chr17	+	34058668	34070540	3205
ENSG00000(	176.0846	207.1375	184.7179	523.6038	579.8722	552.3604	-1.5388	3.16E-21	3.36E-20	PCTP	chr17	+	53828340	53920191	3932
ENSG00000(	124.295	99.95588	116.1084	437.4601	372.775	340.2935	-1.7467	9.08E-19	8.69E-18	TOM1L1	chr17	+	52976748	53039310	2500
ENSG00000(	186.4425	257.7176	278.3963	295.1358	277.05	250.6993	-0.19073	0.33271	0.46074	C17orf80	chr17	+	71228372	71245091	3635
ENSG00000(	632.8689	657.5411	697.9699	628.4744	670.9949	585.239	0.07671	0.57089	0.68999	TOB1	chr17	-	48939584	48945339	2229
ENSG00000(	1017.148	902.0115	1088.516	920.6138	1072.303	1004.441	0.005175	0.96857	0.98169	VPS53	chr17	-	411908	624957	13106
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	SPATA22	chr17	-	3343313	3417146	1704
ENSG00000(	1078.259	1127.213	949.9779	597.7623	760.2768	870.4608	0.50117	0.001174	0.003257	SGSM2	chr17	+	2240792	2284352	4863
ENSG00000(	2150.304	2008.752	2388.139	2230.747	2421.657	2069.708	-0.03807	0.75024	0.83426	NPEPPS	chr17	+	45600306	45700642	5074
ENSG00000(	3.107376	1.204288	1.319414	0	11.96562	2.465895	-1.0043	0.38504	0.5159	SKAP1	chr17	-	46210802	46507637	1687
ENSG00000(	26.93059	21.67718	19.79121	22.47227	20.2495	27.12484	-0.02539	0.95798	0.97513	LRRC46	chr17	+	45908993	45915079	2239
ENSG00000(	172.9772	210.7504	147.7743	185.7707	220.9037	258.9189	-0.32063	0.13748	0.22739	SCRN2	chr17	-	45915058	45918699	1779
ENSG00000(	287.9501	335.9963	427.4901	532.5927	654.4271	520.3038	-0.69881	8.17E-05	0.000269	SSH2	chr17	-	27952956	28257294	9327
ENSG00000(	22.78742	28.90291	14.51355	0.749076	0.920432	4.109825	3.192	4.00E-05	0.000138	RHBDL3	chr17	+	30593195	30651680	4661
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	SPACA3	chr17	+	31297394	31324895	949
ENSG00000(	119.1161	98.75159	101.5949	90.63814	91.12277	84.66239	0.26211	0.30179	0.42683	ARSG	chr17	+	66255323	66418872	4642

ENSG00000(	343.8829	375.7378	442.0036	0	0	0	9.5078	8.07E-25	9.89E-24	ABCA8	chr17	-	66863433	66951533	5677
ENSG00000(	1935.895	1920.839	1636.073	1221.742	1057.576	1251.853	0.63605	5.38E-07	2.30E-06	G6PC3	chr17	+	42148103	42153709	3027
ENSG00000(	8737.941	8299.951	10835.03	7093.745	7585.28	5855.678	0.43965	0.001041	0.002911	CLTC	chr17	+	57697219	57773671	7760
ENSG00000(	233.0532	251.6961	281.0351	100.3761	92.0432	104.3895	1.3566	4.22E-11	2.57E-10	BCAS3	chr17	+	58754814	59470199	4556
ENSG00000(	571.7571	528.6823	506.6549	644.205	482.3064	619.7615	-0.11973	0.44157	0.57142	PTRH2	chr17	-	57751997	57784987	4114
ENSG00000(	1439.751	1560.757	1651.906	2067.449	2272.547	1876.546	-0.41763	0.000625	0.001808	SS18	chr18	-	23596578	23671181	3053
ENSG00000(	21.75163	24.08575	10.55531	71.91125	73.63456	79.7306	-1.9422	7.64E-07	3.20E-06	TAF4B	chr18	+	23805900	23971649	5260
ENSG00000(	558.2918	550.3595	567.3479	585.028	759.3564	581.9512	-0.19918	0.18834	0.29327	AFG3L2	chr18	-	12328943	12377313	3367
ENSG00000(	72.50543	55.39724	30.34652	42.69731	34.05598	46.852	0.35564	0.36095	0.49051	SLMO1	chr18	+	12407895	12432237	2001
ENSG00000(	532.397	435.9522	379.9912	495.888	412.3535	429.0657	0.013462	0.93632	0.96165	IMPA2	chr18	+	11981024	12030876	1616
ENSG00000(	17.60846	8.430014	17.15238	32.21025	33.13555	18.90519	-0.92206	0.084798	0.15299	GNAL	chr18	+	11688955	11885684	6535
ENSG00000(	1734.951	1810.044	2122.937	1232.978	1162.506	1086.638	0.70056	2.39E-08	1.17E-07	SLC39A6	chr18	-	33688495	33709348	3543
ENSG00000(	508.5738	523.8652	696.6505	881.6619	856.9222	753.7418	-0.52782	0.000673	0.001939	RPRD1A	chr18	-	33564350	33647539	4438
ENSG00000(	300.3797	386.5764	257.2857	391.0174	291.7769	350.1571	-0.12949	0.50159	0.62965	C18orf21	chr18	+	33552046	33559241	1581
ENSG00000(	2190.7	2174.944	2780.005	2640.491	2679.378	2326.161	-0.09792	0.44989	0.57966	GALNT1	chr18	+	33161081	33291798	3847
ENSG00000(	44.53905	97.54731	71.24834	44.94453	63.50981	38.63235	0.52568	0.14784	0.24096	ASXL3	chr18	+	31158579	31331156	11344
ENSG00000(	0	0	0	16.47966	29.45382	14.79537	-5.1871	2.51E-06	9.98E-06	ADCYAP1	chr18	+	904944	912173	3346
ENSG00000(	0	0	0	1.498151	9.20432	0	-2.3793	0.076334	0.13974	MEP1B	chr18	+	29765032	29800367	2312
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	SLC25A52	chr18	-	29339525	29340843	1319
ENSG00000(	78.72018	98.75159	67.2901	128.841	170.2799	133.1583	-0.80967	0.001834	0.00492	GAREM	chr18	-	29704840	30050447	7033
ENSG00000(	196.8005	215.5675	300.8263	273.4126	303.7426	211.245	-0.14653	0.49414	0.62286	ESCO1	chr18	-	19109242	19180845	4773
ENSG00000(	964.3223	877.9257	1006.713	568.5483	648.9046	523.5917	0.70923	3.16E-07	1.38E-06	OSBPL1A	chr18	-	21742008	21977844	4195
ENSG00000(	13.46529	10.83859	21.11062	35.20655	43.2603	41.09825	-1.3608	0.004002	0.010115	GATA6	chr18	+	19749404	19782491	3770
ENSG00000(	10.35792	9.634302	22.43003	310.1173	722.5391	388.7894	-4.8738	4.85E-20	4.92E-19	GREB1L	chr18	+	18822203	19102947	6318
ENSG00000(	125.3308	133.6759	129.3026	288.3941	207.0972	193.1618	-0.82321	0.000225	0.000696	C18orf8	chr18	+	21083473	21111746	2162
ENSG00000(	1370.353	1386.135	1224.416	2213.518	2401.407	2597.409	-0.85511	7.07E-13	4.89E-12	PELP1	chr17	-	4574679	4607632	4105
ENSG00000(	617.332	538.3166	646.5128	689.8986	687.5627	609.076	-0.14032	0.32121	0.44841	NPC1	chr18	-	21086307	21166862	5157
ENSG00000(	23.82321	36.12863	25.06886	0	0	0	6.0798	1.53E-08	7.55E-08	SLC14A1	chr18	+	43304092	43332485	3971
ENSG00000(	172.9772	142.106	120.0667	330.3423	281.6522	305.7709	-1.0661	1.08E-07	4.95E-07	ARRB2	chr17	+	4613784	4624794	1895
ENSG00000(	0	0	1.319414	0.749076	0	2.465895	-0.62289	0.64524	NA	ZMYND15	chr17	+	4643319	4649411	2411
ENSG00000(	285.8786	273.3733	217.7033	817.9905	705.9713	779.2227	-1.5596	5.83E-23	6.65E-22	WRAP53	chr17	+	7589389	7606820	4011
ENSG00000(	2113.015	1938.903	2030.578	1659.202	2391.282	2502.883	-0.10678	0.47302	0.60209	MINK1	chr17	+	4736683	4801356	5299
ENSG00000(	1290.597	1068.203	909.0761	277.158	250.3575	319.7444	1.9408	2.06E-32	3.37E-31	SAT2	chr17	-	7529552	7531194	1563
ENSG00000(	59.04014	38.53721	23.74945	50.93714	37.73771	36.16646	-0.03175	0.93871	0.9628	ASGR1	chr17	-	7076750	7082883	2083
ENSG00000(	0	0	1.319414	0.749076	0	0.821965	-0.12362	0.92519	NA	PIK3R5	chr17	-	8782233	8869029	4488
ENSG00000(	1242.95	1097.106	997.4768	1881.678	1521.474	1696.536	-0.60951	5.12E-06	1.96E-05	TP53	chr17	-	7565097	7590856	2653
ENSG00000(	135.6887	162.5788	146.4549	72.66033	86.52061	93.704	0.80849	0.000865	0.002449	CCDC40	chr17	+	78010435	78074412	4294
ENSG00000(	4324.431	4300.511	3389.574	4915.434	4916.948	5093.717	-0.31209	0.009322	0.021828	ARHGDIA	chr17	-	79825597	79829282	1906
ENSG00000(	37.28851	33.72006	46.17948	911.6249	996.8279	1208.288	-4.7109	1.36E-109	1.19E-107	TMC6	chr17	-	76106539	76128488	5268
ENSG00000(	2795.602	2845.732	1990.995	227.719	268.7661	304.949	3.2413	1.89E-89	1.18E-87	SLC16A3	chr17	+	80186273	80219005	4830
ENSG00000(	10.35792	10.83859	2.638828	11.23613	11.96562	22.19305	-0.84714	0.2285	0.34184	CARD14	chr17	+	78143791	78183130	4537
ENSG00000(	145.0109	152.9445	131.9414	22.47227	34.05598	23.01502	2.4137	7.02E-16	5.83E-15	TTYH2	chr17	+	72209653	72258155	3661
ENSG00000(	290.0217	362.4906	258.6051	55.43159	52.46462	69.04505	2.3468	1.00E-24	1.23E-23	RAB40B	chr17	-	80612849	80656604	3859
ENSG00000(	1713.2	1716.11	1564.825	2715.399	2559.721	2789.749	-0.69001	3.55E-10	2.02E-09	EIF4A3	chr17	-	78109013	78120982	3593

ENSG00000(	2946.828	2955.322	2826.184	2606.034	2714.354	2962.362	0.075636	0.48204	0.61119	CSNK1D	chr17	-	80196899	80231607	6094
ENSG00000(	1087.581	875.5172	803.523	1508.638	1107.28	1441.726	-0.54992	0.000425	0.001262	ANAPC11	chr17	+	79848666	79858867	2136
ENSG00000(	1929.68	1947.333	1742.946	1750.59	2081.097	1712.153	0.020325	0.86876	0.91759	TBCD	chr17	+	80709940	80900724	4094
ENSG00000(	535.5044	522.6609	424.8512	588.7734	634.1776	752.9199	-0.41081	0.008976	0.021098	FN3KRP	chr17	+	80674559	80688204	1849
ENSG00000(	953.9643	787.6042	827.2724	632.9688	508.9989	540.8529	0.6083	2.94E-05	0.000103	NARF	chr17	+	80416056	80446143	2598
ENSG00000(	862.8147	761.1098	785.0512	830.7248	873.49	829.3626	-0.0716	0.57257	0.69134	RPTOR	chr17	+	78518619	78940171	6408
ENSG00000(	1079.295	817.7114	1010.671	1375.303	1536.201	1259.25	-0.51827	0.00024	0.000741	FOXK2	chr17	+	80477589	80602538	5265
ENSG00000(	467.1421	514.2309	439.3648	250.1912	215.3811	275.3582	0.93472	2.08E-08	1.02E-07	TRIM65	chr17	-	73876416	73893084	3439
ENSG00000(	236.1606	173.4174	213.745	115.3576	115.9744	189.0519	0.56445	0.020352	0.04405	CBX8	chr17	-	77765931	77775482	3791
ENSG00000(	1501.898	1489.704	1174.278	14.98151	18.40864	20.54912	6.2327	3.24E-162	6.10E-160	SECTM1	chr17	-	80278900	80291950	2235
ENSG00000(	15.53688	13.24716	21.11062	11.98521	16.56778	20.54912	0.020146	0.97166	0.98351	RNF157	chr17	-	74138534	74236454	4955
ENSG00000(	429.8536	340.8134	345.6864	416.486	531.0893	692.0945	-0.54972	0.004242	0.010668	AZI1	chr17	-	79163393	79196799	3673
ENSG00000(	9.322127	3.612863	17.15238	44.94453	42.33987	32.05663	-1.9199	0.000385	0.001153	ZNF750	chr17	-	80787311	80798454	3713
ENSG00000(	1451.144	1460.801	1506.771	2283.182	2093.062	2285.884	-0.59176	7.41E-08	3.44E-07	WDR45B	chr17	-	80572438	80606429	2587
ENSG00000(	487.858	476.8979	424.8512	167.7929	179.4842	184.1201	1.3833	7.42E-17	6.45E-16	CBX4	chr17	-	77806955	77813228	2664
ENSG00000(	2.071584	10.83859	5.277655	35.20655	69.95283	72.33291	-3.1592	1.47E-08	7.28E-08	RNF165	chr18	+	43906772	44043103	7596
ENSG00000(	719.8754	687.6483	803.523	550.5705	372.775	383.8576	0.75307	1.00E-05	3.72E-05	DYM	chr18	-	46570039	46987717	2703
ENSG00000(	0	0	0	76.40571	61.66894	55.89361	-6.7839	3.39E-11	2.07E-10	MAPK4	chr18	+	48086448	48258194	4770
ENSG00000(	49.71801	30.10719	35.62417	83.14739	54.30549	69.86702	-0.82575	0.020531	0.044384	ELAC1	chr18	+	48494361	48514491	2235
ENSG00000(	1108.297	1146.482	1118.863	1031.477	976.5783	977.3163	0.17577	0.13299	0.22149	MBD1	chr18	-	47793252	47808144	4905
ENSG00000(	1002.647	1141.665	1192.75	728.8505	805.378	732.3707	0.55635	1.81E-05	6.50E-05	SMAD4	chr18	+	48494410	48611415	8769
ENSG00000(	3.107376	0	0	18.72689	39.57858	45.20807	-4.339	1.99E-07	8.87E-07	TNFRSF11A	chr18	+	59992520	60058516	8138
ENSG00000(	101.5076	105.9773	104.2337	211.2393	320.3103	206.3132	-1.232	1.54E-07	6.96E-07	ZCCHC2	chr18	+	60190240	60254942	5959
ENSG00000(	2.071584	8.430014	1.319414	5.992604	2.761296	9.041614	-0.50752	0.59895	0.7143	FBXO15	chr18	-	71740588	71815100	3187
ENSG00000(	3.107376	0	0	6.74168	0	0.821965	-0.76978	0.55887	0.67942	CBLN2	chr18	-	70203915	70305756	3336
ENSG00000(	812.0609	975.4731	993.5186	758.8135	673.7562	680.587	0.39361	0.004138	0.010427	PMAIP1	chr18	+	57567180	57571538	1948
ENSG00000(	1732.88	1718.519	1411.773	865.1823	832.0705	944.4377	0.87887	1.41E-11	8.87E-11	LEPREL4	chr17	-	39958199	39968856	2791
ENSG00000(	1361.031	1363.254	1188.792	1474.181	1276.639	1389.121	-0.08096	0.51089	0.63812	NT5C3B	chr17	-	39981335	39992523	1729
ENSG00000(	755.0923	836.98	588.4585	496.6371	629.5755	627.1592	0.31512	0.055211	0.10597	FAM134C	chr17	-	40731531	40762641	4149
ENSG00000(	2806.996	2828.872	2657.299	1618.003	2047.041	1888.875	0.57787	1.69E-06	6.85E-06	PIP4K2B	chr17	-	36921942	36956379	5734
ENSG00000(	557.256	566.0152	581.8615	1319.871	1382.489	1396.518	-1.2631	2.40E-25	3.00E-24	ERBB2	chr17	+	37844167	37886679	4930
ENSG00000(	0	0	0	80.15108	65.35067	64.11326	-6.8873	1.40E-11	8.84E-11	GRB7	chr17	+	37894180	37903544	2243
ENSG00000(	201.9794	197.5032	157.0102	198.505	144.5078	200.5594	0.03394	0.87604	0.92233	MIEN1	chr17	-	37884749	37887040	1999
ENSG00000(	2.071584	2.408575	6.597069	13.48336	16.56778	11.50751	-1.7517	0.026866	0.056463	PNMT	chr17	+	37824234	37826728	1253
ENSG00000(	1.035792	0	2.638828	0.749076	0	0	0.96773	0.47383	NA	ARL5C	chr17	-	37313147	37324102	2777
ENSG00000(	29.00217	14.45145	15.83297	0.749076	0	1.64393	3.98	8.33E-06	3.12E-05	STAC2	chr17	-	37366789	37382125	3362
ENSG00000(	33089.41	31000.77	30206.66	3836.016	3081.606	3404.579	3.1858	6.55E-178	1.49E-175	IGFBP4	chr17	+	38599702	38613983	2200
ENSG00000(	22811.25	23604.04	19102.47	4397.823	4919.709	5784.989	2.1124	8.28E-61	2.95E-59	FKBP10	chr17	+	39968932	39979465	2826
ENSG00000(	1375.532	1169.363	994.838	2516.145	1869.397	2103.408	-0.8709	5.79E-09	2.97E-08	TXNL4A	chr18	-	77732867	77793949	1448
ENSG00000(	10.35792	9.634302	6.597069	1.498151	1.840864	4.93179	1.4803	0.097065	0.1711	CACNA1A	chr19	-	13317256	13734804	8392
ENSG00000(	6.214751	22.88147	6.597069	5.243529	3.681728	11.50751	0.72574	0.3534	0.48307	CTB-55O6.8	chr19	+	14183348	14185874	2187
ENSG00000(	635.9762	587.6924	461.7948	961.0639	828.3888	915.6689	-0.67873	6.75E-06	2.56E-05	SAMD1	chr19	-	14198652	14201848	2164
ENSG00000(	2568.764	2209.868	2215.296	2416.518	3568.515	3273.886	-0.40295	0.005627	0.013802	BRD4	chr19	-	15347647	15443356	5852
ENSG00000(	253.769	223.9975	211.1062	528.0983	440.8869	443.0391	-1.0297	1.27E-09	6.91E-09	SLC39A3	chr19	-	2732202	2740150	2940

ENSG00000(	2590.516	2439.887	2567.579	181.2763	208.9381	216.1768	3.641	2.09E-176	4.63E-174	NFIC	chr19	+	3359561	3469215	8068
ENSG00000(	490.9654	320.3405	245.411	228.468	167.5186	136.4462	0.98189	9.07E-05	0.000297	TPGS1	chr19	+	507299	519654	2873
ENSG00000(	48.68222	48.17151	32.98534	174.5346	173.0412	174.2566	-1.9791	1.29E-13	9.40E-13	PPAP2C	chr19	-	281043	291393	1262
ENSG00000(	208.1942	193.8903	226.9392	184.2726	234.7102	256.4531	-0.10161	0.6121	0.72568	PRDM15	chr21	-	43218385	43299591	7072
ENSG00000(	6898.374	6807.838	5302.724	4041.263	4038.856	4539.712	0.58993	2.66E-06	1.05E-05	PFKL	chr21	+	45719934	45747259	6007
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	FEM1A	chr19	+	4791728	4795571	3844
ENSG00000(	1014.04	855.0443	663.6651	486.8991	388.4223	554.0044	0.82238	4.09E-06	1.58E-05	MVB12A	chr19	+	17516531	17544533	2216
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CIB3	chr19	-	16272179	16284336	711
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	MED26	chr19	-	16589878	16739015	2567
ENSG00000(	3115.662	3027.579	2542.51	2370.075	2200.753	2441.236	0.30851	0.009517	0.022246	SH3GL1	chr19	-	4360367	4400544	2516
ENSG00000(	361.4914	311.9105	250.6886	592.5188	597.3604	612.3639	-0.95635	5.69E-09	2.92E-08	DUS3L	chr19	-	5784843	5791249	2301
ENSG00000(	1007.826	959.8173	874.7713	1383.543	1461.646	1569.953	-0.63304	2.76E-07	1.21E-06	DPP9	chr19	-	4675236	4724685	4295
ENSG00000(	885.6021	853.84	782.4124	806.7544	875.3308	753.7418	0.051116	0.69631	0.7931	CCDC97	chr19	+	41816094	41830788	3322
ENSG00000(	55.93276	54.19295	36.94359	17.97781	25.7721	20.54912	1.1743	0.004525	0.011308	TMEM91	chr19	+	41856816	41889988	1843
ENSG00000(	88.04231	74.66584	118.7472	77.15478	100.3271	57.53754	0.25641	0.39927	0.53034	ZFP14	chr19	-	36827162	36870101	5682
ENSG00000(	335.5966	399.8235	349.6447	215.7338	214.4607	256.4531	0.6567	0.00017	0.000536	SIRT3	chr11	-	215458	236931	2627
ENSG00000(	15637.35	16030.27	12702	1000.765	819.1845	832.6505	4.0543	1.70E-219	5.96E-217	IFITM3	chr11	-	319669	327537	808
ENSG00000(	467.1421	558.7895	278.3963	26.21764	38.65814	50.13986	3.4727	2.18E-36	4.05E-35	ATHL1	chr11	+	289135	296107	4418
ENSG00000(	302.4512	221.5889	253.3274	581.2826	690.324	628.8032	-1.2815	1.22E-14	9.40E-14	HUNK	chr21	+	33245628	33416946	7385
ENSG00000(	268702	266171.7	237807.2	871.1749	970.1353	1030.744	8.0588	0	0	COL6A1	chr21	+	47401651	47424964	4238
ENSG00000(	1082.403	1081.45	1017.268	630.7216	559.6227	555.6483	0.86318	1.79E-11	1.12E-10	IFNAR1	chr21	+	34696734	34732168	6139
ENSG00000(	2525.261	2484.446	2239.045	2244.979	2018.507	2349.998	0.13219	0.25244	0.37018	SOD1	chr21	+	33031935	33041244	1746
ENSG00000(	192521.6	192376.5	149837.9	950.5769	1059.417	1259.25	7.3358	0	0	COL6A2	chr21	+	47518011	47552763	3461
ENSG00000(	44.53905	51.78437	29.0271	319.1062	355.2868	370.7062	-3.026	1.54E-36	2.87E-35	SIK1	chr21	-	44834395	44847008	4712
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	DNMT3L	chr21	-	45666222	45682099	1706
ENSG00000(	2602.945	2412.188	2264.114	1558.077	1236.14	1316.788	0.82226	8.06E-11	4.81E-10	SCYL1	chr11	+	65292548	65306175	2715
ENSG00000(	469.2137	511.8223	463.1142	411.2425	451.0117	410.1605	0.18274	0.21234	0.32243	TMEM50B	chr21	-	34804792	34852318	3062
ENSG00000(	18900.09	18533.99	21593.53	10218.89	11285.42	10648.56	0.87508	2.13E-16	1.81E-15	APP	chr21	-	27252861	27543446	3578
ENSG00000(	131.5456	108.3859	139.8579	400.7554	471.2612	345.2253	-1.6711	3.84E-17	3.39E-16	DOPEY2	chr21	+	37529080	37666572	7685
ENSG00000(	1550.58	1393.361	1682.253	927.3555	1173.551	932.1082	0.60804	1.00E-05	3.71E-05	URB1	chr21	-	33683329	33765335	10832
ENSG00000(	2027.045	1866.646	1729.751	2498.916	2202.594	2391.918	-0.33406	0.004165	0.010486	AKT1	chr14	-	1.05E+08	1.05E+08	8396
ENSG00000(	9.322127	6.021439	0	0	0	0	3.3109	0.011256	0.025875	IL19	chr1	+	2.07E+08	2.07E+08	1473
ENSG00000(	4042.696	3876.602	3174.51	1235.975	918.5911	1072.664	1.7762	4.07E-37	7.74E-36	EMP3	chr19	+	48824766	48833810	876
ENSG00000(	2152.376	2030.429	2220.573	5014.312	4190.727	4492.038	-1.0953	4.32E-22	4.76E-21	SAE1	chr19	+	47616531	47713886	2306
ENSG00000(	10.35792	12.04288	15.83297	1.498151	0.920432	0.821965	3.0532	0.000849	0.002408	NTN5	chr19	-	49164664	49176338	2426
ENSG00000(	30.03797	31.31148	14.51355	111.6123	141.7465	175.0785	-2.4437	4.41E-13	3.10E-12	LMTK3	chr19	-	48988528	49016446	5113
ENSG00000(	92.18548	108.3859	112.1502	265.9218	188.6886	233.438	-1.1348	4.60E-07	1.98E-06	GEMIN7	chr19	+	45582453	45594782	1657
ENSG00000(	0	0	0	6.74168	23.93123	15.61733	-4.7681	2.71E-05	9.54E-05	CBLC	chr19	+	45281126	45303891	1579
ENSG00000(	446.4263	379.3506	427.4901	767.8024	672.8358	849.9117	-0.86721	7.73E-09	3.92E-08	WTIP	chr19	+	34971874	34997258	7714
ENSG00000(	183.3352	209.5461	134.5802	24.71949	33.13555	58.35951	2.1557	8.31E-12	5.32E-11	ADAMTS10	chr19	-	8645126	8675620	4230
ENSG00000(	0	8.430014	0	0	0	0	2.183	0.10757	0.18626	SLC6A3	chr5	-	1392909	1445545	3932
ENSG00000(	594.5446	486.5322	399.7824	937.0935	909.3868	808.8135	-0.83672	1.67E-07	7.48E-07	RNPEPL1	chr2	+	2.42E+08	2.42E+08	3944
ENSG00000(	475.4285	399.8235	405.06	632.9688	518.2032	685.5187	-0.5181	0.001174	0.003255	CAPN10	chr2	+	2.42E+08	2.42E+08	4406
ENSG00000(	0	1.204288	0	2.247227	5.522592	4.93179	-2.2428	0.07313	0.13466	MYO1F	chr19	-	8585674	8642461	4303

ENSG00000(	70.43385	69.84869	134.5802	90.63814	138.0648	73.15488	-0.13639	0.67615	0.77787	ERVK3-1	chr19	+	58816715	58827023	3889
ENSG00000(	0	0	0	4.494453	0	0	-1.1446	0.38559	NA	NLRP12	chr19	-	54296857	54327648	3801
ENSG00000(	0	0	0	0	6.443024	4.93179	-2.5023	0.060732	0.11484	CACNG8	chr19	+	54466294	54493469	8747
ENSG00000(	984.0023	950.183	783.7318	1466.69	1287.684	1430.219	-0.6202	2.94E-06	1.16E-05	ZNF787	chr19	-	56598732	56632649	1928
ENSG00000(	308.666	327.5663	314.0205	430.7184	391.1836	461.1223	-0.43256	0.005942	0.014498	C19orf52	chr19	+	11039409	11044211	1425
ENSG00000(	0	0	0	110.8632	173.9616	170.9687	-7.873	1.61E-15	1.31E-14	FBN3	chr19	-	8130286	8214730	9362
ENSG00000(	3079.409	2873.43	2407.93	3065.217	3092.652	3247.583	-0.16898	0.15916	0.25607	CARM1	chr19	+	10982189	11033453	3032
ENSG00000(	796.524	773.1527	663.6651	202.9995	241.1532	241.6577	1.7001	1.20E-27	1.66E-26	EVI5L	chr19	+	7895119	7929862	3855
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	TM4SF5	chr17	+	4675179	4686506	930
ENSG00000(	3.107376	12.04288	7.916483	1.498151	1.840864	0	2.2636	0.030649	0.063334	SLC47A1	chr17	+	19398698	19482347	3280
ENSG00000(	1258.487	1165.751	1005.393	1787.294	1589.586	1925.864	-0.62643	2.05E-06	8.21E-06	PSMB6	chr17	+	4699439	4701790	844
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	GPR32	chr19	+	51273721	51274989	1269
ENSG00000(	0	1.204288	0	0	1.840864	2.465895	-0.87156	0.52062	NA	SIGLEC10	chr19	-	51913275	51921057	3109
ENSG00000(	18.64425	14.45145	21.11062	23.97042	14.72691	25.48091	-0.23964	0.64946	0.75586	ACPT	chr19	+	51293672	51298481	1347
ENSG00000(	176.0846	169.8046	209.7868	281.6524	275.2092	191.5178	-0.42862	0.042995	0.085258	ZNF473	chr19	+	50528971	50556671	4828
ENSG00000(	10.35792	7.225726	14.51355	42.69731	37.73771	40.27628	-1.8522	0.000212	0.000658	FAM71E1	chr19	-	50970042	50980010	1281
ENSG00000(	30834.49	30663.57	22276.98	13450.4	13824.89	17578.54	0.89878	4.87E-10	2.73E-09	RPS11	chr19	+	49999622	50002946	1133
ENSG00000(	59038.07	60560.02	48568.94	32545.83	25114.91	30296.8	0.93294	2.46E-13	1.76E-12	RPL13A	chr19	+	49990811	49995565	2312
ENSG00000(	273.4491	269.7604	204.5091	298.8811	218.1424	261.3848	-0.05708	0.7733	0.85104	CTU1	chr19	-	51600863	51611627	2087
ENSG00000(	1461.502	1304.244	1146.571	1365.565	984.8622	1160.614	0.15573	0.29327	0.41757	NOSIP	chr19	-	50058968	50093519	2615
ENSG00000(	0	0	0	16.47966	14.72691	12.32947	-4.7292	2.78E-05	9.75E-05	IGLON5	chr19	+	51815102	51833608	2606
ENSG00000(	4740.82	4242.706	3294.576	23.97042	22.09037	40.27628	7.107	5.04E-258	2.76E-255	RCN3	chr19	+	50030875	50050219	1859
ENSG00000(	176.0846	163.7831	233.5362	221.7264	219.9832	202.2034	-0.16941	0.40702	0.53794	ZNF614	chr19	-	52516018	52533493	4818
ENSG00000(	222.6953	244.4704	168.885	1.498151	0	2.465895	6.8678	4.70E-31	7.41E-30	SLC2A5	chr1	-	9095166	9148537	4165
ENSG00000(	2284.957	2006.343	2068.841	1399.273	2128.039	1785.308	0.25969	0.079175	0.14407	RERE	chr1	-	8412457	8877702	8026
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	MMEL1	chr1	-	2522078	2564481	2902
ENSG00000(	2.071584	0	0	0	1.840864	0	0.093542	0.94384	NA	C1orf222	chr1	-	1853396	1935276	4710
ENSG00000(	16.57267	18.06432	10.55531	0	0	0	5.1679	4.86E-06	1.87E-05	PRDM16	chr1	+	2985732	3355185	8721
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	CELA2A	chr1	+	15783223	15798586	919
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	PADI3	chr1	+	17575593	17610728	3189
ENSG00000(	35.21692	21.67718	36.94359	2.996302	2.761296	2.465895	3.2858	5.47E-07	2.34E-06	FHAD1	chr1	+	15573768	15726858	5090
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	PADI1	chr1	+	17531621	17572500	3846
ENSG00000(	1559.903	1443.941	1643.99	5305.702	4387.699	4564.371	-1.6144	3.48E-42	7.66E-41	EPHA2	chr1	-	16450832	16482582	3964
ENSG00000(	132.5814	158.966	113.4696	304.8737	297.2995	354.2669	-1.2315	7.86E-10	4.34E-09	ARHGEF19	chr1	-	16524349	16539140	3029
ENSG00000(	1572.332	1553.531	1397.259	1099.643	874.4104	1000.331	0.60298	3.40E-06	1.33E-05	EFHD2	chr1	+	15736391	15756839	2419
ENSG00000(	518.9317	479.3065	467.0725	656.9393	500.715	600.8564	-0.26258	0.086313	0.15527	PEX14	chr1	+	10532345	10690815	1985
ENSG00000(	8086.427	7861.59	8011.48	6681.005	6194.507	6066.923	0.33847	0.000645	0.001863	PGD	chr1	+	10458649	10480201	1959
ENSG00000(	2.071584	0	3.958241	0	0.920432	0	1.4353	0.28803	0.41168	MYOM3	chr1	-	24382525	24438665	5809
ENSG00000(	5875.012	5642.088	4429.272	2181.308	1725.81	1777.088	1.4842	4.98E-27	6.68E-26	SH3BGRL3	chr1	+	26605667	26608007	1655
ENSG00000(	1.035792	7.225726	6.597069	222.4754	179.4842	216.1768	-5.2786	3.76E-31	5.93E-30	CNKSR1	chr1	+	26503894	26516377	2673
ENSG00000(	23447.22	23675.09	20150.09	12402.44	12415.71	15008.26	0.75489	1.73E-10	1.00E-09	RPL11	chr1	+	24018269	24022915	994
ENSG00000(	4.143168	0	0	3.745378	11.96562	0	-1.3273	0.27632	0.39785	IL22RA1	chr1	-	24446261	24469611	2798
ENSG00000(	1.035792	0	0	0	2.761296	0	-0.44657	0.73574	NA	ZNF593	chr1	+	26496362	26498551	1885
ENSG00000(	495.1085	521.4566	694.0116	222.4754	222.7445	225.2184	1.3439	8.04E-15	6.28E-14	C1orf216	chr1	-	36179476	36185073	3218

ENSG00000(	1231.557	1205.492	1328.65	1188.034	1213.129	1092.391	0.10775	0.36584	0.49572	KIAA0319L	chr1	-	35899091	36023551	4789
ENSG00000(	1381.746	1312.674	967.1303	138.579	254.9597	256.4531	2.4831	1.83E-33	3.12E-32	EVA1B	chr1	-	36787632	36789755	1054
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	C1orf94	chr1	+	34632484	34684732	2287
ENSG00000(	0	0	0	3.745378	9.20432	9.863579	-3.7351	0.002115	0.005612	DMRTA2	chr1	-	50883222	50889172	3137
ENSG00000(	127.4024	113.203	134.5802	584.2789	510.8398	470.9859	-2.0535	7.08E-30	1.07E-28	PLK4	chr4	+	1.29E+08	1.29E+08	3841
ENSG00000(	630.7973	581.671	538.3208	423.2277	561.4635	477.5616	0.26138	0.093175	0.16543	MAP3K6	chr1	-	27681675	27693383	4309
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	FCN3	chr1	-	27695603	27701315	1030
ENSG00000(	431.9252	475.6936	452.5589	557.3122	441.8074	475.9177	-0.11821	0.4412	0.57099	GPN2	chr1	-	27205773	27216788	1529
ENSG00000(	32.10955	52.98866	29.0271	364.0507	329.5147	413.4484	-3.2509	6.69E-39	1.34E-37	SYTL1	chr1	+	27668513	27680421	2681
ENSG00000(	871.101	859.8614	757.3435	415.7369	512.6806	421.668	0.88157	1.50E-09	8.07E-09	WDTC1	chr1	+	27561007	27635110	5149
ENSG00000(	132.5814	133.6759	130.622	59.92604	68.11197	43.56414	1.1997	9.85E-06	3.66E-05	NBPF3	chr1	+	21766621	21811498	4401
ENSG00000(	6090.456	5975.676	6169.579	1913.888	4986.901	3998.859	0.72734	0.058632	0.1115	HSPG2	chr1	-	22148738	22263790	14327
ENSG00000(	189.5499	225.2018	125.3443	435.2129	276.1296	356.7328	-0.9752	2.27E-05	8.04E-05	ITGB3BP	chr1	-	63906441	64059392	1285
ENSG00000(	8677.865	8266.231	8619.73	10021.88	10807.71	10009.89	-0.27026	0.005861	0.014318	SERBP1	chr1	-	67873493	67896098	6676
ENSG00000(	366.6703	446.7907	369.4359	410.4934	372.775	277.0022	0.15656	0.39373	0.52453	BCL10	chr1	-	85731931	85742773	2819
ENSG00000(	1891.356	1622.176	1742.946	6194.855	5542.841	5829.375	-1.7374	4.79E-55	1.48E-53	CYR61	chr1	+	86046444	86049645	2290
ENSG00000(	437.1042	467.2636	589.778	466.6741	462.0569	347.6912	0.22454	0.20038	0.30791	PRKACB	chr1	+	84543745	84704181	4513
ENSG00000(	456.7842	429.9307	595.0556	633.7179	563.3044	547.4286	-0.23686	0.14193	0.23345	PIGK	chr1	-	77554675	77685115	4596
ENSG00000(	20.71584	14.45145	19.79121	2857.723	2313.966	2779.063	-7.1122	8.16E-187	2.04E-184	TINAGL1	chr1	+	32042116	32053288	4759
ENSG00000(	196.8005	185.4603	168.885	26.21764	30.37426	37.81039	2.5234	1.14E-20	1.19E-19	ADC	chr1	+	33546705	33586131	5848
ENSG00000(	25382.08	26748.43	18838.59	17856.46	14009.9	16549.44	0.55023	9.23E-05	0.000302	RPS8	chr1	+	45240923	45244451	1115
ENSG00000(	446.4263	397.4149	414.2959	1454.705	1286.764	1217.33	-1.6489	5.30E-34	9.23E-33	KIF2C	chr1	+	45205490	45233439	2955
ENSG00000(	670.1574	615.391	628.041	5345.403	8165.152	7674.686	-3.4574	5.69E-117	5.73E-115	PTPRF	chr1	+	43990858	44089343	7727
ENSG00000(	2.071584	1.204288	6.597069	2.996302	2.761296	2.465895	0.19493	0.857	0.90911	BEST4	chr1	-	45249257	45253377	2047
ENSG00000(	249.6258	215.5675	230.8974	50.18806	65.35067	45.20807	2.1038	8.94E-19	8.56E-18	MOB3C	chr1	-	47073387	47082563	5725
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CYP4B1	chr1	+	47223510	47285085	2171
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	TMEM61	chr1	+	55446465	55457966	1097
ENSG00000(	1210.841	1083.859	1042.337	1338.598	1345.672	1508.306	-0.32775	0.00815	0.019321	LMO4	chr1	+	87794151	87812788	3587
ENSG00000(	31.07376	13.24716	25.06886	30.7121	14.72691	11.50751	0.26975	0.62921	0.73955	SYPL2	chr1	+	1.1E+08	1.1E+08	3624
ENSG00000(	342.8471	356.4692	374.7135	895.1453	838.5135	787.4424	-1.2291	1.47E-18	1.39E-17	MTF2	chr1	+	93544792	93604638	4125
ENSG00000(	24.85901	32.51577	34.30476	192.5124	149.11	147.1317	-2.3953	6.58E-16	5.48E-15	SLC44A3	chr1	+	95285898	95360802	2388
ENSG00000(	296.2365	270.9647	343.0476	1152.078	1723.969	1295.417	-2.1883	2.79E-38	5.50E-37	IGSF3	chr1	-	1.17E+08	1.17E+08	7254
ENSG00000(	746.806	699.6912	836.5083	509.3714	673.7562	517.0159	0.42464	0.005961	0.014543	ZNF697	chr1	-	1.2E+08	1.2E+08	5041
ENSG00000(	421.5673	445.5865	472.3501	452.4416	431.6826	323.8542	0.14758	0.38192	0.51261	CTTNBP2NI	chr1	+	1.13E+08	1.13E+08	5897
ENSG00000(	108.7581	91.52587	114.789	50.18806	77.31629	100.2797	0.46446	0.12174	0.20633	STRIP1	chr1	+	1.11E+08	1.11E+08	3363
ENSG00000(	1127.977	1172.976	1124.141	2065.95	1654.016	1901.205	-0.71368	9.18E-09	4.61E-08	PSMA5	chr1	-	1.1E+08	1.1E+08	3729
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	FNDC7	chr1	+	1.09E+08	1.09E+08	3332
ENSG00000(	15.53688	19.2686	7.916483	8.988907	9.20432	9.041614	0.61474	0.35124	0.48095	C1orf162	chr1	+	1.12E+08	1.12E+08	2308
ENSG00000(	0	0	0	2.996302	1.840864	0	-1.3549	0.31496	NA	CD53	chr1	+	1.11E+08	1.11E+08	1505
ENSG00000(	1.035792	0	5.277655	0	0	0	1.9229	0.15616	0.25219	PROK1	chr1	+	1.11E+08	1.11E+08	1338
ENSG00000(	30.03797	16.86003	51.45714	183.5235	271.5274	231.7941	-2.7775	5.98E-19	5.78E-18	CELSR2	chr1	+	1.1E+08	1.1E+08	10534
ENSG00000(	4581.308	4896.634	4912.178	36.7047	48.7829	50.13986	6.714	0	0	ITGA10	chr1	+	1.46E+08	1.46E+08	5269
ENSG00000(	0	0	0	20.97412	25.7721	16.4393	-5.2588	1.54E-06	6.26E-06	GJA5	chr1	-	1.47E+08	1.47E+08	3177
ENSG00000(	331.4534	297.4591	387.9077	289.1432	378.2976	340.2935	0.013116	0.94121	0.96466	GPR161	chr1	-	1.68E+08	1.68E+08	2676

ENSG00000(	1773.276	1808.84	1707.321	1086.909	966.4536	901.6955	0.83793	5.36E-12	3.49E-11	ALDH9A1	chr1	-	1.66E+08	1.66E+08	2696
ENSG00000(	159.512	127.6545	129.3026	2092.168	2217.321	2119.848	-3.9311	2.40E-164	4.62E-162	ATP1B1	chr1	+	1.69E+08	1.69E+08	2608
ENSG00000(	494.0727	556.3809	592.4168	648.6994	670.9949	604.9662	-0.2291	0.10465	0.18203	TIPRL	chr1	+	1.68E+08	1.68E+08	1630
ENSG00000(	233.0532	251.6961	229.578	177.5309	152.7917	198.0935	0.43136	0.026622	0.05603	NME7	chr1	-	1.69E+08	1.69E+08	4298
ENSG00000(	791.345	775.5613	924.9091	1307.886	1286.764	1092.391	-0.56476	2.85E-05	9.99E-05	POGK	chr1	+	1.67E+08	1.67E+08	6254
ENSG00000(	185.4068	181.8474	155.6908	502.6297	420.6374	486.6032	-1.4232	2.96E-16	2.50E-15	MPC2	chr1	-	1.68E+08	1.68E+08	2177
ENSG00000(	205.0868	189.0732	254.6469	415.7369	352.5255	341.1154	-0.77348	2.78E-05	9.76E-05	CREG1	chr1	-	1.67E+08	1.68E+08	1974
ENSG00000(	1024.398	1128.418	1022.546	793.271	689.4036	629.6251	0.586	1.62E-05	5.86E-05	DCAF6	chr1	+	1.68E+08	1.68E+08	3349
ENSG00000(	0	0	0	2.247227	2.761296	4.93179	-2.4799	0.060179	0.114	GPA33	chr1	-	1.67E+08	1.67E+08	2802
ENSG00000(	67.32647	52.98866	48.81831	47.94084	16.56778	22.19305	0.93229	0.029606	0.06143	TBX19	chr1	+	1.68E+08	1.68E+08	2822
ENSG00000(	497.1801	491.3494	581.8615	1071.178	963.6923	1015.949	-0.95742	1.44E-12	9.79E-12	UCK2	chr1	+	1.66E+08	1.66E+08	4669
ENSG00000(	1596.155	1686.003	1558.228	1761.077	1332.786	1572.419	0.052176	0.68843	0.78717	TMCO1	chr1	-	1.66E+08	1.66E+08	2224
ENSG00000(	0	0	7.916483	0.749076	0.920432	0	1.2921	0.33227	0.46038	XCL1	chr1	+	1.69E+08	1.69E+08	1367
ENSG00000(	236.1606	217.9761	236.1751	1096.647	1334.626	1027.456	-2.3167	2.53E-51	7.22E-50	POU2F1	chr1	+	1.67E+08	1.67E+08	14332
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	MAEL	chr1	+	1.67E+08	1.67E+08	2355
ENSG00000(	0	2.408575	0	3.745378	1.840864	0.821965	-0.88725	0.49839	0.62672	ILDR2	chr1	-	1.67E+08	1.67E+08	2572
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	DPT	chr1	-	1.69E+08	1.69E+08	1786
ENSG00000(	2074.691	1773.916	1614.962	1852.464	1581.302	1983.401	0.012711	0.9251	0.9546	MGST3	chr1	+	1.66E+08	1.66E+08	2456
ENSG00000(	3.107376	6.021439	1.319414	26.21764	27.61296	23.83698	-2.6773	0.000106	0.000343	ADCY10	chr1	-	1.68E+08	1.68E+08	5055
ENSG00000(	523.0749	538.3166	488.1831	758.8135	735.4252	722.5072	-0.51488	0.00011	0.000357	RFWD2	chr1	-	1.76E+08	1.76E+08	3033
ENSG00000(	3.107376	9.634302	2.638828	75.65663	75.47542	60.00344	-3.6325	5.26E-12	3.42E-11	PVRL4	chr1	-	1.61E+08	1.61E+08	3502
ENSG00000(	946.7138	916.463	829.9113	772.2969	708.7326	675.6552	0.32009	0.014678	0.032845	UFC1	chr1	+	1.61E+08	1.61E+08	1114
ENSG00000(	178.1562	166.1917	121.3861	162.5494	132.5422	151.2415	0.063334	0.78198	0.85646	PPOX	chr1	+	1.61E+08	1.61E+08	2471
ENSG00000(	0	0	1.319414	11.98521	6.443024	4.93179	-3.0778	0.007734	0.018454	FCGR2A	chr1	+	1.61E+08	1.61E+08	2412
ENSG00000(	139.8319	102.3645	125.3443	761.8098	607.4851	544.9627	-2.3667	8.49E-35	1.52E-33	NUF2	chr1	+	1.63E+08	1.63E+08	1969
ENSG00000(	505.4664	531.0909	672.901	1464.443	1133.052	1045.539	-1.0898	2.21E-11	1.37E-10	RGS5	chr1	-	1.63E+08	1.63E+08	5862
ENSG00000(	1377.603	1268.115	1364.274	1327.362	1246.265	1600.366	-0.05781	0.65799	0.76277	SDHC	chr1	+	1.61E+08	1.61E+08	1420
ENSG00000(	817.2398	802.0556	700.6087	1218.746	1360.398	1788.596	-0.90903	4.14E-09	2.16E-08	PFDN2	chr1	-	1.61E+08	1.61E+08	677
ENSG00000(	9.322127	3.612863	14.51355	9.737982	4.60216	5.753754	0.39461	0.61925	0.73162	NR1I3	chr1	-	1.61E+08	1.61E+08	1473
ENSG00000(	357.3482	234.8361	317.9787	367.7961	279.8113	355.0888	-0.13881	0.47729	0.60641	USP21	chr1	+	1.61E+08	1.61E+08	2514
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	F13B	chr1	-	1.97E+08	1.97E+08	2217
ENSG00000(	1264.702	1194.653	1207.264	1911.641	1469.009	1612.695	-0.44484	0.000624	0.001806	PRCC	chr1	+	1.57E+08	1.57E+08	2103
ENSG00000(	188.5141	187.8689	118.7472	247.1949	224.5854	263.8507	-0.56358	0.009364	0.021916	RRNAD1	chr1	+	1.57E+08	1.57E+08	2254
ENSG00000(	981.9307	924.893	816.7171	661.4337	871.6491	1109.653	0.04432	0.79757	0.86812	MRPL24	chr1	-	1.57E+08	1.57E+08	990
ENSG00000(	196.8005	215.5675	242.7721	233.7116	238.3919	252.3432	-0.14683	0.42629	0.55663	PIGM	chr1	-	1.6E+08	1.6E+08	4322
ENSG00000(	7.250543	2.408575	2.638828	5.243529	2.761296	7.397684	-0.2647	0.78146	0.85609	CASQ1	chr1	+	1.6E+08	1.6E+08	1956
ENSG00000(	572.7929	596.1224	572.6256	1155.824	966.4536	986.3579	-0.83449	4.60E-10	2.59E-09	ISG20L2	chr1	-	1.57E+08	1.57E+08	3303
ENSG00000(	2000.114	2111.116	1535.798	4228.531	3990.993	4300.52	-1.1454	1.83E-18	1.72E-17	CRABP2	chr1	-	1.57E+08	1.57E+08	992
ENSG00000(	4177.349	4210.19	3687.762	5972.379	6882.99	6955.467	-0.7127	2.77E-10	1.58E-09	HDGF	chr1	-	1.57E+08	1.57E+08	2380
ENSG00000(	891.8168	814.0985	1044.976	910.1268	947.1245	842.514	0.026386	0.84726	0.90271	ABL2	chr1	-	1.79E+08	1.79E+08	12144
ENSG00000(	820.3472	821.3242	1072.683	834.4702	914.9094	739.7684	0.12373	0.409	0.53982	XPR1	chr1	+	1.81E+08	1.81E+08	8474
ENSG00000(	135.6887	122.8373	145.1355	100.3761	97.56579	81.37453	0.52624	0.029506	0.06126	RGS16	chr1	-	1.83E+08	1.83E+08	2427
ENSG00000(	709.5175	693.6697	845.7442	450.9435	494.272	410.1605	0.72801	9.00E-07	3.75E-06	TOR1AIP1	chr1	+	1.8E+08	1.8E+08	3044
ENSG00000(	0	3.612863	0	0.749076	0	0.821965	0.57209	0.6732	NA	FAM163A	chr1	+	1.8E+08	1.8E+08	2909

ENSG0000(	215.4447	183.0517	270.4798	151.3133	188.6886	119.1849	0.53912	0.019863	0.043118	HMCN1	chr1	+	1.86E+08	1.86E+08	18208
ENSG0000(	1216.02	1159.729	1426.286	328.8442	426.16	303.3051	1.8402	8.48E-32	1.37E-30	RGL1	chr1	+	1.84E+08	1.84E+08	5113
ENSG0000(	80.79177	90.32158	96.31721	154.3096	145.4283	133.9803	-0.69546	0.003674	0.00935	LYPLAL1	chr1	+	2.19E+08	2.19E+08	2169
ENSG0000(	527.2181	549.1552	599.0139	2.996302	0	0	8.4565	1.28E-45	3.12E-44	LHX9	chr1	+	1.98E+08	1.98E+08	7413
ENSG0000(	196.8005	164.9874	212.4256	197.7559	226.4263	150.4196	-0.00036	0.99867	0.99905	PRUNE	chr1	+	1.51E+08	1.51E+08	2997
ENSG0000(	177.1204	208.3418	176.8014	839.7137	774.0833	811.2794	-2.1027	1.07E-42	2.40E-41	TUFT1	chr1	+	1.52E+08	1.52E+08	3111
ENSG0000(	1357.923	1393.361	1293.026	3200.051	2387.601	2419.865	-0.98318	4.17E-13	2.93E-12	SF3B4	chr1	-	1.5E+08	1.5E+08	2085
ENSG0000(	1090.689	1071.816	895.882	161.0512	173.0412	143.8439	2.671	1.65E-66	6.70E-65	ECM1	chr1	+	1.5E+08	1.5E+08	3066
ENSG0000(	670.1574	744.2498	558.112	591.0206	662.711	720.8632	-0.00028	0.99852	0.99905	ZNF687	chr1	+	1.51E+08	1.51E+08	5378
ENSG0000(	372.8851	358.8777	269.1604	453.9398	487.829	547.4286	-0.56799	0.000903	0.00255	TARS2	chr1	+	1.5E+08	1.5E+08	2729
ENSG0000(	11.39371	20.47289	6.597069	953.5732	1533.44	1499.264	-6.5979	2.42E-103	1.96E-101	CGN	chr1	+	1.51E+08	1.52E+08	5091
ENSG0000(	1052.365	1023.645	907.7567	1259.196	1330.945	1291.307	-0.37766	0.001859	0.004983	SNX27	chr1	+	1.52E+08	1.52E+08	7197
ENSG0000(	413.281	443.1779	410.3377	250.9403	459.2956	258.097	0.3877	0.071096	0.13154	SETDB1	chr1	+	1.51E+08	1.51E+08	4437
ENSG0000(	296.2365	331.1791	245.411	622.4818	520.9645	601.6783	-0.99491	1.84E-09	9.84E-09	ADAMTSL4	chr1	+	1.51E+08	1.51E+08	4197
ENSG0000(	3359.073	3405.726	3956.922	3573.839	3816.111	3631.441	-0.03995	0.71947	0.81106	MCL1	chr1	-	1.51E+08	1.51E+08	3932
ENSG0000(	479.5717	451.6079	426.1707	45.69361	52.46462	50.13986	3.1807	4.67E-57	1.52E-55	CTSK	chr1	-	1.51E+08	1.51E+08	1692
ENSG0000(	587.294	557.5852	630.6798	322.1025	356.2072	360.0206	0.77197	1.45E-07	6.55E-07	RFX5	chr1	-	1.51E+08	1.51E+08	3576
ENSG0000(	1826.101	1901.57	1795.722	908.6286	915.8298	984.714	0.97373	1.26E-17	1.14E-16	PI4KB	chr1	-	1.51E+08	1.51E+08	3983
ENSG0000(	1319.599	1301.835	1323.372	1387.288	1488.339	1355.42	-0.10064	0.37578	0.50624	PIP5K1A	chr1	+	1.51E+08	1.51E+08	3767
ENSG0000(	939.4633	1030.87	1138.654	2227.002	2302	2090.257	-1.0891	2.60E-19	2.56E-18	ANP32E	chr1	-	1.5E+08	1.5E+08	3453
ENSG0000(	311.7734	269.7604	339.0893	136.3317	134.3831	132.3364	1.1851	4.45E-10	2.51E-09	FAM63A	chr1	-	1.51E+08	1.51E+08	2817
ENSG0000(	83.89914	114.4073	56.73479	80.90016	125.1788	110.9653	-0.30479	0.31489	0.44158	ANXA9	chr1	+	1.51E+08	1.51E+08	1826
ENSG0000(	572.7929	517.8437	422.2124	132.5864	121.497	143.0219	1.9216	7.02E-26	8.98E-25	SELENBP1	chr1	-	1.51E+08	1.51E+08	2840
ENSG0000(	1413.856	1240.416	1291.706	862.935	800.7758	729.0829	0.72026	1.73E-08	8.54E-08	CERS2	chr1	-	1.51E+08	1.51E+08	2505
ENSG0000(	2122.338	2156.879	1894.678	3216.53	3784.816	4492.038	-0.89398	3.15E-11	1.93E-10	ENSA	chr1	-	1.51E+08	1.51E+08	2818
ENSG0000(	378.064	413.0707	348.3252	181.2763	137.1444	167.6808	1.2211	3.40E-11	2.08E-10	AC027612.	chr2	-	91823266	91847975	1104
ENSG0000(	535.5044	655.1325	525.1267	51.68621	40.49901	56.71558	3.5013	7.34E-67	3.00E-65	SEMA6C	chr1	-	1.51E+08	1.51E+08	5262
ENSG0000(	302.4512	357.6735	304.7846	671.1717	402.2288	429.0657	-0.63707	0.001466	0.003992	MRPL9	chr1	-	1.52E+08	1.52E+08	1296
ENSG0000(	866.9578	979.0859	872.1325	367.7961	515.4419	399.475	1.0817	3.94E-12	2.59E-11	ARNT	chr1	-	1.51E+08	1.51E+08	4887
ENSG0000(	1234.664	1371.684	1393.301	1183.539	1407.341	1200.891	0.076813	0.54233	0.66494	POGZ	chr1	-	1.51E+08	1.51E+08	6626
ENSG0000(	81.82756	91.52587	50.13772	47.94084	56.14635	68.22309	0.37481	0.25543	0.37371	C1orf56	chr1	+	1.51E+08	1.51E+08	2096
ENSG0000(	3.107376	9.634302	0	6.74168	0.920432	1.64393	0.34904	0.75255	0.83619	OAZ3	chr1	+	1.52E+08	1.52E+08	3790
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	HORMAD1	chr1	-	1.51E+08	1.51E+08	1879
ENSG0000(	389.4578	368.512	370.7553	298.1321	336.8781	323.0322	0.23714	0.13163	0.2195	GOLPH3L	chr1	-	1.51E+08	1.51E+08	2999
ENSG0000(	284.8428	254.1047	246.7304	163.2985	141.7465	170.9687	0.71941	0.000178	0.00056	GABPB2	chr1	+	1.51E+08	1.51E+08	8964
ENSG0000(	180.2278	169.8046	180.7597	220.9773	217.222	226.8623	-0.32383	0.086254	0.15518	IKBKE	chr1	+	2.07E+08	2.07E+08	3269
ENSG0000(	50.7538	54.19295	63.33186	42.69731	57.06678	23.83698	0.43733	0.25409	0.37218	SYT14	chr1	+	2.1E+08	2.1E+08	5189
ENSG0000(	2.071584	0	0	11.98521	14.72691	17.26126	-3.5187	0.000381	0.00114	KCNH1	chr1	-	2.11E+08	2.11E+08	3102
ENSG0000(	107.7224	108.3859	118.7472	1096.647	1019.839	784.1545	-3.1032	3.14E-67	1.29E-65	DTL	chr1	+	2.12E+08	2.12E+08	4573
ENSG0000(	365.6345	281.8033	328.534	28.46487	30.37426	37.81039	3.3115	3.20E-43	7.30E-42	DYRK3	chr1	+	2.07E+08	2.07E+08	2329
ENSG0000(	1408.677	1334.351	1105.669	977.5436	820.1049	733.1927	0.60321	4.31E-05	0.000148	EIF2D	chr1	-	2.07E+08	2.07E+08	2094
ENSG0000(	331.4534	297.4591	370.7553	665.1791	532.9301	499.7547	-0.76296	5.76E-06	2.20E-05	INTS7	chr1	-	2.12E+08	2.12E+08	4447
ENSG0000(	136.7245	144.5145	142.4967	26.21764	57.06678	33.70056	1.8434	2.02E-09	1.08E-08	VASH2	chr1	+	2.13E+08	2.13E+08	4224
ENSG0000(	65.25489	52.98866	64.65128	206.7449	213.5402	198.9155	-1.7447	1.90E-13	1.37E-12	TAF1A	chr1	-	2.23E+08	2.23E+08	1911

ENSG00000(	294.1649	349.2434	255.9663	1500.398	1361.319	1434.329	-2.2486	1.58E-54	4.85E-53	SMYD2	chr1	+	2.14E+08	2.15E+08	4732
ENSG00000(	0	4.817151	1.319414	18.72689	16.56778	26.30288	-3.0027	0.000262	0.000804	SUSD4	chr1	-	2.23E+08	2.24E+08	3480
ENSG00000(	79.75598	67.44011	72.56776	1019.492	784.2081	863.0632	-3.5814	1.15E-82	6.48E-81	DUSP10	chr1	-	2.22E+08	2.22E+08	2676
ENSG00000(	66.29068	48.17151	52.77655	62.92235	52.46462	58.35951	-0.05197	0.87325	0.92046	HHIPL2	chr1	-	2.23E+08	2.23E+08	2575
ENSG00000(	809.9893	808.0771	948.6585	1367.812	1269.276	1176.232	-0.57094	1.14E-05	4.20E-05	TP53BP2	chr1	-	2.24E+08	2.24E+08	4741
ENSG00000(	2433.075	2408.575	2231.129	546.8252	636.9389	669.0794	1.9295	2.41E-54	7.34E-53	ATP8B2	chr1	+	1.54E+08	1.54E+08	5861
ENSG00000(	0	0	0	1.498151	1.840864	4.93179	-2.195	0.10101	0.17689	FLG2	chr1	-	1.52E+08	1.52E+08	9122
ENSG00000(	3676.025	3498.456	3018.819	2087.674	1599.711	1603.654	0.94344	4.10E-12	2.69E-11	ADAM15	chr1	+	1.55E+08	1.55E+08	4508
ENSG00000(	1919.322	1840.152	1539.756	1799.279	1616.279	1893.807	-0.0023	0.98557	0.99136	JTB	chr1	-	1.54E+08	1.54E+08	1287
ENSG00000(	9349.058	9121.275	7616.976	1271.93	1512.27	1823.94	2.4948	4.96E-71	2.19E-69	RAB13	chr1	-	1.54E+08	1.54E+08	2123
ENSG00000(	7843.016	7682.151	7432.258	14129.81	12557.45	12693.6	-0.77743	1.87E-14	1.43E-13	TPM3	chr1	-	1.54E+08	1.54E+08	4041
ENSG00000(	7.250543	6.021439	11.87472	8.988907	15.64734	12.32947	-0.52012	0.45513	0.58483	NUP210L	chr1	-	1.54E+08	1.54E+08	5889
ENSG00000(	382.2072	434.7479	423.5318	417.9842	405.9105	460.3004	-0.05109	0.73667	0.82369	SNAPIN	chr1	+	1.54E+08	1.54E+08	1205
ENSG00000(	334.5608	297.4591	242.7721	202.9995	232.8693	262.2068	0.32728	0.089476	0.16001	SLC27A3	chr1	+	1.54E+08	1.54E+08	4504
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	S100A7	chr1	-	1.53E+08	1.53E+08	479
ENSG00000(	3952.582	3917.548	4094.141	4401.568	4529.446	4162.43	-0.12996	0.19922	0.30683	UBAP2L	chr1	+	1.54E+08	1.54E+08	3988
ENSG00000(	3045.228	2721.69	2737.784	4707.94	4313.144	4486.285	-0.66614	4.93E-10	2.76E-09	SLC39A1	chr1	-	1.54E+08	1.54E+08	2723
ENSG00000(	1040.971	1052.547	884.0072	1406.015	963.6923	1167.19	-0.24778	0.10466	0.18203	HAX1	chr1	+	1.54E+08	1.54E+08	1284
ENSG00000(	58.00435	48.17151	29.0271	84.64554	103.0884	80.55256	-0.96206	0.003555	0.009065	CREB3L4	chr1	+	1.54E+08	1.54E+08	1752
ENSG00000(	49.71801	39.74149	35.62417	5.243529	6.443024	0.821965	3.1654	8.27E-08	3.82E-07	EFNA3	chr1	+	1.55E+08	1.55E+08	1782
ENSG00000(	3351.823	3396.091	3124.372	1841.977	1649.414	1694.07	0.92726	2.09E-17	1.87E-16	C1orf43	chr1	-	1.54E+08	1.54E+08	1708
ENSG00000(	599.7235	629.8425	608.2498	463.6778	566.9861	543.3188	0.22383	0.11798	0.20107	GATAD2B	chr1	-	1.54E+08	1.54E+08	7478
ENSG00000(	2520.082	2651.842	2443.554	6560.404	5385.448	5613.198	-1.2031	9.91E-26	1.26E-24	ILF2	chr1	-	1.54E+08	1.54E+08	1659
ENSG00000(	511.6812	503.3923	523.8073	645.7031	609.326	590.1708	-0.2617	0.054445	0.10467	RIT1	chr1	-	1.56E+08	1.56E+08	3445
ENSG00000(	1367.245	1458.392	1405.176	1289.908	1211.289	1129.38	0.21997	0.061537	0.11606	INTS3	chr1	+	1.54E+08	1.54E+08	5741
ENSG00000(	1.035792	1.204288	0	0	0	1.64393	0.19975	0.8819	NA	PKLR	chr1	-	1.55E+08	1.55E+08	2479
ENSG00000(	109.7939	110.7945	79.16483	67.4168	92.0432	81.37453	0.31848	0.25146	0.36902	HCN3	chr1	+	1.55E+08	1.55E+08	3718
ENSG00000(	0	0	1.319414	20.97412	35.89685	23.01502	-4.8463	8.71E-07	3.64E-06	FLG	chr1	-	1.52E+08	1.52E+08	12747
ENSG00000(	10.35792	1.204288	3.958241	50.18806	34.05598	40.27628	-2.8057	3.16E-06	1.24E-05	ACTA1	chr1	-	2.3E+08	2.3E+08	1491
ENSG00000(	199.9078	234.8361	183.3985	364.7998	251.2779	326.3201	-0.60628	0.002372	0.00624	C1orf131	chr1	-	2.31E+08	2.31E+08	2657
ENSG00000(	3026.584	3026.375	3159.996	1666.693	2346.181	2111.628	0.58809	1.01E-05	3.75E-05	GALNT2	chr1	+	2.3E+08	2.3E+08	4454
ENSG00000(	109.7939	152.9445	167.5656	310.8664	298.22	300.8392	-1.0805	1.12E-07	5.09E-07	TTC13	chr1	-	2.31E+08	2.31E+08	3253
ENSG00000(	681.5511	688.8526	639.9157	286.8959	246.6758	212.0669	1.425	4.42E-19	4.30E-18	SCCPDH	chr1	+	2.47E+08	2.47E+08	2503
ENSG00000(	377.0283	340.8134	558.112	109.365	131.6218	101.1017	1.8869	4.44E-18	4.12E-17	LYST	chr1	-	2.36E+08	2.36E+08	13480
ENSG00000(	15.53688	26.49433	14.51355	116.8558	99.40666	87.95025	-2.3841	8.56E-11	5.09E-10	MLK4	chr1	+	2.33E+08	2.34E+08	5809
ENSG00000(	1260.559	1176.589	1745.584	915.3703	935.1589	709.3557	0.70505	2.05E-05	7.32E-05	CEP170	chr1	-	2.43E+08	2.43E+08	6828
ENSG00000(	1477.039	1589.66	1219.138	2286.928	2057.166	2054.09	-0.57633	8.11E-06	3.05E-05	ACP1	chr2	+	264140	278283	1552
ENSG00000(	606.9741	700.8955	537.0014	566.3011	520.9645	598.3905	0.12998	0.38512	0.51598	SNAP47	chr1	+	2.28E+08	2.28E+08	2403
ENSG00000(	2358.498	2402.554	2502.928	4728.914	4053.583	3906.799	-0.80367	2.22E-12	1.48E-11	SRP9	chr1	+	2.26E+08	2.26E+08	1596
ENSG00000(	320.0597	320.3405	352.2835	545.327	544.8957	477.5616	-0.65822	1.59E-05	5.75E-05	NVL	chr1	-	2.24E+08	2.25E+08	3123
ENSG00000(	526.1823	568.4238	542.2791	480.9065	552.2592	514.55	0.081051	0.56565	0.685	SDE2	chr1	-	2.26E+08	2.26E+08	3975
ENSG00000(	1450.109	1453.575	1476.424	4034.521	3309.873	3562.396	-1.3141	9.58E-30	1.45E-28	DEGS1	chr1	+	2.24E+08	2.24E+08	2101
ENSG00000(	564.5066	472.0808	653.1098	686.9023	659.0293	662.5037	-0.24958	0.097622	0.17193	FBXO28	chr1	+	2.24E+08	2.24E+08	5451
ENSG00000(	9496.14	8904.503	8136.825	9417.378	6972.272	6928.342	0.1861	0.16431	0.26261	ARF1	chr1	+	2.28E+08	2.28E+08	2006

ENSG00000(	626.6541	649.1111	666.304	916.1194	945.2837	1060.335	-0.58833	6.02E-06	2.29E-05	CNIH4	chr1	+	2.25E+08	2.25E+08	4125
ENSG00000(	863.8504	829.7542	997.4768	229.2171	312.9469	254.8091	1.7515	4.09E-28	5.77E-27	ITPKB	chr1	-	2.27E+08	2.27E+08	6150
ENSG00000(	4691.102	4425.757	3450.267	2539.366	1936.589	2201.222	0.90983	1.36E-10	7.95E-10	GUK1	chr1	+	2.28E+08	2.28E+08	2549
ENSG00000(	1181.839	1086.268	1741.626	546.0761	670.9949	492.357	1.2245	8.64E-12	5.52E-11	CDC42BPA	chr1	-	2.27E+08	2.28E+08	10855
ENSG00000(	128.4382	74.66584	142.4967	56.92974	72.71413	67.40112	0.80234	0.007295	0.017489	CNIH3	chr1	+	2.25E+08	2.25E+08	2558
ENSG00000(	324.2029	335.9963	216.3839	567.7993	565.1452	859.7753	-1.1756	9.17E-09	4.61E-08	C1orf35	chr1	-	2.28E+08	2.28E+08	3554
ENSG00000(	479.5717	598.531	575.2644	773.046	773.1629	628.8032	-0.39568	0.009119	0.021401	MBOAT2	chr2	-	8992820	9143942	7751
ENSG00000(	2515.939	2196.621	2704.798	4349.133	4708.93	4044.889	-0.81938	6.72E-12	4.34E-11	PARP1	chr1	-	2.27E+08	2.27E+08	3958
ENSG00000(	137.7603	140.9017	130.622	289.8922	240.2328	256.4531	-0.93791	1.94E-06	7.79E-06	PSEN2	chr1	+	2.27E+08	2.27E+08	2465
ENSG00000(	212.3373	198.7075	200.5509	227.719	173.9616	216.1768	-0.01584	0.93587	0.96144	PYCR2	chr1	-	2.26E+08	2.26E+08	3149
ENSG00000(	728.1617	715.3469	916.9926	2404.533	2495.291	2256.294	-1.5978	2.30E-34	4.04E-33	LBR	chr1	-	2.26E+08	2.26E+08	3774
ENSG00000(	51.7896	61.41867	38.263	269.6672	322.1512	364.9524	-2.6318	1.33E-27	1.83E-26	WNT9A	chr1	-	2.28E+08	2.28E+08	3971
ENSG00000(	2425.825	2414.597	1976.482	429.2203	457.4547	438.9293	2.358	3.58E-74	1.68E-72	EPHX1	chr1	+	2.26E+08	2.26E+08	1776
ENSG00000(	0	0	0	8.988907	1.840864	1.64393	-2.7758	0.033395	0.068248	REN	chr1	-	2.04E+08	2.04E+08	1456
ENSG00000(	129.474	105.9773	117.4278	850.2007	936.0793	904.9834	-2.9172	1.86E-72	8.46E-71	SOX13	chr1	+	2.04E+08	2.04E+08	3579
ENSG00000(	94.25706	101.1602	92.35896	50.18806	58.90765	39.45432	0.94495	0.001475	0.004014	ETNK2	chr1	-	2.04E+08	2.04E+08	2486
ENSG00000(	459.8916	692.4654	386.5882	5.992604	9.20432	1.64393	6.404	7.37E-64	2.83E-62	PPFIA4	chr1	+	2.03E+08	2.03E+08	6434
ENSG00000(	7.250543	10.83859	11.87472	112.3613	92.0432	93.704	-3.2538	3.09E-15	2.47E-14	PLEKHA6	chr1	-	2.04E+08	2.04E+08	5091
ENSG00000(	1.035792	0	0	0	1.840864	0	-0.17777	0.89006	NA	PTPN7	chr1	-	2.02E+08	2.02E+08	3765
ENSG00000(	20.71584	12.04288	25.06886	55.43159	92.0432	71.51095	-1.877	3.99E-06	1.55E-05	SYT2	chr1	-	2.03E+08	2.03E+08	7614
ENSG00000(	604.9025	621.4125	567.3479	859.1897	758.436	948.5475	-0.51539	0.000217	0.000675	ARL8A	chr1	-	2.02E+08	2.02E+08	1793
ENSG00000(	1866.497	1938.903	1810.236	50.93714	57.98722	64.11326	5.0062	2.45E-218	8.46E-216	OSR1	chr2	-	19551246	19558414	4175
ENSG00000(	3.107376	8.430014	3.958241	1.498151	0	0.821965	2.046	0.073973	0.13602	GDF7	chr2	+	20866424	20873418	4162
ENSG00000(	6166.069	5868.494	5545.496	4668.988	4323.269	4058.863	0.42916	6.40E-05	0.000214	PDIA6	chr2	-	10923517	10978103	2682
ENSG00000(	3171.595	3175.707	2871.044	2160.334	2191.549	2073.817	0.52013	1.22E-06	5.03E-06	RHOB	chr2	+	20646835	20649200	2366
ENSG00000(	13.46529	16.86003	9.235896	30.7121	20.2495	18.90519	-0.78313	0.15886	0.25566	ATP6V1C2	chr2	+	10861775	10925236	3102
ENSG00000(	871.101	918.8715	928.8673	1084.661	994.0666	985.5359	-0.17297	0.15714	0.25329	HNRPLL	chr2	-	38789120	38830728	4173
ENSG00000(	267.2343	256.5133	249.3692	108.616	121.497	164.393	0.96582	5.54E-06	2.12E-05	GALM	chr2	+	38893052	38968379	2484
ENSG00000(	90.1139	85.50443	124.0249	92.13629	73.63456	87.12828	0.23644	0.38839	0.5192	CAMKMT	chr2	+	44589089	44999731	1495
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	ABCG8	chr2	+	44066103	44105605	2665
ENSG00000(	1903.786	1988.279	2496.331	1432.232	1623.642	1336.515	0.53874	8.26E-05	0.000272	EML4	chr2	+	42396490	42559688	5549
ENSG00000(	3335.25	3245.555	3004.305	11300.55	8894.134	9928.514	-1.6488	1.30E-44	3.06E-43	CALM2	chr2	-	47272677	47403740	4502
ENSG00000(	35.21692	51.78437	18.47179	179.7781	108.611	147.9537	-2.0108	3.29E-09	1.73E-08	CHAC2	chr2	+	53994929	54002333	1321
ENSG00000(	14244.21	14983.75	10662.18	14230.94	11031.38	13747.36	0.032142	0.82103	0.88423	RPS27A	chr2	+	55459039	55462989	1159
ENSG00000(	51.7896	55.39724	72.56776	68.91495	55.22592	66.57916	-0.09101	0.77438	0.85191	WDPCP	chr2	-	63348518	64054977	5408
ENSG00000(	232.0174	264.9433	385.2688	353.5637	376.4567	302.4831	-0.2291	0.25748	0.37607	VPS54	chr2	-	64120035	64246206	3594
ENSG00000(	378.064	298.6634	478.9472	417.9842	709.6531	481.6714	-0.47459	0.024934	0.052846	ASXL2	chr2	-	25960557	26101385	8943
ENSG00000(	155.3688	192.686	189.9956	256.1838	220.9037	216.1768	-0.3673	0.063303	0.11902	ETAA1	chr2	+	67624451	67637677	3418
ENSG00000(	689.8374	686.444	551.515	1682.424	1589.586	2025.322	-1.453	3.31E-24	3.96E-23	SNRPG	chr2	-	70508494	70520903	1093
ENSG00000(	0	1.204288	13.19414	0.749076	4.60216	4.109825	0.46174	0.67924	0.78006	ABHD1	chr2	+	27346682	27353680	1400
ENSG00000(	129.474	144.5145	141.1773	275.6598	253.1188	327.142	-1.0402	1.71E-07	7.66E-07	MEIS1	chr2	+	66660584	66801001	5111
ENSG00000(	0	0	1.319414	0	0.920432	3.28786	-0.84165	0.53503	NA	TRIM43B	chr2	-	96142715	96150479	1668
ENSG00000(	0	0	5.277655	2.996302	0	0	0.41319	0.75997	0.84134	TRIM43	chr2	+	96257766	96265526	1682
ENSG00000(	945.678	994.7417	965.8109	1429.236	1165.267	1201.713	-0.38525	0.002743	0.007136	CIAO1	chr2	+	96931870	96939087	3588

ENSG00000(	303.487	248.0833	262.5633	139.3281	171.2004	166.8589	0.76943	7.91E-05	0.000262	ZNF514	chr2	-	95813075	95831158	5593
ENSG00000(	3626.307	3653.809	4003.101	5335.665	5810.687	4524.917	-0.47309	8.42E-05	0.000277	SNRNP200	chr2	-	96940074	96971297	7165
ENSG00000(	929.1053	1022.44	876.0908	853.197	784.2081	766.8933	0.23334	0.071199	0.1317	MRPS5	chr2	-	95752952	95815179	3680
ENSG00000(	22.78742	16.86003	18.47179	9.737982	21.16994	6.575719	0.61258	0.31189	0.43818	ANKRD53	chr2	+	71205510	71212626	2182
ENSG00000(	206.1226	228.8147	159.6491	482.4047	364.4911	502.2206	-1.1746	1.56E-09	8.39E-09	TPRKB	chr2	-	73956231	73964527	819
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	NAT8	chr2	-	73867959	73869520	947
ENSG00000(	566.5782	584.0795	738.8717	527.3492	790.6511	560.5801	0.008402	0.96221	0.97815	EXOC6B	chr2	-	72403113	73053170	5918
ENSG00000(	655.6563	669.584	592.4168	290.6413	373.6954	363.3085	0.89914	7.94E-09	4.02E-08	SFXN5	chr2	-	73169165	73302747	4140
ENSG00000(	1546.437	1519.811	1604.407	1769.316	1292.287	1279.799	0.10447	0.46311	0.59246	TEX261	chr2	-	71213068	71222075	3579
ENSG00000(	4.143168	2.408575	0	6.74168	4.60216	6.575719	-1.1664	0.25613	0.37445	DQX1	chr2	-	74745258	74753463	2689
ENSG00000(	487.858	497.3708	439.3648	432.9657	310.1856	348.5131	0.38136	0.023332	0.049788	DUSP11	chr2	-	73989311	74007284	2175
ENSG00000(	203.0152	181.8474	213.745	87.64184	122.4175	110.9653	0.89572	6.15E-05	0.000206	ST6GAL2	chr2	-	1.07E+08	1.08E+08	7275
ENSG00000(	84.93494	98.75159	88.40072	70.4131	57.98722	73.97684	0.41963	0.13447	0.2235	NPHP1	chr2	-	1.11E+08	1.11E+08	10006
ENSG00000(	109.7939	98.75159	88.40072	0.749076	4.60216	0	5.5589	3.24E-20	3.31E-19	MALL	chr2	-	1.11E+08	1.11E+08	3061
ENSG00000(	45.57484	24.08575	22.43003	93.63444	95.72493	98.63579	-1.601	3.99E-06	1.55E-05	THNSL2	chr2	+	88469835	88486146	3649
ENSG00000(	1014.04	1156.116	1106.988	1352.081	1443.237	1246.099	-0.30211	0.014456	0.03241	RALB	chr2	+	1.21E+08	1.21E+08	2344
ENSG00000(	0	0	0	38.20285	41.41944	28.76877	-6.0082	1.29E-08	6.41E-08	C1QL2	chr2	-	1.2E+08	1.2E+08	2043
ENSG00000(	145.0109	128.8588	170.2044	377.5341	294.5382	365.7744	-1.2215	5.43E-10	3.03E-09	TMEM177	chr2	+	1.2E+08	1.2E+08	1738
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	NT5DC4	chr2	+	1.13E+08	1.14E+08	2448
ENSG00000(	263.0911	249.2876	174.1626	223.9736	223.665	222.7525	0.037755	0.85148	0.90523	RABL2A	chr2	+	1.14E+08	1.14E+08	2904
ENSG00000(	1182.874	1085.063	1423.647	1645.719	1557.371	1351.31	-0.30299	0.02853	0.059487	SLC20A1	chr2	+	1.13E+08	1.13E+08	3381
ENSG00000(	42.46747	14.45145	44.86007	46.44268	35.89685	31.23467	-0.15483	0.73251	0.82115	FBLN7	chr2	+	1.13E+08	1.13E+08	4598
ENSG00000(	0	0	1.319414	1.498151	0	9.041614	-1.8199	0.16582	0.26453	RP11-395L	chr2	+	1.14E+08	1.14E+08	768
ENSG00000(	159.512	136.0845	151.7326	287.645	185.9273	180.8323	-0.54625	0.018578	0.040599	ZC3H8	chr2	-	1.13E+08	1.13E+08	1813
ENSG00000(	22.78742	34.92434	17.15238	35.20655	34.97642	32.8786	-0.44611	0.31738	0.44424	LIPT1	chr2	+	99771418	99779620	1543
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	TRIM43CP	chr2	-	97691718	97697373	1028
ENSG00000(	2.071584	3.612863	0	1.498151	1.840864	3.28786	-0.14948	0.90155	0.93886	CNGA3	chr2	+	98962618	99015064	3841
ENSG00000(	70.43385	103.5687	79.16483	222.4754	156.4734	138.9121	-1.0263	0.000117	0.000378	FAHD2B	chr2	-	97749320	97760619	1388
ENSG00000(	15.53688	36.12863	38.263	32.21025	15.64734	11.50751	0.56001	0.29713	0.42161	LYG1	chr2	-	99900701	99921205	1038
ENSG00000(	692.9448	590.101	771.8571	91.38722	90.20234	69.86702	3.0162	8.61E-60	2.98E-58	AFF3	chr2	-	1E+08	1.01E+08	8135
ENSG00000(	1493.612	1534.263	1706.002	1190.281	1365.001	961.699	0.42753	0.002759	0.007173	UBXN4	chr2	+	1.36E+08	1.37E+08	4006
ENSG00000(	0	0	0	84.64554	86.52061	76.44274	-7.1053	2.12E-12	1.42E-11	NXPH2	chr2	-	1.39E+08	1.4E+08	1052
ENSG00000(	156.4046	172.2131	219.0227	375.2868	404.0696	327.964	-1.0146	1.08E-07	4.93E-07	SPOPL	chr2	+	1.39E+08	1.39E+08	6025
ENSG00000(	0	0	0	0	9.20432	1.64393	-2.396	0.074141	0.13624	THSD7B	chr2	+	1.38E+08	1.38E+08	6111
ENSG00000(	4.143168	0	2.638828	5.243529	11.04518	15.61733	-1.8991	0.04168	0.082986	GPR17	chr2	+	1.28E+08	1.28E+08	2598
ENSG00000(	515.8244	480.5108	395.8241	812.747	845.877	935.3961	-0.8929	1.43E-09	7.73E-09	POLR2D	chr2	-	1.29E+08	1.29E+08	2327
ENSG00000(	719.8754	675.6054	792.9677	767.8024	927.7955	718.3973	-0.14089	0.33109	0.45898	AMMECR1L	chr2	-	1.29E+08	1.29E+08	4658
ENSG00000(	7.250543	9.634302	21.11062	230.7153	161.0756	180.0103	-3.8781	2.87E-26	3.73E-25	GALNT13	chr2	+	1.55E+08	1.55E+08	5536
ENSG00000(	472.3211	513.0266	595.0556	1401.52	1428.51	1291.307	-1.3814	1.18E-24	1.44E-23	PKP4	chr2	+	1.59E+08	1.6E+08	5777
ENSG00000(	253.769	226.4061	269.1604	256.9329	218.1424	210.423	0.12625	0.49722	0.62564	SCRN3	chr2	+	1.75E+08	1.75E+08	3037
ENSG00000(	1052.365	965.8388	1043.656	557.3122	532.0097	443.8611	0.99518	6.99E-13	4.83E-12	KIAA1715	chr2	-	1.77E+08	1.77E+08	7610
ENSG00000(	9.322127	7.225726	3.958241	67.4168	72.71413	77.2647	-3.2677	7.41E-12	4.76E-11	ZNF385B	chr2	-	1.8E+08	1.81E+08	3288
ENSG00000(	258.948	249.2876	267.841	113.8595	152.7917	104.3895	1.0613	4.67E-07	2.01E-06	TMEFF2	chr2	-	1.93E+08	1.93E+08	3364
ENSG00000(	245.4827	230.019	217.7033	1555.081	1436.794	1254.318	-2.6054	1.40E-71	6.28E-70	CDCA7	chr2	+	1.74E+08	1.74E+08	3176

ENSG00000(	194.7289	163.7831	221.6615	373.0396	423.3987	367.4183	-1.0006	3.54E-08	1.70E-07	DLX1	chr2	+	1.73E+08	1.73E+08	2640
ENSG00000(	630.7973	643.0896	870.8131	362.5526	451.9321	309.8808	0.92746	2.53E-07	1.12E-06	UBR3	chr2	+	1.71E+08	1.71E+08	8005
ENSG00000(	14.50109	12.04288	7.916483	38.20285	22.09037	32.8786	-1.3683	0.010553	0.024398	PHOSPHO2	chr2	+	1.71E+08	1.71E+08	1125
ENSG00000(	876.28	852.6357	1133.376	753.57	842.1953	685.5187	0.32567	0.030152	0.062457	GULP1	chr2	+	1.89E+08	1.89E+08	7427
ENSG00000(	418.4599	399.8235	678.1787	116.8558	202.495	111.7872	1.7827	4.90E-13	3.43E-12	FAM171B	chr2	+	1.88E+08	1.88E+08	5819
ENSG00000(	8700.652	8478.186	8399.388	15592.01	16859.55	15115.11	-0.89377	1.63E-19	1.61E-18	HSPD1	chr2	-	1.98E+08	1.98E+08	2455
ENSG00000(	111.8655	90.32158	121.3861	196.2578	191.4499	193.9837	-0.84157	0.000131	0.000422	CCDC150	chr2	+	1.98E+08	1.98E+08	3685
ENSG00000(	107.7224	80.68728	92.35896	265.9218	278.8909	248.2334	-1.4847	3.07E-12	2.03E-11	METTL21A	chr2	-	2.08E+08	2.08E+08	4805
ENSG00000(	4.143168	9.634302	1.319414	1.498151	5.522592	4.109825	0.38368	0.69931	0.79556	UNC80	chr2	+	2.11E+08	2.11E+08	13562
ENSG00000(	0	0	7.916483	20.97412	33.13555	20.54912	-2.9845	0.000217	0.000675	PTH2R	chr2	+	2.09E+08	2.1E+08	2713
ENSG00000(	4.143168	6.021439	2.638828	0.749076	0	4.109825	1.0721	0.34654	0.47608	CPO	chr2	+	2.08E+08	2.08E+08	1209
ENSG00000(	188.5141	192.686	362.8388	80.90016	184.0864	110.9653	0.97394	0.001162	0.003227	NBEAL1	chr2	+	2.04E+08	2.04E+08	10938
ENSG00000(	218.5521	303.4805	294.2293	256.1838	225.5058	222.7525	0.20789	0.27934	0.40157	KANSL1L	chr2	-	2.11E+08	2.11E+08	4754
ENSG00000(	208.1942	221.5889	196.5927	440.4564	402.2288	404.4067	-0.98956	2.76E-09	1.45E-08	SPAG16	chr2	+	2.14E+08	2.15E+08	4751
ENSG00000(	27.96638	13.24716	58.05421	41.19916	52.46462	43.56414	-0.46109	0.31648	0.44331	ABCA12	chr2	-	2.16E+08	2.16E+08	9100
ENSG00000(	571.7571	520.2523	564.7091	503.3788	480.4655	432.3535	0.22565	0.11749	0.20039	SUMF1	chr3	-	3742498	4508965	3150
ENSG00000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	NYAP2	chr2	+	2.26E+08	2.27E+08	4828
ENSG00000(	457.82	493.758	559.4314	400.7554	393.9449	375.638	0.36575	0.015497	0.034478	RHBDD1	chr2	+	2.28E+08	2.28E+08	5151
ENSG00000(	7.250543	7.225726	7.916483	522.1057	470.3408	530.1674	-5.9811	7.83E-63	2.91E-61	CXCR7	chr2	+	2.37E+08	2.37E+08	2203
ENSG00000(	1.035792	4.817151	0	0.749076	0.920432	0	1.0607	0.42644	0.55667	TRPM8	chr2	+	2.35E+08	2.35E+08	5621
ENSG00000(	67.32647	52.98866	58.05421	89.13999	67.19154	54.24968	-0.23581	0.46473	0.59381	HES6	chr2	-	2.39E+08	2.39E+08	1600
ENSG00000(	4.143168	1.204288	1.319414	0.749076	0.920432	0	1.2762	0.3271	0.45476	ESPNL	chr2	+	2.39E+08	2.39E+08	4836
ENSG00000(	193.6931	172.2131	168.885	104.1215	141.7465	121.6508	0.54191	0.014667	0.032824	ANKMY1	chr2	-	2.41E+08	2.42E+08	4640
ENSG00000(	625.6183	616.5953	610.8886	1091.403	1073.224	1046.361	-0.79127	1.17E-10	6.92E-10	COPS7B	chr2	+	2.33E+08	2.33E+08	3299
ENSG00000(	315.9165	296.2548	361.5194	493.6408	468.4999	400.2969	-0.4843	0.003241	0.008331	DIS3L2	chr2	+	2.33E+08	2.33E+08	4671
ENSG00000(	4.143168	3.612863	1.319414	8.239831	2.761296	9.041614	-0.96667	0.31159	0.43784	CPNE9	chr3	+	9745491	9771592	2068
ENSG00000(	99.43602	116.8159	137.219	795.5182	886.376	923.8886	-2.8775	8.28E-64	3.16E-62	FANCD2	chr3	+	10068098	10143614	5219
ENSG00000(	256.8764	275.7819	286.3128	399.2573	266.0048	313.1686	-0.25841	0.17313	0.27446	TAMM41	chr3	-	11831916	11888393	2768
ENSG00000(	2585.337	2594.036	2572.857	491.3936	971.9762	845.8019	1.7405	3.38E-21	3.59E-20	VGLL4	chr3	-	11597544	11762220	3725
ENSG00000(	760.2713	798.4428	847.0636	906.3814	994.987	886.9001	-0.21276	0.094716	0.16761	RAB5A	chr3	+	19988571	20026667	2536
ENSG00000(	1979.398	1771.507	1670.378	993.2742	927.7955	1023.346	0.87922	4.86E-13	3.41E-12	FAM134A	chr2	+	2.2E+08	2.2E+08	4618
ENSG00000(	2208.308	1994.3	1646.628	1023.237	1006.953	1172.944	0.86719	2.48E-10	1.42E-09	CTDSP1	chr2	+	2.19E+08	2.19E+08	2638
ENSG00000(	579.0077	606.961	740.1911	1489.162	1434.953	1514.059	-1.2033	1.47E-19	1.46E-18	RQCD1	chr2	+	2.19E+08	2.19E+08	4079
ENSG00000(	37.28851	24.08575	38.263	863.6841	874.4104	780.0447	-4.6278	1.37E-101	1.06E-99	4-Mar	chr2	-	2.17E+08	2.17E+08	4447
ENSG00000(	488.8938	557.5852	431.4483	637.4633	682.9605	664.9696	-0.42356	0.003826	0.009705	STK11IP	chr2	+	2.2E+08	2.2E+08	3615
ENSG00000(	1252.272	1324.716	1059.489	626.9762	627.7346	668.2575	0.91759	5.59E-12	3.63E-11	GMPPA	chr2	+	2.2E+08	2.2E+08	4942
ENSG00000(	16.57267	15.65574	6.597069	44.94453	80.99802	60.00344	-2.1717	2.36E-06	9.40E-06	GRIP2	chr3	-	14530619	14583588	7751
ENSG00000(	223.7311	225.2018	244.0915	411.2425	343.3211	344.4033	-0.66451	0.000118	0.00038	EAF1	chr3	+	15468862	15484120	4690
ENSG00000(	10.35792	1.204288	11.87472	208.243	239.3123	173.4346	-4.6175	1.17E-30	1.81E-29	CNTN4	chr3	+	2140497	3099645	5198
ENSG00000(	664.9784	741.8412	812.7589	1194.776	1048.372	941.9718	-0.5212	0.000237	0.000732	DYNC1LI1	chr3	-	32567463	32612366	4791
ENSG00000(	424.6747	441.9736	477.6278	259.9292	267.8457	221.1086	0.84041	2.79E-07	1.23E-06	RBMS3	chr3	+	29322473	30051886	8208
ENSG00000(	2.071584	0	1.319414	3.745378	1.840864	3.28786	-0.98467	0.41824	0.54889	GADL1	chr3	-	30767692	30936257	4509
ENSG00000(	140.8677	78.2787	114.789	552.0687	585.3947	486.6032	-2.2635	2.53E-28	3.60E-27	OSBPL10	chr3	-	31699382	32119072	7723
ENSG00000(	196.8005	243.2661	178.1209	423.2277	281.6522	346.8692	-0.76344	0.000176	0.000555	GTDC2	chr3	-	43120724	43147568	2544

ENSG00000	0	3.612863	0	27.7158	33.13555	18.90519	-3.9377	3.95E-06	1.53E-05	CCBP2	chr3	+	42846244	42949597	3605
ENSG00000	1.035792	0	0	7.490755	11.04518	7.397684	-3.2868	0.003978	0.010061	FAM198A	chr3	+	43020759	43101703	3121
ENSG00000	138.7961	103.5687	112.1502	349.0692	258.6414	391.2553	-1.4822	1.25E-11	7.93E-11	CSRNP1	chr3	-	39183346	39196053	3148
ENSG00000	1021.291	904.4201	819.356	706.3782	649.825	598.3905	0.48949	0.000482	0.001421	SLC25A38	chr3	+	39424839	39438842	2123
ENSG00000	33.14534	32.51577	32.98534	302.6265	530.1688	416.7362	-3.6256	2.02E-42	4.50E-41	ITGA9	chr3	+	37493606	37865005	7889
ENSG00000	13.46529	10.83859	5.277655	1.498151	0	5.753754	1.7345	0.066519	0.12423	SLC22A14	chr3	+	38323785	38360066	2277
ENSG00000	1227.413	1164.546	1564.825	1068.182	1236.14	1000.331	0.2587	0.075408	0.13825	GOLGA4	chr3	+	37284668	37408242	7772
ENSG00000	387.3862	468.4679	469.7113	1703.398	1675.186	1413.78	-1.8512	6.43E-40	1.33E-38	CTDSPL	chr3	+	37903451	38025960	4640
ENSG00000	155.3688	166.1917	143.8161	214.2356	168.4391	167.6808	-0.24141	0.25624	0.37456	STAC	chr3	+	36421836	36589499	3227
ENSG00000	1240.879	1112.762	1373.51	270.4163	277.05	304.949	2.1224	5.31E-51	1.51E-49	IQSEC1	chr3	-	12938719	13114617	5279
ENSG00000	67.32647	50.58008	47.4989	42.69731	47.86246	35.34449	0.39325	0.26585	0.38585	CAND2	chr3	+	12837971	12913415	4573
ENSG00000	17327.76	17835.5	13648.02	12727.54	9369.998	11176.26	0.55138	6.14E-05	0.000206	RPL32	chr3	-	12875984	12883087	2117
ENSG00000	3429.507	3452.693	4328.997	720.6107	886.376	667.4355	2.2957	3.19E-59	1.09E-57	PTPRG	chr3	+	61547243	62283288	9021
ENSG00000	1132.121	1213.922	1315.456	1612.76	1794.842	1466.385	-0.41218	0.001172	0.003252	IL17RD	chr3	-	57124010	57204334	8720
ENSG00000	344.9187	374.5335	391.8659	406.748	372.775	373.1721	-0.05443	0.72534	0.81581	SHQ1	chr3	-	72798428	72911065	4024
ENSG00000	294.1649	285.4162	222.9809	317.608	324.9125	357.5547	-0.31331	0.076749	0.14025	SLC25A26	chr3	+	66119285	66438530	3869
ENSG00000	691.909	770.7441	860.2578	1036.721	1029.963	1022.524	-0.41186	0.001631	0.004412	UBA3	chr3	-	69103881	69129559	2154
ENSG00000	3018.298	3039.622	3091.386	1364.067	1319.899	1274.868	1.2066	3.41E-30	5.21E-29	ARL6IP5	chr3	+	69134095	69155217	2101
ENSG00000	662.9068	732.2069	943.3809	440.4564	426.16	397.0091	0.88313	3.14E-08	1.51E-07	TMF1	chr3	-	69068978	69101484	6886
ENSG00000	587.294	596.1224	808.8006	57.67882	62.58938	45.20807	3.5698	8.26E-68	3.46E-66	LRIG1	chr3	-	66429221	66551687	5283
ENSG00000	1.035792	0	0	0	1.840864	0	-0.17777	0.89006	NA	LRTM1	chr3	-	54952264	55001115	1423
ENSG00000	989.1813	1016.419	1085.878	393.2647	510.8398	388.7894	1.2553	1.54E-17	1.39E-16	LIMD1	chr3	+	45596886	45727830	11331
ENSG00000	170.9057	196.2989	191.315	147.5679	202.495	153.7074	0.14915	0.48453	0.61371	ZNF660	chr3	+	44619715	44641186	5834
ENSG00000	221.6595	226.4061	242.7721	170.0401	123.3379	129.8705	0.69893	0.00081	0.002307	NFKBIZ	chr3	+	1.02E+08	1.02E+08	3923
ENSG00000	2253.883	2208.664	2811.671	258.4311	214.4607	175.0785	3.4748	4.47E-107	3.80E-105	COL8A1	chr3	+	99357319	99518070	5705
ENSG00000	942.5706	838.1843	976.3662	311.6154	350.6846	273.7143	1.5549	1.54E-25	1.95E-24	NXPE3	chr3	+	1.01E+08	1.02E+08	8152
ENSG00000	2.071584	0	0	0	0	0	0.74702	0.55047	NA	GPR128	chr3	+	1E+08	1E+08	3140
ENSG00000	420.5315	321.5448	395.8241	25.46857	36.81728	27.94681	3.638	3.69E-52	1.08E-50	MYH15	chr3	-	1.08E+08	1.08E+08	7074
ENSG00000	2913.683	2825.259	3650.818	1519.125	2170.379	1542.828	0.84115	5.00E-08	2.36E-07	PHLDB2	chr3	+	1.11E+08	1.12E+08	6127
ENSG00000	558.2918	532.2952	568.6673	439.7073	387.5019	420.0241	0.40972	0.004278	0.010746	ABHD10	chr3	+	1.12E+08	1.12E+08	2590
ENSG00000	7.250543	19.2686	9.235896	10.48706	18.40864	18.08323	-0.37142	0.56028	0.68074	TAGLN3	chr3	+	1.12E+08	1.12E+08	1488
ENSG00000	3.107376	2.408575	9.235896	0	0	1.64393	2.2395	0.063579	0.11944	PLA1A	chr3	+	1.19E+08	1.19E+08	1786
ENSG00000	425.7105	302.2762	471.0307	412.7406	436.2848	331.2519	0.022536	0.90539	0.94157	RABL3	chr3	-	1.2E+08	1.2E+08	3883
ENSG00000	35.21692	13.24716	54.09597	92.88537	82.83888	103.5676	-1.4222	0.000242	0.000747	ADPRH	chr3	+	1.19E+08	1.19E+08	4546
ENSG00000	3.107376	3.612863	5.277655	27.7158	38.65814	22.19305	-2.7142	3.51E-05	0.000122	IGSF11	chr3	-	1.19E+08	1.19E+08	3558
ENSG00000	508.5738	578.0581	546.2373	827.7285	551.3388	605.7881	-0.28226	0.093901	0.16647	ATG3	chr3	-	1.12E+08	1.12E+08	3010
ENSG00000	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	NR1I2	chr3	+	1.19E+08	1.2E+08	4417
ENSG00000	951.8928	871.9043	794.2871	452.4416	627.7346	592.6367	0.6462	3.19E-05	0.000111	BOC	chr3	+	1.13E+08	1.13E+08	5750
ENSG00000	1766.025	1743.809	1738.987	1194.776	1123.847	1281.443	0.54282	2.10E-06	8.43E-06	SRPRB	chr3	+	1.34E+08	1.34E+08	2016
ENSG00000	2.071584	2.408575	3.958241	325.8479	334.1168	269.6045	-6.5354	3.68E-36	6.81E-35	TMEM108	chr3	+	1.33E+08	1.33E+08	4833
ENSG00000	81.82756	93.93444	113.4696	0	3.681728	3.28786	5.1756	4.22E-20	4.29E-19	AGTR1	chr3	+	1.48E+08	1.48E+08	2412
ENSG00000	10.35792	9.634302	21.11062	82.39831	184.0864	87.95025	-3.0435	1.46E-12	9.88E-12	MED12L	chr3	+	1.51E+08	1.51E+08	10744
ENSG00000	1965.933	2108.708	1789.125	1791.04	1214.05	1270.758	0.45367	0.002911	0.007534	EIF2A	chr3	+	1.5E+08	1.5E+08	2198
ENSG00000	1.035792	0	0	5.243529	1.840864	4.109825	-2.1229	0.095781	0.16924	ALDH1L1	chr3	-	1.26E+08	1.26E+08	4604

ENSG00000(	235.1248	230.019	357.5611	364.7998	441.8074	378.9258	-0.52707	0.007207	0.01731	OSBPL11	chr3	-	1.25E+08	1.25E+08	4191
ENSG00000(	215.4447	211.9546	245.411	186.5198	195.1316	147.9537	0.34269	0.088239	0.1581	TRPC1	chr3	+	1.42E+08	1.43E+08	4324
ENSG00000(	67.32647	61.41867	88.40072	137.0808	121.497	91.23811	-0.68486	0.015403	0.034292	NCEH1	chr3	-	1.72E+08	1.72E+08	4687
ENSG00000(	0	4.817151	0	2.996302	7.363456	6.575719	-1.4101	0.20949	0.31916	FAM86B2	chr8	-	12282913	12293915	1268
ENSG00000(	2911.611	2939.666	3894.909	2430.001	2901.202	2266.979	0.35801	0.011948	0.027293	LPP	chr3	+	1.88E+08	1.89E+08	18278
ENSG00000(	348.0261	360.082	354.9223	200.7522	207.0972	216.9987	0.76371	4.73E-06	1.82E-05	TMEM44	chr3	-	1.94E+08	1.94E+08	2490
ENSG00000(	342.8471	354.0606	317.9787	408.9952	443.6482	389.6114	-0.28944	0.06328	0.11898	KIAA0226	chr3	-	1.97E+08	1.97E+08	6955
ENSG00000(	91.14969	96.34302	73.88717	90.63814	99.40666	139.734	-0.32924	0.23309	0.34682	AMT	chr3	-	49454211	49460186	3272
ENSG00000(	414.3168	426.3179	430.1289	375.2868	303.7426	278.6461	0.40492	0.015622	0.03472	TCTA	chr3	+	49449639	49453908	2146
ENSG00000(	149.154	130.0631	135.8996	161.0512	152.7917	156.1733	-0.17698	0.4067	0.53759	NICN1	chr3	-	49460379	49466759	2616
ENSG00000(	6.214751	0	3.958241	8.988907	3.681728	2.465895	-0.46622	0.65305	0.75872	UCN2	chr3	-	48599160	48601206	1481
ENSG00000(	246.5185	258.9219	308.7428	511.6186	616.6894	539.209	-1.0323	3.10E-10	1.77E-09	VPRBP	chr3	-	51433298	51534010	4529
ENSG00000(	1507.077	1620.971	1283.79	2062.954	1783.797	2374.657	-0.49435	0.000387	0.001157	MANF	chr3	+	51422478	51426828	1509
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC062028.	chr2	-	11239977	11272947	1635
ENSG00000(	89.0781	81.89156	83.12307	41.19916	47.86246	44.38611	0.92026	0.002371	0.006237	CCDC39	chr3	-	1.8E+08	1.81E+08	4451
ENSG00000(	0	0	2.638828	8.988907	8.283888	2.465895	-2.2535	0.048301	0.094165	STXBP5L	chr3	+	1.21E+08	1.21E+08	9496
ENSG00000(	6.214751	18.06432	5.277655	41.94823	35.89685	46.03004	-1.9865	0.000203	0.000632	EAF2	chr3	+	1.22E+08	1.22E+08	992
ENSG00000(	0	0	0	44.94453	44.18074	36.16646	-6.2075	3.00E-09	1.58E-08	ILDR1	chr3	-	1.22E+08	1.22E+08	2659
ENSG00000(	17.60846	6.021439	15.83297	0.749076	2.761296	0	3.0155	0.001407	0.003848	TM4SF19	chr3	-	1.96E+08	1.96E+08	1582
ENSG00000(	0	0	3.958241	1.498151	0	0.821965	0.3778	0.78033	0.85524	MUC4	chr3	-	1.95E+08	1.96E+08	17110
ENSG00000(	2086.085	1925.656	2654.661	877.1675	1344.751	938.6839	1.0731	1.91E-10	1.11E-09	SLIT2	chr4	+	20254883	20622184	6390
ENSG00000(	585.2224	574.4452	505.3355	949.0787	809.0597	805.5256	-0.62043	9.93E-06	3.69E-05	EIF2B5	chr3	+	1.84E+08	1.84E+08	3460
ENSG00000(	23.82321	10.83859	0	0	4.60216	9.863579	1.0757	0.27867	0.40079	AHSG	chr3	+	1.86E+08	1.86E+08	1711
ENSG00000(	50.7538	90.32158	60.69303	189.5161	128.8605	147.9537	-1.2007	2.24E-05	7.98E-05	ECE2	chr3	+	1.84E+08	1.84E+08	3445
ENSG00000(	8.286335	13.24716	9.235896	6.74168	10.12475	7.397684	0.31937	0.65559	0.76063	VWA5B2	chr3	+	1.84E+08	1.84E+08	4120
ENSG00000(	402.9231	387.7806	354.9223	216.4828	235.6306	347.6912	0.51659	0.008813	0.020745	DGKQ	chr4	-	952675	980683	4636
ENSG00000(	519.9675	496.1665	638.5963	703.3819	736.3456	617.2957	-0.31416	0.037762	0.076114	FIP1L1	chr4	+	54243810	55161439	3180
ENSG00000(	32.10955	38.53721	32.98534	3.745378	2.761296	6.575719	2.8284	1.61E-06	6.54E-06	SLC26A1	chr4	-	972861	987228	3660
ENSG00000(	306.5944	349.2434	277.0769	856.1934	824.7071	1003.619	-1.5193	3.62E-23	4.16E-22	LYAR	chr4	-	4269428	4291896	1569
ENSG00000(	179.192	146.9231	209.7868	205.9958	208.0176	220.2866	-0.24339	0.23285	0.34652	CENPC1	chr4	-	68337521	68411324	3885
ENSG00000(	627.6899	693.6697	973.7274	1.498151	0	0	9.4501	1.85E-41	3.99E-40	EPHA5	chr4	-	66185281	66536213	8266
ENSG00000(	99.43602	99.95588	159.6491	5.992604	0.920432	9.041614	4.325	3.16E-21	3.37E-20	CORIN	chr4	-	47596015	47840123	5378
ENSG00000(	729.1975	658.7454	942.0614	248.6931	325.8329	305.7709	1.3991	6.99E-16	5.81E-15	ATP10D	chr4	+	47487305	47595503	6655
ENSG00000(	565.5424	491.3494	511.9325	470.4194	374.6158	627.1592	0.091085	0.61958	0.7319	OCIAD2	chr4	-	48887036	48908954	1886
ENSG00000(	25.8948	45.76293	31.66593	14.23244	11.96562	16.4393	1.2289	0.01196	0.027318	SLC10A4	chr4	+	48485360	48491213	1790
ENSG00000(	821.383	881.5386	827.2724	205.9958	253.1188	226.8623	1.8795	3.79E-37	7.24E-36	SCD5	chr4	-	83550692	83720010	3101
ENSG00000(	4.143168	4.817151	5.277655	140.0771	78.23672	96.1699	-4.3115	1.62E-17	1.45E-16	PLAC8	chr4	-	84011201	84058228	2253
ENSG00000(	559.3276	546.7466	560.7509	1302.642	1104.518	1283.909	-1.1448	1.70E-18	1.61E-17	ENOPH1	chr4	+	83351715	83382244	2025
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	GC	chr4	-	72607410	72669758	1972
ENSG00000(	88.04231	79.48299	91.03955	205.2467	173.9616	203.0253	-1.1642	2.98E-07	1.30E-06	TRMT10A	chr4	-	1E+08	1E+08	3694
ENSG00000(	225.8026	242.0618	294.2293	269.6672	250.3575	217.8207	0.043404	0.81872	0.88294	KLHL8	chr4	-	88081255	88141760	5621
ENSG00000(	98.40023	86.70872	104.2337	84.64554	78.23672	84.66239	0.22163	0.39843	0.52949	SNCA	chr4	-	90645250	90759466	3173
ENSG00000(	456.7842	434.7479	480.2666	317.608	265.0844	222.7525	0.76358	1.12E-05	4.13E-05	TBCK	chr4	-	1.07E+08	1.07E+08	5383
ENSG00000(	2143.053	2171.331	2493.692	1505.642	1615.358	1353.776	0.60401	8.11E-07	3.39E-06	CAMK2D	chr4	-	1.14E+08	1.15E+08	5947

ENSG00000(	264.1269	295.0505	299.5069	629.9725	440.8869	421.668	-0.79621	1.81E-05	6.52E-05	CISD2	chr4	+	1.04E+08	1.04E+08	2327
ENSG00000(	234.089	320.3405	324.5758	53.93344	29.45382	32.05663	2.8882	7.24E-28	1.01E-26	DDIT4L	chr4	-	1.01E+08	1.01E+08	2604
ENSG00000(	281.7354	207.1375	300.8263	52.43529	104.0088	82.19649	1.7169	2.94E-11	1.81E-10	ANK2	chr4	+	1.14E+08	1.14E+08	14196
ENSG00000(	70.43385	85.50443	91.03955	128.841	96.64536	80.55256	-0.31138	0.27192	0.39255	TIFA	chr4	-	1.13E+08	1.13E+08	3072
ENSG00000(	65.25489	56.60152	73.88717	149.8151	144.5078	155.3514	-1.1917	2.39E-06	9.49E-06	SPATA5	chr4	+	1.24E+08	1.24E+08	3341
ENSG00000(	324.2029	351.652	311.3817	2010.519	2125.277	1737.634	-2.5658	1.12E-79	6.03E-78	CCNA2	chr4	-	1.23E+08	1.23E+08	2797
ENSG00000(	381.1714	370.9206	341.7282	358.8072	479.5451	356.7328	-0.12477	0.46805	0.59732	METTL14	chr4	+	1.2E+08	1.2E+08	3887
ENSG00000(	133.6172	128.8588	145.1355	1628.49	1895.169	1471.317	-3.6044	4.31E-117	4.37E-115	USP53	chr4	+	1.2E+08	1.2E+08	6072
ENSG00000(	940.499	1153.708	1448.716	806.7544	879.0126	601.6783	0.62775	0.000353	0.001063	SETD7	chr4	-	1.4E+08	1.4E+08	7365
ENSG00000(	180.2278	151.7403	237.4945	358.0581	329.5147	311.5247	-0.81007	4.39E-05	0.000151	NAF1	chr4	-	1.64E+08	1.64E+08	2329
ENSG00000(	66.29068	72.25726	105.5531	53.93344	39.57858	36.16646	0.89031	0.007878	0.018759	1-Mar	chr4	-	1.64E+08	1.65E+08	5877
ENSG00000(	114.9729	96.34302	65.97069	320.6043	317.549	279.4681	-1.7056	2.72E-14	2.06E-13	SFRP2	chr4	-	1.55E+08	1.55E+08	2032
ENSG00000(	8966.851	9700.538	7961.343	6204.593	5440.674	5924.723	0.5988	1.32E-07	5.97E-07	RPS3A	chr4	+	1.52E+08	1.52E+08	1526
ENSG00000(	64.2191	77.07441	75.20659	16.47966	9.20432	11.50751	2.4691	1.23E-09	6.69E-09	RNF175	chr4	-	1.55E+08	1.55E+08	3203
ENSG00000(	437.1042	470.8765	523.8073	692.8949	659.9497	564.6899	-0.4218	0.004942	0.012256	PDGFC	chr4	-	1.58E+08	1.58E+08	4165
ENSG00000(	286.9144	313.1148	295.5487	356.56	383.8201	327.142	-0.25235	0.12219	0.20701	CBR4	chr4	-	1.7E+08	1.7E+08	3443
ENSG00000(	0	1.204288	0	0	0.920432	0.821965	-0.17164	0.89643	NA	GLRA3	chr4	-	1.76E+08	1.76E+08	8770
ENSG00000(	95.29286	79.48299	91.03955	71.16218	66.2711	84.66239	0.25658	0.35614	0.48566	CYP4V2	chr4	+	1.87E+08	1.87E+08	8646
ENSG00000(	33.14534	42.15007	40.90183	11.98521	8.283888	9.041614	1.9096	0.00011	0.000357	ROPN1L	chr5	+	10441636	10472141	1291
ENSG00000(	890.781	867.0872	782.4124	977.5436	1058.497	1460.632	-0.45882	0.00379	0.009622	NDUFS6	chr5	+	1801514	1816719	1082
ENSG00000(	2195.879	2129.181	2365.709	999.2668	1133.052	977.3163	1.1036	1.39E-20	1.44E-19	6-Mar	chr5	+	10353815	10435491	4734
ENSG00000(	7.250543	10.83859	3.958241	7.490755	4.60216	6.575719	0.21579	0.79163	0.86382	NKD2	chr5	+	1008944	1039058	2155
ENSG00000(	48.68222	55.39724	46.17948	4.494453	3.681728	9.041614	3.0019	6.14E-09	3.14E-08	CDH18	chr5	-	19473060	20575982	3542
ENSG00000(	131.5456	120.4288	120.0667	8.988907	18.40864	3.28786	3.5426	1.66E-18	1.56E-17	ADAMTS16	chr5	+	5140443	5320417	4979
ENSG00000(	630.7973	570.8324	550.1955	319.8553	313.8673	303.3051	0.90096	1.05E-09	5.74E-09	SRD5A1	chr5	+	6633456	6669675	2308
ENSG00000(	819.3114	816.5071	1146.571	1454.705	2133.561	1593.79	-0.89435	1.35E-07	6.10E-07	MYO10	chr5	-	16665395	16936372	8038
ENSG00000(	6.214751	8.430014	17.15238	73.4094	115.054	83.01846	-3.0388	4.48E-12	2.93E-11	FAM105A	chr5	+	14581884	14615116	3597
ENSG00000(	14929.9	15314.93	12142.57	6531.19	7916.636	10502.25	0.76216	9.37E-07	3.90E-06	RPL37	chr5	-	40825364	40835437	7686
ENSG00000(	628.7257	596.1224	661.0263	4281.716	3792.18	3784.326	-2.6482	3.49E-113	3.24E-111	SKP2	chr5	+	36152091	36184421	3759
ENSG00000(	4082.056	4140.341	4839.61	143.0734	109.5314	92.88204	5.2189	4.09E-252	2.18E-249	OSMR	chr5	+	38845960	38945698	5539
ENSG00000(	0	0	0	10.48706	1.840864	9.863579	-3.6592	0.002943	0.007614	UGT3A1	chr5	-	35951112	36001130	5122
ENSG00000(	1463.574	1399.382	1568.783	2973.081	2375.635	2380.41	-0.8012	3.26E-10	1.85E-09	PLK2	chr5	-	57749809	57756087	2960
ENSG00000(	0	0	0	5.992604	10.12475	11.50751	-4.0403	0.000656	0.001893	FAM159B	chr5	+	63986135	64013917	847
ENSG00000(	0	1.204288	1.319414	2.996302	2.761296	0	-0.74241	0.5741	0.6928	GZMA	chr5	+	54398476	54406080	894
ENSG00000(	3644.952	3655.013	4933.288	1064.436	1565.655	1010.195	1.7424	4.65E-25	5.75E-24	PIK3R1	chr5	+	67511548	67597649	7011
ENSG00000(	456.7842	399.8235	563.3897	7007.602	6778.061	5866.364	-3.7828	6.33E-166	1.27E-163	HAPLN1	chr5	-	82933624	83017432	5607
ENSG00000(	645.2984	555.1766	754.7047	522.1057	778.6855	600.0344	0.041089	0.81305	0.87865	LHFPL2	chr5	-	77781038	78065844	5043
ENSG00000(	710.5532	714.1426	683.4563	493.6408	512.6806	498.9327	0.48534	0.000237	0.000732	SSBP2	chr5	-	80708840	81047616	8780
ENSG00000(	0	0	0	22.47227	8.283888	23.83698	-5.0219	7.03E-06	2.65E-05	BHMT	chr5	+	78407602	78428108	2497
ENSG00000(	5.17896	1.204288	2.638828	17.22874	13.80648	18.08323	-2.1907	0.005164	0.012764	ANKRD31	chr5	-	74364100	74532703	6036
ENSG00000(	8.286335	10.83859	6.597069	290.6413	420.6374	257.275	-5.1245	8.55E-43	1.92E-41	IQGAP2	chr5	+	75699074	76003957	5844
ENSG00000(	19.68005	21.67718	9.235896	10.48706	3.681728	5.753754	1.2434	0.071836	0.1327	CRHBP	chr5	+	76248538	76276983	1980
ENSG00000(	801.7029	840.5928	956.575	688.4004	856.9222	685.5187	0.21966	0.12754	0.21403	RASA1	chr5	+	86563705	86687748	4979
ENSG00000(	5.17896	3.612863	3.958241	20.22504	32.21512	32.8786	-2.5596	8.11E-05	0.000268	LIX1	chr5	-	96427574	96478576	4023

ENSG00000(	56.96855	63.82725	67.2901	98.87797	75.47542	73.15488	-0.39606	0.18268	0.28629	GIN1	chr5	-	1.02E+08	1.02E+08	3325
ENSG00000(	644.2626	708.1212	1044.976	511.6186	669.1541	495.6448	0.51285	0.00614	0.014944	PPIP5K2	chr5	+	1.02E+08	1.03E+08	5817
ENSG00000(	8316.373	8030.191	8547.162	1816.508	1927.385	1667.767	2.1985	1.26E-95	8.92E-94	PAM	chr5	+	1.02E+08	1.02E+08	5432
ENSG00000(	673.2647	591.3053	977.6856	532.5927	713.3348	549.8945	0.31832	0.089199	0.15958	BDP1	chr5	+	70751442	70863649	11073
ENSG00000(	42.46747	87.913	77.84541	194.0106	125.1788	156.1733	-1.1864	5.90E-05	0.000198	GTF2H2	chr5	-	70330784	70363516	2077
ENSG00000(	706.4101	751.4755	836.5083	656.1902	594.5991	555.6483	0.34256	0.014289	0.032098	SLC30A5	chr5	+	68389473	68426896	4360
ENSG00000(	8972.029	9259.768	7956.065	7955.182	6173.337	7462.619	0.27783	0.022997	0.04911	BTF3	chr5	+	72794233	72801460	1237
ENSG00000(	204.051	223.9975	281.0351	198.505	221.8241	173.4346	0.25258	0.21334	0.32365	FBXL17	chr5	-	1.07E+08	1.08E+08	5188
ENSG00000(	6.214751	8.430014	9.235896	22.47227	7.363456	22.19305	-1.0615	0.11733	0.20023	SPATA9	chr5	-	94987885	95034415	2169
ENSG00000(	0	0	0	4.494453	6.443024	8.219649	-3.486	0.004746	0.01181	TSLP	chr5	+	1.1E+08	1.1E+08	2621
ENSG00000(	377.0283	357.6735	362.8388	301.1284	346.0824	292.6195	0.2245	0.16392	0.26223	TNFAIP8	chr5	+	1.19E+08	1.19E+08	3591
ENSG00000(	1241.914	1246.438	1473.785	351.3164	432.603	337.0056	1.8173	1.33E-35	2.43E-34	FEM1C	chr5	-	1.15E+08	1.15E+08	5813
ENSG00000(	230.9816	245.6747	275.7575	274.1617	248.5166	224.3964	0.007712	0.96638	0.98027	COMMD10	chr5	+	1.15E+08	1.16E+08	1469
ENSG00000(	989.1813	1117.579	1109.627	928.8537	711.4939	811.2794	0.38917	0.005076	0.012563	ATG12	chr5	-	1.15E+08	1.15E+08	4333
ENSG00000(	58.00435	62.62296	73.88717	30.7121	46.94203	27.12484	0.87959	0.01463	0.032756	MEGF10	chr5	+	1.27E+08	1.27E+08	7594
ENSG00000(	15.53688	25.29004	21.11062	465.1759	681.1197	505.5084	-4.6996	1.02E-65	4.06E-64	ADAMTS19	chr5	+	1.29E+08	1.29E+08	5234
ENSG00000(	1733.916	1593.273	1859.054	903.3851	794.3328	731.5488	1.091	4.44E-17	3.91E-16	YIPF5	chr5	-	1.44E+08	1.44E+08	3147
ENSG00000(	32.10955	13.24716	38.263	43.44638	55.22592	41.09825	-0.72142	0.097152	0.17123	ARHGAP26	chr5	+	1.42E+08	1.43E+08	9200
ENSG00000(	66.29068	84.30014	62.01245	5787.358	5887.083	5905.818	-6.3487	0	0	CXCL14	chr5	-	1.35E+08	1.35E+08	1971
ENSG00000(	0	0	0	63.67142	112.2927	78.90863	-7.1241	2.16E-12	1.44E-11	LECT2	chr5	-	1.35E+08	1.35E+08	1077
ENSG00000(	0	0	0	56.92974	80.07758	63.2913	-6.8226	2.48E-11	1.53E-10	SLC25A48	chr5	+	1.35E+08	1.35E+08	2062
ENSG00000(	1110.369	1000.763	1167.681	1635.981	1806.808	1480.359	-0.58503	4.69E-06	1.81E-05	DDX46	chr5	+	1.34E+08	1.34E+08	5689
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	IL9	chr5	-	1.35E+08	1.35E+08	591
ENSG00000(	777.8797	767.1313	881.3684	835.9683	756.5951	896.7637	-0.03802	0.77703	0.85319	RNF145	chr5	-	1.59E+08	1.59E+08	3613
ENSG00000(	12.4295	4.817151	10.55531	2.247227	0.920432	2.465895	1.9782	0.032632	0.066877	C1QTNF2	chr5	-	1.6E+08	1.6E+08	2414
ENSG00000(	3.107376	0	6.597069	4.494453	7.363456	9.863579	-0.99922	0.30164	0.42673	GABRB2	chr5	-	1.61E+08	1.61E+08	7385
ENSG00000(	482.679	457.6293	576.5838	483.1537	434.4439	415.0923	0.18436	0.23572	0.35008	FBXO38	chr5	+	1.48E+08	1.48E+08	4424
ENSG00000(	166.7625	157.7617	154.3714	112.3613	115.9744	100.2797	0.54107	0.014658	0.032813	PCYOX1L	chr5	+	1.49E+08	1.49E+08	4887
ENSG00000(	0	2.408575	2.638828	0	1.840864	3.28786	-0.02515	0.98442	0.99094	GLRA1	chr5	-	1.51E+08	1.51E+08	1803
ENSG00000(	1673.84	1424.672	1198.028	1409.76	1123.847	1158.971	0.21841	0.14107	0.23226	TNIP1	chr5	-	1.5E+08	1.5E+08	3268
ENSG00000(	2607.088	2696.4	3109.858	5216.562	5005.309	4323.535	-0.78867	6.02E-11	3.62E-10	G3BP1	chr5	+	1.51E+08	1.51E+08	10240
ENSG00000(	196.8005	132.4716	219.0227	126.5938	116.8949	107.6774	0.63657	0.00791	0.018829	ZNF300	chr5	-	1.5E+08	1.5E+08	4155
ENSG00000(	9.322127	7.225726	3.958241	216.4828	216.3015	230.1502	-4.8684	6.02E-35	1.08E-33	N4BP3	chr5	+	1.78E+08	1.78E+08	6080
ENSG00000(	1351.708	1342.781	1252.124	926.6065	1276.639	1518.169	0.085101	0.59735	0.71301	NHP2	chr5	-	1.78E+08	1.78E+08	865
ENSG00000(	262.0554	249.2876	216.3839	560.3085	548.5775	547.4286	-1.18	5.25E-14	3.91E-13	RMND5B	chr5	+	1.78E+08	1.78E+08	4250
ENSG00000(	1257.451	1360.845	1154.487	1088.407	1117.404	1022.524	0.22482	0.067351	0.12559	BOD1	chr5	-	1.73E+08	1.73E+08	1562
ENSG00000(	135.6887	120.4288	191.315	0	6.443024	2.465895	5.5135	5.06E-27	6.77E-26	CPLX2	chr5	+	1.75E+08	1.75E+08	5023
ENSG00000(	1415.928	1406.608	2115.02	521.3566	807.2189	630.4471	1.328	3.75E-13	2.65E-12	TENM2	chr5	+	1.67E+08	1.68E+08	9427
ENSG00000(	0	1.204288	0	24.71949	23.0108	23.83698	-4.7154	2.12E-06	8.49E-06	KCNMB1	chr5	-	1.7E+08	1.7E+08	1733
ENSG00000(	2.071584	0	0	60.67512	61.66894	67.40112	-5.5912	6.31E-12	4.08E-11	FAM50B	chr6	+	3849620	3851551	1932
ENSG00000(	21.75163	34.92434	42.22124	23.97042	22.09037	17.26126	0.61506	0.1873	0.29199	MYLK4	chr6	-	2663863	2751200	5798
ENSG00000(	3.107376	1.204288	1.319414	8.988907	7.363456	6.575719	-1.6889	0.082808	0.1498	C6ORF50	chr6	+	3982909	3984372	1464
ENSG00000(	1.035792	6.021439	1.319414	2.247227	4.60216	5.753754	-0.48031	0.6498	0.75611	FAM217A	chr6	-	4049668	4087578	2265
ENSG00000(	166.7625	164.9874	159.6491	363.3016	266.9253	295.0854	-0.90935	2.99E-06	1.18E-05	TBC1D7	chr6	-	13275081	13328776	1544

ENSG00000(	253.769	308.2977	266.5216	301.1284	231.0284	240.0138	0.098904	0.59664	0.71243	FARS2	chr6	+	5261277	5771813	1692
ENSG00000(	81.82756	93.93444	104.2337	147.5679	151.8713	113.4312	-0.55866	0.025651	0.054175	GFOD1	chr6	-	13358062	13487894	8751
ENSG00000(	194.7289	198.7075	244.0915	394.7628	358.9685	284.3999	-0.70269	0.000261	0.000801	CDKAL1	chr6	+	20534688	21232635	3272
ENSG00000(	13.46529	3.612863	11.87472	2.247227	0.920432	0	2.6175	0.009634	0.02249	PCDHB18	chr5	+	1.41E+08	1.41E+08	3164
ENSG00000(	7.250543	1.204288	5.277655	0.749076	0	2.465895	1.5714	0.17641	0.27841	PSD2	chr5	+	1.39E+08	1.39E+08	4513
ENSG00000(	1.035792	2.408575	0	2.996302	0	5.753754	-0.90991	0.47099	0.59994	LRRTM2	chr5	-	1.38E+08	1.38E+08	2216
ENSG00000(	1039.935	995.9459	1015.949	1187.285	1071.383	1242.811	-0.19808	0.10432	0.18157	ZMAT2	chr5	+	1.4E+08	1.4E+08	1634
ENSG00000(	0	4.817151	0	3.745378	1.840864	5.753754	-0.91438	0.44438	0.57398	GFRA3	chr5	-	1.38E+08	1.38E+08	2039
ENSG00000(	17.60846	28.90291	17.15238	70.4131	56.14635	50.96182	-1.448	0.000378	0.001131	KLHL3	chr5	-	1.37E+08	1.37E+08	6981
ENSG00000(	0	0	0	39.701	39.57858	42.74218	-6.1744	3.76E-09	1.96E-08	DCDC2	chr6	-	24171984	24358280	4707
ENSG00000(	43.50326	56.60152	56.73479	11.98521	1.840864	0	2.8752	0.005067	0.012543	TRIM7	chr5	-	1.81E+08	1.81E+08	4357
ENSG00000(	551.0413	614.1867	591.0974	649.4485	648.9046	858.1314	-0.29579	0.053813	0.10359	TRIM41	chr5	+	1.81E+08	1.81E+08	7015
ENSG00000(	348.0261	438.3607	324.5758	366.2979	315.7082	359.1987	0.092553	0.59144	0.70783	HIGD2A	chr5	+	1.76E+08	1.76E+08	668
ENSG00000(	865.922	933.323	824.6336	749.0755	689.4036	811.2794	0.22121	0.094032	0.16664	FAM193B	chr5	-	1.77E+08	1.77E+08	4604
ENSG00000(	0	3.612863	1.319414	31.46117	32.21512	29.59074	-3.8739	6.19E-07	2.63E-06	PLA2G7	chr6	-	46671938	46703430	1882
ENSG00000(	2543.905	2435.07	2575.496	7110.974	7071.679	6256.797	-1.4338	2.15E-41	4.62E-40	TNFRSF21	chr6	-	47199268	47277641	3595
ENSG00000(	522.0391	523.8652	464.4337	1047.957	1172.63	1277.333	-1.2073	1.28E-18	1.21E-17	RNF44	chr5	-	1.76E+08	1.76E+08	4155
ENSG00000(	438.14	474.4894	502.6967	277.907	338.719	329.6079	0.57908	0.000284	0.000867	MUT	chr6	-	49398073	49430904	3749
ENSG00000(	0	0	0	3.745378	1.840864	0.821965	-1.8318	0.17592	0.27779	RASGEF1C	chr5	-	1.8E+08	1.8E+08	2395
ENSG00000(	50.7538	49.3758	50.13772	175.2837	163.8369	217.8207	-1.8728	4.44E-13	3.12E-12	DOK3	chr5	-	1.77E+08	1.77E+08	2292
ENSG00000(	554.1487	532.2952	440.6842	1082.414	953.5675	966.6307	-0.97124	6.84E-12	4.40E-11	ABT1	chr6	+	26597180	26600278	2255
ENSG00000(	3992.978	3722.453	3839.494	2653.226	2626.913	2715.772	0.53051	1.83E-07	8.20E-07	PPP1R18	chr6	-	30644166	30655672	4599
ENSG00000(	548.9697	552.7681	651.7904	220.2282	371.8545	328.786	0.92629	1.12E-06	4.62E-06	DAAM2	chr6	+	39760142	39872648	6221
ENSG00000(	224.7668	202.3203	254.6469	428.4712	466.659	369.0622	-0.88799	4.81E-07	2.07E-06	PRIM2	chr6	+	57179603	57513375	2290
ENSG00000(	121.1877	104.773	93.67838	0	1.840864	0	6.7581	1.70E-18	1.61E-17	MLIP	chr6	+	53794780	54131078	5743
ENSG00000(	0	0	0	1.498151	4.60216	4.93179	-2.6203	0.045586	0.089616	HMGCLL1	chr6	-	55299167	55444012	2532
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	LGSN	chr6	-	63985856	64029882	5213
ENSG00000(	418.4599	342.0177	533.0432	428.4712	510.8398	406.8726	-0.05799	0.75006	0.8341	SCUBE3	chr6	+	35182190	35220856	7356
ENSG00000(	65.25489	132.4716	65.97069	32.95932	36.81728	35.34449	1.3034	0.000285	0.00087	ANO7	chr2	+	2.42E+08	2.42E+08	4128
ENSG00000(	0	1.204288	0	0	0	4.109825	-0.75943	0.57378	NA	CRIP3	chr6	-	43267448	43276535	962
ENSG00000(	1.035792	0	13.19414	2.996302	1.840864	0	1.1171	0.35214	0.48186	TCTE1	chr6	-	44246480	44265458	3067
ENSG00000(	3458.509	3480.392	3311.729	4205.31	3591.526	3760.49	-0.17292	0.11224	0.19282	RPL7L1	chr6	+	42847356	42857663	4476
ENSG00000(	153.2972	144.5145	134.5802	303.3756	259.5618	197.2716	-0.8079	0.000194	0.000606	NFKBIE	chr6	-	44225903	44233500	2556
ENSG00000(	24.85901	14.45145	13.19414	11.23613	23.0108	9.863579	0.25518	0.67042	0.77314	CYP39A1	chr6	-	46517541	46620523	2176
ENSG00000(	1686.269	1554.735	1547.672	1390.284	1179.073	1061.157	0.3984	0.002468	0.006468	TPBG	chr6	+	83072923	83080545	6484
ENSG00000(	20.71584	31.31148	25.06886	62.92235	60.74851	49.3179	-1.1464	0.003012	0.007781	IRAK1BP1	chr6	+	79577189	79608320	1157
ENSG00000(	149.154	154.1488	402.4212	137.0808	373.6954	201.3814	-0.01282	0.98276	0.99023	PHIP	chr6	-	79650263	79787953	5781
ENSG00000(	90.1139	83.09585	71.24834	68.16587	93.88406	100.2797	-0.0954	0.73756	0.82414	PRSS35	chr6	+	84222194	84235423	2604
ENSG00000(	142.9393	119.2245	208.4674	693.644	652.5863	552.3604	-2.0065	5.97E-24	7.10E-23	MMS22L	chr6	-	97590037	97731093	8643
ENSG00000(	36.25272	40.94578	44.86007	295.1358	241.1532	247.4114	-2.667	7.50E-27	1.00E-25	FAXC	chr6	-	99728536	99797938	2017
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	GABRR1	chr6	-	89887220	89940997	3110
ENSG00000(	1610.656	1578.821	1340.524	368.5452	339.6394	305.7709	2.1538	2.87E-54	8.72E-53	PNRC1	chr6	+	89790470	89794879	2065
ENSG00000(	163.6551	195.0946	195.2732	804.5071	765.7994	635.3789	-1.9887	1.03E-32	1.71E-31	PM20D2	chr6	+	89855769	89875284	4708
ENSG00000(	844.1704	821.3242	762.6212	651.6957	676.5175	682.2309	0.27259	0.033029	0.067571	RARS2	chr6	-	88224096	88299721	1818

ENSG00000(	0	0	0	5.992604	6.443024	2.465895	-3.0881	0.015198	0.03388	SCML4	chr6	-	1.08E+08	1.08E+08	4297
ENSG00000(	88.04231	121.6331	139.8579	49.43899	54.30549	60.00344	1.0778	0.000187	0.000586	C6orf170	chr6	-	1.21E+08	1.22E+08	5323
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CLVS2	chr6	+	1.23E+08	1.23E+08	3025
ENSG00000(	371.8493	474.4894	525.1267	718.3635	732.6639	641.1326	-0.60977	0.000124	0.000398	RNF217	chr6	+	1.25E+08	1.25E+08	11325
ENSG00000(	30.03797	50.58008	32.98534	5.992604	8.283888	2.465895	2.6406	4.09E-06	1.58E-05	RSPO3	chr6	+	1.27E+08	1.28E+08	2697
ENSG00000(	416.3883	376.9421	515.8908	397.7591	384.7406	332.8958	0.22866	0.17802	0.28042	ARHGAP18	chr6	-	1.3E+08	1.3E+08	4462
ENSG00000(	341.8113	313.1148	323.2564	2069.696	1869.397	2258.76	-2.6565	3.27E-89	2.04E-87	ABRACL	chr6	+	1.39E+08	1.39E+08	845
ENSG00000(	195.7647	221.5889	199.2315	465.925	481.3859	451.2587	-1.1776	4.97E-13	3.48E-12	SLC18B1	chr6	-	1.33E+08	1.33E+08	2368
ENSG00000(	22.78742	37.33292	27.70769	242.7005	155.553	173.4346	-2.6757	1.95E-18	1.83E-17	MTFR2	chr6	-	1.37E+08	1.37E+08	1793
ENSG00000(	126.3666	150.536	220.3421	549.8215	601.0421	427.4218	-1.6621	4.52E-15	3.58E-14	SLC2A12	chr6	-	1.34E+08	1.34E+08	4468
ENSG00000(	264.1269	231.2232	300.8263	271.1653	317.549	287.6877	-0.13808	0.44182	0.57155	SHPRH	chr6	-	1.46E+08	1.46E+08	11660
ENSG00000(	476.4643	457.6293	431.4483	687.6514	682.0401	626.3373	-0.54522	8.70E-05	0.000286	AIG1	chr6	+	1.43E+08	1.44E+08	3393
ENSG00000(	1123.834	1068.203	1037.059	1146.835	856.0018	1100.611	0.056648	0.68537	0.78467	DYNLT1	chr6	-	1.59E+08	1.59E+08	2891
ENSG00000(	253.769	223.9975	230.8974	238.206	282.5726	227.6843	-0.07595	0.6806	0.78119	TIAM2	chr6	+	1.55E+08	1.56E+08	6981
ENSG00000(	1141.443	1045.322	1533.159	860.6878	911.2277	819.499	0.51914	0.000645	0.001863	TMEM181	chr6	+	1.59E+08	1.59E+08	5390
ENSG00000(	2.071584	1.204288	1.319414	2.247227	21.16994	9.863579	-2.37	0.016105	0.035716	PNLDC1	chr6	+	1.6E+08	1.6E+08	1921
ENSG00000(	880.4231	888.7643	932.8255	1468.937	1243.504	1223.084	-0.54211	2.12E-05	7.56E-05	WTAP	chr6	+	1.6E+08	1.6E+08	3656
ENSG00000(	1133.156	1248.846	1450.036	1238.971	1341.99	1078.418	0.065658	0.63479	0.74395	ZMYM4	chr1	+	35734568	35887659	6994
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	VIP	chr6	+	1.53E+08	1.53E+08	1584
ENSG00000(	342.8471	350.4477	448.6007	1165.562	1125.688	1131.024	-1.582	4.15E-28	5.84E-27	C6orf211	chr6	+	1.52E+08	1.52E+08	2576
ENSG00000(	5.17896	8.430014	5.277655	0.749076	2.761296	4.93179	0.99365	0.30486	0.43016	SLC22A3	chr6	+	1.61E+08	1.61E+08	5627
ENSG00000(	2.071584	0	0	45.69361	58.90765	30.4127	-5.0993	2.17E-09	1.16E-08	VWDE	chr7	-	12370511	12443567	5936
ENSG00000(	1904.821	1787.163	2053.008	1818.006	1934.748	1897.917	0.023741	0.83294	0.89313	GNA12	chr7	-	2767746	2883958	4378
ENSG00000(	840.0272	863.4743	759.9823	1529.612	1697.277	1951.345	-1.0685	8.86E-16	7.31E-15	C7orf50	chr7	-	1036622	1177896	2621
ENSG00000(	72.50543	77.07441	93.67838	560.3085	754.7542	641.1326	-2.997	4.63E-53	1.37E-51	SDK1	chr7	+	3341080	4308632	10397
ENSG00000(	222.6953	246.879	158.3297	256.9329	247.5962	269.6045	-0.29777	0.14025	0.23115	WASH2P	chr2	+	1.14E+08	1.14E+08	2800
ENSG00000(	177.1204	217.9761	208.4674	358.8072	226.4263	221.1086	-0.41866	0.059781	0.11336	CCZ1B	chr7	-	6836440	6866401	2885
ENSG00000(	471.2853	432.3393	402.4212	731.8468	623.1325	583.5951	-0.56718	0.000191	0.000598	C7orf26	chr7	+	6629648	6648357	2182
ENSG00000(	358.384	376.9421	397.1435	253.9366	299.1404	272.0704	0.45541	0.005352	0.013179	RBAK	chr7	+	5023349	5112854	6551
ENSG00000(	340.7755	333.5877	347.0058	165.5457	169.3595	157.8173	1.0475	1.75E-09	9.38E-09	CREB5	chr7	+	28338940	28865511	8532
ENSG00000(	1013.004	1081.45	1219.138	688.4004	809.0597	558.1142	0.68667	8.34E-06	3.12E-05	EGFR	chr7	+	55086714	55324313	9821
ENSG00000(	442.2831	370.9206	381.3106	1635.981	1695.436	1782.02	-2.0908	6.95E-58	2.30E-56	CDCA5	chr11	-	64833772	64851636	2587
ENSG00000(	125.3308	85.50443	108.1919	21242.28	20139.97	19456.73	-7.5476	0	0	IGFBP3	chr7	-	45951949	45961473	2262
ENSG00000(	1259.523	1148.89	1537.117	1059.942	1267.435	1108.831	0.19866	0.15862	0.2554	PURB	chr7	-	44915896	44924960	9065
ENSG00000(	5.17896	9.634302	3.958241	17.22874	0.920432	6.575719	-0.3597	0.68659	0.78561	AC004453.	chr7	+	44507441	44507939	499
ENSG00000(	4.143168	8.430014	2.638828	2.247227	0.920432	0.821965	1.5255	0.16043	0.25777	IGFBP1	chr7	+	45927956	45933267	1653
ENSG00000(	14.50109	19.2686	15.83297	32.95932	31.29469	16.4393	-0.67733	0.1925	0.29832	SRCRB4D	chr7	-	76018651	76039012	2801
ENSG00000(	4127.631	3960.902	3591.444	5997.848	4255.157	4466.557	-0.33287	0.015852	0.035217	MDH2	chr7	+	75677369	75696826	2209
ENSG00000(	235.1248	240.8575	220.3421	306.3719	206.1768	266.3166	-0.16244	0.40962	0.5404	POMZP3	chr7	-	76239303	76256578	1587
ENSG00000(	3.107376	2.408575	0	3.745378	0	4.109825	-0.35289	0.7745	0.85197	AC006014.	chr7	-	75021229	75024708	980
ENSG00000(	751.9849	809.2813	686.0952	669.6735	585.3947	531.8113	0.32969	0.022864	0.048852	GBAS	chr7	+	56019486	56067874	4255
ENSG00000(	3965.011	3804.345	4384.412	7271.276	6557.158	6576.541	-0.74657	6.04E-12	3.91E-11	CCT6A	chr7	+	56119323	56131682	2719
ENSG00000(	604.9025	611.7782	501.3772	1180.543	1106.359	1051.293	-0.95464	2.10E-12	1.41E-11	PSPH	chr7	-	56078744	56119297	2178
ENSG00000(	4.143168	0	2.638828	0	1.840864	1.64393	0.65312	0.61101	0.72484	TRIM50	chr7	-	72726535	72742085	2047

ENSG00000(	153.2972	208.3418	188.6762	271.9144	277.9705	214.5328	-0.47372	0.020375	0.044092	ZNF92	chr7	+	64838712	64866038	3210
ENSG00000(	188.5141	181.8474	174.1626	79.40201	84.67974	93.704	1.0728	1.79E-06	7.21E-06	ATXN7L1	chr7	-	1.05E+08	1.06E+08	5417
ENSG00000(	389.4578	392.5978	444.6424	354.3127	355.2868	331.2519	0.23511	0.12909	0.21598	TMEM168	chr7	-	1.12E+08	1.12E+08	4189
ENSG00000(	234.089	225.2018	234.8557	222.4754	231.0284	256.4531	-0.03213	0.85846	0.91006	C7orf43	chr7	-	99752043	99756338	2520
ENSG00000(	1483.254	1425.877	1205.944	1091.403	1185.516	1523.101	0.11526	0.43716	0.5668	SLC12A9	chr7	+	1E+08	1E+08	4462
ENSG00000(	1125.906	1010.397	770.5376	696.6403	894.6599	1095.679	0.11444	0.51998	0.64594	GIGYF1	chr7	-	1E+08	1E+08	6530
ENSG00000(	445.3905	396.2107	440.6842	179.0291	175.8025	182.4762	1.2502	5.35E-14	3.98E-13	TRIM4	chr7	-	99474581	99517223	3383
ENSG00000(	1134.192	1172.976	1064.767	1240.469	1385.25	1385.833	-0.24948	0.03744	0.075569	MEPCE	chr7	+	1E+08	1E+08	3022
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	ZAN	chr7	+	1E+08	1E+08	8834
ENSG00000(	317.9881	251.6961	281.0351	411.9916	393.9449	363.3085	-0.45554	0.006584	0.015922	TMEM209	chr7	-	1.3E+08	1.3E+08	3545
ENSG00000(	33.14534	26.49433	9.235896	40.45008	40.49901	36.98842	-0.73643	0.11751	0.20041	AGBL3	chr7	+	1.35E+08	1.35E+08	3767
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	STRA8	chr7	+	1.35E+08	1.35E+08	993
ENSG00000(	280.6996	215.5675	335.1311	139.3281	211.6994	212.0669	0.55941	0.013034	0.029511	ZC3HAV1L	chr7	-	1.39E+08	1.39E+08	1753
ENSG00000(	156.4046	120.4288	187.3568	89.88907	153.7121	98.63579	0.43803	0.10231	0.17868	TMEM140	chr7	+	1.35E+08	1.35E+08	1680
ENSG00000(	683.6227	645.4982	753.3853	820.9868	769.4811	707.7118	-0.14267	0.29366	0.41795	TLK2	chr17	+	60536019	60692842	3608
ENSG00000(	31.07376	24.08575	25.06886	796.2673	820.1049	866.351	-4.9062	5.13E-105	4.27E-103	EPHA1	chr7	-	1.43E+08	1.43E+08	3363
ENSG00000(	469.2137	511.8223	481.586	909.3777	821.0253	807.9915	-0.79413	4.03E-09	2.10E-08	NOM1	chr7	+	1.57E+08	1.57E+08	6077
ENSG00000(	0	0	0	8.239831	7.363456	6.575719	-3.7195	0.00215	0.005698	CNPY1	chr7	-	1.55E+08	1.55E+08	2378
ENSG00000(	401.8873	349.2434	449.9201	1363.317	1528.838	1333.227	-1.8107	4.32E-38	8.46E-37	NCAPG2	chr7	-	1.58E+08	1.58E+08	5253
ENSG00000(	3.107376	12.04288	1.319414	270.4163	373.6954	286.0438	-5.6668	1.93E-40	4.05E-39	NLGN4X	chrX	-	5758678	6146904	5870
ENSG00000(	541.7192	539.5209	635.9574	295.8848	369.0932	281.112	0.85752	1.72E-07	7.72E-07	SHROOM2	chrX	+	9754496	9917483	7447
ENSG00000(	0	0	0	0	6.443024	2.465895	-2.142	0.1126	0.19333	RAB19	chr7	+	1.4E+08	1.4E+08	1093
ENSG00000(	599.7235	534.7037	704.567	580.5336	595.5195	698.6702	-0.02858	0.85205	0.90563	C7orf55-LU	chr7	+	1.39E+08	1.39E+08	2837
ENSG00000(	661.871	651.5197	688.734	200.7522	180.4047	156.9953	1.8876	1.61E-32	2.64E-31	DENND2A	chr7	-	1.4E+08	1.4E+08	3735
ENSG00000(	1.035792	3.612863	3.958241	20.22504	15.64734	16.4393	-2.3936	0.002154	0.005707	TMEM27	chrX	-	15645441	15683154	1578
ENSG00000(	1441.822	1206.696	1376.149	1360.321	1191.039	1121.16	0.13173	0.31244	0.43886	SH3KBP1	chrX	-	19552093	19905719	4731
ENSG00000(	314.8807	293.8462	362.8388	489.8954	508.0785	447.1489	-0.57202	0.000313	0.000948	TMEM47	chrX	-	34645181	34675405	4054
ENSG00000(	126.3666	173.4174	154.3714	10.48706	7.363456	6.575719	4.1213	2.23E-28	3.19E-27	LANCL3	chrX	+	37430822	37543716	10298
ENSG00000(	120.1519	133.6759	215.0644	181.2763	260.4823	202.2034	-0.45759	0.064433	0.1208	SYTL5	chrX	+	37865835	37988072	4828
ENSG00000(	955.0001	809.2813	1141.293	724.3561	937.9202	755.3858	0.26447	0.094026	0.16664	CASK	chrX	-	41374187	41782716	8298
ENSG00000(	155.3688	189.0732	238.8139	809.7507	887.2964	743.0563	-2.062	2.39E-32	3.90E-31	KDM6A	chrX	+	44732757	44971847	5438
ENSG00000(	22.78742	30.10719	13.19414	2.247227	13.80648	10.68554	1.241	0.059444	0.1128	SPIN2A	chrX	-	57160963	57164058	2468
ENSG00000(	19723.55	18025.78	18579.98	6727.448	8308.74	8319.107	1.268	2.28E-28	3.26E-27	MSN	chrX	+	64887537	64961791	3942
ENSG00000(	0	0	0	3.745378	2.761296	1.64393	-2.1888	0.1018	0.17801	AKAP4	chrX	-	49955406	49965664	2886
ENSG00000(	11.39371	0	0	12.73428	9.20432	2.465895	-0.86919	0.40266	0.53379	CCNB3	chrX	+	49967364	50094909	4693
ENSG00000(	317.9881	283.0076	292.9099	278.6561	255.8801	283.5779	0.12769	0.44882	0.5786	HDAC8	chrX	-	71549366	71792953	2338
ENSG00000(	2961.329	2973.386	3059.721	241.9514	267.8457	199.7375	3.6569	1.73E-168	3.50E-166	SLC16A2	chrX	+	73641085	73753752	4363
ENSG00000(	3.107376	0	6.597069	7.490755	5.522592	8.219649	-0.9768	0.31121	0.43747	ZNF157	chrX	+	47229982	47273704	2318
ENSG00000(	91.14969	116.8159	83.12307	125.8447	127.94	122.4728	-0.36643	0.1398	0.2305	ZNF182	chrX	-	47834250	47863377	3586
ENSG00000(	382.2072	320.3405	345.6864	241.9514	227.3467	242.4797	0.5569	0.000982	0.002758	CHST7	chrX	+	46433219	46457843	2289
ENSG00000(	261.0196	251.6961	242.7721	275.6598	206.1768	199.7375	0.14654	0.45075	0.58041	KRBOX4	chrX	+	46306292	46356857	2774
ENSG00000(	1663.482	1613.746	1451.355	1448.712	1061.258	1283.087	0.3169	0.021541	0.046344	NDUFB11	chrX	-	47001615	47004903	1388
ENSG00000(	153.2972	138.4931	175.482	106.3687	157.3939	116.719	0.29615	0.21351	0.32383	ZNF41	chrX	-	47305278	47342345	4531
ENSG00000(	12.4295	16.86003	18.47179	11.23613	10.12475	2.465895	0.92892	0.17738	0.27954	RAB41	chrX	+	69501943	69504852	1074

ENSG00000(	1399.355	1263.298	1366.913	1258.447	1324.502	1207.466	0.08848	0.44998	0.57974	ZMYM3	chrX	-	70459474	70474996	6067
ENSG00000(	676.3721	676.8097	792.9677	418.7332	621.2916	466.8761	0.50917	0.00231	0.006088	TAF1	chrX	+	70586114	70752224	7708
ENSG00000(	9067.322	8782.87	9022.151	7093.745	7430.648	6994.921	0.32014	0.000895	0.002528	NONO	chrX	+	70503042	70521018	3215
ENSG00000(	321.0955	263.739	277.0769	592.5188	654.4271	663.3257	-1.1419	1.27E-13	9.26E-13	CCDC120	chrX	+	48911101	48927509	3973
ENSG00000(	13.46529	22.88147	23.74945	22.47227	23.0108	16.4393	-0.04924	0.92455	0.95436	LPAR4	chrX	+	78003206	78012591	2611
ENSG00000(	727.1259	658.7454	688.734	1277.174	936.0793	1182.808	-0.70933	1.02E-06	4.24E-06	EBP	chrX	+	48379546	48387104	1775
ENSG00000(	2446.54	2643.412	3169.232	1206.012	1456.123	1084.172	1.1374	1.34E-15	1.10E-14	OGT	chrX	+	70752933	70795747	7243
ENSG00000(	1732.88	1698.046	1852.457	1463.694	1774.593	1768.047	0.077739	0.52624	0.65104	SNX12	chrX	-	70279094	70288273	2376
ENSG00000(	9.322127	13.24716	5.277655	17.22874	11.96562	32.05663	-1.0655	0.096927	0.17092	ITGB1BP2	chrX	+	70521584	70525221	1439
ENSG00000(	0	0	0	0	3.681728	1.64393	-1.4596	0.2805	NA	IL2RG	chrX	-	70327254	70331958	2035
ENSG00000(	24.85901	45.76293	62.01245	26.96672	22.09037	23.01502	0.84489	0.055758	0.10678	ACRC	chrX	+	70798261	70833433	3213
ENSG00000(	351.1335	327.5663	444.6424	719.1125	889.1373	706.0679	-1.0403	2.48E-10	1.43E-09	ZNF711	chrX	+	84498997	84528368	4844
ENSG00000(	305.5586	338.4048	369.4359	286.8959	241.1532	268.7825	0.34243	0.046249	0.090691	DIAPH2	chrX	+	95939662	96859996	9333
ENSG00000(	0	0	0	0.749076	2.761296	3.28786	-1.9076	0.15797	0.25445	NXF3	chrX	-	1.02E+08	1.02E+08	2276
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RIPPLY1	chrX	-	1.06E+08	1.06E+08	1172
ENSG00000(	515.8244	520.2523	554.1538	721.3598	670.0745	692.0945	-0.38985	0.00355	0.009056	PRPS1	chrX	+	1.07E+08	1.07E+08	2073
ENSG00000(	14.50109	25.29004	21.11062	99.62705	85.60018	83.84042	-2.1146	7.57E-09	3.84E-08	CXorf57	chrX	+	1.06E+08	1.06E+08	3861
ENSG00000(	6.214751	8.430014	9.235896	0.749076	3.681728	1.64393	1.7078	0.072427	0.13355	FRMPD3	chrX	+	1.07E+08	1.07E+08	7155
ENSG00000(	258.948	251.6961	308.7428	102.6234	114.1336	96.99186	1.3771	1.48E-11	9.28E-11	DOCK11	chrX	+	1.18E+08	1.18E+08	6664
ENSG00000(	143.9751	131.2674	150.4132	55.43159	38.65814	34.52253	1.7021	1.78E-09	9.56E-09	IGSF1	chrX	-	1.3E+08	1.31E+08	5180
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	ARHGAP36	chrX	+	1.3E+08	1.3E+08	3083
ENSG00000(	37.28851	44.55865	22.43003	931.85	685.7218	646.8864	-4.3946	2.85E-75	1.38E-73	GPC3	chrX	-	1.33E+08	1.33E+08	2568
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	GPR119	chrX	-	1.3E+08	1.3E+08	1193
ENSG00000(	3758.889	3951.268	3765.607	5483.233	5110.238	5000.013	-0.44182	1.48E-05	5.38E-05	RBMX	chrX	-	1.36E+08	1.36E+08	4887
ENSG00000(	240.3037	266.1476	311.3817	323.6006	308.3447	310.7027	-0.20718	0.23264	0.34636	MCPH1	chr8	+	6264113	6501144	3158
ENSG00000(	576.9361	427.5221	588.4585	685.4041	705.0509	586.061	-0.30992	0.054045	0.10401	MFHAS1	chr8	-	8640864	8751155	6414
ENSG00000(	89.0781	102.3645	85.7619	159.5531	133.4626	162.7491	-0.71284	0.002799	0.007269	FBXO25	chr8	+	356428	421225	2360
ENSG00000(	249.6258	290.2333	217.7033	576.0391	405.9105	530.1674	-0.99274	7.34E-08	3.41E-07	FAM58A	chrX	-	1.53E+08	1.53E+08	1303
ENSG00000(	791.345	845.41	767.8988	871.1749	681.1197	921.4227	-0.04144	0.77646	0.85305	NSDHL	chrX	+	1.52E+08	1.52E+08	1929
ENSG00000(	103.5792	93.93444	100.2754	276.4089	294.5382	258.097	-1.4675	5.51E-13	3.84E-12	ZNF185	chrX	+	1.52E+08	1.52E+08	4421
ENSG00000(	1266.773	1269.319	1225.735	966.3075	740.0273	774.291	0.59836	1.12E-05	4.14E-05	CETN2	chrX	-	1.52E+08	1.52E+08	1454
ENSG00000(	3.107376	0	0	4.494453	21.16994	12.32947	-2.8822	0.004253	0.010689	GABRQ	chrX	+	1.52E+08	1.52E+08	6174
ENSG00000(	42481.97	41982.67	33055.27	22817.59	18028.5	22912.27	0.88011	2.79E-11	1.72E-10	RPL10	chrX	+	1.54E+08	1.54E+08	2318
ENSG00000(	17.60846	18.06432	25.06886	202.2504	210.7789	160.2832	-3.2063	7.16E-25	8.81E-24	CSGALNAC1	chr8	-	19261672	19615540	4232
ENSG00000(	1359.995	1238.008	1575.38	1896.659	1910.817	1835.448	-0.43487	0.000449	0.001329	ATP6V1B2	chr8	+	20054878	20084330	6907
ENSG00000(	662.9068	656.3368	712.4834	626.2272	572.5087	494.8229	0.26108	0.069628	0.12915	CCDC25	chr8	-	27590835	27630170	3619
ENSG00000(	337.6682	296.2548	283.674	224.7227	216.3015	231.7941	0.44727	0.010394	0.024078	HMBOX1	chr8	+	28747911	28922281	4082
ENSG00000(	20.71584	27.69862	26.38828	29.21395	26.69253	27.94681	-0.16509	0.71409	0.80698	GNRH1	chr8	-	25276776	25282170	1760
ENSG00000(	363.563	357.6735	354.9223	274.1617	291.7769	312.3467	0.29274	0.067835	0.12638	BIN3	chr8	-	22477931	22526661	3589
ENSG00000(	0	3.612863	0	1.498151	0	2.465895	-0.08537	0.94933	0.96942	DOK2	chr8	-	21766384	21771371	1936
ENSG00000(	703.3027	609.3696	707.2058	558.8104	703.21	678.1211	0.058916	0.6879	0.78671	SLC25A37	chr8	+	23386318	23432976	4823
ENSG00000(	735.4123	894.7858	868.1743	837.4665	844.0361	839.2262	-0.01391	0.91587	0.94865	CHMP7	chr8	+	23101150	23119512	3403
ENSG00000(	306.5944	332.3834	426.1707	720.6107	804.4576	778.4008	-1.1119	1.99E-12	1.34E-11	DOCK5	chr8	+	25042238	25275598	10075
ENSG00000(	111.8655	83.09585	109.5113	1.498151	2.761296	4.109825	4.9911	1.72E-21	1.85E-20	STAR	chr8	-	38001167	38008783	3448

ENSG00000(	292.0933	276.9862	238.8139	848.7026	780.5263	757.8517	-1.5558	3.21E-25	4.00E-24	PROSC	chr8	+	37620111	37637283	2556
ENSG00000(	812.0609	787.6042	969.7691	737.8394	807.2189	708.5338	0.18818	0.1724	0.27348	ERLIN2	chr8	+	37594117	37616619	6073
ENSG00000(	4.143168	9.634302	5.277655	0	0	2.465895	2.2544	0.046209	0.090636	SNTG1	chr8	+	50822349	51706678	3504
ENSG00000(	7.250543	4.817151	0	5.243529	9.20432	1.64393	-0.31903	0.75323	0.83675	PXDNL	chr8	-	52232138	52722005	4805
ENSG00000(	23.82321	37.33292	15.83297	257.682	164.7573	251.5213	-3.0832	9.95E-23	1.13E-21	RGS20	chr8	+	54764368	54871863	2104
ENSG00000(	967.4296	824.9371	1223.097	1152.078	1241.663	867.995	-0.11332	0.50275	0.63072	TACC1	chr8	+	38585704	38710546	7838
ENSG00000(	802.7387	703.304	724.3582	914.6212	802.6167	841.6921	-0.19745	0.13382	0.22264	GOLGA7	chr8	+	41347915	41368499	2027
ENSG00000(	525.1465	559.9938	511.9325	250.1912	225.5058	207.1352	1.2208	1.49E-14	1.14E-13	PPAPDC1B	chr8	-	38120648	38126761	2185
ENSG00000(	123.2592	172.2131	105.5531	913.1231	953.5675	906.6273	-2.7767	3.11E-56	9.94E-55	GINS4	chr8	+	41386725	41402565	3873
ENSG00000(	539.6476	508.2094	766.5794	502.6297	693.0853	496.4668	0.099675	0.5932	0.70931	WHSC1L1	chr8	-	38132544	38239790	5431
ENSG00000(	2.071584	2.408575	0	3.745378	0.920432	2.465895	-0.46936	0.70207	0.79743	DNAJC5B	chr8	+	66933795	67012751	2480
ENSG00000(	15.53688	2.408575	2.638828	663.6809	527.4075	568.7997	-5.9757	3.99E-20	4.06E-19	CRH	chr8	-	67088620	67090960	1540
ENSG00000(	11.39371	7.225726	1.319414	2125.876	1705.56	1822.296	-7.9284	5.58E-114	5.35E-112	TRIM55	chr8	+	67039131	67087720	2912
ENSG00000(	7.250543	15.65574	25.06886	205.9958	164.7573	129.8705	-3.3548	8.39E-20	8.42E-19	ADHFE1	chr8	+	67342420	67383836	2229
ENSG00000(	56.96855	54.19295	60.69303	126.5938	100.3271	117.541	-0.9953	0.000314	0.000953	MRPS28	chr8	-	80830952	80942524	850
ENSG00000(	66.29068	96.34302	48.81831	143.8225	66.2711	97.81383	-0.53543	0.11364	0.19484	LACTB2	chr8	-	71547553	71581409	1508
ENSG00000(	449.5337	463.6508	448.6007	1669.689	1407.341	1439.261	-1.726	1.51E-39	3.09E-38	TERF1	chr8	+	73921099	73960357	3598
ENSG00000(	35475.87	36803.03	29335.85	24745.71	21298.8	24109.05	0.53351	6.21E-06	2.36E-05	RPL7	chr8	-	74202506	74208024	1526
ENSG00000(	8.286335	3.612863	7.916483	0.749076	3.681728	1.64393	1.4525	0.14432	0.23642	SLC26A7	chr8	+	92221722	92410378	5263
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	ATP6V0D2	chr8	+	86999552	87166457	2446
ENSG00000(	2.071584	0	2.638828	407.4971	437.2052	399.475	-7.5582	1.25E-35	2.27E-34	SYBU	chr8	-	1.11E+08	1.11E+08	3435
ENSG00000(	2.071584	4.817151	0	7.490755	0.920432	4.93179	-0.74863	0.50078	0.62891	DPYS	chr8	-	1.05E+08	1.05E+08	2127
ENSG00000(	2564.621	2448.317	2739.103	1799.279	1637.449	1423.643	0.67179	4.97E-08	2.35E-07	MTDH	chr8	+	98656407	98740998	6177
ENSG00000(	521.0033	462.4465	550.1955	206.7449	266.0048	230.1502	1.1232	1.88E-11	1.17E-10	LRP12	chr8	-	1.06E+08	1.06E+08	5008
ENSG00000(	104.615	113.203	105.5531	317.608	239.3123	229.3282	-1.2752	4.67E-09	2.42E-08	EBAG9	chr8	+	1.11E+08	1.11E+08	2379
ENSG00000(	17.60846	8.430014	22.43003	3.745378	8.283888	3.28786	1.544	0.033511	0.068449	RSPO2	chr8	-	1.09E+08	1.09E+08	3111
ENSG00000(	460.9274	417.8878	440.6842	827.7285	622.212	810.4574	-0.77451	5.53E-07	2.36E-06	POLR2K	chr8	+	1.01E+08	1.01E+08	1021
ENSG00000(	0	0	0	516.1131	636.9389	511.2622	-9.525	5.26E-25	6.49E-24	MAL2	chr8	+	1.2E+08	1.2E+08	2819
ENSG00000(	4963.515	4994.181	4400.245	5076.485	3735.113	3601.85	0.20929	0.13088	0.21842	EIF3H	chr8	-	1.18E+08	1.18E+08	3959
ENSG00000(	306.5944	308.2977	261.2439	358.0581	294.5382	324.6761	-0.15665	0.36182	0.49152	UTP23	chr8	+	1.18E+08	1.18E+08	3693
ENSG00000(	642.191	644.2939	606.9303	903.3851	705.0509	859.7753	-0.38193	0.007109	0.017098	NDUFB9	chr8	+	1.26E+08	1.26E+08	1319
ENSG00000(	319.0239	404.6407	278.3963	289.8922	240.2328	275.3582	0.31302	0.094878	0.16784	TATDN1	chr8	-	1.26E+08	1.26E+08	2016
ENSG00000(	31.07376	13.24716	38.263	0	0	0	6.0055	3.18E-08	1.53E-07	GSDMC	chr8	-	1.31E+08	1.31E+08	2714
ENSG00000(	0	0	0	12.73428	3.681728	4.109825	-3.5596	0.003971	0.010044	FAM135B	chr8	-	1.39E+08	1.4E+08	6962
ENSG00000(	381.1714	355.2649	354.9223	309.3682	297.2995	310.7027	0.25018	0.11183	0.19217	ZNF7	chr8	+	1.46E+08	1.46E+08	5641
ENSG00000(	267.2343	303.4805	296.8681	435.962	497.0333	489.8911	-0.71207	6.57E-06	2.49E-05	ARHGAP39	chr8	-	1.46E+08	1.46E+08	4697
ENSG00000(	2.071584	2.408575	2.638828	5.243529	8.283888	11.50751	-1.5672	0.09162	0.16319	SLC39A4	chr8	-	1.46E+08	1.46E+08	2778
ENSG00000(	107.7224	95.13873	83.12307	128.0919	92.0432	143.8439	-0.34341	0.19581	0.30249	NAPRT1	chr8	-	1.45E+08	1.45E+08	1965
ENSG00000(	523.0749	447.995	514.5714	934.8463	793.4124	685.5187	-0.69811	6.65E-06	2.52E-05	VLDLR	chr9	+	2621834	2654480	3590
ENSG00000(	604.9025	625.0253	671.5816	892.8981	630.4959	644.4205	-0.19009	0.23618	0.35061	AK3	chr9	-	4711155	4742043	2736
ENSG00000(	889.7452	928.5058	1095.113	804.5071	791.5715	619.7615	0.39278	0.008154	0.019328	UHRF2	chr9	+	6413151	6507054	3723
ENSG00000(	128.4382	140.9017	147.7743	20.22504	29.45382	36.16646	2.2558	1.04E-13	7.63E-13	NFIB	chr9	-	14081842	14398982	8198
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CER1	chr9	-	14719722	14722715	1215
ENSG00000(	4121.416	3738.109	4078.308	1991.792	1459.805	1620.093	1.2316	3.89E-21	4.12E-20	PLIN2	chr9	-	19108373	19149288	1972

ENSG00000(	369.7777	350.4477	440.6842	892.149	889.1373	739.7684	-1.1168	2.29E-13	1.64E-12	HAUS6	chr9	-	19053141	19103117	6536
ENSG00000(	445.3905	480.5108	507.9743	182.7744	222.7445	202.2034	1.2347	9.50E-14	6.95E-13	CDKN2B	chr9	-	22002902	22009362	3911
ENSG00000(	848.3136	690.0569	556.7926	522.1057	431.6826	599.2124	0.43124	0.015134	0.033758	CDKN2A	chr9	-	21967751	21995300	1283
ENSG00000(	72.50543	72.25726	83.12307	136.3317	120.5766	102.7456	-0.655	0.012593	0.02861	C9orf72	chr9	-	27546544	27573864	4808
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	IFNK	chr9	+	27524312	27526496	1140
ENSG00000(	455.7484	441.9736	409.0183	285.3978	224.5854	186.586	0.90242	1.09E-06	4.52E-06	ZCCHC7	chr9	+	37120536	37358146	2793
ENSG00000(	187.4783	219.1804	284.9934	327.346	312.9469	311.5247	-0.46293	0.015548	0.034576	FBXO10	chr9	-	37510889	37588871	4575
ENSG00000(	2805.96	2777.087	2314.252	1012.75	857.8426	1015.127	1.449	1.65E-29	2.46E-28	SIGMAR1	chr9	-	34634719	34637806	1743
ENSG00000(	78.72018	111.9988	117.4278	126.5938	126.0992	165.2149	-0.44099	0.084472	0.15246	CBWD5	chr9	-	70432004	70497240	3326
ENSG00000(	323.1671	399.8235	415.6153	1110.879	1259.151	1046.361	-1.5828	1.36E-26	1.79E-25	CEP78	chr9	+	80850978	80894606	11198
ENSG00000(	82.86335	52.98866	91.03955	47.94084	98.48622	78.08667	0.018924	0.95521	0.97352	NTRK2	chr9	+	87283466	87638505	8226
ENSG00000(	12.4295	4.817151	29.0271	38.95193	35.89685	41.92021	-1.298	0.014712	0.03291	IDNK	chr9	+	86237964	86259045	1623
ENSG00000(	58.00435	69.84869	42.22124	44.94453	44.18074	23.01502	0.59105	0.12706	0.21339	SHC3	chr9	-	91628060	91793682	2394
ENSG00000(	175.0488	157.7617	184.7179	161.8003	181.3251	207.9571	-0.0899	0.66385	0.76786	AUH	chr9	-	93976097	94124195	1577
ENSG00000(	870.0652	729.7984	961.8526	1503.395	1591.427	1216.508	-0.74902	3.93E-07	1.70E-06	HIATL1	chr9	+	97136833	97223324	3420
ENSG00000(	210.2658	214.3632	151.7326	486.8991	448.2504	517.0159	-1.3238	2.00E-13	1.44E-12	C9orf3	chr9	+	97488983	97849441	2941
ENSG00000(	0	0	0	6.74168	4.60216	9.863579	-3.6393	0.002899	0.007506	LPPR1	chr9	+	1.04E+08	1.04E+08	2495
ENSG00000(	1083.438	998.3545	1192.75	1091.403	2155.652	1635.71	-0.57316	0.002373	0.006243	ZNF462	chr9	+	1.1E+08	1.1E+08	10414
ENSG00000(	569.6855	574.4452	501.3772	839.7137	611.1668	779.2227	-0.43737	0.004863	0.012074	INIP	chr9	-	1.15E+08	1.15E+08	4233
ENSG00000(	932.2127	886.3558	1071.364	1768.567	1673.345	1528.855	-0.78156	8.49E-10	4.68E-09	UGCG	chr9	+	1.15E+08	1.15E+08	4007
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	ACTL7B	chr9	-	1.12E+08	1.12E+08	2369
ENSG00000(	267.2343	350.4477	420.893	365.5489	418.7966	349.3351	-0.12852	0.49188	0.62092	SNX30	chr9	+	1.16E+08	1.16E+08	7622
ENSG00000(	1278.167	1310.265	1213.861	1768.567	1604.313	1472.139	-0.34893	0.004014	0.010139	STOM	chr9	-	1.24E+08	1.24E+08	3010
ENSG00000(	10381.74	9665.613	9111.872	4655.505	4824.905	4894.801	1.0191	2.36E-23	2.74E-22	GSN	chr9	+	1.24E+08	1.24E+08	6454
ENSG00000(	459.8916	480.5108	401.1018	725.8542	505.3172	489.0691	-0.35763	0.043772	0.086572	MRRF	chr9	+	1.25E+08	1.25E+08	1947
ENSG00000(	72.50543	49.3758	46.17948	860.6878	895.5803	807.1696	-3.8946	6.93E-89	4.27E-87	NR6A1	chr9	-	1.27E+08	1.28E+08	7031
ENSG00000(	15.53688	7.225726	7.916483	1.498151	5.522592	0	1.8583	0.048477	0.09447	CRB2	chr9	+	1.26E+08	1.26E+08	5550
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	OR5C1	chr9	+	1.26E+08	1.26E+08	1088
ENSG00000(	743.6986	696.0783	757.3435	342.3275	370.9341	434.8194	0.93392	2.66E-10	1.53E-09	ALAD	chr9	-	1.16E+08	1.16E+08	3247
ENSG00000(	479.5717	523.8652	521.1684	310.8664	290.8565	252.3432	0.83208	1.36E-07	6.14E-07	ASTN2	chr9	-	1.19E+08	1.2E+08	4747
ENSG00000(	56.96855	67.44011	48.81831	59.17697	52.46462	58.35951	0.027077	0.93313	0.95995	WDR31	chr9	-	1.16E+08	1.16E+08	4878
ENSG00000(	632.8689	646.7025	701.9281	1138.595	915.8298	890.188	-0.57122	5.97E-05	0.000201	POLE3	chr9	-	1.16E+08	1.16E+08	2396
ENSG00000(	8741.048	8307.177	8528.691	5226.3	5253.826	5172.625	0.70758	1.77E-13	1.28E-12	SURF4	chr9	-	1.36E+08	1.36E+08	2984
ENSG00000(	6.214751	6.021439	1.319414	70.4131	50.62376	50.13986	-3.4575	6.42E-10	3.57E-09	GBGT1	chr9	-	1.36E+08	1.36E+08	2948
ENSG00000(	398.7799	349.2434	320.6175	309.3682	300.9813	431.5316	0.037791	0.83933	0.89727	SURF1	chr9	-	1.36E+08	1.36E+08	1093
ENSG00000(	97.36444	104.773	88.40072	389.5193	250.3575	267.9606	-1.6324	1.20E-12	8.16E-12	SURF2	chr9	+	1.36E+08	1.36E+08	842
ENSG00000(	780.9871	862.27	733.5941	963.3112	948.045	1035.676	-0.3093	0.016168	0.035842	SURF6	chr9	-	1.36E+08	1.36E+08	2505
ENSG00000(	950.857	939.3444	795.6065	1253.952	1317.138	1503.374	-0.59879	6.60E-06	2.50E-05	MED22	chr9	-	1.36E+08	1.36E+08	4380
ENSG00000(	1039.935	909.2372	876.0908	1006.758	974.7375	1094.857	-0.12163	0.34647	0.47603	REXO4	chr9	-	1.36E+08	1.36E+08	2360
ENSG00000(	48400.48	47825.88	36589.98	27073.84	22066.44	26360.41	0.81297	5.51E-10	3.07E-09	RPL7A	chr9	+	1.36E+08	1.36E+08	1164
ENSG00000(	1269.881	1156.116	1110.946	1730.365	1596.029	1724.482	-0.51249	1.37E-05	4.98E-05	GTF3C5	chr9	+	1.36E+08	1.36E+08	2404
ENSG00000(	462.999	405.845	394.5047	432.2166	404.9901	378.9258	0.055978	0.71724	0.80967	ASB6	chr9	-	1.32E+08	1.32E+08	2330
ENSG00000(	880.4231	823.7328	733.5941	1115.373	990.3848	1114.584	-0.39994	0.002291	0.006041	PTGES2	chr9	-	1.31E+08	1.31E+08	2331
ENSG00000(	1719.415	1704.067	1347.121	1437.476	1102.678	1533.787	0.22713	0.13057	0.21806	NTMT1	chr9	+	1.32E+08	1.32E+08	1487

ENSG00000(	4235.353	4040.385	3513.599	2269.699	2211.798	2288.35	0.79919	1.25E-12	8.50E-12	CIZ1	chr9	-	1.31E+08	1.31E+08	3154
ENSG00000(	725.0543	644.2939	628.041	220.2282	259.5618	236.7259	1.4768	7.24E-22	7.92E-21	SLC25A25	chr9	+	1.31E+08	1.31E+08	3714
ENSG00000(	603.8667	633.4553	497.419	1656.955	1520.554	1856.819	-1.5319	4.16E-28	5.85E-27	SH3GLB2	chr9	-	1.32E+08	1.32E+08	4828
ENSG00000(	398.7799	431.135	426.1707	449.4453	392.104	498.9327	-0.09491	0.54374	0.66614	FAM73B	chr9	+	1.32E+08	1.32E+08	4345
ENSG00000(	44.53905	31.31148	22.43003	14.98151	20.2495	28.76877	0.60875	0.20489	0.31338	PTGES	chr9	-	1.33E+08	1.33E+08	1868
ENSG00000(	486.8222	527.478	414.2959	497.3862	410.5127	514.55	0.006256	0.96898	0.98173	LRSAM1	chr9	+	1.3E+08	1.3E+08	3376
ENSG00000(	30.03797	15.65574	26.38828	0.749076	2.761296	0	3.9299	2.02E-06	8.12E-06	HMCN2	chr9	+	1.33E+08	1.33E+08	4802
ENSG00000(	1922.43	2107.504	2323.488	1088.407	1634.687	1460.632	0.6012	6.67E-05	0.000223	GPR107	chr9	+	1.33E+08	1.33E+08	7353
ENSG00000(	243.4111	268.5562	174.1626	456.187	354.3663	510.4402	-0.93816	3.09E-06	1.21E-05	C9orf142	chr9	+	1.4E+08	1.4E+08	958
ENSG00000(	0	1.204288	2.638828	0	0	4.109825	-0.07122	0.95773	0.97504	IDI2	chr10	-	1064847	1071799	1359
ENSG00000(	349.0619	333.5877	253.3274	403.7517	400.3879	400.2969	-0.35951	0.034732	0.070655	INPP5E	chr9	-	1.39E+08	1.39E+08	3394
ENSG00000(	0	0	0	0	1.840864	2.465895	-1.2108	0.36631	NA	LCN9	chr9	+	1.39E+08	1.39E+08	798
ENSG00000(	3042.121	2840.915	3297.215	2017.26	2798.113	2123.135	0.4032	0.00348	0.008896	SEC16A	chr9	-	1.39E+08	1.39E+08	8806
ENSG00000(	328.346	295.0505	271.7992	698.1384	569.7474	621.4055	-1.0724	1.07E-11	6.76E-11	WDR85	chr9	-	1.4E+08	1.4E+08	1847
ENSG00000(	1721.486	1764.282	1655.864	1443.469	2193.389	1657.903	-0.0415	0.77995	0.85499	NOTCH1	chr9	-	1.39E+08	1.39E+08	9371
ENSG00000(	12.4295	16.86003	3.958241	12.73428	13.80648	14.79537	-0.2839	0.66879	0.77175	CACNA1B	chr9	+	1.41E+08	1.41E+08	9796
ENSG00000(	1233.628	1041.709	1492.257	796.2673	1116.484	1029.922	0.35545	0.028405	0.059246	NACC2	chr9	-	1.39E+08	1.39E+08	6802
ENSG00000(	19.68005	28.90291	26.38828	351.3164	346.0824	328.786	-3.7514	3.57E-47	9.03E-46	PROSER2	chr10	+	11865338	11914276	3333
ENSG00000(	245.4827	220.3847	259.9245	474.9139	537.5323	421.668	-0.97854	7.80E-09	3.95E-08	USP6NL	chr10	-	11502509	11653753	4811
ENSG00000(	42.46747	68.6444	54.09597	17.97781	23.93123	39.45432	0.99674	0.015908	0.035326	COMMD3	chr10	+	22604903	22609235	2290
ENSG00000(	256.8764	261.3304	222.9809	230.7153	221.8241	295.9074	-0.01312	0.94532	0.9672	MSRB2	chr10	+	23384435	23410942	1803
ENSG00000(	120.1519	95.13873	102.9143	358.8072	264.164	277.8241	-1.4901	4.07E-12	2.67E-11	PDSS1	chr10	+	26986588	27035727	1626
ENSG00000(	873.1726	798.4428	905.1179	1079.418	866.1265	879.5025	-0.13322	0.33439	0.46239	FAM171A1	chr10	-	15253642	15413061	3952
ENSG00000(	390.4935	346.8349	426.1707	517.6112	443.6482	463.5882	-0.2928	0.06135	0.11577	FAM188A	chr10	-	15820169	15902519	2452
ENSG00000(	9.322127	6.021439	11.87472	0	0	0	4.3868	0.000235	0.000727	SLC39A12	chr10	+	18240768	18332221	2808
ENSG00000(	0	0	0	2.996302	5.522592	1.64393	-2.4988	0.058193	0.11084	TMEM236	chr10	+	17794251	17842867	5464
ENSG00000(	2142.018	1989.483	2134.811	2278.688	1923.703	1915.178	0.034302	0.77208	0.85017	RSU1	chr10	-	16632610	16859527	3919
ENSG00000(	3.107376	2.408575	1.319414	0	0	3.28786	0.69447	0.59024	0.70695	ST8SIA6	chr10	-	17360382	17496329	2276
ENSG00000(	1005.754	905.6244	1147.89	679.4115	676.5175	554.8263	0.67664	3.09E-06	1.21E-05	PARD3	chr10	-	34398488	35104253	6005
ENSG00000(	2070.548	1889.527	2386.82	89.88907	127.0196	102.7456	4.3025	2.45E-161	4.53E-159	ZEB1	chr10	+	31607424	31818742	6267
ENSG00000(	24.85901	32.51577	50.13772	3.745378	6.443024	6.575719	2.5574	8.51E-06	3.18E-05	FAM13C	chr10	-	61005890	61122939	3456
ENSG00000(	553.1129	551.5638	538.3208	358.8072	330.4351	355.0888	0.65146	6.30E-06	2.40E-05	NRBF2	chr10	+	64893050	64914783	1850
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	A1CF	chr10	-	52566322	52645435	2230
ENSG00000(	0	4.817151	0	7.490755	20.2495	4.109825	-2.2405	0.028902	0.060176	CDHR1	chr10	+	85954410	85979377	5428
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	LRIT1	chr10	-	85991349	86001217	2228
ENSG00000(	932.2127	847.8186	1026.504	927.3555	973.8171	936.218	-0.01605	0.90014	0.93787	POLR3A	chr10	-	79734907	79789303	6640
ENSG00000(	953.9643	979.0859	1062.128	749.0755	798.0145	688.8066	0.4206	0.001085	0.003026	HERC4	chr10	-	69681665	69835105	6391
ENSG00000(	15.53688	36.12863	27.70769	3.745378	0.920432	2.465895	3.174	9.28E-06	3.46E-05	C10orf11	chr10	+	77360998	78319925	3923
ENSG00000(	444.3547	439.565	474.989	398.5082	474.0225	477.5616	0.009711	0.94893	0.96932	CAMK2G	chr10	-	75572259	75634343	3908
ENSG00000(	1.035792	4.817151	5.277655	5.992604	0.920432	0.821965	0.38514	0.72839	0.81801	ADIRF	chr10	+	88727949	88730672	917
ENSG00000(	1889.284	1820.883	1939.538	1779.804	1456.123	1448.302	0.26927	0.029526	0.061295	GLUD1	chr10	-	88810243	88854623	3039
ENSG00000(	37.28851	57.80581	64.65128	10952.98	9697.672	9949.885	-7.5726	0	0	ANKRD1	chr10	-	92671853	92681033	1979
ENSG00000(	119.1161	150.536	207.148	15.73059	14.72691	6.575719	3.6142	3.13E-23	3.60E-22	HTR7	chr10	-	92500578	92617671	3344
ENSG00000(	355.2766	342.0177	303.4652	968.5547	658.1089	791.5522	-1.2675	5.22E-14	3.89E-13	RPP30	chr10	+	92631473	92668312	4272

ENSG00000(	421.5673	549.1552	402.4212	363.3016	347.0029	300.8392	0.43952	0.010968	0.025273	FRA10AC1	chr10	-	95427640	95462329	4780
ENSG00000(	2036.367	2121.955	2562.302	738.5885	913.989	718.3973	1.4994	9.97E-27	1.32E-25	ADD3	chr10	+	1.12E+08	1.12E+08	4337
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	HABP2	chr10	+	1.15E+08	1.15E+08	3009
ENSG00000(	0	1.204288	1.319414	49.43899	36.81728	33.70056	-4.9228	7.40E-09	3.76E-08	VAX1	chr10	-	1.19E+08	1.19E+08	4494
ENSG00000(	855.5641	782.787	808.8006	821.7359	798.0145	782.5106	0.027008	0.82879	0.89005	DNAJB12	chr10	-	74092588	74114988	4360
ENSG00000(	2392.679	2172.535	2599.245	3883.208	4282.77	3693.91	-0.72589	5.16E-10	2.89E-09	EIF4EBP2	chr10	+	72164135	72188374	7257
ENSG00000(	460.9274	505.8008	535.682	528.0983	707.8122	547.4286	-0.24633	0.122	0.2067	TCF7L2	chr10	+	1.15E+08	1.15E+08	4073
ENSG00000(	1255.38	1104.332	1444.758	2653.226	3643.99	2619.602	-1.2251	5.65E-16	4.72E-15	MKI67	chr10	-	1.3E+08	1.3E+08	12678
ENSG00000(	2.071584	2.408575	0	0	0	0	1.5041	0.26224	NA	CYP17A1	chr10	-	1.05E+08	1.05E+08	2230
ENSG00000(	322.1313	280.599	385.2688	1922.877	1521.474	1386.655	-2.2834	7.01E-45	1.66E-43	INA	chr10	+	1.05E+08	1.05E+08	3231
ENSG00000(	135.6887	115.6116	68.60952	62.17327	96.64536	132.3364	0.14053	0.66274	0.76688	FUOM	chr10	-	1.35E+08	1.35E+08	867
ENSG00000(	362.5272	340.8134	259.9245	93.63444	111.3723	87.95025	1.7113	5.26E-16	4.41E-15	LRRC27	chr10	+	1.34E+08	1.34E+08	8147
ENSG00000(	107.7224	89.11729	36.94359	56.92974	104.9292	105.2115	-0.17877	0.62399	0.73559	MTG1	chr10	+	1.35E+08	1.35E+08	2730
ENSG00000(	4.143168	0	2.638828	0	0	0	2.0639	0.1282	0.21482	NKX6-2	chr10	-	1.35E+08	1.35E+08	1061
ENSG00000(	42.46747	43.35436	34.30476	23.97042	12.88605	20.54912	1.0302	0.020965	0.045255	PAOX	chr10	+	1.35E+08	1.35E+08	1858
ENSG00000(	1247.093	1059.773	1088.516	1051.702	919.5116	1076.774	0.15564	0.23205	0.34563	GSTO1	chr10	+	1.06E+08	1.06E+08	1052
ENSG00000(	94.25706	45.76293	104.2337	164.0475	210.7789	178.3664	-1.166	3.22E-05	0.000112	TAF5	chr10	+	1.05E+08	1.05E+08	3268
ENSG00000(	1001.611	1012.806	1186.153	1626.243	2132.641	1424.465	-0.69344	6.99E-06	2.64E-05	PPRC1	chr10	+	1.04E+08	1.04E+08	5330
ENSG00000(	933.2485	861.0657	1019.907	362.5526	324.9125	249.0554	1.5808	1.54E-22	1.73E-21	ITPRIP	chr10	-	1.06E+08	1.06E+08	4362
ENSG00000(	63.18331	101.1602	96.31721	62.17327	92.0432	63.2913	0.25664	0.40346	0.53451	CNNM2	chr10	+	1.05E+08	1.05E+08	4053
ENSG00000(	1695.591	1566.778	1541.075	2215.765	2448.349	2362.327	-0.54713	9.78E-07	4.06E-06	PDCD11	chr10	+	1.05E+08	1.05E+08	6453
ENSG00000(	7543.672	7719.484	8965.417	55.43159	55.22592	57.53754	7.1472	0	0	ADAM12	chr10	-	1.28E+08	1.28E+08	7938
ENSG00000(	687.7658	757.497	560.7509	353.5637	313.8673	267.9606	1.0966	7.69E-11	4.59E-10	RGS10	chr10	-	1.21E+08	1.21E+08	852
ENSG00000(	351.1335	327.5663	431.4483	688.4004	572.5087	526.8795	-0.68709	4.19E-05	0.000144	BTBD10	chr11	-	13409548	13484844	2504
ENSG00000(	3505.12	3290.114	3144.163	2583.562	2347.102	2365.615	0.44536	4.10E-05	0.000141	ADM	chr11	+	10326227	10328944	1889
ENSG00000(	56.96855	69.84869	88.40072	9.737982	15.64734	9.863579	2.5532	1.10E-09	6.01E-09	GAS2	chr11	+	22647188	22834601	2286
ENSG00000(	2.071584	4.817151	2.638828	21.72319	7.363456	13.9734	-1.9669	0.015901	0.035314	SLC5A12	chr11	-	26688566	26744974	6250
ENSG00000(	570.7213	629.8425	616.1662	948.3296	773.1629	806.3476	-0.47667	0.000627	0.001814	LIN7C	chr11	-	27516123	27528320	4688
ENSG00000(	317.9881	315.5234	418.2542	11.98521	11.04518	4.109825	5.1947	1.66E-57	5.47E-56	LRRC4C	chr11	-	40135753	41481323	4054
ENSG00000(	96.32865	115.6116	105.5531	200.0032	179.4842	193.9837	-0.85	9.85E-05	0.000322	IMMP1L	chr11	-	31453948	31531192	1067
ENSG00000(	386.3504	360.082	339.0893	660.6846	548.5775	618.1176	-0.74845	7.08E-07	2.98E-06	PGAP2	chr11	+	3818954	3847601	2062
ENSG00000(	193.6931	215.5675	134.5802	225.4717	187.7681	244.1236	-0.26981	0.22136	0.33307	TUT1	chr11	-	62342517	62359649	3363
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	SCGB1A1	chr11	+	62172575	62190667	466
ENSG00000(	1.035792	0	0	0.749076	0.920432	0.821965	-0.44823	0.73997	NA	SYT8	chr11	+	1848709	1858751	3534
ENSG00000(	33.14534	31.31148	38.263	14.23244	34.05598	12.32947	0.74387	0.13276	0.22115	ZNF214	chr11	-	7020549	7041599	2681
ENSG00000(	61.11172	59.0101	64.65128	137.8299	77.31629	73.15488	-0.63694	0.046892	0.091786	ZNF215	chr11	+	6947635	7005863	3448
ENSG00000(	1516.399	1722.131	1806.277	1862.951	1543.564	1468.029	0.048484	0.7138	0.80669	HSD17B12	chr11	+	43577986	43878167	4292
ENSG00000(	258.948	314.3191	248.0498	226.2208	191.4499	234.26	0.33044	0.079738	0.14497	APIP	chr11	-	34874641	34938046	4583
ENSG00000(	1857.175	1807.636	1833.985	451.6926	389.3427	348.5131	2.2024	4.81E-62	1.76E-60	PAMR1	chr11	-	35453370	35551848	3143
ENSG00000(	1338.243	1107.945	1174.278	2279.437	1913.578	2248.896	-0.82906	8.29E-11	4.94E-10	DGKZ	chr11	+	46354455	46402104	5737
ENSG00000(	2931.291	2742.163	2312.932	3442.002	2609.425	2576.038	-0.11097	0.43235	0.5622	EIF3M	chr11	+	32605344	32627808	5051
ENSG00000(	4622.739	4879.774	4247.193	1988.796	3932.085	4419.705	0.40465	0.23244	0.34613	TNKS1BP1	chr11	-	57067112	57092426	5952
ENSG00000(	0	4.817151	0	5.992604	7.363456	5.753754	-1.5806	0.14787	0.24097	GLYAT	chr11	-	58407899	58499447	1735
ENSG00000(	12.4295	8.430014	10.55531	438.2092	336.8781	295.9074	-4.9986	1.69E-48	4.51E-47	SERPING1	chr11	+	57364860	57382326	2231

ENSG00000(	2741.741	2589.219	2303.696	4825.545	4349.962	4210.104	-0.80821	2.48E-12	1.65E-11	SSRP1	chr11	-	57093459	57103351	6296
ENSG00000(	175.0488	181.8474	225.6198	31.46117	19.32907	28.76877	2.8289	1.47E-23	1.72E-22	SLC43A1	chr11	-	57252007	57283259	2598
ENSG00000(	58.00435	49.3758	50.13772	89.13999	214.4607	122.4728	-1.4082	1.90E-05	6.83E-05	PTPRJ	chr11	+	48002113	48189670	5122
ENSG00000(	674.3005	605.7567	617.4856	558.0613	405.9105	441.3952	0.43076	0.006402	0.015527	C11orf49	chr11	+	46958240	47185936	2141
ENSG00000(	1194.268	1089.88	989.5603	1234.477	1215.891	1348.022	-0.21307	0.090458	0.1614	ARFGAP2	chr11	-	47185848	47198676	2976
ENSG00000(	2437.218	2193.008	2485.776	2415.02	3773.771	3305.121	-0.41433	0.005745	0.014067	CELF1	chr11	-	47487496	47587121	7666
ENSG00000(	477.5001	519.048	410.3377	659.1865	531.0893	801.4158	-0.49931	0.00382	0.009689	C11orf73	chr11	+	86013253	86056969	1694
ENSG00000(	16.57267	3.612863	1.319414	42.69731	45.10117	47.67397	-2.4692	2.67E-05	9.40E-05	CCDC81	chr11	+	86085778	86134151	2636
ENSG00000(	2064.333	2056.923	2716.673	2125.127	2752.092	1949.701	0.002166	0.98871	0.99328	SESN3	chr11	-	94898704	94965705	9531
ENSG00000(	2119.23	2083.418	2979.236	1619.501	1798.524	1547.76	0.53035	0.000317	0.00096	ENDOD1	chr11	+	94822974	94865809	4687
ENSG00000(	436.0684	456.425	606.9303	565.552	543.9753	486.6032	-0.09218	0.57405	0.69278	CCDC82	chr11	-	96085933	96123087	3745
ENSG00000(	62.14751	51.78437	51.45714	7.490755	15.64734	0.821965	2.6879	9.69E-07	4.03E-06	KLHL35	chr11	-	75133438	75141674	2497
ENSG00000(	3044.192	2787.926	3632.346	341.5785	582.6335	479.2055	2.7447	6.75E-59	2.28E-57	TENM4	chr11	-	78363876	79151992	14000
ENSG00000(	34398.65	33941.65	29645.91	16068.42	14138.76	15714.33	1.0917	5.63E-24	6.71E-23	SERPINH1	chr11	+	75273101	75283828	3391
ENSG00000(	811.0251	620.2082	728.3164	207.4939	203.4155	181.6542	1.8596	2.45E-30	3.77E-29	CAPN5	chr11	+	76777979	76837201	4397
ENSG00000(	386.3504	487.7365	389.2271	453.9398	409.5922	378.1039	0.024067	0.88316	0.92688	INTS4	chr11	-	77589766	77705724	3459
ENSG00000(	1096.904	1044.117	1324.691	934.0972	769.4811	724.1511	0.51075	0.000501	0.001474	PAK1	chr11	-	77032752	77185680	3737
ENSG00000(	41217.27	40337.62	31541.91	25320.25	23187.52	31831.41	0.49209	0.000431	0.00128	RPS3	chr11	+	75110530	75133324	2097
ENSG00000(	522.0391	485.328	654.4292	325.8479	395.7858	346.8692	0.63458	0.000131	0.000422	ZC3H12C	chr11	+	1.1E+08	1.1E+08	9542
ENSG00000(	83.89914	56.60152	75.20659	237.4569	155.553	233.438	-1.5229	4.49E-09	2.33E-08	TTC12	chr11	+	1.13E+08	1.13E+08	2985
ENSG00000(	137.7603	150.536	167.5656	75.65663	87.44104	68.22309	0.97058	7.25E-05	0.000241	NCAM1	chr11	+	1.13E+08	1.13E+08	5837
ENSG00000(	46.61064	40.94578	39.58241	71.91125	46.0216	89.59418	-0.69468	0.050637	0.09818	DRD2	chr11	-	1.13E+08	1.13E+08	2789
ENSG00000(	133.6172	155.3531	203.1897	232.2134	254.0392	138.9121	-0.34497	0.17203	0.27305	NPAT	chr11	-	1.08E+08	1.08E+08	6117
ENSG00000(	1453.216	1405.404	1762.737	704.8801	852.32	683.0528	1.042	1.70E-13	1.23E-12	ATM	chr11	+	1.08E+08	1.08E+08	13147
ENSG00000(	449.5337	627.4339	552.8344	800.7618	640.6207	600.0344	-0.32562	0.051885	0.1003	AASDHPPT	chr11	+	1.06E+08	1.06E+08	5145
ENSG00000(	12.4295	10.83859	6.597069	160.3022	116.8949	127.4046	-3.659	1.07E-20	1.12E-19	GLB1L2	chr11	+	1.34E+08	1.34E+08	5621
ENSG00000(	11.39371	6.021439	32.98534	13.48336	22.09037	19.72716	-0.13682	0.82628	0.88809	SLX4IP	chr20	+	10415951	10617477	1407
ENSG00000(	1619.979	1537.875	1337.886	1758.08	1461.646	1625.025	-0.10733	0.40007	0.53123	LAMTOR1	chr11	-	71796941	71814433	1346
ENSG00000(	240.3037	174.6217	183.3985	13.48336	2.761296	9.041614	4.4411	1.18E-33	2.03E-32	P4HA3	chr11	-	73946846	74022702	2627
ENSG00000(	11.39371	6.021439	19.79121	2.247227	6.443024	9.863579	0.91484	0.23719	0.35182	GRIK4	chr11	+	1.2E+08	1.21E+08	5802
ENSG00000(	0	3.612863	0	2042.729	1982.611	2131.355	-10.022	1.27E-58	4.25E-57	ST14	chr11	+	1.3E+08	1.3E+08	3539
ENSG00000(	2846.356	2759.023	2849.934	3477.958	5124.965	4616.977	-0.64285	3.31E-06	1.30E-05	HYOU1	chr11	-	1.19E+08	1.19E+08	4530
ENSG00000(	567.614	617.7996	443.323	9.737982	9.20432	9.863579	5.7471	4.65E-82	2.61E-80	ADAM33	chr20	-	3648612	3662893	3677
ENSG00000(	229.9458	211.9546	212.4256	329.5932	315.7082	289.3317	-0.51133	0.003323	0.008529	CSRP2BP	chr20	+	18118499	18169031	3927
ENSG00000(	493.0369	468.4679	377.3523	323.6006	266.0048	332.0738	0.53703	0.001797	0.00483	DAK	chr11	+	61100682	61120767	4696
ENSG00000(	2063.297	2096.665	1946.135	2901.919	3346.691	3471.158	-0.66912	5.96E-09	3.05E-08	MTA2	chr11	-	62360686	62369312	3058
ENSG00000(	281.7354	267.3519	230.8974	549.0724	354.3663	405.2287	-0.74263	0.000119	0.000384	TMEM138	chr11	+	61129473	61136981	2839
ENSG00000(	3784.784	3487.617	3943.728	1395.528	1471.771	1328.295	1.4164	1.98E-37	3.80E-36	FADS1	chr11	-	61567099	61596790	4523
ENSG00000(	2.071584	1.204288	1.319414	0.749076	0.920432	0	0.86578	0.51619	0.64279	TMC2	chr20	+	2517253	2622430	3169
ENSG00000(	36.25272	87.913	34.30476	16.47966	12.88605	15.61733	1.755	0.000222	0.000688	ROM1	chr11	+	62379194	62382592	1878
ENSG00000(	663.9426	700.8955	589.778	341.5785	377.3771	464.4102	0.72238	6.62E-06	2.51E-05	EML3	chr11	-	62369690	62380237	3665
ENSG00000(	750.9491	563.6067	642.5545	1064.436	1770.911	1572.419	-1.1648	5.63E-11	3.40E-10	INCENP	chr11	+	61891445	61920635	3964
ENSG00000(	47.64643	44.55865	44.86007	0.749076	2.761296	4.109825	3.9556	1.55E-10	9.04E-10	ZP1	chr11	+	60635035	60643166	1954
ENSG00000(	8.286335	39.74149	26.38828	0.749076	6.443024	9.041614	2.0298	0.005473	0.01345	PLCH2	chr1	+	2357419	2436969	6986

ENSG0000(	162.6193	186.6646	189.9956	137.0808	104.0088	86.30632	0.71048	0.002894	0.007493	FRG1B	chr20	+	29611857	29634010	1029
ENSG0000(	1300.955	1294.609	1275.873	1886.172	2035.996	1924.22	-0.59339	7.39E-08	3.43E-07	CPSF7	chr11	-	61170121	61197503	3687
ENSG0000(	1963.861	1826.904	1552.95	958.0676	825.6275	1034.032	0.9211	1.65E-11	1.03E-10	B3GAT3	chr11	-	62382768	62389647	2056
ENSG0000(	2889.859	2508.531	2801.115	4242.764	3685.41	3656.1	-0.49768	1.63E-05	5.90E-05	EI24	chr11	+	1.25E+08	1.25E+08	2447
ENSG0000(	11.39371	21.67718	46.17948	34.45748	80.07758	46.852	-1.0046	0.038387	0.077236	CCDC15	chr11	+	1.25E+08	1.25E+08	3924
ENSG0000(	633.9046	572.0367	514.5714	1001.514	941.6019	843.336	-0.69222	9.26E-07	3.85E-06	CHEK1	chr11	+	1.25E+08	1.26E+08	3502
ENSG0000(	195.7647	208.3418	203.1897	123.5975	94.8045	56.71558	1.1289	2.01E-05	7.18E-05	FEZ1	chr11	-	1.25E+08	1.25E+08	1926
ENSG0000(	4.143168	2.408575	3.958241	7.490755	3.681728	7.397684	-0.7126	0.44262	0.57227	ESAM	chr11	-	1.25E+08	1.25E+08	2336
ENSG0000(	9.322127	19.2686	17.15238	6.74168	10.12475	1.64393	1.2029	0.10202	0.1783	KIRREL3	chr11	-	1.26E+08	1.27E+08	3808
ENSG0000(	0	0	0	65.16957	60.74851	55.07165	-6.6965	6.65E-11	3.99E-10	MPZL2	chr11	-	1.18E+08	1.18E+08	2620
ENSG0000(	879.3873	876.7215	969.7691	453.9398	486.9085	497.2888	0.92019	3.57E-12	2.35E-11	SIDT2	chr11	+	1.17E+08	1.17E+08	4406
ENSG0000(	424.6747	351.652	358.8805	310.8664	299.1404	284.3999	0.34417	0.035953	0.07286	TMEM25	chr11	+	1.18E+08	1.18E+08	3241
ENSG0000(	3605.592	3555.057	3509.641	11323.03	10660.44	13617.49	-1.7351	5.73E-50	1.58E-48	TAGLN	chr11	+	1.17E+08	1.17E+08	3298
ENSG0000(	7.250543	4.817151	3.958241	449.4453	749.2316	698.6702	-6.6854	2.88E-59	9.84E-58	JPH2	chr20	-	42740335	42816218	4787
ENSG0000(	15.53688	12.04288	6.597069	0.749076	0.920432	3.28786	2.4215	0.007891	0.018786	DUSP15	chr20	-	30435440	30458550	1732
ENSG0000(	793.4166	691.2612	608.2498	743.832	582.6335	570.4437	0.14193	0.37106	0.50161	COMMD7	chr20	-	31290493	31331814	1907
ENSG0000(	5.17896	4.817151	1.319414	6.74168	5.522592	5.753754	-0.56605	0.54171	0.66457	KIAA1755	chr20	-	36838890	36889174	6429
ENSG0000(	10.35792	10.83859	22.43003	3.745378	0.920432	3.28786	2.1823	0.007029	0.016919	SPATA25	chr20	-	44515128	44516274	757
ENSG0000(	204.051	192.686	207.148	512.3677	413.274	507.1524	-1.2426	3.40E-13	2.41E-12	DSN1	chr20	-	35380194	35402230	2447
ENSG0000(	2310.852	2143.632	2607.162	1235.226	2048.882	1530.499	0.55111	0.000709	0.002038	SOGA1	chr20	-	35405845	35492089	14371
ENSG0000(	2.071584	8.430014	0	0	6.443024	1.64393	0.29594	0.80369	0.87263	CNBD2	chr20	+	34556512	34618622	2531
ENSG0000(	1487.397	1431.898	1472.466	1049.455	1170.789	1324.185	0.30889	0.014329	0.032163	LSM14B	chr20	+	60697517	60710434	2594
ENSG0000(	1101.047	1046.526	1110.946	1642.723	1645.732	1576.529	-0.57721	3.27E-07	1.43E-06	YTHDF1	chr20	-	61826781	61847586	3301
ENSG0000(	161.5835	227.6104	204.5091	272.6635	308.3447	253.9872	-0.49154	0.012479	0.028392	CABLES2	chr20	-	60963688	60982341	3785
ENSG0000(	336.6324	398.6192	294.2293	574.5409	408.6718	521.1258	-0.5453	0.002353	0.006196	ORAOV1	chr11	-	69467844	69490184	3776
ENSG0000(	191.6215	178.2346	141.1773	245.6968	150.9508	175.0785	-0.16062	0.49365	0.62254	TRPT1	chr11	-	63991271	63993726	1809
ENSG0000(	322.1313	307.0934	196.5927	195.5087	219.9832	243.3016	0.32774	0.12292	0.20802	NUDT22	chr11	+	63993413	63998158	2055
ENSG0000(	9.322127	24.08575	11.87472	23.22134	29.45382	40.27628	-1.0005	0.059103	0.11225	FERMT3	chr11	+	63974150	63991354	2489
ENSG0000(	1393.14	1283.771	1302.261	1897.408	2232.048	2302.324	-0.69074	1.39E-08	6.93E-08	PLCB3	chr11	+	64018995	64036622	4469
ENSG0000(	905.2821	841.7971	898.5208	1177.547	1064.94	1066.088	-0.32218	0.008656	0.020417	MRPL49	chr11	+	64889655	64894843	2526
ENSG0000(	595.5803	653.9282	543.5985	300.3793	196.9724	251.5213	1.2517	1.94E-12	1.30E-11	CDC42EP2	chr11	+	65082289	65089900	2128
ENSG0000(	1472.896	1677.573	1380.107	1588.789	1145.017	1656.259	0.044868	0.7663	0.8458	FAU	chr11	-	64888100	64889945	1484
ENSG0000(	93.22127	101.1602	56.73479	549.8215	601.9625	604.1442	-2.7813	2.15E-43	4.94E-42	TM7SF2	chr11	+	64879317	64883856	2094
ENSG0000(	2126.481	2053.311	1559.547	1120.617	1027.202	1121.982	0.81006	4.41E-09	2.29E-08	VPS51	chr11	+	64856796	64879332	2714
ENSG0000(	12.4295	3.612863	9.235896	8.239831	15.64734	14.79537	-0.55601	0.4333	0.56311	TBX6	chr16	-	30097114	30103208	2162
ENSG0000(	1992.864	1889.527	1611.004	2851.731	2637.958	3240.186	-0.66626	1.77E-07	7.93E-07	PPP4C	chr16	+	30087299	30096698	1490
ENSG0000(	33365.96	33341.91	25331.43	26318.77	20230.17	20716.8	0.45121	0.001095	0.00305	ALDOA	chr16	+	30064411	30081778	2534
ENSG0000(	2.071584	0	2.638828	0.749076	4.60216	0.821965	-0.25782	0.83724	0.89602	FAM57B	chr16	-	30035748	30064299	2313
ENSG0000(	3.107376	0	1.319414	5.992604	4.60216	6.575719	-1.5347	0.15473	0.25026	DOC2A	chr16	-	30016830	30034591	3749
ENSG0000(	153.2972	160.1703	151.7326	173.0365	202.495	274.5363	-0.47889	0.031444	0.064773	HIRIP3	chr16	-	30003645	30007757	3385
ENSG0000(	2153.411	2150.858	2097.868	1257.698	1885.045	2190.537	0.26296	0.11142	0.19152	TAOK2	chr16	+	29984962	30003582	5169
ENSG0000(	1079.295	1115.17	905.1179	705.6292	508.9989	549.0726	0.81008	1.92E-07	8.58E-07	TMEM219	chr16	+	29952206	29984373	1292
ENSG0000(	4361.72	4460.682	5454.457	11561.23	12313.54	10738.15	-1.2754	1.05E-26	1.39E-25	HMGA2	chr12	+	66217911	66360075	8094
ENSG0000(	5.17896	1.204288	0	0.749076	0	0.821965	1.2026	0.36509	0.49491	MMP3	chr11	-	1.03E+08	1.03E+08	2016

ENSG00000(	3.107376	0	6.597069	454.6889	428.0009	330.4299	-6.7489	2.73E-42	6.05E-41	CNKSR2	chrX	+	21392536	21672813	5668
ENSG00000(	0	1.204288	0	3.745378	10.12475	5.753754	-2.8402	0.016673	0.036855	CNTN5	chr11	+	98891683	1E+08	6258
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	KLRF1	chr12	+	9980077	9997606	1244
ENSG00000(	106.6866	138.4931	94.99779	72.66033	57.06678	53.42772	0.88127	0.001975	0.005267	CLEC1A	chr12	-	10222153	10264226	2685
ENSG00000(	295.2007	354.0606	405.06	5.243529	5.522592	7.397684	5.7519	6.00E-58	1.99E-56	MKX	chr10	-	27961803	28034989	3847
ENSG00000(	19.68005	21.67718	31.66593	214.9847	278.8909	201.3814	-3.2257	8.48E-28	1.18E-26	MPP7	chr10	-	28339922	28623415	5080
ENSG00000(	10.35792	3.612863	6.597069	0.749076	0.920432	1.64393	2.1522	0.039035	0.078337	C10orf68	chr10	+	32832297	33171802	2729
ENSG00000(	4.143168	1.204288	2.638828	2.247227	4.60216	0	0.18146	0.87779	0.92368	GRIN2B	chr12	-	13714144	14133053	6238
ENSG00000(	17789.73	17789.74	21065.76	15601.75	16724.25	12543.18	0.33545	0.008776	0.020665	ITGB1	chr10	-	33189247	33294720	3784
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	ANXA8L1	chr10	-	47011753	47174093	1954
ENSG00000(	0	0	0	2.247227	0.920432	1.64393	-1.4644	0.28023	NA	TRIM48	chr11	+	55029658	55038595	1445
ENSG00000(	0	2.408575	1.319414	8.239831	6.443024	8.219649	-2.1572	0.038727	0.077811	PCDH15	chr10	-	55562531	57387702	9258
ENSG00000(	105.6508	89.11729	48.81831	81.64923	90.20234	97.81383	-0.13658	0.65753	0.76231	CTF1	chr16	+	30907928	30914881	1664
ENSG00000(	532.397	635.8639	546.2373	1040.466	682.0401	789.0863	-0.54999	0.001069	0.002986	CWC15	chr11	-	94695787	94706776	1575
ENSG00000(	2.071584	3.612863	0	0.749076	1.840864	0	0.71817	0.58556	0.70302	FCGR1A	chr1	+	1.5E+08	1.5E+08	2180
ENSG00000(	978.8233	940.5487	1171.639	464.4268	452.8525	323.0322	1.312	1.35E-15	1.10E-14	ARID5B	chr10	+	63661059	63856703	7891
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	KLHL1	chr13	-	70274726	70682591	4115
ENSG00000(	15.53688	10.83859	9.235896	202.2504	219.9832	198.0935	-4.0325	3.28E-32	5.34E-31	CDH8	chr16	-	61681146	62070939	9721
ENSG00000(	220.6237	275.7819	257.2857	285.3978	251.2779	280.29	-0.1185	0.5099	0.63719	DCUN1D2	chr13	-	1.14E+08	1.14E+08	3164
ENSG00000(	1716.307	1592.068	1642.67	1054.698	1154.222	1011.839	0.61977	1.34E-07	6.07E-07	TMCO3	chr13	+	1.14E+08	1.14E+08	3050
ENSG00000(	229.9458	268.5562	248.0498	168.542	150.0304	159.4612	0.63789	0.000834	0.002367	TMEM218	chr11	-	1.25E+08	1.25E+08	4547
ENSG00000(	90.1139	78.2787	79.16483	97.37982	110.4518	104.3895	-0.32841	0.20518	0.31373	TIRAP	chr11	+	1.26E+08	1.26E+08	2245
ENSG00000(	79.75598	119.2245	69.92893	114.6086	75.47542	101.1017	-0.11578	0.69372	0.79116	N6AMT2	chr13	-	21302870	21348097	1042
ENSG00000(	509.6096	385.3721	658.3875	596.2641	749.2316	539.209	-0.27803	0.1468	0.23974	LATS2	chr13	-	21547171	21635686	5511
ENSG00000(	2266.313	2349.565	2034.536	1812.763	1899.772	2151.082	0.18163	0.12977	0.21691	SAP18	chr13	+	21714653	21723221	2298
ENSG00000(	102.5434	69.84869	149.0938	129.5901	146.3487	128.2265	-0.32992	0.23165	0.34518	LPHN3	chr4	+	62066976	62938184	6767
ENSG00000(	95.29286	145.7188	112.1502	50.93714	61.66894	37.81039	1.217	5.48E-05	0.000185	KIAA1328	chr18	+	34409069	34812135	5881
ENSG00000(	65.25489	105.9773	88.40072	20.97412	19.32907	32.05663	1.8051	6.84E-07	2.88E-06	FAM124A	chr13	+	51796503	51858377	4761
ENSG00000(	1.035792	7.225726	0	7.490755	9.20432	3.28786	-1.0503	0.30572	0.43121	CTAGE5	chr14	+	39734488	39856156	3860
ENSG00000(	29.00217	24.08575	7.916483	301.8774	265.0844	280.29	-3.7153	4.00E-35	7.19E-34	HNMT	chr2	+	1.39E+08	1.39E+08	3291
ENSG00000(	408.102	391.3935	345.6864	359.5563	486.9085	460.3004	-0.18703	0.26902	0.38944	LYPD1	chr2	-	1.33E+08	1.33E+08	1891
ENSG00000(	6.214751	9.634302	3.958241	1480.173	1244.424	1430.219	-7.5606	1.31E-99	9.93E-98	LYPD6B	chr2	+	1.5E+08	1.5E+08	1719
ENSG00000(	441.2474	499.7794	448.6007	151.3133	194.2112	234.26	1.2564	2.18E-11	1.35E-10	PDCD4	chr10	+	1.13E+08	1.13E+08	3654
ENSG00000(	60.07593	48.17151	48.81831	41.94823	43.2603	38.63235	0.34078	0.32892	0.45664	ADRA2A	chr10	+	1.13E+08	1.13E+08	3869
ENSG00000(	1.035792	3.612863	6.597069	11.98521	11.04518	1.64393	-0.99717	0.28956	0.41328	GPM6A	chr4	-	1.77E+08	1.77E+08	2854
ENSG00000(	44.53905	16.86003	32.98534	30.7121	35.89685	34.52253	-0.0894	0.84102	0.89827	WDR17	chr4	+	1.77E+08	1.77E+08	7397
ENSG00000(	0	0	5.277655	4.494453	0	1.64393	-0.17099	0.89565	0.93537	SPATA4	chr4	-	1.77E+08	1.77E+08	2115
ENSG00000(	97.36444	86.70872	80.48424	43.44638	20.2495	28.76877	1.4829	2.30E-05	8.16E-05	VEGFC	chr4	-	1.78E+08	1.78E+08	2067
ENSG00000(	141.9035	91.52587	135.8996	27.7158	15.64734	18.08323	2.5353	1.49E-13	1.08E-12	CCDC102B	chr18	+	66382446	66722426	2711
ENSG00000(	0	2.408575	0	1.498151	0.920432	2.465895	-0.61136	0.64596	0.75302	CD226	chr18	-	67498394	67629039	2638
ENSG00000(	0	0	1.319414	5.243529	0	0	-0.96444	0.4771	0.60629	CNDP1	chr18	+	72201675	72254448	4111
ENSG00000(	9.322127	13.24716	15.83297	6.74168	13.80648	8.219649	0.3906	0.5611	0.68128	FSIP1	chr15	-	39892232	40075031	2805
ENSG00000(	53.86118	46.96722	58.05421	11.98521	20.2495	19.72716	1.5797	0.000163	0.000517	DLG2	chr11	-	83166055	85338966	7890
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	CCDC83	chr11	+	85566144	85631064	2358

ENSG00000(	0	0	0	4.494453	0.920432	0	-1.4809	0.27346	NA	RGS18	chr1	+	1.92E+08	1.92E+08	2150
ENSG00000(	2911.611	2654.25	2669.174	17709.64	17610.63	17155.23	-2.6679	1.79E-158	3.10E-156	PRSS23	chr11	+	86502101	86663952	5323
ENSG00000(	554.1487	647.9068	692.6922	538.5853	683.881	533.4552	0.10911	0.48568	0.6148	MTMR12	chr5	-	32227100	32313115	5187
ENSG00000(	9.322127	7.225726	7.916483	291.3904	260.4823	286.0438	-4.993	1.27E-42	2.84E-41	PPP1R1C	chr2	+	1.83E+08	1.83E+08	3004
ENSG00000(	5361.259	5269.963	5317.238	11200.18	9513.585	9667.951	-0.92841	3.54E-18	3.30E-17	CCT5	chr5	+	10250033	10266524	3675
ENSG00000(	152.2614	158.966	199.2315	145.3207	150.9508	120.0069	0.28987	0.19268	0.29852	FAM173B	chr5	-	10226442	10250009	1928
ENSG00000(	1240.879	1280.158	1498.854	740.8357	914.9094	650.9962	0.79909	9.06E-08	4.17E-07	DOCK1	chr10	+	1.29E+08	1.29E+08	6797
ENSG00000(	282.7712	258.9219	390.5465	117.6049	137.1444	98.63579	1.3899	2.90E-10	1.66E-09	DIXDC1	chr11	+	1.12E+08	1.12E+08	5896
ENSG00000(	617.332	637.0682	683.4563	1328.86	1479.134	1279.799	-1.075	2.76E-17	2.45E-16	DLAT	chr11	+	1.12E+08	1.12E+08	4458
ENSG00000(	10.35792	21.67718	15.83297	17.97781	22.09037	13.9734	-0.17108	0.76315	0.84363	PIH1D2	chr11	-	1.12E+08	1.12E+08	1838
ENSG00000(	794.4524	775.5613	811.4395	547.5742	633.2572	556.4703	0.45463	0.000653	0.001886	C11orf57	chr11	+	1.12E+08	1.12E+08	3739
ENSG00000(	1001.611	908.0329	663.6651	1116.872	1302.411	1520.635	-0.61056	0.000222	0.000688	TIMM8B	chr11	-	1.12E+08	1.12E+08	1155
ENSG00000(	1.035792	1.204288	9.235896	23.22134	15.64734	21.37109	-2.23	0.003632	0.009252	IL18	chr11	-	1.12E+08	1.12E+08	1697
ENSG00000(	0	0	0	0.749076	2.761296	2.465895	-1.7341	0.2007	0.30828	TEX12	chr11	+	1.12E+08	1.12E+08	1147
ENSG00000(	261.0196	246.879	208.4674	800.7618	708.7326	801.4158	-1.6815	2.11E-27	2.89E-26	PTS	chr11	+	1.12E+08	1.12E+08	1069
ENSG00000(	1102.083	1050.139	1138.654	668.9245	717.937	602.5003	0.72483	2.06E-08	1.01E-07	PIP4K2A	chr10	-	22823778	23003484	3802
ENSG00000(	0	0	0	0.749076	3.681728	0	-1.2286	0.35939	NA	C2orf50	chr2	+	11273179	11286916	2684
ENSG00000(	0	1.204288	0	4427.036	5795.96	3813.917	-11.78	2.67E-57	8.77E-56	FREM2	chr13	+	39261266	39460074	14876
ENSG00000(	109.7939	79.48299	125.3443	167.0438	232.8693	163.571	-0.83293	0.000865	0.00245	FOXO1	chr13	-	41129804	41240734	5735
ENSG00000(	1281.275	1262.094	1779.889	2481.687	2757.614	2334.38	-0.80738	2.97E-08	1.43E-07	CRIM1	chr2	+	36583069	36778278	5912
ENSG00000(	3311.427	3169.685	3826.3	916.8685	1002.35	806.3476	1.915	8.29E-51	2.34E-49	SEC24D	chr4	-	1.2E+08	1.2E+08	4065
ENSG00000(	175.0488	202.3203	154.3714	187.2689	180.4047	181.6542	-0.0459	0.82123	0.8844	ABCB9	chr12	-	1.23E+08	1.23E+08	6051
ENSG00000(	176.0846	209.5461	192.6344	61.42419	90.20234	77.2647	1.3303	2.47E-08	1.20E-07	RILPL2	chr12	-	1.24E+08	1.24E+08	1435
ENSG00000(	1136.264	1065.795	984.2827	1638.228	1822.455	1797.637	-0.7202	1.98E-09	1.06E-08	DHX37	chr12	-	1.25E+08	1.25E+08	4550
ENSG00000(	6177.463	6174.383	6780.467	6499.729	5159.942	5187.421	0.1829	0.12957	0.21663	UBC	chr12	-	1.25E+08	1.25E+08	3745
ENSG00000(	106.6866	148.1274	171.5238	21.72319	40.49901	18.90519	2.3649	1.83E-12	1.23E-11	ITPR1	chr3	+	4535032	4889524	10197
ENSG00000(	63.18331	89.11729	43.54065	15.73059	20.2495	34.52253	1.4413	0.000584	0.001699	PRSS53	chr16	-	31094746	31100949	5489
ENSG00000(	457.82	413.0707	701.9281	854.6952	823.7866	638.6667	-0.55824	0.003575	0.009113	SLC7A11	chr4	-	1.39E+08	1.39E+08	9645
ENSG00000(	137.7603	125.2459	104.2337	431.4675	411.4331	336.1837	-1.6694	2.64E-17	2.35E-16	CCRN4L	chr4	+	1.4E+08	1.4E+08	1767
ENSG00000(	0	9.634302	7.916483	16.47966	15.64734	7.397684	-1.0735	0.1922	0.29795	ENKUR	chr10	-	25270908	25305089	3382
ENSG00000(	0	1.204288	0	5.243529	11.04518	4.109825	-2.8928	0.014328	0.032163	GPR158	chr10	+	25463991	25891155	6959
ENSG00000(	1.035792	7.225726	0	5.243529	4.60216	4.109825	-0.60874	0.5713	0.69031	CACNA2D4	chr12	-	1901123	2028002	5936
ENSG00000(	372.8851	398.6192	315.3399	322.1025	254.0392	233.438	0.42254	0.022037	0.04731	DCP1B	chr12	-	2055220	2113701	2086
ENSG00000(	151.2256	137.2888	171.5238	113.8595	216.3015	179.1884	-0.14346	0.56905	0.68823	CACNA1C	chr12	+	2079952	2802108	8425
ENSG00000(	10.35792	7.225726	19.79121	27.7158	49.70333	26.30288	-1.4203	0.008701	0.02051	KCNA6	chr12	+	4918342	4960277	5977
ENSG00000(	8.286335	9.634302	3.958241	453.1907	557.7818	486.6032	-5.9581	5.13E-61	1.85E-59	THRB	chr3	-	24158651	24536773	7459
ENSG00000(	291.0575	314.3191	321.937	590.2715	482.3064	529.3454	-0.78816	4.96E-07	2.13E-06	NGLY1	chr3	-	25760435	25831530	3196
ENSG00000(	117.0445	121.6331	79.16483	143.0734	100.3271	115.0751	-0.17045	0.52071	0.64651	OXSM	chr3	+	25824408	25836025	1519
ENSG00000(	365.6345	387.7806	498.7384	306.3719	364.4911	330.4299	0.31996	0.064448	0.12081	UEVLD	chr11	-	18551156	18610294	4156
ENSG00000(	17.60846	28.90291	26.38828	5.243529	11.96562	5.753754	1.5888	0.008636	0.020381	TMEM86A	chr11	+	18714669	18726332	3595
ENSG00000(	205.0868	223.9975	183.3985	378.2832	368.1728	432.3535	-0.93967	7.91E-08	3.66E-07	C12orf45	chr12	+	1.05E+08	1.05E+08	1131
ENSG00000(	2845.32	2995.064	3026.735	578.2863	700.4487	565.5119	2.2618	1.09E-74	5.20E-73	C12orf23	chr12	+	1.07E+08	1.07E+08	3362
ENSG00000(	611.1172	597.3267	654.4292	80.90016	101.2475	73.15488	2.8588	4.28E-57	1.40E-55	BTBD11	chr12	+	1.08E+08	1.08E+08	5767
ENSG00000(	1234.664	1097.106	1246.846	809.7507	844.0361	660.0378	0.62777	5.08E-06	1.95E-05	UBE3B	chr12	+	1.1E+08	1.1E+08	5722

ENSG0000(	1272.988	1333.147	1708.641	334.8368	527.4075	377.2819	1.7934	1.30E-24	1.58E-23	ANK3	chr10	-	61788159	62493248	14771
ENSG0000(	190.5857	168.6003	270.4798	371.5415	500.715	389.6114	-0.99945	1.11E-06	4.60E-06	IPMK	chr10	-	59951278	60027694	6133
ENSG0000(	6.214751	18.06432	13.19414	9.737982	24.85166	12.32947	-0.30604	0.63792	0.74625	RAD9B	chr12	+	1.11E+08	1.11E+08	2843
ENSG0000(	3235.814	3150.417	2852.573	725.8542	1112.802	964.9868	1.7165	5.51E-31	8.63E-30	PLBD2	chr12	+	1.14E+08	1.14E+08	2573
ENSG0000(	935.3201	940.5487	1132.057	512.3677	1265.594	904.1614	0.16251	0.6606	0.765	DLG5	chr10	-	79550549	79686378	7415
ENSG0000(	3.107376	2.408575	0	0	0.920432	0	1.3534	0.31736	0.44424	MAT1A	chr10	-	82031576	82049440	3410
ENSG0000(	89.0781	108.3859	106.8725	110.1141	147.2691	100.2797	-0.23083	0.37167	0.50217	SLC2A13	chr12	-	40148823	40499891	7003
ENSG0000(	324.2029	299.8676	378.6718	711.6218	799.8554	665.7916	-1.116	5.33E-13	3.71E-12	GXYLT1	chr12	-	42475647	42538681	7497
ENSG0000(	1320.635	1354.824	1600.449	1610.512	1443.237	1397.34	-0.05881	0.64343	0.75086	TWF1	chr12	-	44187526	44200178	3320
ENSG0000(	1423.178	1498.134	1523.923	282.4015	445.4891	306.5929	2.0984	1.16E-37	2.23E-36	DIP2C	chr10	-	320130	735683	7894
ENSG0000(	852.4567	840.5928	901.1596	1749.091	1589.586	1421.177	-0.87424	5.41E-12	3.52E-11	EIF4E	chr4	-	99792835	99851788	11523
ENSG0000(	167.7983	172.2131	249.3692	343.8257	583.5539	408.5166	-1.1746	1.27E-07	5.74E-07	MAGI1	chr3	-	65339200	66024509	7415
ENSG0000(	83.89914	77.07441	100.2754	355.8109	277.9705	271.2484	-1.785	3.96E-16	3.34E-15	TEX30	chr13	-	1.03E+08	1.03E+08	1689
ENSG0000(	589.3656	612.9824	719.0805	534.0909	584.4743	445.505	0.29526	0.057576	0.10983	CSNK1G3	chr5	+	1.23E+08	1.23E+08	4462
ENSG0000(	3.107376	2.408575	1.319414	0.749076	0.920432	0.821965	1.0108	0.42028	0.55106	AGAP11	chr10	+	88728247	88784489	4560
ENSG0000(	113.9371	142.106	182.0791	281.6524	294.5382	296.7293	-0.99477	1.67E-06	6.77E-06	SRFBP1	chr5	+	1.21E+08	1.21E+08	2855
ENSG0000(	17.60846	13.24716	23.74945	14.98151	21.16994	14.79537	0.095494	0.86244	0.91288	AKAP6	chr14	+	32798479	33300567	8686
ENSG0000(	50.7538	30.10719	42.22124	2.996302	7.363456	4.109825	2.9694	1.70E-07	7.63E-07	NPAS3	chr14	+	33404139	34273382	5847
ENSG0000(	753.0207	720.1641	840.4666	685.4041	636.9389	634.5569	0.23999	0.072025	0.13296	FAM177A1	chr14	+	35514113	35582336	3395
ENSG0000(	211.3015	246.879	254.6469	262.9255	230.108	189.8739	0.058852	0.76497	0.84492	MBIP	chr14	-	36767770	36789882	1642
ENSG0000(	122.2234	93.93444	137.219	104.8706	97.56579	75.62077	0.34109	0.19798	0.30518	MIPOL1	chr14	+	37667118	38021566	7434
ENSG0000(	1683.162	1647.466	1897.317	1099.643	1023.52	979.7822	0.75045	5.23E-10	2.93E-09	EXT2	chr11	+	44117099	44266979	3454
ENSG0000(	416.3883	443.1779	389.2271	273.4126	232.8693	325.4981	0.58309	0.000829	0.002355	TMEM18	chr2	-	667335	677439	2762
ENSG0000(	6.214751	4.817151	5.277655	23.97042	10.12475	4.109825	-1.1128	0.16302	0.26107	KCTD14	chr11	-	77726761	77757237	1691
ENSG0000(	1.035792	2.408575	5.277655	0	0	0.821965	2.013	0.12483	0.21044	THRSP	chr11	+	77774907	77779397	1174
ENSG0000(	132.5814	107.1816	150.4132	280.1543	197.8929	300.0172	-0.99155	1.27E-05	4.65E-05	NDUFC2	chr11	-	77779350	77791265	2518
ENSG0000(	40.39588	32.51577	26.38828	199.2541	211.6994	202.2034	-2.5872	1.22E-21	1.33E-20	ME3	chr11	-	86152150	86383678	2311
ENSG0000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	MSGN1	chr2	+	17997763	17998368	606
ENSG0000(	4577.164	4499.219	6321.311	256.9329	352.5255	268.7825	4.1198	4.81E-147	7.11E-145	ADAMTS12	chr5	-	33523640	33892297	8774
ENSG0000(	175.0488	201.116	189.9956	239.7042	215.3811	191.5178	-0.1925	0.3265	0.4542	NUBPL	chr14	+	31959162	32330430	5032
ENSG0000(	543.7907	585.2838	789.0094	426.224	417.8761	342.7594	0.68787	7.24E-05	0.00024	NEK7	chr1	+	1.98E+08	1.98E+08	4149
ENSG0000(	1.035792	0	1.319414	2.247227	1.840864	1.64393	-0.82312	0.52593	0.65083	ATP6V1G3	chr1	-	1.98E+08	1.99E+08	678
ENSG0000(	335.5966	388.9849	533.0432	504.1278	517.2828	385.5015	-0.16358	0.39224	0.52311	FER	chr5	+	1.08E+08	1.09E+08	12119
ENSG0000(	633.9046	574.4452	712.4834	400.7554	277.9705	249.8773	1.0413	2.17E-08	1.06E-07	VIPAS39	chr14	-	77893018	77924295	2934
ENSG0000(	849.3494	779.1742	1101.711	606.7512	911.2277	587.7049	0.37335	0.042062	0.08364	ANKRD50	chr4	-	1.26E+08	1.26E+08	8794
ENSG0000(	581.0793	575.6495	633.3186	505.626	536.6119	473.4518	0.23915	0.087462	0.15702	UPF2	chr10	-	11962021	12085169	5569
ENSG0000(	790.3092	791.217	740.1911	1608.265	1259.151	1356.242	-0.86137	1.18E-10	6.96E-10	CDC123	chr10	+	12237964	12292588	1542
ENSG0000(	154.333	139.6974	127.9831	306.3719	230.108	250.6993	-0.89305	1.45E-05	5.29E-05	SCLT1	chr4	-	1.3E+08	1.3E+08	3673
ENSG0000(	18.64425	32.51577	26.38828	185.7707	189.609	161.1051	-2.7666	2.53E-20	2.60E-19	CCDC3	chr10	-	12938627	13141652	3180
ENSG0000(	69.39806	72.25726	58.05421	122.8484	71.7937	107.6774	-0.59206	0.047393	0.092656	C4orf33	chr4	+	1.3E+08	1.3E+08	2862
ENSG0000(	344.9187	343.222	373.3941	550.5705	656.268	510.4402	-0.69155	1.09E-05	4.04E-05	FRMD4A	chr10	-	13685706	14504141	6815
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	SLC25A31	chr4	+	1.29E+08	1.29E+08	1835
ENSG0000(	8.286335	0	17.15238	8.239831	6.443024	1.64393	0.5411	0.56624	0.68549	PTPRO	chr12	+	15475331	15750333	5301
ENSG0000(	3666.703	3467.144	4489.965	583.5299	678.3584	484.9593	2.7269	1.02E-77	5.31E-76	EPS8	chr12	-	15773092	16035263	4061

ENSG0000(	290.0217	242.0618	244.0915	209.7412	273.3683	231.7941	0.12177	0.5194	0.64554	ACAD8	chr11	+	1.34E+08	1.34E+08	3315
ENSG0000(	179.192	196.2989	182.0791	304.1247	220.9037	263.8507	-0.50021	0.010862	0.025054	THYN1	chr11	-	1.34E+08	1.34E+08	1299
ENSG0000(	1142.478	1060.977	1155.806	695.1421	656.268	701.1361	0.70893	8.42E-09	4.24E-08	VPS26B	chr11	+	1.34E+08	1.34E+08	3691
ENSG0000(	285.8786	290.2333	332.4923	1005.259	1026.282	951.0134	-1.7122	2.22E-34	3.91E-33	NCAPD3	chr11	-	1.34E+08	1.34E+08	5531
ENSG0000(	426.7463	373.3292	403.7406	427.7221	449.1708	389.6114	-0.07195	0.63895	0.74707	VTI1A	chr10	+	1.14E+08	1.15E+08	4131
ENSG0000(	585.2224	474.4894	540.9597	747.5774	668.2336	714.2875	-0.41068	0.003918	0.00992	QDPR	chr4	-	17461884	17513857	1648
ENSG0000(	387.3862	431.135	637.2769	151.3133	199.7337	137.2681	1.5661	3.78E-13	2.67E-12	FAM160B1	chr10	+	1.17E+08	1.17E+08	5806
ENSG0000(	36.25272	48.17151	54.09597	258.4311	299.1404	233.438	-2.5018	9.46E-24	1.12E-22	ANO4	chr12	+	1.01E+08	1.02E+08	3909
ENSG0000(	62.14751	54.19295	64.65128	62.17327	67.19154	65.75719	-0.10664	0.7271	0.8172	TEX9	chr15	+	56536207	56738195	4440
ENSG0000(	371.8493	360.082	445.9619	686.9023	674.6767	671.5453	-0.78707	7.67E-08	3.56E-07	QTRTD1	chr3	+	1.14E+08	1.14E+08	4023
ENSG0000(	140.8677	78.2787	133.2608	46.44268	36.81728	50.96182	1.3722	1.18E-05	4.34E-05	MMAA	chr4	+	1.47E+08	1.47E+08	7068
ENSG0000(	901.139	818.9156	907.7567	430.7184	600.1217	485.7813	0.79216	1.91E-07	8.53E-07	ZNF827	chr4	-	1.47E+08	1.47E+08	7463
ENSG0000(	1639.659	1533.058	1741.626	873.4221	1130.29	980.6041	0.71857	5.24E-08	2.47E-07	EDNRA	chr4	+	1.48E+08	1.48E+08	4135
ENSG0000(	11.39371	1.204288	7.916483	4.494453	15.64734	8.219649	-0.4009	0.63004	0.74012	NR3C2	chr4	-	1.49E+08	1.49E+08	5909
ENSG0000(	1.035792	3.612863	1.319414	3.745378	0.920432	0	0.22799	0.85647	0.90907	AKR1C6P	chr10	-	4914093	4934167	983
ENSG0000(	75.61281	55.39724	46.17948	14.98151	23.0108	12.32947	1.7833	2.59E-05	9.14E-05	AKR1C2	chr10	-	5029967	5060223	3381
ENSG0000(	1017.148	1164.546	902.479	361.8035	305.5834	338.6495	1.6105	2.20E-27	3.00E-26	DPYSL4	chr10	+	1.34E+08	1.34E+08	2729
ENSG0000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	VENTX	chr10	+	1.35E+08	1.35E+08	2911
ENSG0000(	45.57484	33.72006	27.70769	28.46487	34.97642	31.23467	0.18162	0.66104	0.76539	ADAM8	chr10	-	1.35E+08	1.35E+08	3279
ENSG0000(	19.68005	16.86003	17.15238	5.992604	21.16994	13.9734	0.37672	0.5344	0.65887	ITIH2	chr10	+	7745232	7791483	3193
ENSG0000(	236.1606	184.256	242.7721	279.4052	301.9017	267.1386	-0.35313	0.05778	0.11015	KIN	chr10	-	7795188	7829990	2081
ENSG0000(	113.9371	52.98866	120.0667	96.63075	46.0216	58.35951	0.50022	0.1617	0.25935	PIGF	chr2	-	46808076	46844258	3454
ENSG0000(	65.25489	62.62296	67.2901	21.72319	27.61296	26.30288	1.3461	0.000191	0.000597	ANKAR	chr2	+	1.91E+08	1.91E+08	4410
ENSG0000(	295.2007	267.3519	296.8681	241.2023	260.4823	235.9039	0.22041	0.20028	0.30777	INPP1	chr2	+	1.91E+08	1.91E+08	2162
ENSG0000(	23.82321	90.32158	48.81831	86.89276	95.72493	92.06007	-0.74445	0.048565	0.094616	MFSD6	chr2	+	1.91E+08	1.91E+08	4797
ENSG0000(	3053.515	3331.06	3322.284	403.7517	422.4783	357.5547	3.0299	8.42E-139	1.12E-136	RNF144A	chr2	+	7057523	7208417	5743
ENSG0000(	266.1985	268.5562	357.5611	180.5272	327.6738	174.2566	0.38509	0.10982	0.18928	ASAP2	chr2	+	9346894	9545812	5712
ENSG0000(	366.6703	367.3078	449.9201	402.2536	428.9213	340.2935	0.013984	0.93333	0.96001	ADAM17	chr2	-	9628615	9695921	4349
ENSG0000(	307.6302	303.4805	419.5736	201.5013	187.7681	163.571	0.89132	4.95E-06	1.90E-05	FLI1	chr11	+	1.29E+08	1.29E+08	5370
ENSG0000(	12.4295	6.021439	7.916483	8.988907	4.60216	20.54912	-0.3376	0.65096	0.75715	TMEM45B	chr11	+	1.3E+08	1.3E+08	2234
ENSG0000(	317.9881	308.2977	469.7113	834.4702	1215.891	886.0782	-1.4168	6.65E-14	4.91E-13	WWC2	chr4	+	1.84E+08	1.84E+08	8826
ENSG0000(	129.474	93.93444	116.1084	1054.698	687.5627	679.765	-2.8163	3.30E-42	7.28E-41	MLF1IP	chr4	-	1.86E+08	1.86E+08	1998
ENSG0000(	1923.466	1902.775	1977.801	302.6265	301.9017	226.8623	2.7961	5.05E-89	3.13E-87	ACSL1	chr4	-	1.86E+08	1.86E+08	3948
ENSG0000(	198.872	198.7075	205.8285	2164.079	1986.292	2266.979	-3.4032	1.36E-141	1.87E-139	SLC25A4	chr4	+	1.86E+08	1.86E+08	1666
ENSG0000(	25.8948	26.49433	35.62417	20.22504	16.56778	32.05663	0.33695	0.47697	0.60623	AMN1	chr12	-	31824071	31882108	2110
ENSG0000(	149.154	179.4389	267.841	244.9477	251.2779	250.6993	-0.32769	0.1375	0.22741	BICD1	chr12	+	32259769	32536567	8811
ENSG0000(	656.6921	759.9056	621.4439	667.4263	662.711	561.402	0.10753	0.45962	0.58906	SAV1	chr14	-	51098776	51135049	3063
ENSG0000(	30.03797	24.08575	29.0271	77.90386	84.67974	80.55256	-1.5207	9.06E-06	3.38E-05	CCDC122	chr13	-	44398045	44453827	3467
ENSG0000(	48.68222	25.29004	30.34652	17.97781	25.7721	34.52253	0.41144	0.37086	0.5014	SERP2	chr13	+	44947801	44971850	962
ENSG0000(	1376.567	1256.072	1483.021	538.5853	589.9969	489.8911	1.3436	8.12E-24	9.61E-23	NBAS	chr2	-	15307032	15701454	7281
ENSG0000(	22.78742	28.90291	22.43003	29.96302	11.96562	13.15144	0.40179	0.45136	0.58094	ZNF385D	chr3	-	21459915	22414812	4498
ENSG0000(	46.61064	42.15007	50.13772	731.8468	763.0381	771.8251	-4.009	1.24E-92	8.24E-91	TDO2	chr4	+	1.57E+08	1.57E+08	3139
ENSG0000(	408.102	458.8336	463.1142	919.8648	768.5607	639.4887	-0.8062	6.06E-07	2.57E-06	GUF1	chr4	+	44680444	44702943	4449
ENSG0000(	18.64425	24.08575	21.11062	0	0	1.64393	4.4534	1.57E-06	6.37E-06	SLC35F4	chr14	-	58030640	58448912	2700

ENSG00000(	2.071584	1.204288	3.958241	58.42789	57.06678	45.20807	-4.2109	9.54E-11	5.66E-10	GABRA2	chr4	-	46250444	46477247	5812
ENSG00000(	3122.913	3069.729	4273.581	805.2562	864.2856	600.0344	2.1974	2.03E-42	4.51E-41	SACS	chr13	-	23902965	24007841	15639
ENSG00000(	1.035792	7.225726	1.319414	3.745378	3.681728	4.109825	-0.22388	0.83136	0.892	PABPC3	chr13	+	25670300	25673389	3090
ENSG00000(	203.0152	174.6217	266.5216	493.6408	506.2376	444.683	-1.1627	2.29E-10	1.32E-09	CENPJ	chr13	-	25457171	25497018	4347
ENSG00000(	51.7896	44.55865	51.45714	66.66772	31.29469	41.92021	0.072115	0.84906	0.90389	FBXO4	chr5	+	41925356	41941845	1731
ENSG00000(	167.7983	152.9445	180.7597	164.7966	165.6778	167.6808	0.008869	0.96527	0.9799	C5orf28	chr5	-	43444354	43483995	2950
ENSG00000(	117.0445	95.13873	68.60952	39.701	37.73771	24.65895	1.4403	2.44E-05	8.64E-05	CCL28	chr5	-	43376747	43412493	3126
ENSG00000(	395.6725	443.1779	527.7655	481.6556	402.2288	360.0206	0.13243	0.44243	0.57208	PARP8	chr5	+	49961733	50142356	7177
ENSG00000(	447.4621	413.0707	423.5318	170.7892	176.7229	138.0901	1.398	1.73E-15	1.41E-14	GFRA1	chr10	-	1.18E+08	1.18E+08	9216
ENSG00000(	782.0229	733.4112	873.4519	964.0602	1012.475	877.0366	-0.25625	0.053583	0.10319	CACUL1	chr10	-	1.2E+08	1.21E+08	6733
ENSG00000(	4611.346	4773.797	6521.862	1713.885	1960.52	1564.199	1.5977	5.59E-28	7.81E-27	DST	chr6	-	56322785	56819426	24269
ENSG00000(	274.4849	255.309	296.8681	86.89276	69.95283	65.75719	1.8771	3.13E-18	2.92E-17	BEND6	chr6	+	56819773	56892140	3497
ENSG00000(	1424.214	1478.865	1460.591	1632.985	1705.56	1622.559	-0.18483	0.092252	0.16406	TIAL1	chr10	-	1.21E+08	1.21E+08	2321
ENSG00000(	2068.476	1942.516	1926.344	1739.353	1546.326	1380.901	0.34671	0.004866	0.012081	BAG3	chr10	+	1.21E+08	1.21E+08	2571
ENSG00000(	0	0	0	6.74168	4.60216	4.109825	-3.1605	0.01238	0.028189	GLT1D1	chr12	+	1.29E+08	1.29E+08	3010
ENSG00000(	1.035792	1.204288	0	0	3.681728	0.821965	-0.54523	0.68482	0.78423	TMEM132D	chr12	-	1.3E+08	1.3E+08	5776
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RBM46	chr4	+	1.56E+08	1.56E+08	3626
ENSG00000(	12.4295	13.24716	9.235896	30.7121	22.09037	24.65895	-1.0989	0.043328	0.085808	SCHIP1	chr3	+	1.6E+08	1.6E+08	5949
ENSG00000(	1921.394	1923.247	1646.628	226.9699	210.7789	188.23	3.1243	7.07E-112	6.42E-110	LIX1L	chr1	+	1.45E+08	1.46E+08	3979
ENSG00000(	16.57267	18.06432	22.43003	5.992604	11.04518	5.753754	1.2548	0.04665	0.091378	NBPF11	chr1	-	1.46E+08	1.46E+08	5642
ENSG00000(	1646.909	1459.597	1579.338	5.243529	0	6.575719	8.3978	2.55E-113	2.38E-111	KCNE4	chr2	+	2.24E+08	2.24E+08	3291
ENSG00000(	118.0803	151.7403	143.8161	374.5378	364.4911	379.7478	-1.4326	1.03E-14	7.95E-14	AP1S3	chr2	-	2.25E+08	2.25E+08	2515
ENSG00000(	309.7018	334.792	467.0725	232.9625	254.0392	141.378	0.81574	0.000378	0.001131	RABGAP1L	chr1	+	1.74E+08	1.75E+08	6821
ENSG00000(	129.474	120.4288	100.2754	47.19176	49.70333	64.93523	1.1042	9.16E-05	0.0003	CCDC74B	chr2	-	1.31E+08	1.31E+08	3385
ENSG00000(	1.035792	3.612863	3.958241	104.8706	82.83888	94.52597	-4.833	6.36E-17	5.54E-16	TMEM56	chr1	+	95582894	95663163	6822
ENSG00000(	74.57702	116.8159	130.622	88.39091	60.74851	101.1017	0.35154	0.2403	0.35556	MZT2B	chr2	+	1.31E+08	1.31E+08	933
ENSG00000(	0	1.204288	1.319414	0	0.920432	1.64393	-0.02084	0.98774	NA	TUBA3E	chr2	-	1.31E+08	1.31E+08	1540
ENSG00000(	7.250543	8.430014	15.83297	1.498151	4.60216	7.397684	1.0962	0.18386	0.2879	ASTN1	chr1	-	1.77E+08	1.77E+08	7122
ENSG00000(	3460.581	3312.996	4013.657	2851.731	3664.24	3027.297	0.17643	0.17197	0.27296	FAM168B	chr2	-	1.32E+08	1.32E+08	5285
ENSG00000(	238.2321	219.1804	295.5487	264.4237	670.0745	438.1073	-0.85793	0.000769	0.002197	PTPN14	chr1	-	2.15E+08	2.15E+08	5552
ENSG00000(	411.2094	352.8563	350.9641	468.9213	435.3643	453.7246	-0.28213	0.065631	0.12277	AC093838.	chr2	+	1.32E+08	1.32E+08	3785
ENSG00000(	1282.31	1230.782	1827.388	799.2636	1113.723	807.1696	0.6714	0.000109	0.000354	MGAT5	chr2	+	1.35E+08	1.35E+08	8252
ENSG00000(	0	4.817151	1.319414	1.498151	4.60216	3.28786	-0.46722	0.68962	0.78808	TMEM163	chr2	-	1.35E+08	1.35E+08	5078
ENSG00000(	291.0575	322.7491	366.797	245.6968	208.9381	170.9687	0.64226	0.00093	0.002619	GPATCH11	chr2	+	37311594	37326387	3906
ENSG00000(	18.64425	21.67718	46.17948	417.2351	361.7298	317.2785	-3.6524	4.56E-39	9.20E-38	HSPB8	chr12	+	1.2E+08	1.2E+08	2150
ENSG00000(	184.371	202.3203	197.9121	330.3423	256.8005	372.3501	-0.7133	0.000246	0.000758	GEMIN6	chr2	+	38978676	39009598	1210
ENSG00000(	7.250543	6.021439	1.319414	349.0692	189.609	186.586	-5.4095	2.94E-31	4.65E-30	TMEM178A	chr2	+	39892122	39945103	1662
ENSG00000(	0	0	1.319414	17.97781	20.2495	18.90519	-4.3845	1.71E-05	6.19E-05	POU4F1	chr13	-	79173227	79177673	3795
ENSG00000(	160.5477	118.0202	147.7743	368.5452	364.4911	372.3501	-1.3658	3.20E-13	2.27E-12	RNF219	chr13	-	79188426	79233314	3529
ENSG00000(	1.035792	0	0	2.996302	11.04518	10.68554	-3.1841	0.006108	0.01488	CYSLTR2	chr13	+	49280951	49283498	2548
ENSG00000(	2.071584	3.612863	1.319414	2.996302	7.363456	3.28786	-0.7749	0.45962	0.58906	GRID2	chr4	+	93225550	94695707	5340
ENSG00000(	0	0	0	0.749076	4.60216	0.821965	-1.7467	0.19759	0.30468	ARL11	chr13	+	50202435	50208008	3760
ENSG00000(	501.3233	450.4036	605.6109	141.5753	247.5962	130.6924	1.5753	2.21E-12	1.47E-11	SETBP1	chr18	+	42260138	42648475	9899
ENSG00000(	425.7105	402.2321	472.3501	383.5267	355.2868	288.5097	0.33757	0.044062	0.087064	ARL14EP	chr11	+	30344598	30359774	3417

ENSG00000(	496.1443	440.7693	701.9281	316.859	323.0716	284.3999	0.82079	9.06E-06	3.38E-05	EPG5	chr18	-	43427574	43547240	12633
ENSG00000(	211.3015	186.6646	175.482	1896.659	1487.418	1436.795	-3.0582	2.73E-83	1.55E-81	PSTPIP2	chr18	-	43563502	43652238	3000
ENSG00000(	7841.981	7692.99	7248.859	8468.299	7214.346	7083.694	0.001087	0.99214	0.99518	ATP5A1	chr18	-	43664110	43684300	4547
ENSG00000(	293.1291	339.6091	274.4381	691.3967	543.9753	631.2691	-1.0377	1.57E-10	9.14E-10	HAUS1	chr18	+	43684298	43708299	1125
ENSG00000(	292.0933	364.8992	485.5443	805.2562	829.3092	666.6135	-1.009	2.82E-08	1.37E-07	C18orf25	chr18	+	43753519	43846949	5454
ENSG00000(	64.2191	75.87013	64.65128	408.2462	312.9469	390.4333	-2.4272	1.76E-29	2.63E-28	SPC25	chr2	-	1.7E+08	1.7E+08	1354
ENSG00000(	659.7994	679.2183	600.3333	98.1289	109.5314	101.9236	2.6396	1.59E-56	5.12E-55	PDK1	chr2	+	1.73E+08	1.73E+08	2987
ENSG00000(	14.50109	15.65574	21.11062	122.8484	170.2799	108.4994	-2.9267	2.32E-16	1.97E-15	SPON1	chr11	+	13983914	14289646	5372
ENSG00000(	53.86118	51.78437	81.80365	452.4416	544.8957	447.1489	-2.9368	6.84E-42	1.49E-40	PDE3B	chr11	+	14665269	14892350	5521
ENSG00000(	861.7789	792.4213	733.5941	1107.883	940.6815	895.1198	-0.30067	0.02931	0.060924	TCF7L1	chr2	+	85360533	85537511	2968
ENSG00000(	3418.113	3344.307	3774.843	1844.973	2406.93	1924.22	0.76933	1.92E-09	1.03E-08	TGOLN2	chr2	-	85545147	85555548	6489
ENSG00000(	8.286335	14.45145	13.19414	1.498151	3.681728	4.109825	1.7601	0.030993	0.063956	SH2D6	chr2	+	85645844	85664152	1975
ENSG00000(	0	0	1.319414	1.498151	2.761296	0	-0.85965	0.52633	NA	KCNK13	chr14	+	90528109	90652201	2522
ENSG00000(	1164.23	1191.041	1746.904	934.0972	1147.779	854.0216	0.48022	0.004572	0.011419	UHMK1	chr1	+	1.62E+08	1.62E+08	8478
ENSG00000(	131.5456	92.73015	79.16483	185.0217	171.2004	191.5178	-0.83805	0.000551	0.001606	ATG10	chr5	+	81267844	81572676	3033
ENSG00000(	132.5814	99.95588	106.8725	265.9218	208.0176	180.0103	-0.93687	5.77E-05	0.000194	POC5	chr5	-	74969949	75013313	2229
ENSG00000(	146.0467	172.2131	197.9121	246.4459	304.663	218.6427	-0.57531	0.006021	0.014681	SPOCK1	chr5	-	1.36E+08	1.37E+08	4846
ENSG00000(	27.96638	36.12863	36.94359	34.45748	39.57858	32.05663	-0.0717	0.85862	0.9101	FAM151B	chr5	+	79783788	79838382	2185
ENSG00000(	98.40023	140.9017	139.8579	262.1764	202.495	180.0103	-0.76566	0.001135	0.003154	TADA1	chr1	-	1.67E+08	1.67E+08	2539
ENSG00000(	210.2658	236.0404	347.0058	44.19546	41.41944	36.98842	2.6648	1.37E-24	1.67E-23	GUCY1A2	chr11	-	1.07E+08	1.07E+08	5795
ENSG00000(	109.7939	107.1816	147.7743	268.9181	232.8693	201.3814	-0.94535	2.14E-05	7.63E-05	CWF19L2	chr11	-	1.07E+08	1.07E+08	3278
ENSG00000(	133.6172	125.2459	188.6762	83.89646	107.6905	96.1699	0.63053	0.012576	0.028581	JMY	chr5	+	78532012	78623038	9042
ENSG00000(	248.5901	233.6318	254.6469	568.5483	772.2424	569.6217	-1.3679	1.84E-15	1.49E-14	HOMER1	chr5	-	78668459	78810040	5881
ENSG00000(	63.18331	59.0101	89.72014	205.2467	139.9057	154.5294	-1.2327	4.60E-06	1.77E-05	XRCC4	chr5	+	82373317	82649606	1696
ENSG00000(	55.93276	48.17151	71.24834	48.68991	58.90765	47.67397	0.17173	0.6068	0.72126	ZNF547	chr19	+	57874845	57890933	2739
ENSG00000(	170.9057	134.8802	141.1773	92.13629	63.50981	81.37453	0.90536	0.000363	0.001092	ZNF773	chr19	+	58011283	58029772	5832
ENSG00000(	279.6638	348.0392	325.8952	271.1653	333.1964	263.0288	0.13602	0.44747	0.57723	ZNF776	chr19	+	58258164	58269527	5292
ENSG00000(	69.39806	85.50443	56.73479	83.14739	66.2711	75.62077	-0.08757	0.76978	0.84862	ZNF256	chr19	-	58452201	58459043	2172
ENSG00000(	154.333	155.3531	191.315	500.3825	466.659	492.357	-1.5401	2.87E-19	2.81E-18	SUV39H2	chr10	+	14920819	14946314	3087
ENSG00000(	201.9794	236.0404	232.2168	266.6709	229.1876	230.9721	-0.11918	0.5202	0.64608	DCLRE1C	chr10	-	14939358	14996431	3674
ENSG00000(	3.107376	7.225726	6.597069	9.737982	5.522592	3.28786	-0.13158	0.88019	0.92516	OLAH	chr10	+	15074226	15115851	1767
ENSG00000(	80.79177	68.6444	68.60952	175.2837	156.4734	141.378	-1.1056	8.00E-06	3.00E-05	RPP38	chr10	+	15139179	15181817	1457
ENSG00000(	337.6682	391.3935	353.6029	487.6482	373.6954	399.475	-0.22082	0.18512	0.28965	NMT2	chr10	-	15144583	15210692	2907
ENSG00000(	0	2.408575	0	2.996302	0	0	-0.15661	0.90782	NA	ZSCAN1	chr19	+	58545400	58565999	2054
ENSG00000(	84.93494	69.84869	69.92893	84.64554	71.7937	118.3629	-0.28529	0.33364	0.46176	ZNF837	chr19	-	58878985	58892427	2038
ENSG00000(	708.4817	621.4125	754.7047	1338.598	1563.814	1352.954	-1.027	1.34E-14	1.03E-13	USP12	chr13	-	27640293	27746033	4497
ENSG00000(	6.214751	3.612863	14.51355	13.48336	7.363456	4.109825	-0.04968	0.95068	0.97041	ARL5B-AS1	chr10	-	18940195	18948196	689
ENSG00000(	785.1303	762.3141	860.2578	1724.372	1335.547	1286.375	-0.85071	2.83E-09	1.49E-08	CCDC50	chr3	+	1.91E+08	1.91E+08	8429
ENSG00000(	180.2278	167.396	229.578	119.8521	115.9744	95.34793	0.79345	0.000493	0.00145	CAMK4	chr5	+	1.11E+08	1.11E+08	12240
ENSG00000(	14.50109	27.69862	21.11062	86.89276	68.11197	61.64737	-1.7472	8.43E-06	3.15E-05	TRIM36	chr5	-	1.14E+08	1.15E+08	4218
ENSG00000(	1825.065	1861.829	1794.403	1430.734	1658.618	1339.803	0.30735	0.011415	0.02619	ZFP36L2	chr2	-	43449541	43453748	3696
ENSG00000(	657.7279	655.1325	674.2204	441.9546	485.0677	423.3119	0.55639	5.80E-05	0.000195	PAN3	chr13	+	28712643	28869475	4940
ENSG00000(	617.332	673.1968	769.2182	9.737982	2.761296	0	6.4258	2.78E-13	1.98E-12	PLEKHH2	chr2	+	43864412	43995126	6981
ENSG00000(	2580.158	2592.831	2615.078	1125.111	1140.415	1238.701	1.1503	7.31E-26	9.35E-25	PFKM	chr12	+	48498922	48540187	3579

ENSG00000(	1798.135	1858.216	2088.632	5138.658	5426.867	4722.188	-1.41	3.16E-35	5.70E-34	TMEM123	chr11	-	1.02E+08	1.02E+08	3579
ENSG00000(	190.5857	151.7403	200.5509	0	1.840864	0.821965	7.1497	8.23E-26	1.05E-24	GRIA4	chr11	+	1.05E+08	1.06E+08	5621
ENSG00000(	199.9078	181.8474	352.2835	15.73059	25.7721	26.30288	3.3945	7.88E-27	1.05E-25	IGSF10	chr3	-	1.51E+08	1.51E+08	11067
ENSG00000(	117.0445	110.7945	127.9831	46.44268	45.10117	41.09825	1.4073	4.45E-07	1.92E-06	SPEF2	chr5	+	35617946	35814713	6246
ENSG00000(	35.21692	27.69862	18.47179	17.22874	15.64734	17.26126	0.68065	0.17535	0.2771	SPARCL1	chr4	-	88394487	88452213	2994
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	DSPP	chr4	+	88529681	88538062	4331
ENSG00000(	0	0	0	0.749076	1.840864	0	-0.68825	0.58858	NA	DMP1	chr4	+	88571459	88585513	2682
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	MEPE	chr4	+	88742563	88767969	2226
ENSG00000(	1122.798	1162.138	1456.633	762.5589	846.7974	622.2274	0.74281	1.27E-06	5.20E-06	MBNL1	chr3	+	1.52E+08	1.52E+08	6422
ENSG00000(	3.107376	1.204288	2.638828	0	0	0	2.2312	0.098725	0.17353	CAPSL	chr5	-	35904397	35938881	1004
ENSG00000(	670.1574	602.1439	729.6358	292.1395	329.5147	263.8507	1.1736	5.84E-14	4.33E-13	NADKD1	chr5	-	36192694	36242381	3614
ENSG00000(	188.5141	197.5032	193.9538	94.38352	111.3723	72.33291	1.0545	5.92E-06	2.26E-05	GPD1L	chr3	+	32147181	32210205	4060
ENSG00000(	13786.39	15031.92	15394.92	3754.367	4367.45	3678.293	1.9026	4.41E-66	1.77E-64	GJA1	chr6	+	1.22E+08	1.22E+08	3037
ENSG00000(	0	0	0	32.21025	22.09037	12.32947	-5.3111	1.32E-06	5.39E-06	CCNO	chr5	-	54526980	54529508	1726
ENSG00000(	624.5825	623.821	678.1787	933.3481	824.7071	745.5222	-0.37794	0.00662	0.016001	SLC30A6	chr2	+	32390933	32449448	5089
ENSG00000(	534.4686	540.7252	522.4879	728.1014	637.8594	607.4321	-0.30428	0.030257	0.062648	PELO	chr5	+	52083774	52099880	4349
ENSG00000(	58.00435	65.03154	43.54065	6.74168	4.60216	8.219649	2.9785	1.12E-09	6.11E-09	RASGRP3	chr2	+	33661391	33789817	4807
ENSG00000(	606.9741	611.7782	576.5838	699.6366	539.3732	599.2124	-0.03476	0.81269	0.87847	SAR1B	chr5	-	1.34E+08	1.34E+08	6682
ENSG00000(	3.107376	3.612863	5.277655	2.247227	0.920432	4.109825	0.57323	0.58803	0.70527	CATSPER3	chr5	+	1.34E+08	1.34E+08	1362
ENSG00000(	12.4295	32.51577	17.15238	2.247227	16.56778	3.28786	1.3935	0.054785	0.10525	FAM21B	chr10	+	47894023	47949412	4231
ENSG00000(	356.3124	378.1463	402.4212	283.8996	306.5039	263.8507	0.4104	0.011579	0.026526	GPR180	chr13	+	95254157	95286899	8822
ENSG00000(	0	0	2.638828	22.47227	8.283888	22.19305	-3.6948	0.000139	0.000445	TCTEX1D1	chr1	+	67218142	67244470	2001
ENSG00000(	52.82539	43.35436	59.37362	57.67882	46.0216	74.79881	-0.19848	0.56167	0.68169	WDR78	chr1	-	67278568	67390570	4206
ENSG00000(	0	1.204288	1.319414	11.98521	22.09037	19.72716	-3.7614	7.46E-05	0.000247	ANKRD22	chr10	-	90581889	90611575	1596
ENSG00000(	4386.579	4271.609	4128.446	3331.139	2908.565	2622.89	0.52776	7.30E-06	2.75E-05	FARP1	chr13	+	98794816	99102027	8209
ENSG00000(	424.6747	476.8979	500.0578	92.88537	92.0432	84.66239	2.3663	1.67E-38	3.33E-37	IFIT5	chr10	+	91174343	91180758	4015
ENSG00000(	46.61064	38.53721	46.17948	91.38722	137.1444	125.7606	-1.4108	2.90E-06	1.15E-05	SLC16A12	chr10	-	91190051	91316398	4622
ENSG00000(	242.3753	230.019	271.7992	316.1099	311.106	278.6461	-0.28371	0.10337	0.18027	PANK1	chr10	-	91342745	91405215	3367
ENSG00000(	164.6909	158.966	166.2461	38.20285	23.93123	22.19305	2.4993	1.17E-17	1.06E-16	PRDM8	chr4	+	81105033	81125483	4095
ENSG00000(	1.035792	3.612863	5.277655	1.498151	0	2.465895	0.9496	0.42637	0.55666	BMP3	chr4	+	81952119	81978685	5734
ENSG00000(	3920.472	4011.482	3989.907	5715.446	5681.827	6044.73	-0.54829	2.88E-08	1.39E-07	HNRPDL	chr4	-	83343717	83351294	3781
ENSG00000(	23.82321	26.49433	18.47179	0	3.681728	1.64393	3.3948	1.46E-05	5.31E-05	HHEX	chr10	+	94447945	94455403	3490
ENSG00000(	896.9958	834.5714	1409.134	1068.931	1545.405	1121.16	-0.24956	0.1911	0.29667	UTRN	chr6	+	1.45E+08	1.45E+08	12339
ENSG00000(	2.071584	0	0	1.498151	2.761296	0	-0.5204	0.70059	0.7965	GRM1	chr6	+	1.46E+08	1.47E+08	6939
ENSG00000(	863.8504	788.8085	1001.435	651.6957	737.266	573.7315	0.43401	0.003503	0.008948	PTPRK	chr6	-	1.28E+08	1.29E+08	6188
ENSG00000(	587.294	586.4881	498.7384	690.6477	651.6659	711.8216	-0.29475	0.034267	0.069842	GGPS1	chr1	+	2.35E+08	2.36E+08	2895
ENSG00000(	0	0	0	7.490755	11.96562	11.50751	-4.2173	0.000311	0.000945	CNTNAP4	chr16	+	76311176	76593135	4866
ENSG00000(	80.79177	103.5687	141.1773	62.92235	46.94203	47.67397	1.0253	0.000835	0.00237	ZNF117	chr7	-	64438360	64467062	2874
ENSG00000(	70.43385	72.25726	79.16483	5.243529	3.681728	4.109825	3.9371	7.24E-16	6.00E-15	PART1	chr5	+	59783540	59843484	2316
ENSG00000(	0	0	0	7.490755	2.761296	10.68554	-3.5959	0.003484	0.008903	RAB3C	chr5	+	57878048	58155213	8888
ENSG00000(	12.4295	9.634302	36.94359	2.996302	1.840864	0.821965	3.0071	0.000243	0.000748	IFLTD1	chr12	-	25562241	25801513	1729
ENSG00000(	2.071584	0	0	402.2536	385.661	383.8576	-8.084	3.83E-29	5.62E-28	MARVELD2	chr5	+	68710939	68740157	4376
ENSG00000(	401.8873	349.2434	407.6989	516.8621	452.8525	343.5813	-0.18018	0.31343	0.43986	RAD17	chr5	+	68665120	68710628	3233
ENSG00000(	328.346	261.3304	308.7428	373.0396	339.6394	290.9756	-0.15869	0.37072	0.50123	MED21	chr12	+	27175479	27219276	1753

ENSG00000(	2927.148	3258.803	3057.082	793.271	848.6383	716.7534	1.967	2.58E-62	9.51E-61	PLOD2	chr3	-	1.46E+08	1.46E+08	3835
ENSG00000(	734.3765	659.9497	816.7171	128.0919	127.0196	83.84042	2.6927	1.46E-47	3.75E-46	STK32B	chr4	+	5053169	5502725	3582
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	NRSN1	chr6	+	24126350	24155128	2354
ENSG00000(	4.143168	1.204288	1.319414	0	0	0	2.1615	0.11037	0.19002	JAKMIP1	chr4	-	6027926	6202318	2975
ENSG00000(	4675.565	4564.25	4259.068	854.6952	1009.714	987.1799	2.2398	2.28E-84	1.31E-82	ZIC1	chr3	+	1.47E+08	1.47E+08	5241
ENSG00000(	604.9025	632.2511	647.8322	895.1453	852.32	682.2309	-0.36576	0.011741	0.026852	GPR125	chr4	-	22346694	22517677	4557
ENSG00000(	1.035792	0	5.277655	0	0	0	1.9229	0.15616	0.25219	CPB1	chr3	+	1.49E+08	1.49E+08	3574
ENSG00000(	337.6682	414.275	427.4901	563.3048	393.9449	488.2472	-0.29542	0.092336	0.16418	SREK1IP1	chr5	-	64016338	64064512	4509
ENSG00000(	88.04231	96.34302	104.2337	29.96302	23.93123	35.34449	1.6639	2.37E-07	1.05E-06	LGI2	chr4	-	25000469	25032501	6428
ENSG00000(	417.4241	417.8878	386.5882	495.1389	517.2828	456.1905	-0.26352	0.073907	0.13593	CWC27	chr5	+	64064757	64314590	2103
ENSG00000(	44.53905	25.29004	32.98534	2.247227	5.522592	4.109825	2.9671	1.23E-06	5.06E-06	MR1	chr1	+	1.81E+08	1.81E+08	7704
ENSG00000(	61.11172	78.2787	67.2901	113.8595	97.56579	87.95025	-0.53187	0.056767	0.10846	SRP19	chr5	+	1.12E+08	1.12E+08	2841
ENSG00000(	181.2636	190.2775	145.1355	755.0682	585.3947	642.7766	-1.9303	3.26E-28	4.61E-27	CENPH	chr5	+	68485375	68506184	1389
ENSG00000(	297.2723	342.0177	319.2981	571.5446	705.0509	512.9061	-0.89712	7.07E-08	3.29E-07	CDYL	chr6	+	4706393	4955785	3419
ENSG00000(	1212.912	1224.761	949.9779	1224.739	1408.261	1407.204	-0.25226	0.06576	0.123	CARHSP1	chr16	-	8946799	8962866	3026
ENSG00000(	0	1.204288	0	3.745378	3.681728	0	-1.46	0.27523	0.39659	TEKT5	chr16	-	10721358	10788802	1612
ENSG00000(	5.17896	4.817151	7.916483	41.94823	45.10117	33.70056	-2.6409	2.40E-06	9.55E-06	BANK1	chr4	+	1.02E+08	1.03E+08	3544
ENSG00000(	389.4578	339.6091	277.0769	447.9472	331.3555	350.979	-0.16578	0.37285	0.50339	TXNDC11	chr16	-	11772936	11836734	3178
ENSG00000(	3403.612	3333.468	3847.411	785.0312	791.5715	672.3673	2.23	4.61E-75	2.22E-73	DAB2	chr5	-	39371780	39462402	4534
ENSG00000(	10.35792	8.430014	6.597069	0.749076	1.840864	2.465895	2.0039	0.034848	0.070879	ACMSD	chr2	+	1.36E+08	1.36E+08	1936
ENSG00000(	1.035792	0	0	87.64184	47.86246	47.67397	-6.0062	5.63E-11	3.40E-10	ACOXL	chr2	+	1.11E+08	1.12E+08	2714
ENSG00000(	1048.221	1094.698	1143.932	253.9366	295.4587	294.2634	1.9579	9.20E-46	2.25E-44	BCL2L11	chr2	+	1.12E+08	1.12E+08	5086
ENSG00000(	506.5022	450.4036	548.8761	962.5621	1055.736	812.1013	-0.9079	1.20E-09	6.53E-09	ANAPC1	chr2	-	1.13E+08	1.13E+08	8259
ENSG00000(	1603.406	1623.38	1653.225	3801.558	3496.721	3180.182	-1.1008	2.81E-22	3.11E-21	CAST	chr5	+	95865525	96115299	4629
ENSG00000(	583.1508	587.6924	628.041	874.9202	780.5263	747.1661	-0.41749	0.001967	0.005245	SCOC	chr4	+	1.41E+08	1.41E+08	2193
ENSG00000(	13.46529	19.2686	9.235896	14.98151	21.16994	27.12484	-0.5594	0.32477	0.45226	CLGN	chr4	-	1.41E+08	1.41E+08	3043
ENSG00000(	166.7625	125.2459	142.4967	435.2129	324.9125	457.0125	-1.4761	2.51E-13	1.80E-12	CETN3	chr5	-	89688078	89705603	2432
ENSG00000(	1819.886	1935.29	2030.578	3161.099	3144.196	2820.984	-0.65682	4.00E-09	2.08E-08	SMARCA5	chr4	+	1.44E+08	1.44E+08	7923
ENSG00000(	11.39371	14.45145	9.235896	38.95193	24.85166	15.61733	-1.1249	0.048377	0.094292	SYCP2L	chr6	+	10748027	10979553	3130
ENSG00000(	52.82539	37.33292	42.22124	652.4448	680.1992	593.4587	-3.8301	2.30E-75	1.12E-73	BMP6	chr6	+	7727030	7881655	2780
ENSG00000(	6.214751	4.817151	5.277655	5.992604	4.60216	9.863579	-0.29064	0.73067	0.81964	RGPD3	chr2	-	1.07E+08	1.07E+08	5594
ENSG00000(	408.102	407.0492	416.9348	991.776	1145.017	938.6839	-1.3159	3.11E-21	3.31E-20	RASSF3	chr12	+	65004293	65091347	3492
ENSG00000(	7870.983	7271.489	7862.387	8952.202	12509.59	10392.1	-0.46837	0.000251	0.000772	HNRNPU	chr1	-	2.45E+08	2.45E+08	5940
ENSG00000(	1351.708	1333.147	1998.912	1922.877	2045.2	1601.188	-0.24971	0.12228	0.20714	RANBP2	chr2	+	1.09E+08	1.09E+08	11711
ENSG00000(	707.4459	667.1754	984.2827	1255.451	1226.936	979.7822	-0.55292	0.000771	0.002205	AHCTF1	chr1	-	2.47E+08	2.47E+08	8751
ENSG00000(	34.18113	34.92434	34.30476	179.0291	208.0176	137.2681	-2.3144	1.09E-15	8.92E-15	MERTK	chr2	+	1.13E+08	1.13E+08	3954
ENSG00000(	422.6031	454.0165	530.4043	555.065	535.6914	478.3836	-0.1588	0.29979	0.42464	TMEM87B	chr2	+	1.13E+08	1.13E+08	5212
ENSG00000(	0	0	1.319414	35.20655	39.57858	36.16646	-5.322	1.96E-08	9.63E-08	PTPRR	chr12	-	71031853	71314623	3529
ENSG00000(	50.7538	48.17151	73.88717	2.996302	8.283888	12.32947	2.7797	2.76E-08	1.34E-07	NR4A2	chr2	-	1.57E+08	1.57E+08	3472
ENSG00000(	18.64425	1.204288	13.19414	18.72689	9.20432	7.397684	-0.08579	0.91041	0.94496	CCDC148	chr2	-	1.59E+08	1.59E+08	3122
ENSG00000(	427.7821	429.9307	460.4754	5.992604	22.09037	22.19305	4.6886	1.60E-62	5.92E-61	PLA2R1	chr2	-	1.61E+08	1.61E+08	8526
ENSG00000(	1571.296	1483.682	1915.789	2869.708	3285.022	2650.837	-0.82336	7.28E-10	4.04E-09	RBMS1	chr2	-	1.61E+08	1.61E+08	4273
ENSG00000(	1.035792	4.817151	5.277655	0	2.761296	0.821965	1.2149	0.3092	0.43534	SCN3A	chr2	-	1.66E+08	1.66E+08	9123
ENSG00000(	4.143168	4.817151	0	3.745378	4.60216	1.64393	-0.10696	0.92253	0.95302	FEZF2	chr3	-	62355356	62359999	2074

ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	CD96	chr3	+	1.11E+08	1.11E+08	4324
ENSG00000(	33.14534	28.90291	25.06886	15.73059	13.80648	9.863579	1.1045	0.030255	0.062648	SLC25A27	chr6	+	46620678	46645930	2963
ENSG00000(	2.071584	0	3.958241	1.498151	2.761296	0	0.33258	0.79554	0.86654	GPR110	chr6	-	46965440	47010099	9130
ENSG00000(	0	0	0	3.745378	16.56778	11.50751	-4.2064	0.000368	0.001106	GPR115	chr6	+	47653600	47689757	3162
ENSG00000(	510.6454	534.7037	522.4879	1394.779	1245.344	1255.962	-1.311	4.12E-25	5.12E-24	FAM49B	chr8	-	1.31E+08	1.31E+08	4552
ENSG00000(	1832.316	1835.334	2514.803	1879.431	1814.171	1559.267	0.2337	0.10699	0.18545	ASAP1	chr8	-	1.31E+08	1.31E+08	6042
ENSG00000(	416.3883	366.1035	482.9054	627.7253	506.2376	467.698	-0.34042	0.044699	0.088094	TRAPPC8	chr18	-	29409136	29533099	6226
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	FAM81B	chr5	+	94727048	94786158	1560
ENSG00000(	44.53905	22.88147	42.22124	83.89646	58.90765	60.8254	-0.87624	0.017515	0.038553	LINC00467	chr1	+	2.12E+08	2.12E+08	711
ENSG00000(	125.3308	103.5687	131.9414	249.4422	183.166	216.9987	-0.84466	0.000134	0.000428	INO80C	chr18	-	33032194	33077955	3245
ENSG00000(	2537.69	2312.232	2671.813	3286.194	3909.995	3858.303	-0.55436	2.58E-06	1.02E-05	LPCAT1	chr5	-	1456595	1524092	5610
ENSG00000(	825.5261	881.5386	778.4541	1017.994	1121.086	1092.391	-0.3772	0.002507	0.006563	PLEKHG4B	chr5	+	140373	190085	11513
ENSG00000(	683.6227	686.444	581.8615	1378.299	1142.256	1464.741	-1.0264	3.67E-13	2.60E-12	NMRAL1	chr16	-	4511681	4545764	1719
ENSG00000(	193.6931	156.5574	155.6908	678.6624	570.6678	598.3905	-1.8579	1.15E-27	1.58E-26	UBALD1	chr16	-	4658884	4665028	2641
ENSG00000(	7.250543	3.612863	0	1.498151	0	0.821965	1.5262	0.22135	0.33307	C16orf89	chr16	-	5094123	5116111	1872
ENSG00000(	33.14534	25.29004	36.94359	65.16957	83.75931	71.51095	-1.1879	0.000676	0.001946	TMEM251	chr14	+	93651296	93653434	1303
ENSG00000(	474.3927	441.9736	378.6718	477.9102	409.5922	496.4668	-0.09446	0.553	0.67388	ING1	chr13	+	1.11E+08	1.11E+08	2870
ENSG00000(	39.36009	28.90291	15.83297	3.745378	1.840864	8.219649	2.4393	0.000207	0.000646	TEX29	chr13	+	1.12E+08	1.12E+08	835
ENSG00000(	6.214751	13.24716	15.83297	40.45008	27.61296	30.4127	-1.4413	0.006832	0.016479	ADPRHL1	chr13	-	1.14E+08	1.14E+08	1872
ENSG00000(	475.4285	499.7794	386.5882	764.8061	454.6934	479.2055	-0.31766	0.1094	0.18869	CMTM7	chr3	+	32433163	32524559	2066
ENSG00000(	325.2387	293.8462	358.8805	226.9699	226.4263	167.6808	0.65128	0.000622	0.001801	FBXL2	chr3	+	33318517	33445154	3847
ENSG00000(	1274.024	1169.363	1388.023	1612.76	1703.72	1496.798	-0.32866	0.007227	0.017354	UBP1	chr3	-	33429828	33482863	7394
ENSG00000(	467.1421	439.565	563.3897	652.4448	670.9949	641.1326	-0.41846	0.004314	0.010825	RMND5A	chr2	+	86947296	87005164	6301
ENSG00000(	3.107376	0	0	0.749076	5.522592	7.397684	-1.4858	0.21801	0.32937	CD8A	chr2	-	87011729	87035519	3048
ENSG00000(	374.9567	376.9421	344.367	683.1569	583.5539	732.3707	-0.86386	1.18E-08	5.87E-08	RPIA	chr2	+	88991162	89050452	1848
ENSG00000(	325.2387	258.9219	292.9099	420.2314	404.9901	405.2287	-0.4853	0.002866	0.007428	TUBGCP5	chr15	+	22833395	22873892	3849
ENSG00000(	0	3.612863	1.319414	0	0	0	1.6005	0.2346	NA	GOLGA8I	chr15	+	23255242	23268823	5264
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	GOLGA8F	chr15	+	28623767	28637170	5281
ENSG00000(	929.1053	983.9031	1208.583	476.412	486.9085	360.0206	1.2331	1.48E-14	1.13E-13	PTPRD	chr9	-	8314246	10612723	9911
ENSG00000(	276.5564	337.2006	288.9516	137.8299	88.36147	101.9236	1.4457	2.45E-11	1.52E-10	LURAP1L	chr9	+	12775020	12822130	1753
ENSG00000(	295.2007	348.0392	343.0476	144.5716	176.7229	124.1167	1.1418	6.57E-09	3.35E-08	CNKSR3	chr6	-	1.55E+08	1.55E+08	3268
ENSG00000(	216.4805	191.4817	162.2879	427.7221	432.603	388.7894	-1.1222	2.48E-10	1.42E-09	GTF2E1	chr3	+	1.2E+08	1.21E+08	3012
ENSG00000(	910.4611	870.7	726.997	495.888	486.9085	523.5917	0.7346	2.01E-07	8.93E-07	CFDP1	chr16	-	75327596	75467383	1275
ENSG00000(	1549.545	1636.627	1578.019	1355.827	1570.257	1532.965	0.095611	0.41296	0.54346	ZDHHC7	chr16	-	85007787	85045141	3442
ENSG00000(	8.286335	4.817151	6.597069	0	0	0.821965	3.2228	0.006404	0.01553	FAM92B	chr16	-	85131965	85146114	1897
ENSG00000(	67.32647	59.0101	60.69303	63.67142	69.0324	66.57916	-0.08782	0.77058	0.84912	C7orf31	chr7	-	25174316	25219975	3357
ENSG00000(	3.107376	4.817151	1.319414	0	0	0	2.6591	0.046093	0.090462	TMPRSS11I	chr4	-	68686594	68749750	2817
ENSG00000(	304.5228	278.1905	331.1729	33.7084	23.0108	27.12484	3.4075	1.97E-43	4.51E-42	JAZF1	chr7	-	27870192	28220362	3125
ENSG00000(	669.1216	727.3898	653.1098	2009.021	1650.335	1712.153	-1.3871	9.61E-27	1.27E-25	CMIP	chr16	+	81478775	81745367	4357
ENSG00000(	1.035792	2.408575	1.319414	0	0	0	1.6865	0.21314	NA	SPHKAP	chr2	-	2.29E+08	2.29E+08	6917
ENSG00000(	1.035792	0	0	7.490755	11.04518	5.753754	-3.1893	0.005691	0.013943	KCNJ16	chr17	+	68049570	68131749	4014
ENSG00000(	54.89697	34.92434	63.33186	27.7158	14.72691	8.219649	1.5353	0.001334	0.003671	PID1	chr2	-	2.3E+08	2.3E+08	2745
ENSG00000(	2824.605	2604.874	3497.766	2572.325	2867.146	2200.4	0.22389	0.11065	0.19044	TRIP12	chr2	-	2.31E+08	2.31E+08	9874
ENSG00000(	42.46747	46.96722	56.73479	35.20655	25.7721	33.70056	0.60673	0.11085	0.19074	FBXO36	chr2	+	2.31E+08	2.31E+08	3120

ENSG00000(	354.2408	408.2535	348.3252	695.1421	732.6639	631.2691	-0.88751	1.99E-09	1.06E-08	CEBPG	chr19	+	33864236	33873591	4108
ENSG00000(	791.345	667.1754	765.26	991.776	1043.77	1107.187	-0.49731	0.00014	0.000448	KCTD15	chr19	+	34286838	34306666	4916
ENSG00000(	123.2592	169.8046	109.5113	94.38352	66.2711	84.66239	0.70474	0.009016	0.02118	ZNF599	chr19	-	35248979	35264134	3397
ENSG00000(	5.17896	6.021439	17.15238	48.68991	57.98722	77.2647	-2.6356	1.18E-07	5.37E-07	MCOLN2	chr1	-	85391268	85462796	2869
ENSG00000(	1.035792	2.408575	0	2.996302	0	3.28786	-0.56239	0.66384	0.76786	LGI4	chr19	-	35615417	35633355	2891
ENSG00000(	689.8374	594.9181	820.6754	3848.001	2889.236	2666.454	-2.1527	5.39E-42	1.18E-40	DDAH1	chr1	-	85784164	86043933	3920
ENSG00000(	1116.584	1246.438	1381.426	897.3925	1086.11	860.5973	0.39556	0.004642	0.011578	SREK1	chr5	+	65435799	65479443	9353
ENSG00000(	533.4328	482.9194	658.3875	898.1416	1017.077	739.7684	-0.66316	4.88E-05	0.000166	CHD1	chr5	-	98190908	98262240	5918
ENSG00000(	0	0	0	1.498151	2.761296	0	-1.199	0.3707	NA	CLCA3P	chr1	+	87099956	87121059	3412
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	ANKFN1	chr17	+	54188319	54589020	3840
ENSG00000(	93.22127	80.68728	112.1502	163.2985	163.8369	189.8739	-0.85013	0.000301	0.000914	DGKE	chr17	+	54911460	54946036	7768
ENSG00000(	1411.784	1393.361	1567.464	686.1532	652.5863	600.8564	1.1696	1.11E-20	1.16E-19	HS2ST1	chr1	+	87380331	87602334	6736
ENSG00000(	1621.014	1630.606	2064.883	1802.276	2360.908	1954.633	-0.20221	0.15374	0.24915	MSI2	chr17	+	55333212	55762046	7612
ENSG00000(	438.14	461.2422	686.0952	150.5642	137.1444	126.5826	1.9226	1.33E-21	1.44E-20	CACNA2D1	chr7	-	81575760	82073114	7563
ENSG00000(	167.7983	181.8474	211.1062	209.7412	209.8585	206.3132	-0.16063	0.40929	0.54005	ZUFSP	chr6	-	1.17E+08	1.17E+08	2195
ENSG00000(	313.8449	276.9862	302.1458	82.39831	105.8497	96.99186	1.6409	4.98E-16	4.18E-15	HS3ST3A1	chr17	-	13399006	13505244	2527
ENSG00000(	14.50109	6.021439	10.55531	19.47596	8.283888	21.37109	-0.61751	0.34568	0.47517	GDPD1	chr17	+	57297828	57353328	1821
ENSG00000(	1219.127	1248.846	1456.633	1358.823	1500.304	1237.057	-0.06202	0.63355	0.74324	NUS1	chr6	+	1.18E+08	1.18E+08	4676
ENSG00000(	7.250543	6.021439	21.11062	450.9435	627.7346	487.4252	-5.4733	7.02E-62	2.57E-60	SEMA3D	chr7	-	84624869	84816171	6265
ENSG00000(	745.7702	804.4642	852.3413	1240.469	1249.026	1051.293	-0.55899	2.12E-05	7.56E-05	PPP2R5E	chr14	-	63838075	64010092	6659
ENSG00000(	0	2.408575	0	0.749076	0.920432	2.465895	-0.44793	0.73865	0.82493	SLC5A10	chr17	+	18853658	18925908	4436
ENSG00000(	700.1953	684.0354	733.5941	131.0882	120.5766	109.3213	2.5421	3.36E-56	1.07E-54	AK5	chr1	+	77747736	78025651	3929
ENSG00000(	234.089	222.7932	252.008	168.542	185.0068	166.8589	0.44395	0.018823	0.041087	C17orf103	chr17	-	21142183	21156722	4925
ENSG00000(	81.82756	79.48299	87.08131	86.14369	79.15715	78.90863	0.022659	0.93322	0.95995	CABYR	chr18	+	21718942	21741567	2250
ENSG00000(	422.6031	484.1237	533.0432	469.6704	500.715	479.2055	-0.0114	0.93961	0.96348	IMPACT	chr18	+	22006580	22033499	3792
ENSG00000(	29.00217	20.47289	23.74945	0.749076	6.443024	4.109825	2.5383	0.000237	0.00073	ANKRD29	chr18	-	21178890	21242849	3597
ENSG00000(	143.9751	146.9231	143.8161	198.505	186.8477	203.0253	-0.43478	0.030528	0.063125	C6orf57	chr6	+	71276620	71299272	1196
ENSG00000(	3374.61	3322.63	2646.744	642.7068	588.156	514.55	2.4142	8.67E-69	3.68E-67	THY1	chr11	-	1.19E+08	1.19E+08	3554
ENSG00000(	12.4295	15.65574	6.597069	5.243529	14.72691	23.83698	-0.30417	0.65724	0.76213	DNAAF1	chr16	+	84178865	84212373	4708
ENSG00000(	17.60846	24.08575	21.11062	76.40571	41.41944	92.88204	-1.7112	3.89E-05	0.000134	C16orf74	chr16	-	85723690	85784735	1237
ENSG00000(	327.3102	370.9206	431.4483	413.4897	420.6374	344.4033	-0.06297	0.71068	0.8044	TBCEL	chr11	+	1.21E+08	1.21E+08	5142
ENSG00000(	21.75163	3.612863	15.83297	124.3465	186.8477	216.1768	-3.5804	3.99E-20	4.06E-19	JPH3	chr16	+	87635441	87731762	4023
ENSG00000(	1068.937	826.1414	1058.17	301.1284	305.5834	262.2068	1.7597	2.98E-30	4.56E-29	ANKH	chr5	-	14704910	14871887	8203
ENSG00000(	401.8873	364.8992	449.9201	456.187	490.5903	452.9027	-0.20199	0.18649	0.29112	FAM105B	chr5	+	14664773	14699820	7800
ENSG00000(	1080.331	1115.17	1393.301	1220.993	1424.829	1244.455	-0.11671	0.39593	0.52694	UBASH3B	chr11	+	1.23E+08	1.23E+08	6912
ENSG00000(	23.82321	16.86003	14.51355	5.243529	3.681728	5.753754	1.7823	0.008489	0.020055	ROBO4	chr11	-	1.25E+08	1.25E+08	4710
ENSG00000(	163.6551	163.7831	116.1084	152.0623	88.36147	170.9687	0.10719	0.69083	0.78917	ROBO3	chr11	+	1.25E+08	1.25E+08	4569
ENSG00000(	346.9903	345.6306	397.1435	363.3016	335.0372	354.2669	0.048047	0.76119	0.84209	TBRG1	chr11	+	1.24E+08	1.25E+08	4461
ENSG00000(	13.46529	10.83859	19.79121	47.94084	48.7829	30.4127	-1.4864	0.001849	0.00496	NRGN	chr11	+	1.25E+08	1.25E+08	1971
ENSG00000(	37.28851	66.23582	34.30476	56.18067	49.70333	35.34449	-0.0356	0.92694	0.95607	FAM134B	chr5	-	16473147	16617167	3268
ENSG00000(	1828.173	1910	1855.096	1592.535	1597.87	1256.784	0.33007	0.009606	0.022431	TOMM70A	chr3	-	1E+08	1E+08	4409
ENSG00000(	412.2452	376.9421	589.778	6.74168	9.20432	10.68554	5.6192	7.43E-68	3.12E-66	ABI3BP	chr3	-	1E+08	1.01E+08	6783
ENSG00000(	209.23	215.5675	320.6175	364.7998	561.4635	355.0888	-0.77814	0.000404	0.001205	ANGPT1	chr8	-	1.08E+08	1.09E+08	4353
ENSG00000(	407.0662	287.8248	316.6593	238.206	189.609	195.6277	0.69522	0.000358	0.001077	PITPNC1	chr17	+	65373575	65693372	6182

ENSG00000(	530.3255	594.9181	591.0974	784.2821	709.6531	725.795	-0.37155	0.005934	0.014481	CC2D1B	chr1	-	52811395	52831865	5638
ENSG00000(	1297.847	1339.168	1628.157	374.5378	428.9213	372.3501	1.8541	2.45E-39	4.99E-38	PRKCA	chr17	+	64298754	64806861	8751
ENSG00000(	210.2658	175.826	163.6073	74.90755	69.0324	74.79881	1.3208	1.94E-08	9.51E-08	LRRK1	chr15	+	1.01E+08	1.02E+08	7701
ENSG00000(	212.3373	205.9332	245.411	31.46117	46.0216	37.81039	2.5093	3.29E-23	3.78E-22	CEP112	chr17	-	63631656	64188202	3517
ENSG00000(	1.035792	0	3.958241	2.996302	4.60216	0	-0.42834	0.73314	0.82147	GAL3ST2	chr2	+	2.43E+08	2.43E+08	1370
ENSG00000(	18.64425	34.92434	15.83297	5.243529	11.96562	2.465895	1.7168	0.00995	0.023152	ABCA9	chr17	-	66970629	67057205	6514
ENSG00000(	20.71584	42.15007	34.30476	0	0	0	6.2508	4.79E-09	2.48E-08	ABCA6	chr17	-	67074843	67138029	8186
ENSG00000(	17.60846	7.225726	18.47179	7.490755	3.681728	1.64393	1.5861	0.041299	0.082296	ABCA10	chr17	-	67143355	67240987	6362
ENSG00000(	126.3666	104.773	127.9831	105.6197	78.23672	95.34793	0.35733	0.15888	0.25567	ABCA5	chr17	-	67240452	67323385	8220
ENSG00000(	0	0	0	1.498151	0	6.575719	-2.011	0.13747	0.22739	ENPP3	chr6	+	1.32E+08	1.32E+08	3413
ENSG00000(	0	2.408575	7.916483	21.72319	22.09037	27.94681	-2.6213	0.000466	0.001375	C4orf19	chr4	+	37455563	37625117	1949
ENSG00000(	6194.036	5710.732	5327.793	7335.697	5930.343	6500.099	-0.19748	0.091729	0.16332	UCHL1	chr4	+	41258430	41270472	1578
ENSG00000(	1177.695	1098.31	1489.618	606.7512	644.3024	494.8229	1.1049	1.04E-12	7.10E-12	MIA3	chr1	+	2.23E+08	2.23E+08	8142
ENSG00000(	181.2636	168.6003	236.1751	77.90386	80.07758	67.40112	1.3661	1.10E-08	5.50E-08	DISP1	chr1	+	2.23E+08	2.23E+08	4762
ENSG00000(	43.50326	52.98866	40.90183	269.6672	393.0245	331.2519	-2.8295	4.75E-31	7.49E-30	TNIK	chr3	-	1.71E+08	1.71E+08	6970
ENSG00000(	0	1.204288	0	17.22874	29.45382	19.72716	-4.5955	5.07E-06	1.95E-05	TDH	chr8	+	11197146	11225961	1442
ENSG00000(	10.35792	6.021439	9.235896	129.5901	81.91845	59.18147	-3.2917	1.80E-12	1.21E-11	FAM167A	chr8	-	11278972	11332224	4094
ENSG00000(	328.346	326.362	281.0351	230.7153	175.8025	239.1918	0.53185	0.004775	0.011877	NEIL2	chr8	+	11627148	11644855	2671
ENSG00000(	0	2.408575	0	7.490755	15.64734	13.15144	-3.1814	0.001893	0.005064	PGM5	chr9	+	70971815	71145977	4032
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	WNT3A	chr1	+	2.28E+08	2.28E+08	2932
ENSG00000(	843.1346	1051.343	836.5083	380.5304	904.7847	864.7071	0.3383	0.38022	0.5109	OBSCN	chr1	+	2.28E+08	2.29E+08	26927
ENSG00000(	337.6682	322.7491	254.6469	283.1506	314.7877	224.3964	0.15627	0.41681	0.54732	LONRF1	chr8	-	12579403	12613582	3594
ENSG00000(	422.6031	372.1249	356.2417	845.7063	765.7994	793.1961	-1.0584	1.00E-13	7.33E-13	TRIM11	chr1	-	2.29E+08	2.29E+08	5774
ENSG00000(	5054.664	4843.645	6015.207	1682.424	2406.009	1771.334	1.4375	6.79E-23	7.72E-22	ENAH	chr1	-	2.26E+08	2.26E+08	7167
ENSG00000(	137.7603	101.1602	122.7055	304.1247	358.9685	289.3317	-1.3856	1.19E-11	7.52E-11	CCSAP	chr1	-	2.29E+08	2.29E+08	5157
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	ASZ1	chr7	-	1.17E+08	1.17E+08	2900
ENSG00000(	301.4154	275.7819	347.0058	401.5045	620.3712	337.0056	-0.55206	0.00937	0.021928	SH3RF1	chr4	-	1.7E+08	1.7E+08	5272
ENSG00000(	1.035792	2.408575	0	1.498151	2.761296	7.397684	-1.2818	0.28032	0.40256	GBP5	chr1	-	89724633	89738544	4699
ENSG00000(	1466.681	1334.351	1488.299	2474.197	1931.987	2064.776	-0.5923	3.93E-06	1.53E-05	BUB3	chr10	+	1.25E+08	1.25E+08	2731
ENSG00000(	0	0	0	5.243529	3.681728	0	-2.1664	0.10825	0.1871	GPR26	chr10	+	1.25E+08	1.25E+08	7514
ENSG00000(	13.46529	2.408575	6.597069	7.490755	6.443024	4.93179	0.23738	0.777	0.85319	CCDC173	chr2	-	1.71E+08	1.71E+08	2181
ENSG00000(	1.035792	0	0	0	4.60216	4.93179	-1.7939	0.17495	0.27674	MMP21	chr10	-	1.27E+08	1.27E+08	1919
ENSG00000(	37.28851	50.58008	31.66593	0	0	0	6.5497	4.52E-10	2.54E-09	C10orf90	chr10	-	1.28E+08	1.28E+08	3076
ENSG00000(	103.5792	108.3859	116.1084	127.3428	93.88406	83.84042	0.10005	0.70204	0.79743	FAM69A	chr1	-	93307724	93427057	2574
ENSG00000(	2892.967	2992.655	2723.27	3672.717	3342.089	4014.477	-0.35681	0.001655	0.004472	ATP5G3	chr2	-	1.76E+08	1.76E+08	5484
ENSG00000(	0	4.817151	5.277655	8.988907	4.60216	7.397684	-0.92769	0.33795	0.46657	CNTNAP3B	chr9	+	43684902	43924049	7939
ENSG00000(	2.071584	0	1.319414	2.247227	0	4.109825	-0.5825	0.6528	0.75858	FAM27C	chr9	+	44990314	44991483	616
ENSG00000(	51.7896	54.19295	44.86007	17.22874	15.64734	12.32947	1.6943	7.01E-05	0.000233	MAGED4	chrX	+	51927919	51935364	3015
ENSG00000(	54.89697	55.39724	32.98534	160.3022	132.5422	160.2832	-1.6353	7.43E-09	3.77E-08	SRSF12	chr6	-	89805678	89827800	3599
ENSG00000(	33.14534	48.17151	21.11062	122.0993	65.35067	83.84042	-1.3768	0.000222	0.000688	PDLIM3	chr4	-	1.86E+08	1.86E+08	5137
ENSG00000(	51.7896	80.68728	76.526	707.1273	694.9262	511.2622	-3.1839	2.77E-50	7.68E-49	SORBS2	chr4	-	1.87E+08	1.87E+08	6050
ENSG00000(	828.6335	894.7858	820.6754	1474.93	1154.222	1491.866	-0.69463	4.20E-07	1.81E-06	TCEB1	chr8	-	74851404	74884522	2780
ENSG00000(	45.57484	32.51577	46.17948	0.749076	0	1.64393	5.067	1.22E-10	7.17E-10	LY96	chr8	+	74903587	74941322	607
ENSG00000(	3.107376	8.430014	26.38828	2.247227	5.522592	6.575719	1.2454	0.1357	0.22498	CEP170P1	chr4	+	1.19E+08	1.19E+08	4587

ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	PSMA8	chr18	+	23713816	23773319	1876
ENSG00000(	0	0	0	97.37982	93.88406	71.51095	-7.1773	1.19E-12	8.14E-12	TMSB4Y	chrY	+	15815447	15817904	1669
ENSG00000(	102.5434	71.05298	98.95603	984.2853	1202.084	928.8204	-3.4958	1.06E-80	5.75E-79	CXADR	chr21	+	18884700	18965897	6254
ENSG00000(	564.5066	685.2397	609.5692	1239.72	977.4988	945.2597	-0.76515	3.12E-07	1.36E-06	BTG3	chr21	-	18965971	18985265	1485
ENSG00000(	210.2658	240.8575	281.0351	182.0254	236.551	164.393	0.32629	0.11896	0.20233	C21orf91	chr21	-	19161284	19191703	5433
ENSG00000(	1.035792	0	0	14.98151	16.56778	21.37109	-4.3016	3.32E-05	0.000115	CHODL	chr21	+	19273580	19639690	2548
ENSG00000(	62.14751	43.35436	67.2901	87.64184	115.054	95.34793	-0.7755	0.009302	0.021784	NCAM2	chr21	+	22370633	22915650	8135
ENSG00000(	0	0	1.319414	11.98521	6.443024	8.219649	-3.2779	0.003766	0.00957	L3MBTL4	chr18	-	5954705	6415236	4534
ENSG00000(	16.57267	28.90291	40.90183	321.3534	286.2544	203.0253	-3.2131	2.08E-26	2.71E-25	PDE1C	chr7	-	31790793	32338941	8852
ENSG00000(	8.286335	7.225726	10.55531	11.98521	10.12475	3.28786	0.0299	0.96877	0.98169	RABGEF1	chr7	+	66205720	66276451	3733
ENSG00000(	265.1627	236.0404	249.3692	713.869	492.4311	660.0378	-1.3089	9.13E-14	6.69E-13	MRPL39	chr21	-	26957968	26979829	1199
ENSG00000(	188.5141	267.3519	170.2044	8.239831	7.363456	9.041614	4.5787	4.16E-37	7.91E-36	JAM2	chr21	+	27011584	27089874	4337
ENSG00000(	342.8471	404.6407	299.5069	659.1865	506.2376	586.883	-0.74023	1.14E-05	4.20E-05	ATP5J	chr21	-	27088815	27107984	1179
ENSG00000(	395.6725	409.4578	559.4314	408.2462	370.9341	291.7975	0.34549	0.064582	0.12101	GABPA	chr21	+	27106881	27144771	5120
ENSG00000(	5668.889	5757.7	5829.17	1013.499	1087.03	983.07	2.481	5.75E-124	6.34E-122	ADAMTS1	chr21	-	28208606	28217728	4718
ENSG00000(	127.4024	154.1488	158.3297	15.73059	12.88605	9.041614	3.4816	1.82E-24	2.20E-23	ADAMTS5	chr21	-	28290231	28338832	9056
ENSG00000(	220.6237	179.4389	205.8285	246.4459	266.9253	229.3282	-0.29047	0.1234	0.20854	TSEN2	chr3	+	12525931	12581122	3918
ENSG00000(	1.035792	7.225726	7.916483	267.42	221.8241	254.8091	-5.4409	5.91E-36	1.09E-34	SLFN13	chr17	-	33762115	33775856	8469
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	WNT7A	chr3	-	13857755	13921618	4041
ENSG00000(	711.589	720.1641	785.0512	843.4591	917.6707	818.6771	-0.21861	0.090131	0.16098	XPC	chr3	-	14186647	14220283	3832
ENSG00000(	506.5022	434.7479	386.5882	283.8996	294.5382	286.8658	0.61794	0.000174	0.00055	CCDC174	chr3	+	14693271	14714166	2942
ENSG00000(	2.071584	0	0	160.3022	177.6434	166.0369	-6.9359	3.71E-20	3.78E-19	FGD5	chr3	+	14860469	14975895	5720
ENSG00000(	615.2604	663.5625	599.0139	432.2166	401.3084	449.6148	0.54748	0.000105	0.000341	FLCN	chr17	-	17115526	17140502	3638
ENSG00000(	598.6877	523.8652	606.9303	1059.193	727.1413	831.0065	-0.59662	0.000194	0.000606	DPH3	chr3	-	16299485	16306479	3131
ENSG00000(	125.3308	109.5902	133.2608	209.7412	172.1208	177.5444	-0.60149	0.005864	0.014323	OXNAD1	chr3	+	16306706	16378822	3929
ENSG00000(	102.5434	115.6116	88.40072	84.64554	94.8045	89.59418	0.18911	0.4644	0.59356	PLCL2	chr3	+	16844159	17132086	4153
ENSG00000(	764.4144	812.8942	712.4834	1229.982	921.3524	1154.861	-0.52889	0.000224	0.000693	CXXC1	chr18	-	47808713	47814674	2936
ENSG00000(	140.8677	136.0845	117.4278	639.7105	525.5667	595.1026	-2.1466	1.65E-34	2.92E-33	SKA1	chr18	+	47901365	47920543	2905
ENSG00000(	1034.756	1011.602	1211.222	1605.269	1484.657	1458.166	-0.48144	0.000112	0.000364	PPP4R1	chr18	-	9546789	9615238	3925
ENSG00000(	3747.495	3522.542	3113.817	226.2208	217.222	183.2982	4.0403	1.39E-197	3.81E-195	APCDD1	chr18	+	10454625	10488698	2562
ENSG00000(	77.68439	86.70872	114.789	86.14369	157.3939	117.541	-0.3678	0.20046	0.30801	PIEZO2	chr18	-	10666480	11148587	9356
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CCDC144B	chr17	-	18431900	18528930	8682
ENSG00000(	162.6193	164.9874	138.5384	95.88167	133.4626	89.59418	0.5478	0.024403	0.051862	MPPE1	chr18	-	11882621	11909222	4236
ENSG00000(	7.250543	0	6.597069	8.988907	24.85166	13.15144	-1.5769	0.05019	0.097452	CCDC144C	chr17	+	20224477	20306870	5227
ENSG00000(	35.21692	48.17151	42.22124	106.3687	80.07758	100.2797	-1.1805	0.000163	0.000515	USP43	chr17	+	9548015	9633001	3624
ENSG00000(	113.9371	128.8588	139.8579	121.3502	175.8025	166.0369	-0.27368	0.24743	0.36425	RAB6B	chr3	-	1.34E+08	1.34E+08	5526
ENSG00000(	56.96855	40.94578	22.43003	176.7818	171.2004	156.9953	-2.0255	1.78E-11	1.11E-10	EME1	chr17	+	48450581	48458844	2354
ENSG00000(	43.50326	37.33292	40.90183	207.4939	196.9724	138.9121	-2.133	2.69E-14	2.03E-13	EPHB1	chr3	+	1.34E+08	1.35E+08	4672
ENSG00000(	189.5499	114.4073	168.885	19.47596	21.16994	20.54912	2.9121	3.81E-20	3.88E-19	ACSS1	chr20	-	24986868	25039616	4877
ENSG00000(	559.3276	578.0581	639.9157	799.2636	829.3092	778.4008	-0.43746	0.000941	0.002647	ANKRD40	chr17	-	48770551	48785285	4184
ENSG00000(	105.6508	131.2674	126.6637	57.67882	52.46462	74.79881	0.96186	0.000453	0.001341	ZNF18	chr17	-	11880762	11900827	2767
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	CA10	chr17	-	49707674	50237377	3189
ENSG00000(	1677.983	1557.144	1765.376	1188.034	1027.202	955.9452	0.655	2.98E-07	1.31E-06	VOPP1	chr7	-	55503749	55640681	2962
ENSG00000(	84.93494	61.41867	109.5113	77.15478	75.47542	60.8254	0.25547	0.39992	0.53109	APOOL	chrX	+	84258832	84343069	1279

ENSG00000(	1191.161	1358.437	1578.019	490.6445	423.3987	317.2785	1.7371	5.55E-25	6.85E-24	DKK2	chr4	-	1.08E+08	1.08E+08	3638
ENSG00000(	80.79177	84.30014	68.60952	67.4168	66.2711	41.92021	0.40849	0.19381	0.29979	CYP2U1	chr4	+	1.09E+08	1.09E+08	4944
ENSG00000(	0	4.817151	0	2.996302	0.920432	4.109825	-0.52014	0.67709	0.77848	RSPH10B	chr7	-	5965181	6010314	3222
ENSG00000(	206.1226	236.0404	283.674	409.7443	581.713	425.7778	-0.96232	5.51E-07	2.35E-06	FBXL18	chr7	-	5470966	5553429	3498
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	CNTNAP5	chr2	+	1.25E+08	1.26E+08	5284
ENSG00000(	16.57267	10.83859	23.74945	218.7301	313.8673	322.2102	-4.0169	5.78E-37	1.10E-35	PROM2	chr2	+	95940201	95957056	4728
ENSG00000(	49.71801	77.07441	30.34652	35.20655	39.57858	27.12484	0.61437	0.13346	0.22215	AK9	chr6	-	1.1E+08	1.1E+08	6326
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	ODF1	chr8	+	1.04E+08	1.04E+08	1013
ENSG00000(	862.8147	899.6029	1000.116	644.205	495.1924	410.1605	0.82942	6.85E-07	2.89E-06	KLF10	chr8	-	1.04E+08	1.04E+08	3659
ENSG00000(	2.071584	3.612863	5.277655	5.992604	7.363456	7.397684	-0.81874	0.36355	0.49339	PTPRN2	chr7	-	1.57E+08	1.58E+08	4723
ENSG00000(	2499.366	2367.63	2657.299	3981.337	4467.777	3803.232	-0.70221	5.28E-10	2.95E-09	AZIN1	chr8	-	1.04E+08	1.04E+08	4721
ENSG00000(	639.0836	643.0896	645.1933	1074.923	970.1353	801.4158	-0.5613	9.15E-05	0.0003	ATP6V1C1	chr8	+	1.04E+08	1.04E+08	5612
ENSG00000(	206.1226	215.5675	242.7721	208.243	169.3595	184.9421	0.23558	0.22669	0.33967	TMEM55A	chr8	-	92006024	92053292	2970
ENSG00000(	118.0803	148.1274	151.7326	442.7036	335.9577	322.2102	-1.3942	7.88E-12	5.06E-11	OTUD6B	chr8	+	92082424	92099323	3298
ENSG00000(	933.2485	958.613	1126.779	292.1395	338.719	276.1802	1.73	1.87E-31	2.98E-30	CDK19	chr6	-	1.11E+08	1.11E+08	6246
ENSG00000(	1172.516	1046.526	1099.072	1379.048	1185.516	1621.737	-0.33444	0.016135	0.035778	GTF3C6	chr6	+	1.11E+08	1.11E+08	952
ENSG00000(	11697.2	11417.85	11530.36	3470.467	4032.413	3685.691	1.6285	8.14E-56	2.57E-54	MARCKS	chr6	+	1.14E+08	1.14E+08	4273
ENSG00000(	94.25706	95.13873	116.1084	14.98151	17.48821	11.50751	2.749	1.78E-14	1.36E-13	TTC39B	chr9	-	15170843	15307358	3260
ENSG00000(	589.3656	526.2737	694.0116	1223.989	984.8622	1020.058	-0.83432	2.29E-08	1.12E-07	AGPAT5	chr8	+	6565878	6617184	3682
ENSG00000(	1998.043	2026.816	1926.344	2199.286	1930.146	1758.183	0.015326	0.89892	0.9373	MMS19	chr10	-	99218081	99258551	3797
ENSG00000(	637.012	528.6823	476.3084	561.8067	518.2032	600.0344	-0.03121	0.84023	0.89774	PI4K2A	chr10	+	99344131	99436191	4189
ENSG00000(	2897.11	2563.929	2698.201	1456.952	1368.682	1181.986	1.0237	4.58E-17	4.03E-16	MARVELD1	chr10	+	99472930	99477907	3219
ENSG00000(	541.7192	539.5209	486.8637	423.9768	505.3172	548.2506	0.08702	0.57103	0.69009	ZFYVE27	chr10	+	99496878	99520664	3047
ENSG00000(	6.214751	2.408575	0	8.988907	5.522592	3.28786	-0.83749	0.41127	0.54202	GOLGA7B	chr10	+	99609996	99631337	2894
ENSG00000(	0	2.408575	0	2.996302	4.60216	7.397684	-1.932	0.10283	0.17949	GPR78	chr4	+	8560452	8621486	4944
ENSG00000(	151.2256	181.8474	203.1897	185.7707	166.5982	194.8057	-0.03318	0.87315	0.9204	TRMT44	chr4	+	8437867	8495258	4157
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-195B	chr9	+	67968793	67987998	1017
ENSG00000(	298.3081	322.7491	307.4234	325.8479	217.222	261.3848	0.20315	0.28247	0.40514	SLC25A28	chr10	-	1.01E+08	1.01E+08	1448
ENSG00000(	845.2062	857.4529	1099.072	686.1532	784.2081	593.4587	0.43904	0.004655	0.011606	HSPA13	chr21	-	15743436	15755805	3986
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	SAMSN1	chr21	-	15857549	15955723	2185
ENSG00000(	588.3298	633.4553	617.4856	811.9979	713.3348	609.898	-0.21544	0.14341	0.2352	USP25	chr21	+	17102344	17252377	5216
ENSG00000(	185.4068	148.1274	159.6491	198.505	146.3487	167.6808	-0.05528	0.79954	0.86933	GRAMD3	chr5	+	1.26E+08	1.26E+08	3175
ENSG00000(	164.6909	183.0517	182.0791	286.8959	266.9253	314.8126	-0.71195	0.000117	0.000379	ZCCHC10	chr5	-	1.32E+08	1.32E+08	2178
ENSG00000(	185.4068	172.2131	191.315	382.7776	317.549	324.6761	-0.8982	6.78E-07	2.86E-06	C16orf87	chr16	-	46830519	46865323	6640
ENSG00000(	1101.047	1046.526	1083.239	744.5811	851.3996	865.5291	0.39217	0.001828	0.004907	MOV10	chr1	+	1.13E+08	1.13E+08	4689
ENSG00000(	2636.09	2442.295	2113.701	3041.247	2366.431	2650.015	-0.1634	0.21394	0.32429	RHOC	chr1	-	1.13E+08	1.13E+08	2199
ENSG00000(	101.5076	89.11729	71.24834	128.841	96.64536	125.7606	-0.41676	0.11663	0.19925	PPM1J	chr1	-	1.13E+08	1.13E+08	2474
ENSG00000(	2564.621	2674.723	2260.156	2369.326	2544.994	3222.102	-0.11704	0.38916	0.51982	DBI	chr2	+	1.2E+08	1.2E+08	842
ENSG00000(	1827.137	1836.539	2217.935	6254.032	6926.251	5692.107	-1.679	6.51E-42	1.42E-40	SLC16A1	chr1	-	1.13E+08	1.13E+08	4374
ENSG00000(	341.8113	264.9433	344.367	624.729	526.4871	559.7581	-0.84442	2.41E-07	1.07E-06	HEATR3	chr16	+	50099852	50140298	3560
ENSG00000(	16.57267	16.86003	3.958241	5.243529	0	1.64393	2.0892	0.022681	0.048509	TRIM74	chr7	-	72430016	72439997	1350
ENSG00000(	514.7886	570.8324	468.3919	1038.968	693.0853	681.4089	-0.63295	0.000343	0.001034	MKI67IP	chr2	-	1.22E+08	1.22E+08	1734
ENSG00000(	2561.513	2551.886	2340.64	2145.352	1678.868	1740.922	0.42042	0.000866	0.002452	OXA1L	chr14	+	23235731	23241007	1750
ENSG00000(	65.25489	52.98866	56.73479	328.8442	315.7082	314.8126	-2.4347	3.67E-29	5.39E-28	SLC7A7	chr14	-	23242431	23299029	3017

ENSG0000(	4853.721	4847.258	5337.029	4549.885	6714.551	5487.438	-0.15519	0.25882	0.37754	LARP1	chr5	+	1.54E+08	1.54E+08	6595
ENSG0000(	1405.57	1505.36	1424.967	711.6218	600.1217	662.5037	1.1316	1.46E-19	1.45E-18	CNOT8	chr5	+	1.54E+08	1.54E+08	2708
ENSG0000(	174.013	296.2548	166.2461	166.2948	125.1788	147.9537	0.52801	0.033499	0.068432	GRIA1	chr5	+	1.53E+08	1.53E+08	5708
ENSG0000(	1.035792	8.430014	3.958241	14.98151	15.64734	7.397684	-1.3664	0.093483	0.16589	LRGUK	chr7	+	1.34E+08	1.34E+08	3163
ENSG0000(	56.96855	74.66584	67.2901	186.5198	148.1896	156.9953	-1.299	3.00E-07	1.31E-06	SETD9	chr5	+	56205087	56221359	1619
ENSG0000(	351.1335	356.4692	451.2395	444.9509	484.1472	354.2669	-0.14798	0.40094	0.53217	MIER3	chr5	-	56215429	56267502	5240
ENSG0000(	778.9155	708.1212	963.1721	2211.271	2197.071	1719.551	-1.3195	8.50E-19	8.16E-18	NUP205	chr7	+	1.35E+08	1.35E+08	6266
ENSG0000(	150.1898	207.1375	200.5509	229.9662	228.2671	175.9005	-0.18673	0.38128	0.51194	ZKSCAN2	chr16	-	25247322	25269252	7523
ENSG0000(	204.051	255.309	191.315	264.4237	231.0284	212.0669	-0.12077	0.54089	0.66388	C9orf85	chr9	+	74526426	74600970	3321
ENSG0000(	0	3.612863	0	6.74168	6.443024	7.397684	-1.9869	0.06912	0.12837	PIK3AP1	chr10	-	98353069	98480271	4803
ENSG0000(	155.3688	179.4389	164.9267	221.7264	189.609	173.4346	-0.2274	0.26901	0.38944	RBM45	chr2	+	1.79E+08	1.79E+08	1992
ENSG0000(	76.6486	59.0101	137.219	71.16218	138.9852	55.89361	0.035403	0.92342	0.95368	C10orf12	chr10	+	98741041	98745582	4542
ENSG0000(	128.4382	168.6003	249.3692	86.14369	160.1552	93.704	0.67647	0.019852	0.043102	TTN	chr2	-	1.79E+08	1.8E+08	109224
ENSG0000(	8027.387	8047.051	7496.909	7073.52	6840.651	6543.663	0.20416	0.040333	0.080632	PDIA4	chr7	-	1.49E+08	1.49E+08	2903
ENSG0000(	104.615	99.95588	110.8308	78.65293	87.44104	101.1017	0.23727	0.35603	0.48557	KDM8	chr16	+	27214807	27233089	2458
ENSG0000(	0	2.408575	2.638828	1.498151	0.920432	0	0.61675	0.64273	0.75011	PDZD9	chr16	-	21995186	22012433	1331
ENSG0000(	0	0	0	1.498151	7.363456	0	-2.1224	0.11624	0.19866	OTOA	chr16	+	21689835	21772050	4635
ENSG0000(	190.5857	240.8575	216.3839	67.4168	137.1444	110.1433	1.0364	5.44E-05	0.000184	KCTD18	chr2	-	2.01E+08	2.01E+08	2940
ENSG0000(	79.75598	67.44011	120.0667	85.39461	116.8949	82.19649	-0.09116	0.75839	0.84022	FAM126B	chr2	-	2.02E+08	2.02E+08	4778
ENSG0000(	10.35792	12.04288	10.55531	2.996302	5.522592	1.64393	1.5354	0.061374	0.11581	ALS2CR12	chr2	-	2.02E+08	2.02E+08	2075
ENSG0000(	6.214751	0	5.277655	0	6.443024	1.64393	0.40122	0.73171	0.82061	ALS2CR11	chr2	-	2.02E+08	2.02E+08	5512
ENSG0000(	373.9209	331.1791	394.5047	947.5806	695.8466	722.5072	-1.1026	1.37E-11	8.64E-11	TMEM237	chr2	-	2.02E+08	2.03E+08	5592
ENSG0000(	737.4838	678.014	723.0388	262.9255	277.9705	221.1086	1.4849	2.01E-22	2.25E-21	FZD7	chr2	+	2.03E+08	2.03E+08	3851
ENSG0000(	15.53688	22.88147	14.51355	23.22134	9.20432	14.79537	0.14839	0.79892	0.8689	SPAG17	chr1	-	1.18E+08	1.19E+08	6924
ENSG0000(	7.250543	10.83859	6.597069	2.247227	0.920432	0	2.4098	0.018771	0.040986	DEPTOR	chr8	+	1.21E+08	1.21E+08	2569
ENSG0000(	286.9144	315.5234	377.3523	26.96672	27.61296	34.52253	3.429	6.76E-45	1.61E-43	FMN2	chr1	+	2.4E+08	2.41E+08	6434
ENSG0000(	756.1281	739.4327	799.5648	500.3825	666.3928	479.2055	0.47916	0.002041	0.005433	RNF20	chr9	+	1.04E+08	1.04E+08	3936
ENSG0000(	33.14534	36.12863	63.33186	35.20655	66.2711	36.98842	-0.06344	0.87627	0.92253	PPARGC1B	chr5	+	1.49E+08	1.49E+08	10568
ENSG0000(	106.6866	77.07441	84.44248	1224.739	1226.936	992.1117	-3.6594	3.04E-94	2.09E-92	ELMO1	chr7	-	36893961	37488852	4022
ENSG0000(	282.7712	234.8361	414.2959	188.018	288.0952	188.23	0.48468	0.039522	0.079172	SLC26A2	chr5	+	1.49E+08	1.49E+08	8080
ENSG0000(	179.192	131.2674	201.8703	241.2023	235.6306	216.9987	-0.43597	0.03758	0.075819	LSM11	chr5	+	1.57E+08	1.57E+08	6584
ENSG0000(	121.1877	155.3531	127.9831	203.7485	161.0756	203.8473	-0.49076	0.025743	0.054345	MED7	chr5	-	1.57E+08	1.57E+08	2402
ENSG0000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	FAM154A	chr9	-	18927656	19033251	2099
ENSG0000(	2766.6	2404.963	2378.903	1292.155	1143.177	1125.27	1.0823	3.83E-19	3.73E-18	RRAGA	chr9	+	19049372	19051019	1648
ENSG0000(	288.9859	251.6961	340.4088	134.0845	156.4734	117.541	1.1046	7.27E-08	3.38E-07	ACPL2	chr3	+	1.41E+08	1.41E+08	4158
ENSG0000(	3.107376	1.204288	1.319414	2.996302	5.522592	4.109825	-0.90855	0.4017	0.53291	ADCY8	chr8	-	1.32E+08	1.32E+08	5938
ENSG0000(	190.5857	178.2346	203.1897	307.121	314.7877	241.6577	-0.59168	0.001965	0.005241	RASA2	chr3	+	1.41E+08	1.41E+08	5614
ENSG0000(	453.6769	552.7681	498.7384	558.0613	438.1256	373.1721	0.13423	0.44163	0.57145	RMND1	chr6	-	1.52E+08	1.52E+08	1854
ENSG0000(	3.107376	3.612863	7.916483	0.749076	1.840864	4.109825	0.91599	0.38149	0.51217	SLA	chr8	-	1.34E+08	1.34E+08	3447
ENSG0000(	116.0087	155.3531	89.72014	132.5864	107.6905	118.3629	0.009969	0.96935	0.98193	TMBIM4	chr12	-	66517709	66563852	2952
ENSG0000(	714.6964	649.1111	628.041	1385.041	1106.359	1110.475	-0.85198	1.14E-09	6.22E-09	VBP1	chrX	+	1.54E+08	1.54E+08	1686
ENSG0000(	15.53688	7.225726	13.19414	14.23244	22.09037	16.4393	-0.51573	0.39288	0.5236	RAB39B	chrX	-	1.54E+08	1.54E+08	3505
ENSG0000(	64.2191	90.32158	65.97069	9.737982	13.80648	5.753754	2.8445	5.96E-11	3.59E-10	CLIC2	chrX	-	1.55E+08	1.55E+08	2655
ENSG0000(	786.1661	800.8513	1027.823	180.5272	185.9273	169.3248	2.2781	4.58E-45	1.10E-43	AFF2	chrX	+	1.48E+08	1.48E+08	13746

ENSG00000(	181.2636	205.9332	258.6051	131.0882	135.3035	92.06007	0.84069	0.000321	0.000972	MICU3	chr8	+	16884747	16980153	3992
ENSG00000(	38.3243	24.08575	23.74945	191.0143	247.5962	137.2681	-2.6878	2.35E-17	2.10E-16	GRIP1	chr12	-	66741211	67197966	5216
ENSG00000(	703.3027	820.1199	977.6856	688.4004	605.6443	509.6182	0.46814	0.004017	0.010146	VPS37A	chr8	+	17104080	17159936	4906
ENSG00000(	31.07376	37.33292	35.62417	2.247227	1.840864	7.397684	2.9944	1.39E-06	5.67E-06	KIF5A	chr12	+	57943781	57980415	5824
ENSG00000(	123.2592	114.4073	162.2879	67.4168	87.44104	107.6774	0.60047	0.025805	0.054462	TMEM185A	chrX	-	1.49E+08	1.49E+08	3665
ENSG00000(	0	0	0	2.996302	2.761296	0	-1.5727	0.24592	NA	NAT2	chr8	+	18248755	18258728	1322
ENSG00000(	2.071584	3.612863	2.638828	0	0	0	2.5105	0.060897	0.11506	MAGEA8	chrX	+	1.49E+08	1.49E+08	2112
ENSG00000(	1080.331	1117.579	1505.451	152.8114	150.0304	122.4728	3.1088	7.34E-74	3.42E-72	PSD3	chr8	-	18384811	18942240	11693
ENSG00000(	355.2766	343.222	319.2981	304.8737	355.2868	301.6611	0.083447	0.61169	0.72538	C9orf41	chr9	-	77595936	77643339	4130
ENSG00000(	321.0955	374.5335	370.7553	513.1168	448.2504	439.7512	-0.39474	0.012091	0.027588	MCU	chr10	+	74451889	74647452	3224
ENSG00000(	1170.445	1205.492	1092.475	768.5515	1148.699	991.2897	0.25439	0.093343	0.16568	ELMSAN1	chr14	-	74181825	74256988	8091
ENSG00000(	13.46529	3.612863	5.277655	25.46857	10.12475	9.041614	-0.90419	0.22026	0.33199	TTC18	chr10	-	75013517	75118617	6686
ENSG00000(	31.07376	10.83859	31.66593	89.13999	96.64536	86.30632	-1.8466	1.05E-06	4.33E-06	GNA14	chr9	-	80037995	80263223	2482
ENSG00000(	122.2234	103.5687	131.9414	48.68991	38.65814	46.852	1.395	8.86E-07	3.69E-06	FAM161B	chr14	-	74398204	74417117	4078
ENSG00000(	906.3179	932.1187	1360.316	1087.658	1152.381	969.9186	-0.00622	0.96931	0.98193	GNAQ	chr9	-	80331003	80646374	6539
ENSG00000(	3.107376	0	1.319414	14.23244	29.45382	19.72716	-3.3396	8.16E-05	0.000269	WIF1	chr12	-	65444406	65515346	2238
ENSG00000(	0	0	5.277655	6.74168	8.283888	0	-1.1169	0.35669	0.48622	GPR61	chr1	+	1.1E+08	1.1E+08	4921
ENSG00000(	537.576	544.338	881.3684	233.7116	261.4027	230.9721	1.4263	3.73E-13	2.64E-12	MMP16	chr8	-	89044237	89340254	11558
ENSG00000(	331.4534	335.9963	327.2146	1435.978	1088.871	1126.092	-1.8707	1.24E-35	2.26E-34	ADK	chr10	+	75910960	76469061	2083
ENSG00000(	3336.286	2970.978	3810.467	2849.483	2906.724	2783.995	0.24387	0.040457	0.080853	KCNMA1	chr10	-	78629359	79398353	11397
ENSG00000(	193.6931	162.5788	245.411	550.5705	407.7514	341.9374	-1.1078	2.10E-07	9.34E-07	DCK	chr4	+	71858255	71896631	2716
ENSG00000(	107.7224	121.6331	141.1773	59.92604	75.47542	41.92021	1.0517	0.000292	0.000888	ADAMTS3	chr4	-	73146686	73434516	5822
ENSG00000(	470.2495	517.8437	658.3875	405.2499	441.8074	363.3085	0.44075	0.008547	0.020183	DPY19L4	chr8	+	95731931	95806064	6197
ENSG00000(	112.9013	77.07441	81.80365	295.8848	263.2436	271.2484	-1.5943	3.75E-13	2.65E-12	NDUFAF6	chr8	+	95907995	96128683	2549
ENSG00000(	391.5293	422.705	345.6864	629.9725	437.2052	447.1489	-0.38356	0.031907	0.065595	DRAM2	chr1	-	1.12E+08	1.12E+08	2246
ENSG00000(	44.53905	40.94578	55.41538	59.17697	46.94203	53.42772	-0.18161	0.59784	0.7135	C8orf37	chr8	-	96257147	96281429	3334
ENSG00000(	1.035792	0	1.319414	0.749076	0	0	0.56083	0.6714	NA	PPEF2	chr4	-	76781020	76823724	4160
ENSG00000(	0	0	0	0.749076	1.840864	2.465895	-1.5178	0.26323	NA	C15orf26	chr15	+	81299374	81441516	1631
ENSG00000(	0	0	0	167.7929	216.3015	161.9271	-8.111	1.10E-16	9.50E-16	ADAMTSL3	chr15	+	84322838	84708594	7336
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	ART3	chr4	+	76932337	77033955	1577
ENSG00000(	205.0868	187.8689	200.5509	220.9773	196.052	151.2415	0.061938	0.7672	0.84655	WHAMM	chr15	+	83478380	83503611	3852
ENSG00000(	3.107376	1.204288	1.319414	1.498151	4.60216	1.64393	-0.32205	0.78299	0.85708	CXCL13	chr4	+	78432907	78532988	1203
ENSG00000(	175.0488	131.2674	153.052	134.8336	103.0884	95.34793	0.45873	0.058732	0.11167	N6AMT1	chr21	-	30244513	30257693	4865
ENSG00000(	377.0283	270.9647	329.8534	152.8114	159.2347	175.9005	0.99944	2.33E-07	1.03E-06	RWDD2B	chr21	-	30376705	30391699	3094
ENSG00000(	572.7929	673.1968	633.3186	792.5219	702.2896	617.2957	-0.16916	0.24991	0.36725	USP16	chr21	+	30396950	30426809	3835
ENSG00000(	3755.781	3567.1	3669.29	7301.239	6523.102	6464.754	-0.88293	2.90E-17	2.57E-16	CCT8	chr21	-	30428126	30446118	2005
ENSG00000(	17.60846	9.634302	19.79121	33.7084	13.80648	14.79537	-0.3936	0.50032	0.62853	MAP3K7CL	chr21	+	30449792	30548210	2093
ENSG00000(	0	3.612863	1.319414	0	0	0	1.6005	0.2346	NA	NAA11	chr4	-	80146848	80247204	2014
ENSG00000(	561.3992	564.8109	720.3999	437.4601	479.5451	382.2137	0.50459	0.001689	0.004556	BACH1	chr21	+	30566392	31003071	5769
ENSG00000(	2.071584	4.817151	6.597069	7.490755	5.522592	4.93179	-0.37892	0.67453	0.77646	TSPAN7	chrX	+	38420623	38548169	1909
ENSG00000(	204.051	240.8575	275.7575	367.047	589.9969	420.846	-0.93092	4.48E-06	1.73E-05	TIAM1	chr21	-	32490734	32932290	7200
ENSG00000(	702.2669	659.9497	678.1787	1191.03	1324.502	1177.054	-0.85326	8.05E-12	5.16E-11	SCAF4	chr21	-	33043346	33104388	4193
ENSG00000(	94.25706	92.73015	85.7619	78.65293	99.40666	117.541	-0.11223	0.677	0.77848	RPGR	chrX	-	38128416	38186817	4767
ENSG00000(	234.089	238.449	225.6198	125.0956	102.168	101.9236	1.0763	2.02E-07	8.97E-07	CDK20	chr9	-	90581356	90589668	5503

ENSG00000(	105.6508	105.9773	109.5113	257.682	229.1876	218.6427	-1.13	5.88E-08	2.76E-07	PCGF6	chr10	-	1.05E+08	1.05E+08	2230
ENSG00000(	322.1313	270.9647	211.1062	312.3645	247.5962	213.7109	0.057521	0.78478	0.85853	ANKRD9	chr14	-	1.03E+08	1.03E+08	1645
ENSG00000(	111.8655	93.93444	59.37362	161.0512	185.9273	141.378	-0.86371	0.00117	0.003246	SFR1	chr10	+	1.06E+08	1.06E+08	1583
ENSG00000(	3.107376	1.204288	1.319414	89.88907	118.7357	129.8705	-5.4948	1.65E-18	1.56E-17	SORCS3	chr10	+	1.06E+08	1.07E+08	5757
ENSG00000(	182.2994	203.5246	150.4132	528.0983	535.6914	562.224	-1.5917	7.75E-21	8.11E-20	SFXN2	chr10	+	1.04E+08	1.04E+08	2568
ENSG00000(	1178.731	1218.739	1011.99	1244.214	977.4988	1094.035	0.040021	0.77068	0.84912	C14orf2	chr14	-	1.04E+08	1.04E+08	1659
ENSG00000(	3.107376	0	0	0	0	0.821965	0.7418	0.57612	NA	FUT6	chr19	-	5830621	5839742	3137
ENSG00000(	12.4295	9.634302	13.19414	14.23244	8.283888	13.15144	-0.02114	0.97393	0.98483	FGF18	chr5	+	1.71E+08	1.71E+08	1986
ENSG00000(	3.107376	10.83859	6.597069	504.8769	493.3516	463.5882	-6.0651	2.32E-59	7.97E-58	PCDH1	chr5	-	1.41E+08	1.41E+08	4530
ENSG00000(	212.3373	221.5889	249.3692	465.1759	396.7062	399.475	-0.88378	1.96E-07	8.72E-07	SH3RF2	chr5	+	1.45E+08	1.45E+08	5607
ENSG00000(	53.86118	79.48299	64.65128	1730.365	2603.902	2262.047	-5.0377	2.75E-148	4.17E-146	GDF6	chr8	-	97154562	97173020	3697
ENSG00000(	2043.617	2149.654	1827.388	1140.842	998.6687	1394.053	0.76659	5.11E-08	2.41E-07	UQCRB	chr8	-	97238148	97247862	5575
ENSG00000(	160.5477	191.4817	133.2608	410.4934	199.7337	306.5929	-0.91103	0.000245	0.000753	MTERFD1	chr8	-	97251626	97273838	1529
ENSG00000(	2080.906	2028.021	2045.091	2167.825	1788.399	1873.258	0.077673	0.50816	0.63563	PTDSS1	chr8	+	97273943	97349223	5177
ENSG00000(	303.487	263.739	271.7992	113.1104	79.15715	92.06007	1.5482	2.94E-13	2.10E-12	PPP2R2B	chr5	-	1.46E+08	1.46E+08	3477
ENSG00000(	1064.794	1177.793	1124.141	825.4813	733.5843	807.9915	0.50628	4.90E-05	0.000167	RPL30	chr8	-	99037079	99058697	1129
ENSG00000(	10.35792	8.430014	14.51355	2.247227	2.761296	2.465895	1.9199	0.022686	0.048515	KCNS2	chr8	+	99439250	99445076	5219
ENSG00000(	34.18113	32.51577	35.62417	44.94453	24.85166	21.37109	0.15594	0.72361	0.81433	FAM122C	chrX	+	1.34E+08	1.34E+08	2483
ENSG00000(	338.704	363.6949	315.3399	643.4559	532.0097	554.8263	-0.76338	8.00E-07	3.35E-06	SUPV3L1	chr10	+	70939988	70968855	2484
ENSG00000(	444.3547	458.8336	448.6007	576.0391	657.1884	595.1026	-0.43394	0.002067	0.005494	FAM122B	chrX	-	1.34E+08	1.34E+08	4246
ENSG00000(	368722.2	375782.3	328197.6	195606.1	177366.3	170044.8	0.98067	2.84E-20	2.91E-19	EEF1A1	chr6	-	74225473	74233520	4441
ENSG00000(	16.57267	16.86003	17.15238	18.72689	10.12475	15.61733	0.17065	0.76535	0.84506	FBXO43	chr8	-	1.01E+08	1.01E+08	3082
ENSG00000(	0	4.817151	0	16.47966	15.64734	12.32947	-2.772	0.002628	0.006859	HKDC1	chr10	+	70980059	71027315	3689
ENSG00000(	3619.057	3662.239	3328.881	3250.239	3978.107	3917.485	-0.07057	0.54785	0.66959	HK1	chr10	+	71029740	71161638	3992
ENSG00000(	178.1562	152.9445	127.9831	262.1764	282.5726	329.6079	-0.91951	5.70E-06	2.18E-05	TYSND1	chr10	-	71897737	71906432	3644
ENSG00000(	806.8819	687.6483	902.479	708.6255	925.0342	766.8933	-0.00173	0.99095	0.99468	PHF6	chrX	+	1.34E+08	1.34E+08	4759
ENSG00000(	4272.642	4529.326	5887.224	265.9218	341.4803	252.3432	4.0834	5.88E-156	9.59E-154	CD109	chr6	+	74405508	74538040	9401
ENSG00000(	30.03797	31.31148	31.66593	0	0	0	6.2143	5.46E-09	2.81E-08	LRFN2	chr6	-	40359325	40555204	3270
ENSG00000(	1.035792	1.204288	0	3.745378	4.60216	6.575719	-2.0036	0.084875	0.1531	NODAL	chr10	-	72192071	72207707	1665
ENSG00000(	302.4512	317.932	295.5487	120.6012	98.48622	73.97684	1.6314	4.04E-14	3.03E-13	UBE2L6	chr11	-	57319129	57335757	1573
ENSG00000(	1631.372	1707.68	1686.211	1958.083	2054.404	1966.962	-0.25047	0.019885	0.043157	ZDHHC5	chr11	+	57435219	57468659	4666
ENSG00000(	443.3189	423.9093	368.1164	411.9916	343.3211	436.4634	0.05207	0.75066	0.83461	MED19	chr11	-	57471186	57479693	1515
ENSG00000(	2613.303	2577.176	2590.009	1677.18	1637.449	1942.303	0.56456	8.19E-07	3.43E-06	ZFAND3	chr6	+	37787275	38122400	3366
ENSG00000(	2172.056	2271.287	2385.5	2235.241	2054.404	2008.06	0.11613	0.29376	0.41807	NPTN	chr15	-	73852355	73926475	2817
ENSG00000(	672.2289	724.9812	819.356	142.3244	193.2907	156.1733	2.1664	1.11E-37	2.15E-36	KAT6B	chr10	+	76585340	76792380	8287
ENSG00000(	678.4437	675.6054	829.9113	431.4675	392.104	341.1154	0.90246	6.69E-09	3.42E-08	SAMD8	chr10	+	76859344	76941881	6782
ENSG00000(	124.295	169.8046	155.6908	791.7729	977.4988	863.8851	-2.5433	1.30E-50	3.64E-49	RAB11FIP1	chr8	-	37716136	37756985	7811
ENSG00000(	13.46529	6.021439	21.11062	15.73059	57.98722	38.63235	-1.4017	0.014329	0.032163	UNC5D	chr8	+	35092975	35654068	8662
ENSG00000(	27.96638	21.67718	18.47179	3.745378	7.363456	5.753754	1.9139	0.002431	0.006381	GLYATL2	chr11	-	58601542	58671688	1636
ENSG00000(	579.0077	580.4667	504.0161	673.4189	685.7218	673.1893	-0.28699	0.034942	0.071045	UTP14A	chrX	+	1.29E+08	1.29E+08	2488
ENSG00000(	645.2984	715.3469	655.7486	750.5737	752.9134	804.7037	-0.19478	0.13424	0.22323	AIFM1	chrX	-	1.29E+08	1.29E+08	2260
ENSG00000(	29.00217	9.634302	13.19414	227.719	210.7789	234.26	-3.6095	1.40E-28	2.02E-27	MAPK13	chr6	+	36095586	36107842	2052
ENSG00000(	419.4957	428.7264	505.3355	443.4527	359.8889	361.6646	0.2131	0.19089	0.29639	BAG4	chr8	+	38034051	38070819	4453
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	AQP7P3	chr9	+	42858072	42876505	2351

ENSG00000(	3.107376	2.408575	26.38828	6.74168	4.60216	4.109825	0.89937	0.30767	0.4334	IGKV1OR-2	chr9	-	69777099	69777953	350
ENSG00000(	99.43602	87.913	83.12307	198.505	182.2455	174.2566	-1.0269	6.01E-06	2.29E-05	WDR67	chr8	+	1.24E+08	1.24E+08	3502
ENSG00000(	153.2972	127.6545	142.4967	232.9625	190.5294	219.4646	-0.59894	0.003769	0.009573	WDYHV1	chr8	+	1.24E+08	1.24E+08	1491
ENSG00000(	149.154	138.4931	224.3003	1172.303	981.1805	893.4759	-2.5671	3.00E-43	6.86E-42	ATAD2	chr8	-	1.24E+08	1.24E+08	5565
ENSG00000(	19.68005	19.2686	34.30476	4.494453	12.88605	9.041614	1.4021	0.019929	0.043236	FBXO32	chr8	-	1.25E+08	1.25E+08	6744
ENSG00000(	367.7061	298.6634	324.5758	403.7517	293.6178	299.1952	-0.00852	0.96306	0.97854	NSMCE2	chr8	+	1.26E+08	1.26E+08	1195
ENSG00000(	206.1226	198.7075	221.6615	221.7264	249.4371	235.9039	-0.17369	0.34444	0.47364	ZNF689	chr16	-	30613879	30635333	3547
ENSG00000(	562.435	599.7353	517.2102	446.449	482.3064	559.7581	0.17428	0.24803	0.365	PRR14	chr16	+	30662038	30667761	2316
ENSG00000(	2399.93	2170.126	2071.48	1367.063	1771.832	2172.453	0.32193	0.036776	0.074348	FBRS	chr16	+	30669752	30682135	5200
ENSG00000(	158.4762	119.2245	116.1084	54.68252	100.3271	78.90863	0.75125	0.008129	0.019277	FRRS1	chr1	-	1E+08	1E+08	2706
ENSG00000(	305.5586	264.9433	238.8139	586.5262	375.5363	470.9859	-0.81942	1.87E-05	6.70E-05	PHKG2	chr16	+	30759591	30772490	5532
ENSG00000(	806.8819	606.961	861.5772	862.186	779.6059	649.3523	-0.01029	0.9498	0.96986	HIAT1	chr1	+	1.01E+08	1.01E+08	2777
ENSG00000(	44.53905	46.96722	50.13772	283.1506	219.9832	230.1502	-2.3566	1.14E-21	1.24E-20	SASS6	chr1	-	1.01E+08	1.01E+08	3972
ENSG00000(	6.214751	0	0	0	0	0	1.7844	0.18526	0.28968	ITGAD	chr16	+	31404633	31437826	3912
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	GPR112	chrX	+	1.35E+08	1.36E+08	9931
ENSG00000(	22.78742	8.430014	23.74945	205.2467	195.1316	180.8323	-3.35	6.24E-25	7.69E-24	ZIC3	chrX	+	1.37E+08	1.37E+08	3469
ENSG00000(	294.1649	291.4376	300.8263	478.6593	494.272	514.55	-0.7446	7.87E-07	3.30E-06	MALSU1	chr7	+	23338358	23351348	3044
ENSG00000(	587.294	604.5524	712.4834	546.0761	528.328	382.2137	0.38417	0.021985	0.04721	VPS8	chr3	+	1.85E+08	1.85E+08	5047
ENSG00000(	137.7603	225.2018	178.1209	154.3096	142.667	112.6092	0.39563	0.10061	0.17636	GALK2	chr15	+	49447853	49660066	3222
ENSG00000(	0	10.83859	5.277655	11.98521	15.64734	13.9734	-1.2503	0.12361	0.20878	B3GNT7	chr2	+	2.32E+08	2.32E+08	3706
ENSG00000(	0	0	0	15.73059	15.64734	9.041614	-4.6104	5.21E-05	0.000177	MPV17L	chr16	+	15489611	15503458	2153
ENSG00000(	241.3395	254.1047	306.104	875.6693	973.8171	761.9615	-1.7006	2.23E-26	2.91E-25	BUB1B	chr15	+	40453224	40513337	3725
ENSG00000(	207.1584	154.1488	180.7597	204.4976	142.667	179.1884	0.041594	0.85058	0.9049	PDE6D	chr2	-	2.33E+08	2.33E+08	1175
ENSG00000(	5858.439	6056.363	6305.478	4825.545	4372.052	4139.415	0.44921	2.62E-05	9.23E-05	EIF4A2	chr3	+	1.87E+08	1.87E+08	5327
ENSG00000(	467.1421	435.9522	548.8761	557.3122	640.6207	580.3072	-0.29215	0.051677	0.099942	BRPF1	chr3	+	9773413	9789702	4736
ENSG00000(	432.961	526.2737	402.4212	838.2155	694.0057	835.1164	-0.79562	2.61E-07	1.15E-06	RPUSD3	chr3	-	9879533	9886286	2491
ENSG00000(	0	0	0	0.749076	2.761296	1.64393	-1.5386	0.25678	NA	SST	chr3	-	1.87E+08	1.87E+08	618
ENSG00000(	1040.971	1077.838	1121.502	746.8283	783.2876	792.3742	0.47928	7.68E-05	0.000254	TATDN2	chr3	+	10289707	10327480	5342
ENSG00000(	10.35792	10.83859	9.235896	7.490755	8.283888	9.041614	0.27518	0.69673	0.79349	GHRL	chr3	-	10327359	10334631	1425
ENSG00000(	4315.109	4130.707	3715.469	3043.494	2492.53	2856.328	0.53407	6.81E-06	2.58E-05	SEC13	chr3	-	10334815	10362862	2374
ENSG00000(	3.107376	0	0	2.247227	0	3.28786	-0.47351	0.72193	0.81302	FAM92A1P	chr15	+	41455360	41456572	890
ENSG00000(	311.7734	299.8676	325.8952	208.243	179.4842	164.393	0.7588	3.19E-05	0.000111	EXOG	chr3	+	38537618	38583652	2792
ENSG00000(	998.5034	995.9459	918.312	698.8875	578.9517	580.3072	0.64639	1.98E-06	7.95E-06	NTAN1	chr16	-	15131710	15149921	2398
ENSG00000(	7.250543	9.634302	9.235896	937.8426	1334.626	1129.38	-6.9259	2.19E-95	1.54E-93	NMNAT2	chr1	-	1.83E+08	1.83E+08	5663
ENSG00000(	298.3081	290.2333	311.3817	162.5494	147.2691	146.3098	0.97452	9.27E-08	4.27E-07	ZFYVE9	chr1	+	52608046	52812358	4914
ENSG00000(	2.071584	0	5.277655	0	0	0	2.1617	0.11093	0.19077	ATP2B2	chr3	-	10365707	10749716	9101
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	LYZL4	chr3	-	42438570	42452092	904
ENSG00000(	1715.271	1642.648	2539.872	1291.406	1735.935	1289.663	0.44814	0.009012	0.021173	SMG1	chr16	-	18816175	18937776	16115
ENSG00000(	339.7397	435.9522	452.5589	202.9995	252.1984	184.9421	0.93546	7.77E-07	3.26E-06	FCHO2	chr5	+	72251808	72386349	4981
ENSG00000(	592.473	558.7895	576.5838	2961.845	2150.129	2031.075	-2.0413	2.31E-41	4.95E-40	RBPMS	chr8	+	30241944	30429778	3110
ENSG00000(	37.28851	7.225726	32.98534	8.988907	8.283888	2.465895	1.8407	0.006951	0.016752	TMEM171	chr5	+	72416119	72427644	1535
ENSG00000(	163.6551	114.4073	135.8996	1.498151	4.60216	1.64393	5.56	1.04E-26	1.38E-25	TIMP4	chr3	-	12194551	12200851	1650
ENSG00000(	22.78742	19.2686	19.79121	41.94823	34.05598	40.27628	-0.88523	0.042206	0.08387	SYN2	chr3	+	12045876	12232900	3897
ENSG00000(	67.32647	45.76293	83.12307	228.468	132.5422	166.8589	-1.4163	9.27E-07	3.86E-06	NRG1	chr8	+	31496902	32622548	3127

ENSG00000(	311.7734	305.8891	295.5487	497.3862	372.775	401.1189	-0.47625	0.004977	0.012331	C1orf27	chr1	+	1.86E+08	1.86E+08	3823
ENSG00000(	126.3666	119.2245	117.4278	217.981	187.7681	162.7491	-0.64261	0.003513	0.008968	CPT2	chr1	+	53662101	53679869	3094
ENSG00000(	1578.547	1404.199	1526.562	997.0196	983.9418	1093.213	0.55175	4.12E-06	1.60E-05	NECAP2	chr1	+	16767167	16786573	4619
ENSG00000(	114.9729	150.536	205.8285	266.6709	254.0392	221.1086	-0.65607	0.003868	0.009805	LRP8	chr1	-	53711217	53793742	4467
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CDCP2	chr1	-	54598747	54619443	2723
ENSG00000(	211.3015	239.6533	245.411	390.2684	555.0205	429.8877	-0.97749	9.31E-08	4.29E-07	PAXIP1	chr7	-	1.55E+08	1.55E+08	5515
ENSG00000(	84.93494	126.4502	127.9831	30.7121	12.88605	16.4393	2.4347	3.31E-11	2.03E-10	STEAP2	chr7	+	89796904	89867451	6873
ENSG00000(	885.6021	814.0985	881.3684	676.4152	780.5263	766.0713	0.21567	0.098373	0.173	SSBP3	chr1	-	54691105	54879152	2913
ENSG00000(	417.4241	350.4477	501.3772	510.1204	450.0912	435.6414	-0.13841	0.4113	0.54203	CLDN12	chr7	+	90013035	90142716	3587
ENSG00000(	38872.23	37090.86	35581.95	10973.21	12825.3	16551.91	1.4632	2.47E-26	3.21E-25	MMP14	chr14	+	23305766	23318236	3732
ENSG00000(	1328.921	1228.373	1265.318	226.2208	294.5382	250.6993	2.3054	7.98E-59	2.69E-57	FZD1	chr7	+	90893783	90898123	4341
ENSG00000(	671.1932	590.101	579.2227	385.0248	416.0353	345.2253	0.68273	5.50E-06	2.11E-05	GATAD1	chr7	+	92076767	92088150	3361
ENSG00000(	0	0	0	3.745378	0	4.93179	-2.136	0.11352	0.19465	SUSD3	chr9	+	95820989	95847420	1195
ENSG00000(	14.50109	7.225726	7.916483	2.996302	11.96562	7.397684	0.39128	0.61223	0.72568	RP11-66N2	chr14	+	23980969	24029987	2524
ENSG00000(	11.39371	12.04288	3.958241	26.21764	16.56778	14.79537	-0.9981	0.11853	0.2018	TMED6	chr16	-	69377151	69385712	938
ENSG00000(	2.071584	3.612863	1.319414	2.996302	1.840864	4.109825	-0.27882	0.80164	0.8709	CLEC18A	chr16	+	69984810	69998141	3194
ENSG00000(	213.3731	202.3203	186.0373	158.804	185.0068	209.6011	0.12253	0.54457	0.66676	DHRS4	chr14	+	24422795	24438488	1443
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	C1orf158	chr1	+	12806163	12823847	3764
ENSG00000(	0	0	0	0	1.840864	2.465895	-1.2108	0.36631	NA	CLEC18C	chr16	+	70207225	70221264	3660
ENSG00000(	11.39371	21.67718	10.55531	6.74168	5.522592	3.28786	1.3687	0.059575	0.11302	ARMC12	chr6	+	35704809	35716856	1254
ENSG00000(	161.5835	180.6432	134.5802	286.1469	173.9616	207.1352	-0.48221	0.03737	0.075448	DDX19B	chr16	+	70323566	70369186	3386
ENSG00000(	827.5977	752.6798	724.3582	364.7998	462.9773	399.475	0.9087	8.01E-10	4.42E-09	ST3GAL2	chr16	-	70413338	70473140	5345
ENSG00000(	181.2636	161.3746	160.9685	217.981	231.0284	230.1502	-0.42705	0.026059	0.054964	FUK	chr16	+	70488324	70514177	4439
ENSG00000(	46.61064	51.78437	46.17948	0	0	0	6.8158	4.81E-11	2.91E-10	IL34	chr16	+	70613798	70694585	1779
ENSG00000(	393.6009	352.8563	348.3252	354.3127	323.9921	373.1721	0.058701	0.71256	0.80567	DHRS1	chr14	-	24759804	24769039	2660
ENSG00000(	34.18113	56.60152	50.13772	5.992604	5.522592	3.28786	3.1095	8.77E-09	4.41E-08	CACNA1D	chr3	+	53528683	53846490	7721
ENSG00000(	244.4469	187.8689	246.7304	37.45378	47.86246	47.67397	2.3364	5.83E-21	6.14E-20	ARSE	chrX	-	2852699	2886286	2158
ENSG00000(	16.57267	12.04288	11.87472	208.9921	182.2455	189.0519	-3.7675	1.54E-29	2.29E-28	KIT	chr4	+	55524085	55606881	5186
ENSG00000(	1.035792	0	0	61.42419	43.2603	38.63235	-5.6832	1.06E-09	5.80E-09	HYDIN	chr16	-	70841281	71264625	15719
ENSG00000(	155.3688	186.6646	224.3003	137.0808	104.0088	141.378	0.55658	0.016074	0.035651	AASDH	chr4	-	57204456	57253666	3590
ENSG00000(	26.93059	25.29004	19.79121	35.20655	32.21512	31.23467	-0.43778	0.31844	0.44545	ZNF19	chr16	-	71498453	71598992	3213
ENSG00000(	157.4404	127.6545	126.6637	59.92604	69.0324	30.4127	1.3557	1.03E-05	3.83E-05	CACNA2D3	chr3	+	54156574	55108584	3675
ENSG00000(	682.5869	702.0997	852.3413	527.3492	550.4183	446.327	0.55102	0.000272	0.000832	RNF111	chr15	+	59157374	59389618	5913
ENSG00000(	465.0706	376.9421	473.6695	1582.048	1391.693	1338.981	-1.7083	1.07E-33	1.84E-32	CCNB2	chr15	+	59397277	59417244	1556
ENSG00000(	3.107376	0	6.597069	20.97412	22.09037	12.32947	-2.2933	0.003718	0.009453	FAM81A	chr15	+	59664892	59815748	3465
ENSG00000(	2656.806	2496.488	2630.911	659.1865	800.7758	750.454	1.8137	2.26E-51	6.47E-50	MYO1E	chr15	-	59427113	59665099	6193
ENSG00000(	530.3255	616.5953	688.734	786.5293	715.1757	631.2691	-0.21789	0.1507	0.24496	APPL1	chr3	+	57261765	57307496	6058
ENSG00000(	934.2843	868.2914	1187.472	294.3867	302.8221	312.3467	1.7106	1.56E-28	2.25E-27	MUM1L1	chrX	+	1.05E+08	1.05E+08	4308
ENSG00000(	78.72018	87.913	65.97069	181.2763	194.2112	158.6392	-1.1868	8.37E-07	3.50E-06	AFAP1L1	chr5	+	1.49E+08	1.49E+08	4177
ENSG00000(	1426.285	1445.145	1365.593	208.243	162.9165	163.571	2.9745	2.08E-93	1.41E-91	TSC22D3	chrX	-	1.07E+08	1.07E+08	2266
ENSG00000(	855.5641	756.2927	853.6607	973.7982	828.3888	813.7453	-0.08568	0.52644	0.65122	DSCR3	chr21	-	38595721	38640262	5648
ENSG00000(	876.28	783.9913	1000.116	693.644	798.935	685.5187	0.28777	0.042256	0.083941	DYRK1A	chr21	+	38739236	38887680	6384
ENSG00000(	10.35792	16.86003	23.74945	18.72689	19.32907	13.9734	-0.03942	0.94444	0.96675	KCNJ6	chr21	-	38996789	39288749	2534
ENSG00000(	38.3243	25.29004	22.43003	14.98151	8.283888	19.72716	0.96151	0.069276	0.12862	KCNJ15	chr21	+	39529128	39673748	2914

ENSG00000(	5.17896	0	6.597069	0.749076	0.920432	2.465895	1.1268	0.338	0.46658	ERG	chr21	-	39751949	40033704	5034
ENSG00000(	1538.151	1600.498	1493.576	585.7771	497.9537	471.8079	1.5697	3.68E-33	6.23E-32	ETS2	chr21	+	40177231	40196879	3936
ENSG00000(	19.68005	8.430014	10.55531	141.5753	142.667	118.3629	-3.2874	1.17E-18	1.12E-17	TSPAN18	chr11	+	44748015	44953972	4229
ENSG00000(	21.75163	21.67718	22.43003	8.239831	10.12475	9.863579	1.1678	0.041046	0.081895	LCA5L	chr21	-	40777770	40817731	2564
ENSG00000(	1757.739	1814.862	1727.113	1656.206	1513.19	1831.338	0.083415	0.48094	0.61005	SLC35B2	chr6	-	44221833	44225291	2043
ENSG00000(	678.4437	676.8097	679.4981	435.962	659.9497	527.7015	0.32612	0.04508	0.088733	TMEM164	chrX	+	1.09E+08	1.09E+08	5567
ENSG00000(	19.68005	7.225726	18.47179	10.48706	13.80648	7.397684	0.4921	0.45021	0.58	MX1	chr21	+	42792231	42831141	3470
ENSG00000(	4450.798	4224.641	3475.336	740.8357	510.8398	588.5269	2.7137	3.08E-74	1.45E-72	CREB3L1	chr11	+	46299212	46342972	2687
ENSG00000(	314.8807	349.2434	398.463	62.17327	65.35067	72.33291	2.3955	4.00E-31	6.31E-30	C2CD2	chr21	-	43305221	43373999	6345
ENSG00000(	369.7777	284.2119	358.8805	534.8399	549.4979	459.4784	-0.60498	0.000245	0.000753	TAB3	chrX	-	30845559	30993201	7987
ENSG00000(	3215.098	3088.998	2795.838	2238.987	2553.278	2702.621	0.2799	0.018038	0.039536	SLC38A10	chr17	-	79218800	79269347	4300
ENSG00000(	11.39371	13.24716	15.83297	11.98521	7.363456	16.4393	0.15814	0.80364	0.87261	C9orf43	chr9	+	1.16E+08	1.16E+08	2130
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	PALM2-AK/	chr9	+	1.13E+08	1.13E+08	7507
ENSG00000(	1098.975	1063.386	1328.65	280.9033	460.216	319.7444	1.7131	5.48E-22	6.01E-21	ZNF618	chr9	+	1.17E+08	1.17E+08	9109
ENSG00000(	163.6551	164.9874	167.5656	4.494453	0.920432	5.753754	5.2788	1.87E-32	3.06E-31	DGKI	chr7	-	1.37E+08	1.38E+08	5148
ENSG00000(	191.6215	228.8147	175.482	116.1067	113.2131	79.7306	0.94058	6.12E-05	0.000205	C9orf91	chr9	+	1.17E+08	1.17E+08	4578
ENSG00000(	0	0	0	33.7084	12.88605	27.12484	-5.4536	5.68E-07	2.42E-06	SVOPL	chr7	-	1.38E+08	1.38E+08	5761
ENSG00000(	41.43168	56.60152	38.263	35.20655	34.97642	36.98842	0.34011	0.36706	0.49709	SNX22	chr15	+	64443914	64449680	3713
ENSG00000(	378.064	367.3078	478.9472	290.6413	368.1728	297.5513	0.35461	0.04441	0.087611	UBN2	chr7	+	1.39E+08	1.39E+08	14443
ENSG00000(	161.5835	151.7403	254.6469	82.39831	115.9744	106.0335	0.89087	0.000539	0.001575	BRAF	chr7	-	1.4E+08	1.41E+08	2480
ENSG00000(	1.035792	0	0	23.22134	16.56778	14.79537	-4.3443	2.63E-05	9.27E-05	SLC34A2	chr4	+	25656923	25680370	4122
ENSG00000(	5.17896	18.06432	11.87472	47.94084	45.10117	43.56414	-1.9081	0.000129	0.000414	ACAN	chr15	+	89346674	89418585	8840
ENSG00000(	264.1269	208.3418	180.7597	318.3571	301.9017	353.4449	-0.569	0.002952	0.007634	PSMG3	chr7	-	1606966	1610641	1391
ENSG00000(	15.53688	9.634302	3.958241	1.498151	3.681728	0	2.1349	0.028612	0.059641	CABP1	chr12	+	1.21E+08	1.21E+08	3048
ENSG00000(	591.4372	592.5096	568.6673	265.1727	268.7661	189.0519	1.2729	9.44E-14	6.90E-13	WDR19	chr4	+	39184024	39287430	4520
ENSG00000(	797.5598	717.7555	833.8695	710.8727	675.5971	570.4437	0.26252	0.064723	0.12122	SLC37A3	chr7	-	1.4E+08	1.4E+08	3488
ENSG00000(	203.0152	231.2232	195.2732	167.0438	119.6562	117.541	0.63209	0.004184	0.010531	AP3S2	chr15	-	90373831	90437574	5891
ENSG00000(	2637.126	2797.56	3437.073	869.6767	929.6363	764.4274	1.7863	1.25E-39	2.57E-38	FMNL2	chr2	+	1.53E+08	1.54E+08	5575
ENSG00000(	149.154	155.3531	122.7055	125.8447	110.4518	161.9271	0.10134	0.67143	0.77389	GAREML	chr2	+	26395960	26412532	5138
ENSG00000(	641.1552	603.3481	579.2227	909.3777	828.3888	820.321	-0.4865	0.000212	0.000661	SPPL3	chr12	-	1.21E+08	1.21E+08	4148
ENSG00000(	10.35792	1.204288	3.958241	149.066	201.5746	188.23	-4.9028	1.61E-27	2.22E-26	DPYSL5	chr2	+	27070615	27173219	5209
ENSG00000(	0	3.612863	7.916483	0	0.920432	0.821965	1.8283	0.14726	0.24027	DRC1	chr2	+	26624784	26679579	2491
ENSG00000(	148.1182	220.3847	209.7868	283.8996	225.5058	218.6427	-0.33492	0.11722	0.20006	RAB28	chr4	-	13362978	13485989	1810
ENSG00000(	335.5966	286.6205	345.6864	288.3941	305.5834	351.801	0.03339	0.84569	0.90145	FAM213B	chr1	+	2517930	2522908	2765
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	TNFRSF14	chr1	+	2487078	2496821	4255
ENSG00000(	382.2072	372.1249	349.6447	570.7956	484.1472	561.402	-0.54821	0.00028	0.000857	PANK4	chr1	-	2439972	2458039	2649
ENSG00000(	12.4295	39.74149	21.11062	14.23244	34.97642	21.37109	0.053064	0.92248	0.95302	MEGF11	chr15	-	66187417	66546085	6163
ENSG00000(	294.1649	260.1261	284.9934	398.5082	358.9685	319.7444	-0.35868	0.03477	0.070725	C12orf43	chr12	-	1.21E+08	1.21E+08	2533
ENSG00000(	991.2529	1041.709	939.4226	965.5584	800.7758	952.6573	0.12778	0.3303	0.45806	PEX10	chr1	-	2336236	2345236	2038
ENSG00000(	2694.095	2715.669	2376.264	2128.873	2102.267	2011.348	0.31855	0.004106	0.010352	RER1	chr1	+	2323267	2335190	2469
ENSG00000(	25.8948	36.12863	15.83297	53.18436	34.05598	78.90863	-1.0616	0.015762	0.035022	RADIL	chr7	-	4836686	4923350	5669
ENSG00000(	2545.977	2448.317	2411.888	1950.593	1989.974	1848.599	0.35508	0.00085	0.00241	SKI	chr1	+	2160134	2241558	5613
ENSG00000(	1199.447	1247.642	1153.168	1250.956	1089.791	1103.077	0.063664	0.60102	0.71631	WIPI2	chr7	+	5229819	5273457	4476
ENSG00000(	301.4154	263.739	295.5487	272.6635	283.4931	208.7791	0.17015	0.36062	0.4902	LDLRAP1	chr1	+	25870071	25895377	4670

ENSG00000(	959.1433	899.6029	907.7567	588.7734	878.0921	727.439	0.33476	0.030334	0.062774	AGAP1	chr2	+	2.36E+08	2.37E+08	6138
ENSG00000(	21.75163	9.634302	13.19414	7.490755	11.96562	13.15144	0.43682	0.49599	0.62466	KRTCAP3	chr2	+	27665233	27669348	956
ENSG00000(	9.322127	27.69862	21.11062	19.47596	43.2603	24.65895	-0.56883	0.28725	0.41082	ANKRD61	chr7	+	6071007	6076017	1257
ENSG00000(	181.2636	222.7932	216.3839	322.1025	357.1276	288.5097	-0.64003	0.000504	0.001481	PAFAH2	chr1	-	26286258	26324648	3581
ENSG00000(	17.60846	24.08575	34.30476	5.992604	12.88605	9.041614	1.3787	0.017695	0.03889	EXTL1	chr1	+	26346375	26362955	4015
ENSG00000(	0	0	0	1.498151	2.761296	7.397684	-2.6881	0.039872	0.079806	SLC30A2	chr1	-	26363743	26372624	3097
ENSG00000(	872.1368	929.7101	798.2453	472.6667	313.8673	312.3467	1.2356	1.20E-12	8.17E-12	BRE	chr2	+	28112808	28561768	1852
ENSG00000(	3.107376	2.408575	0	2.247227	2.761296	0	0.1111	0.93061	0.95822	TRIM63	chr1	-	26377795	26394927	1770
ENSG00000(	64.2191	63.82725	73.88717	16.47966	34.05598	15.61733	1.5848	7.20E-05	0.000239	WDR66	chr12	+	1.22E+08	1.22E+08	4675
ENSG00000(	1224.306	1183.815	971.0885	1046.459	942.5224	1020.88	0.16725	0.2084	0.31793	MRPL17	chr11	-	6702013	6704632	1969
ENSG00000(	6.214751	9.634302	7.916483	8.239831	6.443024	9.041614	-0.00425	0.99552	0.99709	DUSP2	chr2	-	96808905	96811179	1688
ENSG00000(	5.17896	0	13.19414	629.9725	766.7199	713.4655	-6.1926	3.96E-15	3.15E-14	GRHL3	chr1	+	24645812	24690972	2869
ENSG00000(	324.2029	317.932	254.6469	317.608	240.2328	370.7062	-0.04955	0.80136	0.87075	UBXN11	chr1	-	26607819	26644854	2646
ENSG00000(	4.143168	0	0	0	0.920432	0	0.95689	0.47805	NA	NLRP14	chr11	+	7041677	7092539	3628
ENSG00000(	95.29286	90.32158	134.5802	98.1289	95.72493	68.22309	0.28221	0.3132	0.43968	PTPDC1	chr9	+	96793076	96872138	4517
ENSG00000(	6.214751	6.021439	0	84.64554	45.10117	71.51095	-3.7977	3.15E-11	1.94E-10	GALNT14	chr2	-	31133333	31378068	2733
ENSG00000(	251.6974	257.7176	277.0769	253.9366	223.665	204.6693	0.20226	0.26661	0.38662	NCK1	chr3	+	1.37E+08	1.37E+08	2403
ENSG00000(	5.17896	2.408575	1.319414	14.23244	21.16994	5.753754	-1.9295	0.022482	0.048144	HPD	chr12	-	1.22E+08	1.22E+08	1709
ENSG00000(	9.322127	7.225726	15.83297	191.7633	209.8585	225.2184	-4.2203	1.88E-32	3.08E-31	RHPN1	chr8	+	1.44E+08	1.44E+08	3683
ENSG00000(	762.3428	690.0569	787.69	498.8843	469.4203	450.4368	0.65677	1.76E-06	7.11E-06	TPRG1L	chr1	+	3541566	3546691	2414
ENSG00000(	6.214751	6.021439	2.638828	8.239831	2.761296	0	0.3528	0.73541	0.82299	LRRC43	chr12	+	1.23E+08	1.23E+08	2028
ENSG00000(	195.7647	252.9004	203.1897	270.4163	179.4842	228.5062	-0.06019	0.77557	0.85283	AAED1	chr9	-	99401859	99417585	2863
ENSG00000(	7.250543	3.612863	3.958241	35.20655	23.93123	21.37109	-2.275	0.000416	0.001238	XDH	chr2	-	31557187	31637581	5688
ENSG00000(	215.4447	251.6961	199.2315	233.7116	197.8929	234.26	0.0004	0.99834	0.99905	XKR8	chr1	+	28285973	28294607	2692
ENSG00000(	163.6551	196.2989	131.9414	202.2504	233.7897	216.9987	-0.40361	0.055271	0.10604	CNNM4	chr2	+	97426639	97477628	4800
ENSG00000(	431.9252	455.2208	438.0454	525.102	542.1344	440.5732	-0.1856	0.21881	0.33029	EYA3	chr1	-	28296855	28415207	6085
ENSG00000(	134.6529	142.106	176.8014	92.13629	165.6778	115.0751	0.2816	0.27752	0.39928	DZIP1L	chr3	-	1.38E+08	1.38E+08	3493
ENSG00000(	305.5586	316.7277	269.1604	160.3022	143.5874	173.4346	0.89671	1.75E-06	7.07E-06	TMSB15A	chrX	-	1.02E+08	1.02E+08	685
ENSG00000(	234.089	216.7718	252.008	346.822	346.0824	360.8426	-0.5828	0.000515	0.001512	FANCC	chr9	-	97861336	98079991	4585
ENSG00000(	550.0055	628.6382	676.8593	320.6043	293.6178	235.082	1.1215	2.03E-11	1.26E-10	MRAS	chr3	+	1.38E+08	1.38E+08	4538
ENSG00000(	3931.866	3508.09	3782.759	2938.623	3786.657	3180.182	0.18014	0.14206	0.23358	WASF2	chr1	-	27730730	27816669	5666
ENSG00000(	96.32865	103.5687	121.3861	379.0322	350.6846	375.638	-1.7786	2.10E-20	2.16E-19	ABHD3	chr18	-	19230858	19284766	2080
ENSG00000(	9.322127	8.430014	5.277655	23.97042	19.32907	18.08323	-1.3254	0.033517	0.068457	ESYT3	chr3	+	1.38E+08	1.38E+08	4620
ENSG00000(	123.2592	116.8159	108.1919	309.3682	227.3467	244.9455	-1.1587	5.41E-08	2.54E-07	FAIM	chr3	+	1.38E+08	1.38E+08	3161
ENSG00000(	244.4469	199.9118	195.2732	1032.226	925.0342	1097.323	-2.2447	9.08E-48	2.35E-46	FAM46B	chr1	-	27331511	27339327	2368
ENSG00000(	21.75163	14.45145	42.22124	200.0032	238.3919	252.3432	-3.116	6.16E-24	7.32E-23	CLSTN2	chr3	+	1.4E+08	1.4E+08	4882
ENSG00000(	11265.27	11110.76	11500.01	1523.62	1594.188	1351.31	2.9179	2.02E-164	3.93E-162	COLEC12	chr18	-	319361	500722	4719
ENSG00000(	124.295	116.8159	87.08131	27.7158	21.16994	32.8786	1.9742	1.35E-09	7.34E-09	RNF207	chr1	+	6265535	6281359	3924
ENSG00000(	1436.643	1468.027	1756.14	988.0306	990.3848	875.3926	0.70541	5.62E-08	2.64E-07	CUL4B	chrX	-	1.2E+08	1.2E+08	4902
ENSG00000(	635.9762	675.6054	581.8615	98.1289	91.12277	126.5826	2.5716	5.46E-47	1.37E-45	GPR153	chr1	-	6307406	6321035	4082
ENSG00000(	49.71801	34.92434	27.70769	18.72689	35.89685	16.4393	0.65471	0.16085	0.25827	SLC13A3	chr20	-	45186463	45304714	4017
ENSG00000(	232.0174	278.1905	270.4798	112.3613	126.0992	83.01846	1.272	6.12E-09	3.13E-08	GPRASP2	chrX	+	1.02E+08	1.02E+08	4729
ENSG00000(	25.8948	13.24716	10.55531	4.494453	3.681728	18.08323	0.85715	0.23267	0.34637	RHBDL2	chr1	-	39351479	39407471	2129
ENSG00000(	747.8418	852.6357	885.3266	568.5483	830.2297	662.5037	0.26975	0.088705	0.15883	AUTS2	chr7	+	69063905	70258054	6173

ENSG00000(	69.39806	66.23582	71.24834	103.3724	196.052	138.9121	-1.068	0.000188	0.00059	SHROOM4	chrX	-	50334647	50557302	9556
ENSG00000(	712.6248	717.7555	622.7633	142.3244	101.2475	122.4728	2.4735	5.07E-46	1.24E-44	HIST1H2BD	chr6	+	26158349	26171577	789
ENSG00000(	89.0781	65.03154	77.84541	232.2134	193.2907	216.9987	-1.4565	3.86E-10	2.18E-09	CDC25C	chr5	-	1.38E+08	1.38E+08	2128
ENSG00000(	234.089	258.9219	242.7721	56.92974	91.12277	119.1849	1.4512	9.35E-09	4.69E-08	HIST1H4H	chr6	-	26281283	26285762	1034
ENSG00000(	319.0239	350.4477	286.3128	554.3159	467.5795	473.4518	-0.64333	6.46E-05	0.000216	MITD1	chr2	-	99777890	99797521	3270
ENSG00000(	2680.629	2557.907	2545.149	5480.986	3665.16	4137.771	-0.7692	5.96E-08	2.80E-07	EIF5B	chr2	+	99953816	1E+08	4716
ENSG00000(	2.071584	13.24716	11.87472	18.72689	19.32907	32.8786	-1.3217	0.040325	0.080622	RIBC1	chrX	+	53449639	53458059	1949
ENSG00000(	279.6638	242.0618	274.4381	163.2985	135.3035	185.7641	0.71177	0.000338	0.00102	TMSB15B	chrX	+	1.03E+08	1.03E+08	2279
ENSG00000(	1.035792	0	0	2.247227	1.840864	0.821965	-1.1159	0.40841	0.53916	C2orf62	chr2	+	2.19E+08	2.19E+08	2383
ENSG00000(	576.9361	591.3053	580.5421	1758.829	1480.975	1481.181	-1.43	1.49E-28	2.14E-27	CNOT11	chr2	+	1.02E+08	1.02E+08	2599
ENSG00000(	11.39371	4.817151	11.87472	0	1.840864	0	3.1611	0.003287	0.008442	KCNB1	chr20	-	47984946	48099184	7318
ENSG00000(	1.035792	0	0	12.73428	11.96562	12.32947	-3.8001	0.00046	0.001358	TSPAN33	chr7	+	1.29E+08	1.29E+08	1883
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	NRG2	chr5	-	1.39E+08	1.39E+08	3723
ENSG00000(	277.5922	319.1362	379.9912	260.6783	353.4459	245.7675	0.18231	0.35318	0.48286	AHCYL2	chr7	+	1.29E+08	1.29E+08	5056
ENSG00000(	2924.041	2680.744	2740.422	1842.726	2337.897	2119.026	0.40547	0.000825	0.002346	B4GALT5	chr20	-	48249482	48330415	4722
ENSG00000(	0	0	0	3.745378	0	5.753754	-2.2627	0.092546	0.16448	CD1D	chr1	+	1.58E+08	1.58E+08	2253
ENSG00000(	246.5185	231.2232	207.148	352.8146	332.276	313.9906	-0.54064	0.001791	0.004816	SPATA2	chr20	-	48519928	48532080	4138
ENSG00000(	3.107376	9.634302	7.916483	1.498151	5.522592	0	1.2999	0.20534	0.31395	SNX29P1	chr16	+	21391313	21403412	1209
ENSG00000(	42.46747	75.87013	35.62417	95.13259	69.95283	61.64737	-0.55015	0.12144	0.20587	FAM86C1	chr11	+	71498556	71512282	2110
ENSG00000(	1.035792	0	0	5.992604	6.443024	4.109825	-2.658	0.028397	0.059241	DNAH3	chr16	-	20944433	21170762	12394
ENSG00000(	1.035792	2.408575	1.319414	1.498151	1.840864	3.28786	-0.3512	0.77039	0.84909	CPA2	chr7	+	1.3E+08	1.3E+08	1366
ENSG00000(	1.035792	0	1.319414	2.247227	3.681728	0.821965	-0.98627	0.44325	0.57292	NCF1	chr7	+	74188309	74203659	2354
ENSG00000(	4.143168	7.225726	3.958241	0	0.920432	0.821965	2.3462	0.044368	0.087551	CPA5	chr7	+	1.3E+08	1.3E+08	2573
ENSG00000(	444.3547	502.188	444.6424	612.7438	739.1069	919.7787	-0.70448	2.35E-05	8.34E-05	TSR2	chrX	+	54466834	54471920	1534
ENSG00000(	9.322127	13.24716	10.55531	149.8151	180.4047	134.8022	-3.743	6.97E-24	8.26E-23	PPP1R9A	chr7	+	94536514	94925727	10219
ENSG00000(	1310.277	1124.805	1188.792	1957.334	2263.342	2612.205	-0.91207	1.22E-11	7.69E-11	ZC3H18	chr16	+	88636789	88698374	4654
ENSG00000(	391.5293	317.932	287.6322	334.0877	222.7445	257.275	0.29106	0.14361	0.23546	ZFAND2B	chr2	+	2.2E+08	2.2E+08	2021
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	POM121L2	chr6	-	27253682	27279949	3108
ENSG00000(	108.7581	104.773	112.1502	249.4422	238.3919	226.0404	-1.1264	3.85E-08	1.84E-07	GDPD5	chr11	-	75145685	75236948	4150
ENSG00000(	3.107376	8.430014	7.916483	77.15478	56.14635	60.8254	-3.2275	1.86E-10	1.08E-09	DYNC1I1	chr7	+	95401866	95739634	2950
ENSG00000(	0	0	1.319414	6.74168	3.681728	1.64393	-2.1402	0.089503	0.16001	PFKFB1	chrX	-	54959394	55024967	1929
ENSG00000(	1.035792	0	0	1.498151	0	1.64393	-0.62149	0.64536	NA	ALAS2	chrX	-	55035488	55057497	2027
ENSG00000(	1274.024	1277.749	1106.988	1638.228	1554.61	1617.627	-0.39352	0.000876	0.00248	TMED4	chr7	-	44617493	44621886	2322
ENSG00000(	761.307	788.8085	891.9237	692.8949	825.6275	735.6586	0.11498	0.40077	0.53204	PPP1R15B	chr1	-	2.04E+08	2.04E+08	5227
ENSG00000(	186.4425	158.966	204.5091	205.9958	212.6198	210.423	-0.19358	0.32362	0.451	COPG2	chr7	-	1.3E+08	1.3E+08	895
ENSG00000(	277.5922	338.4048	353.6029	322.1025	387.5019	348.5131	-0.12683	0.4595	0.58903	C11orf30	chr11	+	76155967	76264069	6848
ENSG00000(	1059.615	1164.546	1215.18	963.3112	902.9438	908.2712	0.30824	0.011966	0.027326	AGPAT6	chr8	+	41434706	41482520	6298
ENSG00000(	0	1.204288	0	3.745378	4.60216	4.93179	-2.3181	0.061778	0.11647	PKD1L1	chr7	-	47814250	47988088	9092
ENSG00000(	131.5456	156.5574	178.1209	170.7892	229.1876	188.23	-0.33481	0.12542	0.21119	ZSCAN12	chr6	-	28346732	28367511	5495
ENSG00000(	6293.472	5599.938	4962.315	14380	11989.55	14424.66	-1.2723	6.18E-25	7.62E-24	TAGLN2	chr1	-	1.6E+08	1.6E+08	1604
ENSG00000(	740.5912	688.8526	872.1325	342.3275	420.6374	331.2519	1.0697	1.19E-11	7.50E-11	ELK4	chr1	-	2.06E+08	2.06E+08	10239
ENSG00000(	1.035792	0	0	1.498151	0	0	-0.08447	0.94679	NA	SLAMF8	chr1	+	1.6E+08	1.6E+08	2996
ENSG00000(	76.6486	91.52587	67.2901	119.103	131.6218	133.1583	-0.69681	0.006412	0.015544	SLC45A3	chr1	-	2.06E+08	2.06E+08	3341
ENSG00000(	285.8786	305.8891	304.7846	304.1247	194.2112	314.8126	0.13737	0.49665	0.62521	DUSP23	chr1	+	1.6E+08	1.6E+08	756

ENSG0000(	180.2278	151.7403	142.4967	270.4163	291.7769	276.1802	-0.81305	2.14E-05	7.63E-05	RNF166	chr16	-	88762903	88772829	2419
ENSG0000(	1295.776	1216.331	1169.001	130.3391	90.20234	78.08667	3.6028	5.50E-93	3.68E-91	NBL1	chr1	+	19967048	19984945	2172
ENSG0000(	13.46529	2.408575	0	0	0	1.64393	2.2278	0.074011	0.13607	HTR6	chr1	+	19991780	20006055	1984
ENSG0000(	0	0	0	14.23244	7.363456	18.90519	-4.6011	5.77E-05	0.000194	ITLN2	chr1	-	1.61E+08	1.61E+08	1151
ENSG0000(	6.214751	1.204288	0	2502.661	1914.499	2195.468	-9.2969	7.29E-81	3.99E-79	F11R	chr1	-	1.61E+08	1.61E+08	4835
ENSG0000(	554.1487	608.1653	537.0014	810.4997	792.4919	917.3128	-0.5672	3.27E-05	0.000114	USF1	chr1	-	1.61E+08	1.61E+08	1807
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	PLA2G2F	chr1	+	20465819	20476879	4129
ENSG0000(	161.5835	189.0732	138.5384	341.5785	300.9813	384.6796	-1.0639	4.83E-08	2.29E-07	SPATA2L	chr16	-	89762751	89768113	2335
ENSG0000(	331.4534	268.5562	275.7575	502.6297	356.2072	495.6448	-0.62567	0.000638	0.001844	NIT1	chr1	+	1.61E+08	1.61E+08	2081
ENSG0000(	268.2701	319.1362	316.6593	273.4126	207.0972	244.1236	0.31422	0.087954	0.15774	DEDD	chr1	-	1.61E+08	1.61E+08	2452
ENSG0000(	155.3688	216.7718	170.2044	171.5383	242.0736	249.8773	-0.28854	0.19287	0.29873	ZNF276	chr16	+	89786808	89807311	4589
ENSG0000(	0	1.204288	5.277655	19.47596	19.32907	21.37109	-2.9464	0.000331	0.001002	NPM2	chr8	+	21881636	21894408	1874
ENSG0000(	2.071584	0	0	50.18806	28.53339	27.94681	-4.7713	5.25E-08	2.47E-07	EDA	chrX	+	68835911	69259319	5278
ENSG0000(	5.17896	3.612863	1.319414	2.996302	3.681728	4.109825	-0.05986	0.9535	0.97227	FGF17	chr8	+	21899909	21906320	2578
ENSG0000(	18.64425	10.83859	9.235896	0	1.840864	0	3.6612	0.000302	0.000917	CDA	chr1	+	20915441	20945401	963
ENSG0000(	275.5206	246.879	262.5633	81.64923	64.43024	66.57916	1.869	5.67E-18	5.23E-17	PINK1	chr1	+	20959948	20978004	3821
ENSG0000(	844.1704	761.1098	691.3728	761.0608	693.0853	675.6552	0.10944	0.4256	0.55596	B4GALT3	chr1	-	1.61E+08	1.61E+08	3178
ENSG0000(	25.8948	10.83859	7.916483	76.40571	131.6218	118.3629	-2.766	2.68E-11	1.66E-10	EPB49	chr8	+	21906506	21940038	2772
ENSG0000(	186.4425	171.0089	174.1626	3.745378	2.761296	1.64393	5.8055	4.09E-33	6.90E-32	ADAMTS4	chr1	-	1.61E+08	1.61E+08	4333
ENSG0000(	638.0478	688.8526	494.7802	244.9477	251.2779	300.0172	1.1903	4.94E-12	3.22E-11	FAM160B2	chr8	+	21946670	21962409	4245
ENSG0000(	1791.92	1751.034	1655.864	1317.624	1065.86	1249.387	0.51561	3.23E-05	0.000112	NDUFS2	chr1	+	1.61E+08	1.61E+08	2064
ENSG0000(	0	0	0	2.247227	0	0.821965	-0.85594	0.51054	NA	SLC5A11	chr16	+	24857162	24922949	2745
ENSG0000(	4.143168	3.612863	7.916483	15.73059	8.283888	3.28786	-0.72867	0.38922	0.51982	FCER1G	chr1	+	1.61E+08	1.61E+08	591
ENSG0000(	0	3.612863	0	0	0.920432	0.821965	0.52233	0.70023	NA	APOA2	chr1	-	1.61E+08	1.61E+08	927
ENSG0000(	134.6529	143.3102	142.4967	161.8003	142.667	156.1733	-0.13276	0.53437	0.65887	TOMM40L	chr1	+	1.61E+08	1.61E+08	2708
ENSG0000(	6.214751	7.225726	7.916483	6.74168	9.20432	30.4127	-1.0315	0.1626	0.26052	MPZ	chr1	-	1.61E+08	1.61E+08	1955
ENSG0000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	WFDC8	chr20	-	44179792	44207965	1268
ENSG0000(	1160.087	1146.482	1187.472	2152.843	2161.174	2368.903	-0.93412	7.85E-17	6.82E-16	KIAA1967	chr8	+	22462145	22479027	4853
ENSG0000(	129.474	192.686	171.5238	222.4754	297.2995	196.4496	-0.53444	0.018807	0.041057	CACHD1	chr1	+	64936428	65158741	5547
ENSG0000(	439.1758	464.8551	531.7238	637.4633	660.8702	618.9396	-0.41764	0.003446	0.008815	CDC42SE2	chr5	+	1.31E+08	1.31E+08	4352
ENSG0000(	75.61281	119.2245	108.1919	189.5161	106.7701	171.7907	-0.62746	0.023216	0.049554	RAPGEF6	chr5	-	1.31E+08	1.31E+08	8357
ENSG0000(	153.2972	121.6331	142.4967	366.2979	521.8849	395.3651	-1.6087	8.60E-16	7.10E-15	EPB41	chr1	+	29213603	29446553	5930
ENSG0000(	142.9393	167.396	158.3297	536.3381	511.7602	582.7731	-1.7944	1.83E-26	2.39E-25	MIS18A	chr21	-	33640530	33651380	1575
ENSG0000(	699.1595	756.2927	667.6234	1203.764	868.8878	925.5325	-0.49704	0.000988	0.002773	ALG8	chr11	-	77811982	77850706	1677
ENSG0000(	2712.739	2437.478	1880.165	2050.969	1974.327	2303.146	0.15196	0.28338	0.40622	FBXW5	chr9	-	1.4E+08	1.4E+08	2392
ENSG0000(	45.57484	48.17151	31.66593	104.8706	100.3271	120.0069	-1.3515	8.66E-06	3.24E-05	C21orf59	chr21	-	33964389	33985176	2503
ENSG0000(	209.23	154.1488	282.3545	231.4643	287.1748	218.6427	-0.19113	0.39974	0.53088	SYNJ1	chr21	-	34001069	34100359	7094
ENSG0000(	421.5673	454.0165	568.6673	662.9319	687.5627	585.239	-0.4232	0.007076	0.017023	PAXBP1	chr21	-	34106210	34144169	3995
ENSG0000(	112.9013	96.34302	127.9831	57.67882	45.10117	53.42772	1.0939	0.00011	0.000357	IFNAR2	chr21	+	34602206	34637980	4284
ENSG0000(	1056.508	1034.483	913.0343	1085.41	855.0813	781.6886	0.14162	0.34047	0.46923	MRPL10	chr17	-	45900638	45908900	2013
ENSG0000(	1024.398	1047.73	866.8549	337.084	341.4803	315.6345	1.5604	2.48E-28	3.54E-27	IFNGR2	chr21	+	34775202	34851655	2221
ENSG0000(	941.5348	985.1074	1113.585	2522.137	2475.962	2358.217	-1.2735	2.64E-27	3.58E-26	GART	chr21	-	34876238	34915797	3571
ENSG0000(	2865	2614.509	3716.789	2925.889	3541.822	2864.548	-0.0213	0.88262	0.92672	SON	chr21	+	34914924	34949812	8813
ENSG0000(	114.9729	130.0631	129.3026	514.6149	419.717	417.5582	-1.847	3.34E-23	3.84E-22	DONSON	chr21	-	34947783	34961014	2332

ENSG00000(	688.8016	626.2296	631.9992	218.7301	252.1984	277.0022	1.3774	1.01E-18	9.69E-18	SV2A	chr1	-	1.5E+08	1.5E+08	4416
ENSG00000(	1.035792	0	0	646.4522	651.6659	661.6818	-9.1876	3.38E-31	5.34E-30	LAD1	chr1	-	2.01E+08	2.01E+08	2906
ENSG00000(	219.5879	311.9105	344.367	352.8146	510.8398	376.4599	-0.50078	0.014175	0.031866	STC1	chr8	-	23699428	23712320	3883
ENSG00000(	0	1.204288	1.319414	11.98521	1.840864	5.753754	-2.2862	0.044061	0.087064	TNNI1	chr1	-	2.01E+08	2.01E+08	5413
ENSG00000(	16.57267	9.634302	10.55531	3286.194	3118.424	3484.309	-7.9583	4.19E-186	1.02E-183	CSRP1	chr1	-	2.01E+08	2.01E+08	8475
ENSG00000(	76.6486	65.03154	50.13772	0	0.920432	0	6.5132	3.40E-13	2.41E-12	PRAC	chr17	-	46799084	46799884	383
ENSG00000(	308.666	266.1476	259.9245	14.98151	3.681728	7.397684	4.8797	1.87E-47	4.76E-46	HOXB13	chr17	-	46802125	46806540	3467
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	KCNE2	chr21	+	35736323	35743440	803
ENSG00000(	1002.647	885.1515	800.8842	1300.395	979.3396	1282.265	-0.40413	0.006451	0.015632	ATP5G1	chr17	+	46970127	46973233	2214
ENSG00000(	3000.689	2738.55	3443.67	657.6883	425.2396	482.4934	2.5418	2.26E-58	7.57E-57	RCAN1	chr21	-	35885440	35987441	2816
ENSG00000(	2726.204	2691.583	2762.852	2373.82	2380.237	2258.76	0.22188	0.031697	0.065219	UBE2Z	chr17	+	46985731	47006418	4250
ENSG00000(	127.4024	148.1274	110.8308	7.490755	8.283888	10.68554	3.7944	6.39E-24	7.59E-23	C1orf51	chr1	+	1.5E+08	1.5E+08	1803
ENSG00000(	392.5651	502.188	368.1164	394.7628	414.1944	557.2922	-0.11283	0.53807	0.6619	SNF8	chr17	-	47006678	47022479	2319
ENSG00000(	0	4.817151	1.319414	6.74168	6.443024	6.575719	-1.404	0.17381	0.2753	CLIC6	chr21	+	36041688	36090525	3860
ENSG00000(	42.46747	16.86003	22.43003	104.1215	80.07758	110.1433	-1.7979	1.11E-06	4.58E-06	CCDC24	chr1	+	44457031	44462200	2654
ENSG00000(	714.6964	675.6054	730.9552	644.954	711.4939	607.4321	0.11138	0.40808	0.53893	RUNX1	chr21	-	36160098	37357047	7274
ENSG00000(	1045.114	1106.74	1298.303	6135.678	8978.814	7774.966	-2.7228	1.26E-78	6.67E-77	IGF2BP1	chr17	+	47074774	47133012	8274
ENSG00000(	9.322127	7.225726	3.958241	4.494453	9.20432	3.28786	0.26032	0.76034	0.84156	GIP	chr17	-	47035916	47045958	716
ENSG00000(	257.9122	232.4275	237.4945	197.7559	147.2691	187.408	0.44715	0.023569	0.050263	CBR1	chr21	+	37442239	37445464	1924
ENSG00000(	109.7939	89.11729	65.97069	83.14739	52.46462	79.7306	0.29648	0.33719	0.4657	CBR3	chr21	+	37507210	37518864	1169
ENSG00000(	71.46964	72.25726	64.65128	58.42789	34.05598	22.19305	0.83974	0.026936	0.056601	C2orf81	chr2	-	74641304	74648718	2407
ENSG00000(	0	0	0	4.494453	11.96562	4.109825	-3.5646	0.003814	0.009675	TUBBP5	chr9	+	1.41E+08	1.41E+08	1735
ENSG00000(	0	0	0	85.39461	129.7809	129.8705	-7.5198	5.82E-14	4.32E-13	GJD2	chr15	-	35043233	35047166	2889
ENSG00000(	0	2.408575	0	12614.43	9829.293	9812.617	-12.557	3.59E-83	2.03E-81	ACTC1	chr15	-	35080297	35088340	4106
ENSG00000(	413.281	408.2535	435.4065	338.5821	348.8437	281.112	0.37464	0.019932	0.04324	MORC3	chr21	+	37692487	37758446	4246
ENSG00000(	71.46964	104.773	75.20659	596.2641	515.4419	488.2472	-2.6579	3.73E-40	7.74E-39	CHAF1B	chr21	+	37757676	37789125	2292
ENSG00000(	13.46529	21.67718	13.19414	14.23244	3.681728	10.68554	0.69605	0.29477	0.41908	SIM2	chr21	+	38071433	38122218	4442
ENSG00000(	294.1649	307.0934	390.5465	194.7596	223.665	170.1467	0.74813	0.000106	0.000345	HLCS	chr21	-	38123493	38362536	6466
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	SCUBE1	chr22	-	43599229	43739394	3868
ENSG00000(	30.03797	14.45145	29.0271	331.0914	388.4223	414.2703	-3.9018	1.08E-47	2.78E-46	ARHGAP27	chr17	-	43471275	43511787	4754
ENSG00000(	1274.024	1230.782	1005.393	1204.513	991.3053	1077.596	0.10088	0.46473	0.59381	ADPGK	chr15	-	73043710	73078187	4576
ENSG00000(	15400.15	14567.06	11556.75	4757.379	3882.382	4759.177	1.6279	9.35E-35	1.66E-33	PTMS	chr12	+	6874682	6880116	1139
ENSG00000(	0	0	0	4.494453	0	1.64393	-1.6577	0.22164	0.3333	PADI4	chr1	+	17634690	17690499	2267
ENSG00000(	999.5392	997.1502	1034.42	1612.76	1418.386	1300.349	-0.51438	4.74E-05	0.000162	ADIPOR1	chr1	-	2.03E+08	2.03E+08	2177
ENSG00000(	764.4144	770.7441	765.26	352.8146	388.4223	385.5015	1.0279	4.45E-14	3.33E-13	CYB5R1	chr1	-	2.03E+08	2.03E+08	3033
ENSG00000(	2532.511	2321.867	2002.87	2937.125	2722.638	2993.596	-0.33444	0.005587	0.013714	PSMD4	chr1	+	1.51E+08	1.51E+08	1350
ENSG00000(	462.999	478.1022	401.1018	2777.572	2608.504	2368.081	-2.5233	1.40E-85	8.20E-84	ATP13A2	chr1	-	17312453	17338423	3981
ENSG00000(	18.64425	9.634302	2.638828	12.73428	11.96562	7.397684	-0.03051	0.96699	0.98061	M1AP	chr2	-	74785010	74875465	2543
ENSG00000(	4014.729	3970.537	3153.399	3967.104	3428.609	3547.601	0.02568	0.83776	0.89628	PSMB4	chr1	+	1.51E+08	1.51E+08	2067
ENSG00000(	0	0	0	71.91125	85.60018	84.66239	-7.0748	2.79E-12	1.85E-11	IRX6	chr16	+	55357672	55364672	3128
ENSG00000(	791.345	764.7227	891.9237	800.7618	1008.793	910.7371	-0.15166	0.27511	0.39649	BTG2	chr1	+	2.03E+08	2.03E+08	2712
ENSG00000(	1177.695	1264.502	1415.731	884.6582	1096.235	825.2528	0.45804	0.001306	0.003596	HK2	chr2	+	75061108	75120486	5772
ENSG00000(	336.6324	408.2535	281.0351	4.494453	2.761296	5.753754	6.1398	4.09E-53	1.21E-51	C1R	chr12	-	7187513	7245203	2112
ENSG00000(	2.071584	2.408575	3.958241	3.745378	0	0	0.77919	0.53457	0.65901	CELF3	chr1	-	1.52E+08	1.52E+08	3246

ENSG00000(	131.5456	126.4502	100.2754	455.4379	377.3771	438.1073	-1.8138	2.29E-21	2.46E-20	ALDH4A1	chr1	-	19197926	19229275	3363
ENSG00000(	748.8775	908.0329	936.7838	88.39091	115.9744	115.8971	3.0082	1.60E-67	6.64E-66	STARD9	chr15	+	42867857	43013179	15567
ENSG00000(	122.2234	166.1917	138.5384	161.0512	145.4283	165.2149	-0.14553	0.51158	0.63875	THEM4	chr1	-	1.52E+08	1.52E+08	2406
ENSG00000(	0	0	0	62.17327	104.0088	100.2797	-7.1831	1.27E-12	8.67E-12	TCHH	chr1	-	1.52E+08	1.52E+08	6900
ENSG00000(	505.4664	573.241	734.9135	484.6519	533.8506	364.1305	0.38846	0.033729	0.068866	UBR1	chr15	-	43235095	43398311	7761
ENSG00000(	1080.331	1123.6	1054.212	747.5774	730.823	761.9615	0.53922	7.69E-06	2.89E-05	AMFR	chr16	-	56395364	56459450	3600
ENSG00000(	573.8287	509.4137	476.3084	567.0502	432.603	578.6633	-0.01703	0.9161	0.94881	MED8	chr1	-	43849588	43855479	1924
ENSG00000(	45.57484	37.33292	34.30476	1.498151	14.72691	27.94681	1.3424	0.026522	0.055839	RGL4	chr22	+	24030323	24041363	3779
ENSG00000(	19.68005	16.86003	34.30476	2.996302	3.681728	6.575719	2.2587	0.000672	0.001936	ISL2	chr15	+	76629065	76634817	1881
ENSG00000(	904.2463	843.0014	891.9237	863.6841	824.7071	688.8066	0.15045	0.26831	0.38862	RSPRY1	chr16	+	57220049	57274387	3586
ENSG00000(	18.64425	16.86003	7.916483	26.21764	19.32907	12.32947	-0.386	0.5112	0.63835	CCDC17	chr1	-	46085716	46089729	2988
ENSG00000(	840.0272	891.1729	1034.42	1218.746	1123.847	1039.786	-0.29108	0.029489	0.061235	GPBP1L1	chr1	-	46092976	46153785	3736
ENSG00000(	418.4599	509.4137	472.3501	1748.342	1296.889	1375.969	-1.6553	5.38E-28	7.53E-27	NAE1	chr16	-	66836778	66907159	1909
ENSG00000(	311.7734	401.0278	362.8388	1176.049	813.6619	826.0747	-1.3847	1.96E-15	1.58E-14	TMEM69	chr1	+	46152886	46160115	2439
ENSG00000(	0	0	0	32.95932	50.62376	41.92021	-6.2021	3.26E-09	1.71E-08	GPR114	chr16	+	57576333	57625593	4768
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	CCDC135	chr16	+	57728705	57765717	3041
ENSG00000(	11.39371	15.65574	15.83297	11.98521	11.04518	25.48091	-0.17461	0.77296	0.85085	ACE	chr17	+	61554422	61599205	4858
ENSG00000(	5.17896	2.408575	5.277655	0.749076	5.522592	8.219649	-0.13684	0.88977	0.93161	TEPP	chr16	+	58010339	58022020	2360
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	UROC1	chr3	-	1.26E+08	1.26E+08	3149
ENSG00000(	1038.899	955.0002	1302.261	832.2229	917.6707	752.9199	0.39558	0.007554	0.018061	EFCAB14	chr1	-	47124366	47184824	5767
ENSG00000(	382.2072	375.7378	290.271	2.996302	2.761296	7.397684	6.1699	2.98E-54	9.03E-53	SPON2	chr4	-	1160720	1202750	1869
ENSG00000(	208.1942	179.4389	160.9685	179.0291	164.7573	189.8739	0.042003	0.83759	0.89625	CHCHD6	chr3	+	1.26E+08	1.27E+08	1159
ENSG00000(	2716.882	2463.973	2348.557	3066.715	2968.393	3212.239	-0.29561	0.007377	0.017675	CTBP1	chr4	-	1205236	1243741	4250
ENSG00000(	1.035792	2.408575	6.597069	14.98151	26.69253	28.76877	-2.623	0.000376	0.001127	ANKRD18C	chr9	-	99918852	99983517	2980
ENSG00000(	11.39371	12.04288	18.47179	0	3.681728	2.465895	2.474	0.004244	0.010671	TPPP3	chr16	-	67423712	67427438	1736
ENSG00000(	326.2744	323.9534	290.271	52.43529	33.13555	26.30288	3.0361	1.74E-33	2.98E-32	ZDHHC1	chr16	-	67428322	67450736	2047
ENSG00000(	2235.239	1817.27	2103.146	2050.969	1612.597	1727.77	0.19061	0.15049	0.24464	ATP6V0D1	chr16	-	67471917	67515140	3390
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AGRP	chr16	-	67516474	67517716	764
ENSG00000(	249.6258	258.9219	182.0791	6.74168	19.32907	19.72716	3.8785	1.38E-32	2.29E-31	ZFYVE28	chr4	-	2271309	2420390	4131
ENSG00000(	97.36444	101.1602	67.2901	137.8299	103.0884	143.8439	-0.52598	0.049238	0.095793	RLTPR	chr16	+	67678822	67691472	4687
ENSG00000(	14.50109	3.612863	5.277655	6.74168	11.96562	10.68554	-0.27767	0.71825	0.81024	C16orf86	chr16	+	67700719	67702661	1719
ENSG00000(	261.0196	311.9105	259.9245	29.21395	25.7721	42.74218	3.0609	1.26E-33	2.15E-32	FAM131B	chr7	-	1.43E+08	1.43E+08	5856
ENSG00000(	855.5641	750.2712	715.1223	554.3159	681.1197	586.883	0.35001	0.01512	0.033728	RGS12	chr4	+	3294755	3441640	6240
ENSG00000(	1160.087	1122.396	1008.032	663.6809	698.6079	742.2343	0.64429	4.88E-07	2.09E-06	PSKH1	chr16	+	67927175	67963581	3481
ENSG00000(	8724.475	7579.787	7552.324	8672.797	7383.705	7785.652	0.000927	0.99344	0.99585	ZYX	chr7	+	1.43E+08	1.43E+08	2493
ENSG00000(	1751.524	1536.671	1790.445	697.3893	821.0253	782.5106	1.1404	3.11E-19	3.05E-18	ABR	chr17	-	906758	1132315	5595
ENSG00000(	9.322127	24.08575	9.235896	2.247227	0	2.465895	2.7438	0.002054	0.005463	FAM115D	chr7	+	1.43E+08	1.44E+08	2600
ENSG00000(	2.071584	0	0	14.23244	8.283888	8.219649	-3.0053	0.004409	0.011039	LYPD5	chr19	-	44300081	44331358	2499
ENSG00000(	453.6769	401.0278	461.7948	703.3819	606.5647	544.9627	-0.4936	0.001378	0.003779	CCDC117	chr22	+	29168662	29185283	3985
ENSG00000(	64.2191	104.773	76.526	45.69361	60.74851	50.96182	0.63304	0.04681	0.091639	ZNF230	chr19	+	44507100	44518078	4115
ENSG00000(	47.64643	39.74149	40.90183	7.490755	28.53339	44.38611	0.65621	0.19419	0.30032	CCDC107	chr9	+	35658301	35661508	1324
ENSG00000(	41.43168	45.76293	31.66593	31.46117	29.45382	36.16646	0.28778	0.46822	0.59747	ZNF222	chr19	+	44529494	44537265	1598
ENSG00000(	384.2788	334.792	444.6424	111.6123	126.0992	119.1849	1.6973	4.24E-19	4.12E-18	NPR2	chr9	+	35792151	35809729	3686
ENSG00000(	0	2.408575	0	0	4.60216	4.109825	-1.1569	0.37574	0.50624	ZNF890P	chr7	-	5160870	5184177	1352

ENSG0000(	154.333	126.4502	113.4696	26.21764	40.49901	29.59074	2.0179	2.82E-11	1.73E-10	ZNF221	chr19	+	44455375	44471861	2535
ENSG0000(	32.10955	31.31148	29.0271	19.47596	29.45382	23.01502	0.35769	0.4234	0.55387	ZNF233	chr19	+	44754318	44779470	2938
ENSG0000(	64.2191	72.25726	64.65128	58.42789	80.99802	69.86702	-0.05409	0.85748	0.90943	ZNF235	chr19	-	44732882	44809199	4219
ENSG0000(	650.4773	606.961	687.4146	242.7005	235.6306	202.2034	1.5095	2.17E-22	2.42E-21	GNE	chr9	-	36214438	36277053	5298
ENSG0000(	0	3.612863	0	6.74168	1.840864	11.50751	-1.9172	0.088778	0.15894	TNFRSF13C	chr22	-	42321045	42322822	926
ENSG0000(	4277.821	3824.818	4310.525	1847.22	3267.534	3144.016	0.58587	0.000624	0.001806	ARHGAP35	chr19	+	47421933	47508334	8889
ENSG0000(	23.82321	2.408575	3.958241	3.745378	0	0	2.3771	0.027068	0.056856	PTGIR	chr19	-	47123725	47128375	2107
ENSG0000(	8977.208	8849.106	7717.251	10942.5	9832.975	10205.52	-0.2779	0.009926	0.023104	CALM3	chr19	+	47104331	47114050	2536
ENSG0000(	1214.984	1301.835	1166.362	2263.706	1868.477	2064.776	-0.74931	8.27E-10	4.56E-09	DFFA	chr1	-	10516579	10532583	6032
ENSG0000(	176.0846	162.5788	172.8432	37.45378	50.62376	57.53754	1.7997	5.24E-12	3.41E-11	CCDC28B	chr1	+	32665987	32670988	1415
ENSG0000(	37.28851	48.17151	47.4989	55.43159	53.38506	85.48435	-0.54244	0.12137	0.20579	IQCC	chr1	+	32671236	32674288	2293
ENSG0000(	119.1161	158.966	133.2608	109.365	108.611	139.734	0.19814	0.40943	0.54018	TMEM234	chr1	-	32680073	32687972	2736
ENSG0000(	772.7008	669.584	773.1765	1012.75	1042.849	1052.937	-0.48732	0.000125	0.000401	BSDC1	chr1	-	32830704	32860332	4599
ENSG0000(	10.35792	7.225726	5.277655	8.988907	10.12475	4.109825	-0.00892	0.99093	0.99468	ZBTB8A	chr1	+	33005028	33066591	1943
ENSG0000(	1083.438	1047.73	844.4248	3110.911	2862.544	3453.075	-1.6585	3.40E-36	6.30E-35	ATAD3B	chr1	+	1407143	1433228	4314
ENSG0000(	2105.765	1808.84	1666.42	3113.907	2394.964	2622.068	-0.54118	6.52E-05	0.000218	SSU72	chr1	-	1477053	1510249	2679
ENSG0000(	1059.615	1003.172	963.1721	1465.192	1438.635	1672.699	-0.59514	1.23E-06	5.06E-06	UBE2J2	chr1	-	1189289	1209265	2455
ENSG0000(	274.4849	222.7932	240.1333	184.2726	341.4803	258.097	-0.08368	0.708	0.80261	ZNF362	chr1	+	33722146	33766320	3106
ENSG0000(	26.93059	31.31148	36.94359	11.23613	14.72691	16.4393	1.1265	0.021723	0.046705	FNDC5	chr1	-	33327869	33338083	2732
ENSG0000(	47.64643	63.82725	40.90183	20.22504	33.13555	13.9734	1.1556	0.007607	0.018174	CPAMD8	chr19	-	17003758	17137625	5992
ENSG0000(	479.5717	481.7151	339.0893	2096.662	1723.969	1822.296	-2.1084	3.11E-43	7.09E-42	NR2F6	chr19	-	17342692	17356749	2404
ENSG0000(	18.64425	24.08575	15.83297	70.4131	33.13555	47.67397	-1.333	0.002881	0.007462	ANKLE1	chr19	+	17392454	17398455	3218
ENSG0000(	244.4469	291.4376	273.1187	495.1389	497.0333	607.4321	-0.98138	2.78E-09	1.47E-08	CCDC58	chr3	-	1.22E+08	1.22E+08	769
ENSG0000(	746.806	768.3356	796.9259	1315.377	1231.538	1034.032	-0.63017	2.71E-06	1.07E-05	VMA21	chrX	+	1.51E+08	1.51E+08	4717
ENSG0000(	392.5651	485.328	410.3377	606.7512	771.322	691.2725	-0.68127	1.19E-05	4.38E-05	KALRN	chr3	+	1.24E+08	1.24E+08	10806
ENSG0000(	48.68222	32.51577	47.4989	24.71949	14.72691	24.65895	0.97381	0.025118	0.053184	CILP2	chr19	+	19649057	19657468	4234
ENSG0000(	59.04014	49.3758	47.4989	80.15108	69.95283	87.95025	-0.59978	0.051064	0.098895	FAM86C2P	chr11	-	67559119	67572807	2496
ENSG0000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	ABCG1	chr21	+	43619799	43717354	3475
ENSG0000(	13.46529	9.634302	5.277655	2.996302	0	4.109825	1.7083	0.067635	0.12607	RSPH1	chr21	-	43892596	43916464	2880
ENSG0000(	126.3666	103.5687	150.4132	145.3207	177.6434	199.7375	-0.45607	0.052183	0.1008	SLC37A1	chr21	+	43916128	44001550	3664
ENSG0000(	25.8948	8.430014	27.70769	29.96302	22.09037	27.12484	-0.34025	0.51416	0.64099	PDE9A	chr21	+	44073746	44195619	3412
ENSG0000(	226.8384	192.686	277.0769	522.8547	532.9301	521.9477	-1.177	5.41E-12	3.52E-11	WDR4	chr21	-	44263204	44299678	2205
ENSG0000(	503.3949	437.1564	409.0183	607.5003	481.3859	583.5951	-0.30767	0.051265	0.099252	NDUFV3	chr21	+	44299754	44329783	2029
ENSG0000(	486.8222	485.328	517.2102	414.9879	450.0912	408.5166	0.22521	0.11879	0.20212	PKNOX1	chr21	+	44394620	44454172	5483
ENSG0000(	1630.336	1558.348	1162.404	4300.443	4111.57	4925.214	-1.6108	9.60E-31	1.49E-29	CBS	chr21	-	44473301	44497053	2656
ENSG0000(	1999.078	1907.592	1728.432	3080.948	3319.078	3830.357	-0.85807	2.59E-12	1.72E-11	U2AF1	chr21	-	44513066	44527697	4694
ENSG0000(	12.4295	13.24716	5.277655	11.23613	20.2495	17.26126	-0.60141	0.34817	0.47784	HSF2BP	chr21	-	44949072	45079374	1899
ENSG0000(	819.3114	745.4541	1021.226	1656.955	1578.541	1338.159	-0.8213	2.15E-08	1.05E-07	RRP1B	chr21	+	45079429	45115958	5088
ENSG0000(	2513.867	2425.435	2208.699	1865.947	1810.49	1868.326	0.36614	0.000878	0.002486	PDXK	chr21	+	45138975	45182188	7366
ENSG0000(	3143.628	2763.84	2679.729	2257.714	1906.215	1836.27	0.51614	3.38E-05	0.000117	G6PD	chrX	-	1.54E+08	1.54E+08	2631
ENSG0000(	1671.768	1470.435	1369.552	2279.437	1943.952	2441.236	-0.56104	1.75E-05	6.30E-05	CSTB	chr21	-	45192393	45196326	2163
ENSG0000(	772.7008	734.6155	709.8446	1344.591	1260.992	1369.394	-0.84004	4.13E-12	2.71E-11	RRP1	chr21	+	45209394	45225174	3022
ENSG0000(	211.3015	211.9546	281.0351	464.4268	586.3152	448.7928	-1.0874	2.83E-09	1.49E-08	AGPAT3	chr21	+	45285067	45406417	5767
ENSG0000(	593.5088	538.3166	716.4417	898.8907	973.8171	798.9499	-0.5308	0.000387	0.001157	TRAPPC10	chr21	+	45432200	45526433	6976

ENSG00000(	44.53905	55.39724	48.81831	10.48706	11.04518	7.397684	2.2916	7.55E-07	3.17E-06	GAB3	chrX	-	1.54E+08	1.54E+08	4718
ENSG00000(	1328.921	1471.64	1114.905	944.5843	956.3288	1105.543	0.38063	0.006161	0.014991	C21orf33	chr21	+	45553487	45565605	1674
ENSG00000(	106.6866	69.84869	87.08131	360.3053	472.1816	457.8345	-2.2709	1.08E-26	1.42E-25	ICOSLG	chr21	-	45642874	45660849	7080
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AIRE	chr21	+	45705721	45718531	4306
ENSG00000(	88.04231	90.32158	56.73479	66.66772	67.19154	86.30632	0.097862	0.74671	0.83155	C21orf2	chr21	-	45748827	45759285	4532
ENSG00000(	23.82321	13.24716	23.74945	73.4094	110.4518	81.37453	-2.0776	4.42E-08	2.10E-07	ZNF66	chr19	+	20959110	20991922	1745
ENSG00000(	152.2614	155.3531	158.3297	47.19176	69.95283	77.2647	1.2527	1.73E-06	6.99E-06	LRRC3	chr21	+	45875369	45878739	2529
ENSG00000(	11.39371	2.408575	18.47179	2.247227	6.443024	4.109825	1.1926	0.16175	0.2594	ITGB2	chr21	-	46305868	46351904	4781
ENSG00000(	646.3341	637.0682	504.0161	632.2198	782.3672	1044.717	-0.45695	0.011755	0.02688	FAM207A	chr21	+	46359925	46396904	927
ENSG00000(	673.2647	699.6912	717.7611	635.2161	564.2248	502.2206	0.29527	0.038299	0.077084	RALGDS	chr9	-	1.36E+08	1.36E+08	5817
ENSG00000(	61.11172	42.15007	31.66593	8.988907	7.363456	9.041614	2.3265	3.36E-06	1.31E-05	FTCD	chr21	-	47556176	47575481	1955
ENSG00000(	783.0587	780.3784	580.5421	392.5156	287.1748	257.275	1.188	1.48E-10	8.67E-10	SPATC1L	chr21	-	47581062	47604390	2303
ENSG00000(	5844.974	5467.466	5777.713	3302.674	3871.337	3896.114	0.62567	1.41E-08	7.00E-08	LSS	chr21	-	47608055	47648738	4936
ENSG00000(	640.1194	662.3582	716.4417	809.7507	1258.231	1104.721	-0.64948	6.41E-05	0.000214	VAV2	chr9	-	1.37E+08	1.37E+08	5101
ENSG00000(	1031.649	1097.106	1352.399	620.2346	1083.348	822.7869	0.4609	0.010998	0.025336	MCM3AP	chr21	-	47655047	47706211	6333
ENSG00000(	182.2994	184.256	137.219	577.5372	505.3172	667.4355	-1.7853	1.55E-22	1.74E-21	C21orf58	chr21	-	47720095	47743789	2975
ENSG00000(	988.1455	946.5701	1046.295	1050.953	1531.599	1329.939	-0.39059	0.008246	0.019525	PCNT	chr21	+	47744036	47865682	10560
ENSG00000(	915.64	979.0859	898.5208	692.1458	893.7395	743.0563	0.26264	0.058628	0.1115	DIP2A	chr21	+	47878812	47989926	7293
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	S100B	chr21	-	48018875	48025121	971
ENSG00000(	2689.952	2687.97	2744.381	2048.722	1763.548	2035.185	0.47286	2.43E-05	8.58E-05	PRMT2	chr21	+	48055079	48085036	4031
ENSG00000(	5.17896	8.430014	5.277655	12.73428	11.04518	24.65895	-1.2631	0.072303	0.1334	CLDND2	chr19	-	51870352	51872257	974
ENSG00000(	79.75598	87.913	73.88717	18.72689	23.93123	32.05663	1.6668	2.52E-06	1.00E-05	ADAMTS13	chr9	+	1.36E+08	1.36E+08	4934
ENSG00000(	529.2897	464.8551	469.7113	333.3386	331.3555	369.0622	0.50127	0.001004	0.002814	CACFD1	chr9	+	1.36E+08	1.36E+08	2794
ENSG00000(	255.8406	214.3632	230.8974	258.4311	175.8025	202.2034	0.1375	0.50075	0.62891	SLC2A6	chr9	-	1.36E+08	1.36E+08	3417
ENSG00000(	279.6638	293.8462	283.674	376.785	460.216	446.327	-0.57934	0.000376	0.001128	ZNF761	chr19	+	53935227	53961515	4206
ENSG00000(	107.7224	87.913	117.4278	71.91125	57.98722	85.48435	0.53093	0.058098	0.11068	C9orf116	chr9	-	1.38E+08	1.38E+08	1278
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	LCN1	chr9	+	1.38E+08	1.38E+08	776
ENSG00000(	114.9729	99.95588	155.6908	609.7475	683.881	586.883	-2.3369	6.71E-36	1.24E-34	ZNF714	chr19	+	21264965	21308073	6809
ENSG00000(	4892.045	4825.581	3885.674	584.2789	689.4036	798.1279	2.7084	2.96E-82	1.66E-80	GPSM1	chr9	+	1.39E+08	1.39E+08	3633
ENSG00000(	275.5206	303.4805	269.1604	912.374	866.1265	1029.1	-1.722	4.97E-32	8.04E-31	C19orf47	chr19	-	40825443	40854434	3628
ENSG00000(	12.4295	30.10719	10.55531	2.247227	5.522592	0	2.5006	0.002615	0.006827	HIPK4	chr19	-	40885178	40896094	2452
ENSG00000(	39.36009	63.82725	58.05421	37.45378	29.45382	50.96182	0.43625	0.24811	0.36508	C9orf117	chr9	+	1.3E+08	1.3E+08	2708
ENSG00000(	180.2278	181.8474	141.1773	386.523	276.1296	309.0588	-0.94276	3.21E-06	1.26E-05	TOR2A	chr9	-	1.3E+08	1.3E+08	3496
ENSG00000(	1716.307	1783.55	1537.117	67.4168	90.20234	119.1849	4.1719	1.51E-125	1.68E-123	ST6GALNAC	chr9	-	1.31E+08	1.31E+08	2460
ENSG00000(	1195.304	1082.655	1039.698	650.1976	599.2012	484.1373	0.93405	1.25E-10	7.34E-10	SHKBP1	chr19	+	41082757	41097305	2363
ENSG00000(	186.4425	150.536	157.0102	326.5969	276.1296	337.8276	-0.9225	1.43E-06	5.84E-06	RDH13	chr19	-	55550476	55582659	3022
ENSG00000(	679.4795	751.4755	651.7904	650.1976	574.3496	588.5269	0.19909	0.14724	0.24027	ZER1	chr9	-	1.31E+08	1.32E+08	4259
ENSG00000(	201.9794	203.5246	154.3714	867.4295	653.5067	729.9048	-1.9962	3.94E-30	6.01E-29	ZDHHC12	chr9	-	1.31E+08	1.31E+08	2536
ENSG00000(	69.39806	27.69862	38.263	556.5631	613.0077	670.7234	-3.714	8.00E-54	2.40E-52	PKN3	chr9	+	1.31E+08	1.31E+08	3375
ENSG00000(	25.8948	3.612863	14.51355	0	0.920432	1.64393	3.4558	0.000398	0.001187	SPTBN4	chr19	+	40972148	41082370	8676
ENSG00000(	280.6996	303.4805	183.3985	166.2948	205.2563	190.6959	0.45012	0.038619	0.077615	BRSK1	chr19	+	55793440	55823901	3079
ENSG00000(	10.35792	4.817151	1.319414	0.749076	0.920432	3.28786	1.404	0.19319	0.29904	COX6B2	chr19	-	55860674	55866182	2083
ENSG00000(	3.107376	0	0	0.749076	0	0.821965	0.47233	0.72731	NA	TMEM190	chr19	+	55888204	55889612	593
ENSG00000(	7.250543	7.225726	3.958241	3.745378	4.60216	0.821965	0.86931	0.36513	0.49491	PPAPDC3	chr9	+	1.34E+08	1.34E+08	2095

ENSG00000(	1356.887	1439.124	2235.087	1125.861	1454.283	1085.816	0.45423	0.011313	0.025993	TAOK1	chr17	+	27717482	27878922	12407
ENSG00000(	138.7961	128.8588	130.622	468.9213	285.3339	283.5779	-1.3728	1.56E-09	8.38E-09	MED27	chr9	-	1.35E+08	1.35E+08	1431
ENSG00000(	296.2365	375.7378	298.1875	344.5748	313.8673	372.3501	-0.08805	0.60982	0.7236	DEDD2	chr19	-	42702750	42724292	1894
ENSG00000(	1052.365	1028.462	1174.278	462.1796	582.6335	424.9559	1.1446	1.84E-14	1.40E-13	SIK3	chr11	-	1.17E+08	1.17E+08	6331
ENSG00000(	6.214751	7.225726	5.277655	67.4168	83.75931	69.04505	-3.4312	1.56E-12	1.05E-11	MPZL3	chr11	-	1.18E+08	1.18E+08	3964
ENSG00000(	79.75598	97.54731	77.84541	101.8743	82.83888	112.6092	-0.2203	0.41524	0.54575	NEK8	chr17	+	27052915	27070473	3581
ENSG00000(	42.46747	20.47289	62.01245	156.5568	117.8153	130.6924	-1.6778	5.31E-07	2.27E-06	TLCD1	chr17	-	27051366	27054953	1017
ENSG00000(	1381.746	1380.114	1477.743	1465.941	1638.369	1775.444	-0.20253	0.094754	0.16767	PCSK7	chr11	-	1.17E+08	1.17E+08	9347
ENSG00000(	1991.828	1777.529	1608.365	3079.45	3146.037	3455.541	-0.84572	1.85E-12	1.24E-11	SAFB	chr19	+	5623046	5668489	3471
ENSG00000(	8.286335	18.06432	3.958241	5.992604	19.32907	23.83698	-0.63839	0.36671	0.49676	S100A1	chr1	+	1.54E+08	1.54E+08	2619
ENSG00000(	813.0966	704.5083	825.953	902.636	975.6579	1232.125	-0.40705	0.006323	0.015353	CHTOP	chr1	+	1.54E+08	1.54E+08	2553
ENSG00000(	877.3157	875.5172	730.9552	795.5182	856.9222	1087.46	-0.14023	0.356	0.48557	ZBTB7B	chr1	+	1.55E+08	1.55E+08	3594
ENSG00000(	459.8916	466.0593	409.0183	949.8278	830.2297	1012.661	-1.0614	8.26E-14	6.06E-13	FLAD1	chr1	+	1.55E+08	1.55E+08	2656
ENSG00000(	7583.033	7416.004	8411.263	2383.558	2669.253	2540.694	1.6219	2.70E-51	7.69E-50	SHC1	chr1	-	1.55E+08	1.55E+08	3481
ENSG00000(	804.8103	698.4869	697.9699	557.3122	487.829	511.2622	0.49906	0.000363	0.001092	VPS11	chr11	+	1.19E+08	1.19E+08	3387
ENSG00000(	66.29068	67.44011	88.40072	229.9662	239.3123	194.8057	-1.5732	2.01E-11	1.25E-10	NLRX1	chr11	+	1.19E+08	1.19E+08	4092
ENSG00000(	3082.517	2972.182	3736.58	3050.985	3533.538	3100.452	0.015553	0.90053	0.93815	ADAR	chr1	-	1.55E+08	1.55E+08	6620
ENSG00000(	113.9371	118.0202	108.1919	61.42419	66.2711	34.52253	1.0567	0.000463	0.001367	IL6R	chr1	+	1.54E+08	1.54E+08	5914
ENSG00000(	1108.297	1172.976	1121.502	1277.174	968.2945	1058.691	0.041459	0.75924	0.84088	UBE2Q1	chr1	-	1.55E+08	1.55E+08	3210
ENSG00000(	6.214751	2.408575	1.319414	7.490755	16.56778	15.61733	-1.7486	0.034494	0.070235	CHRNB2	chr1	+	1.55E+08	1.55E+08	5867
ENSG00000(	630.7973	698.4869	552.8344	868.1786	804.4576	945.2597	-0.4743	0.000824	0.002344	CRTC2	chr1	-	1.54E+08	1.54E+08	2644
ENSG00000(	1016.112	906.8287	1023.865	761.0608	568.827	526.8795	0.66309	2.30E-05	8.15E-05	ANO10	chr3	-	43396351	43733086	3212
ENSG00000(	134.6529	190.2775	163.6073	124.3465	144.5078	189.8739	0.088683	0.70968	0.80385	FDPS	chr1	+	1.55E+08	1.55E+08	2017
ENSG00000(	731.2691	773.1527	704.567	819.4887	632.3368	738.1245	0.011609	0.93483	0.96073	RUSC1	chr1	+	1.55E+08	1.55E+08	3403
ENSG00000(	217.5163	256.5133	187.3568	148.317	171.2004	178.3664	0.40935	0.046901	0.091793	GBAP1	chr1	-	1.55E+08	1.55E+08	2918
ENSG00000(	1818.851	1633.014	1579.338	1209.757	1000.51	1072.664	0.6145	1.11E-06	4.59E-06	FAM189B	chr1	-	1.55E+08	1.55E+08	3082
ENSG00000(	45.57484	42.15007	27.70769	29.96302	45.10117	32.8786	0.10462	0.79622	0.86697	PAQR6	chr1	-	1.56E+08	1.56E+08	2117
ENSG00000(	168.8341	175.826	129.3026	309.3682	226.4263	230.1502	-0.68697	0.001389	0.003806	PMF1	chr1	+	1.56E+08	1.56E+08	1068
ENSG00000(	411.2094	494.9623	521.1684	548.3233	523.7258	388.7894	-0.03497	0.83952	0.89731	SLC25A44	chr1	+	1.56E+08	1.56E+08	6952
ENSG00000(	25624.46	23548.64	21313.81	10272.07	11147.35	11499.29	1.0968	9.53E-24	1.12E-22	LMNA	chr1	+	1.56E+08	1.56E+08	3190
ENSG00000(	0	0	0	6.74168	6.443024	13.15144	-3.9643	0.000899	0.002539	CCR5	chr3	+	46411633	46417697	3637
ENSG00000(	117.0445	90.32158	76.526	851.6989	1008.793	1048.827	-3.3313	1.45E-74	6.87E-73	NBEAL2	chr3	+	47021173	47051193	8827
ENSG00000(	462.999	470.8765	341.7282	448.6963	498.8741	653.4621	-0.32444	0.077006	0.14065	CCDC12	chr3	-	46963216	47023500	2412
ENSG00000(	696.0522	820.1199	580.5421	547.5742	551.3388	621.4055	0.28521	0.067114	0.12518	PTH1R	chr3	+	46919236	46945287	2123
ENSG00000(	1029.577	871.9043	895.882	1166.311	1449.68	1389.943	-0.51545	0.000137	0.00044	UBQLN4	chr1	-	1.56E+08	1.56E+08	3576
ENSG00000(	29.00217	48.17151	30.34652	23.97042	31.29469	35.34449	0.24129	0.57182	0.69062	MYL3	chr3	-	46899362	46923659	1012
ENSG00000(	59.04014	55.39724	39.58241	142.3244	136.2239	126.5826	-1.3736	6.77E-07	2.86E-06	PPP1R35	chr7	-	1E+08	1E+08	1031
ENSG00000(	508.5738	580.4667	534.3626	895.8944	1032.725	1177.054	-0.93339	1.23E-10	7.25E-10	GPATCH4	chr1	-	1.57E+08	1.57E+08	2464
ENSG00000(	186.4425	181.8474	106.8725	327.346	231.9489	359.1987	-0.94006	7.66E-05	0.000253	AC004166.	chr7	-	74112305	74306731	1340
ENSG00000(	7.250543	9.634302	6.597069	2.996302	2.761296	2.465895	1.3233	0.13974	0.23044	LRRC71	chr1	+	1.57E+08	1.57E+08	1959
ENSG00000(	23.82321	18.06432	27.70769	149.066	104.9292	103.5676	-2.3278	9.66E-12	6.15E-11	FGFR4	chr5	+	1.77E+08	1.77E+08	3122
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CYP3A4	chr7	-	99354604	99381888	2318
ENSG00000(	2.071584	2.408575	5.277655	5.243529	6.443024	1.64393	-0.3854	0.70405	0.79928	CYP3A7	chr7	-	99302660	99332819	2314
ENSG00000(	2856.714	2805.99	2695.562	3329.641	4153.91	4644.102	-0.53551	4.16E-05	0.000143	NACC1	chr19	+	13228917	13251955	4445

ENSG00000(	2.071584	0	0	1.498151	0	2.465895	-0.46898	0.72919	0.81854	HK3	chr5	-	1.76E+08	1.76E+08	3066
ENSG00000(	46.61064	74.66584	60.69303	90.63814	123.3379	146.3098	-0.97628	0.001104	0.003073	LY6K	chr8	+	1.44E+08	1.44E+08	2724
ENSG00000(	319.0239	396.2107	347.0058	447.1981	479.5451	578.6633	-0.50191	0.002549	0.006665	IER2	chr19	+	13261229	13265722	2934
ENSG00000(	241.3395	311.9105	204.5091	238.206	260.4823	287.6877	-0.05191	0.79393	0.86525	ZNF394	chr7	-	99084142	99097947	2179
ENSG00000(	562.435	566.0152	552.8344	888.4036	783.2876	984.714	-0.65852	2.11E-06	8.45E-06	CPSF4	chr7	+	99036545	99054994	1738
ENSG00000(	3560.017	3422.586	2495.011	4006.805	3335.646	4158.321	-0.27802	0.054917	0.10548	LY6E	chr8	+	1.44E+08	1.44E+08	1419
ENSG00000(	1572.332	1375.297	1046.295	937.0935	600.1217	689.6286	0.83891	2.98E-06	1.17E-05	VPS28	chr8	-	1.46E+08	1.46E+08	2337
ENSG00000(	358.384	372.1249	298.1875	1226.986	1334.626	1486.113	-1.9687	2.10E-42	4.67E-41	TONSL	chr8	-	1.46E+08	1.46E+08	6600
ENSG00000(	21.75163	9.634302	14.51355	0	1.840864	1.64393	3.2655	0.000292	0.000888	PTGER1	chr19	-	14583278	14586174	1421
ENSG00000(	990.2171	887.56	944.7003	642.7068	793.4124	873.7487	0.28923	0.045599	0.089631	MUM1	chr19	+	1285890	1378430	4170
ENSG00000(	334.5608	309.5019	229.578	871.1749	812.7415	1080.884	-1.652	1.28E-21	1.39E-20	RECQL4	chr8	-	1.46E+08	1.46E+08	3897
ENSG00000(	364.5988	363.6949	407.6989	405.9989	407.7514	470.1639	-0.17711	0.25504	0.37322	LRRC14	chr8	+	1.46E+08	1.46E+08	5323
ENSG00000(	268.2701	279.3948	340.4088	110.1141	141.7465	131.5144	1.2058	2.30E-09	1.22E-08	ZNF333	chr19	+	14800613	14844558	4672
ENSG00000(	71.46964	63.82725	67.2901	1391.033	1564.734	1895.451	-4.5585	1.84E-138	2.45E-136	COL26A1	chr7	+	1.01E+08	1.01E+08	3032
ENSG00000(	222.6953	225.2018	134.5802	283.1506	218.1424	234.26	-0.33169	0.13868	0.22905	PPP1R16A	chr8	+	1.46E+08	1.46E+08	4311
ENSG00000(	0	0	0	0.749076	0	3.28786	-1.135	0.39451	NA	FOXH1	chr8	-	1.46E+08	1.46E+08	2503
ENSG00000(	1438.715	1282.566	1322.053	806.7544	859.6835	896.7637	0.65697	7.03E-08	3.27E-07	ORAI2	chr7	+	1.02E+08	1.02E+08	10769
ENSG00000(	241.3395	240.8575	215.0644	194.0106	201.5746	189.8739	0.25254	0.17215	0.27322	ALKBH4	chr7	-	1.02E+08	1.02E+08	2105
ENSG00000(	79.75598	95.13873	43.54065	113.8595	73.63456	83.84042	-0.30605	0.34659	0.47612	SH2B2	chr7	+	1.02E+08	1.02E+08	2061
ENSG00000(	416.3883	438.3607	403.7406	374.5378	379.218	427.4218	0.091379	0.54772	0.66946	C5orf45	chr5	-	1.79E+08	1.79E+08	4145
ENSG00000(	2614.339	2384.49	2384.181	1194.776	1203.925	1167.19	1.0486	1.99E-21	2.14E-20	SQSTM1	chr5	+	1.79E+08	1.79E+08	2986
ENSG00000(	2650.591	2482.037	2233.768	3181.324	2625.992	2603.985	-0.1908	0.12614	0.21214	MGAT4B	chr5	-	1.79E+08	1.79E+08	3027
ENSG00000(	38532.49	37360.62	28688.01	25048.34	23873.24	30748.06	0.39155	0.004143	0.010438	RPL8	chr8	-	1.46E+08	1.46E+08	1041
ENSG00000(	1098.975	1000.763	1080.6	1001.514	1100.837	911.5591	0.077916	0.54231	0.66494	MAML1	chr5	+	1.79E+08	1.79E+08	6559
ENSG00000(	629.7615	566.0152	496.0996	997.0196	862.4448	972.3845	-0.73967	1.89E-07	8.45E-07	LRWD1	chr7	+	1.02E+08	1.02E+08	5491
ENSG00000(	13.46529	30.10719	14.51355	26.21764	9.20432	26.30288	-0.09211	0.87293	0.92025	FBXL13	chr7	-	1.02E+08	1.03E+08	3032
ENSG00000(	230.9816	303.4805	321.937	146.8188	135.3035	113.4312	1.1045	1.35E-07	6.13E-07	NAPEPLD	chr7	-	1.03E+08	1.03E+08	4988
ENSG00000(	3.107376	2.408575	0	0	0.920432	1.64393	0.6991	0.59616	0.71192	SCGB3A1	chr5	-	1.8E+08	1.8E+08	714
ENSG00000(	1312.348	1219.943	1225.735	2272.695	1665.061	1694.07	-0.58226	3.46E-05	0.00012	PSMC2	chr7	+	1.03E+08	1.03E+08	3054
ENSG00000(	2.071584	0	3.958241	5.992604	0	3.28786	-0.46852	0.69899	0.79531	CELF5	chr19	+	3224701	3297074	4268
ENSG00000(	1274.024	1117.579	968.4497	1349.085	1080.587	1105.543	-0.07253	0.61485	0.72803	MFSD12	chr19	-	3538259	3574288	2124
ENSG00000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	AC008103.	chr22	+	18837631	18848562	5920
ENSG00000(	3.107376	8.430014	7.916483	5.243529	4.60216	9.041614	0.025038	0.9763	0.98632	XXbac-B44	chr22	+	20287283	20300739	1240
ENSG00000(	3.107376	0	2.638828	0	0	0.821965	1.4274	0.29154	0.41564	USP41	chr22	-	20704868	20745048	1427
ENSG00000(	29.00217	25.29004	11.87472	20.97412	13.80648	9.041614	0.57043	0.3212	0.44841	TUBA3FP	chr22	-	21357184	21368581	1974
ENSG00000(	413.281	420.2964	286.3128	874.1712	617.6099	772.647	-1.0098	2.52E-08	1.22E-07	YDJC	chr22	-	21982378	21984353	1613
ENSG00000(	1.035792	1.204288	2.638828	3.745378	1.840864	8.219649	-1.2016	0.27617	0.39769	CCDC116	chr22	+	21987007	21991616	2260
ENSG00000(	2651.627	2577.176	2596.606	2371.573	2516.461	2311.365	0.12033	0.25151	0.36905	DVL3	chr3	+	1.84E+08	1.84E+08	5254
ENSG00000(	16092.06	15083.7	14049.12	12712.56	9758.42	10472.66	0.45616	0.000175	0.000551	AP2M1	chr3	+	1.84E+08	1.84E+08	2091
ENSG00000(	1130.049	1171.772	1088.516	812.747	722.5391	761.9615	0.55995	5.55E-06	2.12E-05	ABCF3	chr3	+	1.84E+08	1.84E+08	2844
ENSG00000(	1501.898	1427.081	1564.825	1127.359	1100.837	1075.952	0.44263	0.000111	0.000361	PCYT1A	chr3	-	1.96E+08	1.96E+08	5597
ENSG00000(	51.7896	44.55865	32.98534	75.65663	56.14635	83.01846	-0.71535	0.036288	0.073465	FBXO27	chr19	-	39481354	39523425	2330
ENSG00000(	0	0	0	1592.535	1522.395	1879.012	-10.926	8.13E-36	1.50E-34	DMKN	chr19	-	35988122	36004560	2811
ENSG00000(	8.286335	16.86003	3.958241	40.45008	13.80648	18.90519	-1.2508	0.052311	0.10102	U2AF1L4	chr19	-	36233428	36236346	2582

ENSG00000(	93.22127	79.48299	104.2337	241.9514	219.0628	259.7409	-1.3732	3.18E-10	1.81E-09	BDH1	chr3	-	1.97E+08	1.97E+08	3546
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	NPHS1	chr19	-	36316866	36360189	4276
ENSG00000(	140.8677	103.5687	72.56776	113.1104	77.31629	102.7456	0.11535	0.69285	0.7905	THAP8	chr19	-	36525887	36545664	1825
ENSG00000(	12.4295	9.634302	15.83297	5.243529	4.60216	35.34449	-0.23691	0.74877	0.83302	COX7A1	chr19	-	36641824	36643771	762
ENSG00000(	59.04014	63.82725	91.03955	60.67512	51.54419	55.89361	0.33577	0.29037	0.41433	ZNF382	chr19	+	37095719	37119499	3865
ENSG00000(	448.4979	387.7806	327.2146	1504.144	1208.527	1270.758	-1.7673	7.24E-31	1.13E-29	DUSP14	chr17	+	35849937	35873603	2207
ENSG00000(	31.07376	43.35436	25.06886	14.23244	11.96562	17.26126	1.1533	0.018866	0.04117	LRRC56	chr11	+	537527	554916	2769
ENSG00000(	229.9458	213.1589	224.3003	5.992604	3.681728	4.93179	5.3735	2.64E-42	5.86E-41	PLXDC1	chr17	-	37219556	37310647	6252
ENSG00000(	209.23	249.2876	242.7721	181.2763	156.4734	239.1918	0.27741	0.18792	0.29273	PGAP3	chr17	-	37827375	37853050	3028
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	IKZF3	chr17	-	37921198	38020441	2437
ENSG00000(	13.46529	6.021439	15.83297	13.48336	10.12475	9.863579	0.068387	0.91851	0.9507	GRIN2C	chr17	-	72838162	72857627	6516
ENSG00000(	1222.234	1203.083	913.0343	1249.458	1007.873	1441.726	-0.14705	0.35475	0.48444	FDXR	chr17	-	72858619	72869156	2482
ENSG00000(	2200.022	2070.171	1963.288	1691.413	1513.19	1603.654	0.37396	0.001	0.002804	SAP30BP	chr17	+	73663196	73704142	2786
ENSG00000(	601.7951	563.6067	585.8197	628.4744	635.0981	636.2008	-0.11682	0.37586	0.50631	ACOX1	chr17	-	73937588	73975515	7751
ENSG00000(	546.8981	540.7252	554.1538	704.8801	638.7798	639.4887	-0.27243	0.043039	0.085314	PRPSAP1	chr17	-	74305567	74380602	3660
ENSG00000(	722.9827	727.3898	635.9574	102.6234	92.96363	109.3213	2.7628	2.22E-61	8.05E-60	CYGB	chr17	-	74523438	74547257	2158
ENSG00000(	903.2105	1138.052	979.005	3719.909	2329.613	2546.447	-1.504	1.32E-19	1.32E-18	SRSF2	chr17	-	74730197	74733456	2885
ENSG00000(	104.615	118.0202	89.72014	89.88907	85.60018	85.48435	0.25795	0.318	0.44491	ZNF577	chr19	-	52359055	52394203	3148
ENSG00000(	111.8655	140.9017	100.2754	105.6197	97.56579	95.34793	0.23988	0.33869	0.46725	TMEM143	chr19	-	48835613	48867494	2560
ENSG00000(	3.107376	0	7.916483	2.247227	1.840864	1.64393	0.71045	0.53581	0.66002	CCL5	chr17	-	34198495	34207797	1365
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	TBC1D3G	chr17	-	34745936	34808104	3389
ENSG00000(	4.143168	1.204288	0	0	0.920432	0.821965	0.96156	0.47231	0.60138	KLHL10	chr17	+	39991937	40004636	2057
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	HCRT	chr17	-	40336078	40337470	577
ENSG00000(	306.5944	266.1476	261.2439	571.5446	503.4763	655.928	-1.0481	2.20E-10	1.27E-09	ALDH16A1	chr19	+	49956426	49974305	3995
ENSG00000(	6616.639	6663.324	6521.862	1813.512	1782.877	1872.436	1.8538	1.20E-77	6.20E-76	ITGA5	chr12	-	54789045	54813244	4996
ENSG00000(	363.563	284.2119	361.5194	1262.192	1384.33	1505.84	-2.034	4.55E-44	1.06E-42	ZNF385A	chr12	-	54762917	54785082	2494
ENSG00000(	1.035792	6.021439	1.319414	12.73428	3.681728	4.93179	-1.151	0.24213	0.35781	SIGLEC16	chr19	+	50472857	50479071	2510
ENSG00000(	136.7245	160.1703	112.1502	23.22134	19.32907	32.05663	2.4188	1.73E-14	1.32E-13	MPP3	chr17	-	41878167	41910538	2996
ENSG00000(	73.54123	40.94578	43.54065	29.21395	14.72691	27.12484	1.1222	0.008738	0.020592	NAGS	chr17	+	42081914	42086431	2182
ENSG00000(	580.0435	566.0152	534.3626	828.4776	769.4811	729.9048	-0.46861	0.000467	0.001377	LSM12	chr17	-	42112003	42144987	2484
ENSG00000(	39.36009	28.90291	25.06886	47.94084	55.22592	82.19649	-0.96086	0.012728	0.028878	ASB16	chr17	+	42247815	42256451	2139
ENSG00000(	1777.419	1801.614	1607.046	1997.035	1580.382	1892.985	-0.07699	0.54295	0.66549	EMC10	chr19	+	50979657	50986608	2178
ENSG00000(	686.73	678.014	595.0556	318.3571	302.8221	423.3119	0.90478	4.82E-08	2.28E-07	JOSD2	chr19	-	51009255	51014610	996
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	SHANK1	chr19	-	51165084	51222707	6643
ENSG00000(	995.396	992.3331	778.4541	329.5932	358.9685	343.5813	1.4196	1.40E-21	1.52E-20	FAM171A2	chr17	-	42430583	42441243	3160
ENSG00000(	179.192	168.6003	221.6615	771.5478	776.8446	886.9001	-2.0923	4.18E-38	8.19E-37	DBF4B	chr17	+	42785976	42829632	2998
ENSG00000(	1595.12	1580.025	1331.289	938.5917	747.3908	874.5707	0.81323	2.18E-09	1.16E-08	PLCD3	chr17	-	43186335	43210721	6106
ENSG00000(	779.9513	621.4125	729.6358	280.1543	368.1728	358.3767	1.0801	2.88E-11	1.77E-10	FMNL3	chr12	-	50031724	50101948	11192
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	AQP5	chr12	+	50355653	50359464	1450
ENSG00000(	576.9361	527.478	637.2769	1464.443	1459.805	1390.765	-1.3068	1.20E-24	1.46E-23	RACGAP1	chr12	-	50370706	50426919	3307
ENSG00000(	583.1508	566.0152	913.0343	1035.971	1202.084	999.5093	-0.64961	0.000222	0.000687	LARP4	chr12	+	50786166	50873787	6427
ENSG00000(	432.961	466.0593	337.7699	45.69361	45.10117	72.33291	2.9015	2.40E-36	4.46E-35	GRASP	chr12	+	52400724	52409673	1933
ENSG00000(	834.8483	827.3457	785.0512	797.7655	911.2277	930.4643	-0.10796	0.40326	0.53429	RAVER1	chr19	-	10426888	10444316	4693
ENSG00000(	16.57267	12.04288	10.55531	8.239831	13.80648	13.15144	0.15693	0.80538	0.87386	SYCE2	chr19	-	13009600	13030090	1231

ENSG00000(	321.0955	261.3304	224.3003	871.9239	887.2964	1091.569	-1.8101	2.54E-27	3.45E-26	SPC24	chr19	-	11242196	11266484	2315
ENSG00000(	6.214751	6.021439	1.319414	15.73059	9.20432	7.397684	-1.1106	0.17631	0.27829	IP6K3	chr6	-	33689444	33714762	2822
ENSG00000(	1123.834	1106.74	1025.185	892.8981	1063.099	1157.327	0.065237	0.62848	0.73907	LEMD2	chr6	-	33738979	33756913	4870
ENSG00000(	2.071584	0	0	2.996302	7.363456	4.93179	-2.0267	0.087202	0.15669	ALOX15	chr17	-	4534197	4545589	2784
ENSG00000(	0	3.612863	0	0.749076	3.681728	0	-0.16223	0.9038	0.94052	TREML1	chr6	-	41117080	41122075	1194
ENSG00000(	142.9393	166.1917	153.052	123.5975	127.0196	77.2647	0.4908	0.05056	0.098056	ADCY10P1	chr6	+	41068761	41108571	4567
ENSG00000(	99.43602	63.82725	59.37362	81.64923	81.91845	87.95025	-0.16635	0.57705	0.69533	ZNF653	chr19	-	11594242	11616738	2240
ENSG00000(	56.96855	50.58008	38.263	53.93344	72.71413	61.64737	-0.35487	0.29114	0.41527	MED11	chr17	+	4634723	4636905	833
ENSG00000(	20.71584	36.12863	14.51355	56.18067	49.70333	68.22309	-1.2539	0.00261	0.006816	CXCL16	chr17	-	4636821	4643217	2222
ENSG00000(	8.286335	7.225726	0	0	0	0.821965	2.7272	0.030564	0.063194	SCIMP	chr17	-	5112256	5138155	2383
ENSG00000(	3.107376	9.634302	3.958241	4.494453	12.88605	9.863579	-0.63083	0.44607	0.57565	RNASEK-C1	chr17	+	6915954	6920839	1856
ENSG00000(	3.107376	0	0	0	0	0.821965	0.7418	0.57612	NA	BCL6B	chr17	+	6926339	6933609	3555
ENSG00000(	1.035792	0	0	0	0.920432	3.28786	-0.88129	0.51584	NA	ASGR2	chr17	-	7004641	7019019	1454
ENSG00000(	12.4295	21.67718	22.43003	24.71949	42.33987	32.05663	-0.78905	0.10372	0.18077	TNFSF13	chr17	+	7461609	7464925	2036
ENSG00000(	298.3081	264.9433	266.5216	301.8774	286.2544	514.55	-0.40703	0.062754	0.11815	SENP3	chr17	+	7465192	7475287	2612
ENSG00000(	113.9371	144.5145	72.56776	26.21764	36.81728	41.09825	1.6482	1.07E-06	4.44E-06	FGF11	chr17	+	7341592	7349285	5553
ENSG00000(	109.7939	136.0845	130.622	55.43159	119.6562	161.9271	0.15877	0.61968	0.73198	EIF4A1	chr17	+	7476024	7482323	1756
ENSG00000(	166.7625	146.9231	142.4967	176.0328	180.4047	223.5745	-0.34218	0.10504	0.18262	RPL26	chr17	-	8280838	8286531	1002
ENSG00000(	84.93494	97.54731	98.95603	438.9583	274.2887	388.7894	-1.9603	1.55E-18	1.47E-17	POLR3K	chr16	-	96407	103628	1392
ENSG00000(	522.0391	575.6495	364.1582	730.3487	662.711	891.8319	-0.6401	0.000371	0.001113	SNRNP25	chr16	+	103010	107669	1905
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	C16orf11	chr16	+	610422	615528	2216
ENSG00000(	397.7441	364.8992	255.9663	304.1247	383.8201	535.0992	-0.25945	0.23452	0.34865	WDR90	chr16	+	699311	717833	5589
ENSG00000(	487.858	458.8336	398.463	292.1395	360.8093	331.2519	0.45195	0.005768	0.014119	JMJD8	chr16	-	731671	734529	2205
ENSG00000(	54.89697	60.21439	23.74945	7.490755	26.69253	28.76877	1.1116	0.029436	0.061139	CCDC78	chr16	-	772582	776954	3458
ENSG00000(	4.143168	18.06432	5.277655	8.988907	0	9.041614	0.51473	0.57377	0.69251	SPSB3	chr16	-	1826713	1843701	2316
ENSG00000(	2.071584	4.817151	1.319414	2.247227	4.60216	5.753754	-0.50115	0.63092	0.74096	MEIOB	chr16	-	1883984	1934295	1884
ENSG00000(	0	7.225726	3.958241	0	0	0	2.7876	0.037048	0.074861	HS3ST6	chr16	-	1961464	1968441	1273
ENSG00000(	130.5098	120.4288	122.7055	525.102	395.7858	484.9593	-1.9023	3.71E-24	4.44E-23	C16orf59	chr16	+	2510081	2514964	2156
ENSG00000(	308.666	309.5019	300.8263	1471.933	1354.876	1248.565	-2.1433	3.73E-56	1.18E-54	CCNF	chr16	+	2479395	2508855	4283
ENSG00000(	272.4133	250.4918	230.8974	227.719	241.1532	239.1918	0.092236	0.60475	0.71965	TBC1D24	chr16	+	2525147	2555735	6578
ENSG00000(	131.5456	175.826	105.5531	168.542	171.2004	162.7491	-0.27945	0.2317	0.34523	AMDHD2	chr16	+	2570358	2581423	3273
ENSG00000(	18.64425	25.29004	18.47179	3.745378	7.363456	10.68554	1.4362	0.023139	0.049402	NTN3	chr16	+	2521500	2524146	1986
ENSG00000(	0	0	0	95.13259	81.91845	118.3629	-7.3273	3.20E-13	2.27E-12	CCDC64B	chr16	-	3077683	3086927	3519
ENSG00000(	43.50326	38.53721	51.45714	176.0328	201.5746	177.5444	-2.0397	5.37E-15	4.24E-14	PAQR4	chr16	+	3019246	3023490	2793
ENSG00000(	461.9632	398.6192	383.9494	185.0217	169.3595	187.408	1.1956	3.75E-12	2.47E-11	FLYWCH2	chr16	+	2933187	2949383	1036
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	ZG16B	chr16	+	2880170	2888967	849
ENSG00000(	272.4133	262.5347	277.0769	370.0433	248.5166	291.7975	-0.16631	0.38001	0.51065	ZNF75A	chr16	+	3355406	3368852	3989
ENSG00000(	791.345	714.1426	887.9655	119.103	200.6542	187.408	2.2313	6.53E-32	1.05E-30	ADCY9	chr16	-	4003388	4166186	7725
ENSG00000(	10.35792	9.634302	14.51355	117.6049	175.8025	134.8022	-3.5697	5.84E-21	6.15E-20	SHANK2	chr11	-	70313961	70963623	8987
ENSG00000(	276.5564	201.116	249.3692	413.4897	365.4115	360.8426	-0.64467	0.000318	0.000963	CLPB	chr11	-	72003469	72145692	3240
ENSG00000(	114.9729	146.9231	92.35896	60.67512	168.4391	99.45776	0.11269	0.73088	0.81984	NEU3	chr11	+	74699179	74729938	3519
ENSG00000(	616.2962	586.4881	601.6527	457.6852	294.5382	342.7594	0.71561	3.74E-05	0.000129	CYB561A3	chr11	-	61116217	61129771	4094
ENSG00000(	25.8948	16.86003	13.19414	24.71949	11.04518	22.19305	-0.04536	0.93511	0.96088	PPP1R32	chr11	+	61248592	61258403	1535
ENSG00000(	2.071584	0	0	51.68621	50.62376	59.18147	-5.3661	8.78E-11	5.22E-10	ASRGL1	chr11	+	62104920	62160882	2268

ENSG00000(	2.071584	2.408575	1.319414	0.749076	8.283888	6.575719	-1.1285	0.29586	0.42027	GNG3	chr11	+	62475130	62476673	882
ENSG00000(	1875.819	1692.024	1604.407	1279.421	1275.719	1366.928	0.39902	0.000717	0.002059	UBXN1	chr11	-	62443970	62446567	2073
ENSG00000(	91.14969	79.48299	76.526	234.4606	139.9057	165.2149	-1.1157	1.85E-05	6.64E-05	C11orf48	chr11	-	62430287	62439727	2915
ENSG00000(	621.4751	637.0682	629.3604	568.5483	455.6138	497.2888	0.30916	0.031727	0.065267	TTC9C	chr11	+	62495541	62507765	1833
ENSG00000(	296.2365	283.0076	220.3421	269.6672	260.4823	304.949	-0.05997	0.74535	0.83051	TAF6L	chr11	+	62538775	62554814	2116
ENSG00000(	1567.153	1570.391	1562.186	1849.468	1365.921	1383.367	0.030672	0.82413	0.88643	NXF1	chr11	-	62559595	62573774	4128
ENSG00000(	836.9199	792.4213	717.7611	722.8579	589.0765	610.7199	0.28699	0.043042	0.085314	STX5	chr11	-	62574369	62599560	1794
ENSG00000(	43.50326	50.58008	39.58241	22.47227	4.60216	16.4393	1.5462	0.002119	0.005621	SLC25A45	chr11	-	65142663	65151172	7118
ENSG00000(	31880.64	31198.28	21808.59	19319.41	15593.96	17972.26	0.68076	2.33E-06	9.29E-06	RPL29	chr3	-	52027616	52029958	880
ENSG00000(	20.71584	7.225726	0	0	3.681728	0.821965	2.1274	0.051167	0.099087	ITIH3	chr3	+	52828784	52843025	3007
ENSG00000(	521.0033	617.7996	566.0285	450.1944	531.0893	470.9859	0.23083	0.11826	0.20145	DCP1A	chr3	-	53317448	53381637	5998
ENSG00000(	1091.725	1057.365	947.3391	713.1199	712.4144	678.1211	0.55727	1.10E-05	4.06E-05	SYVN1	chr11	-	64889252	64902004	4547
ENSG00000(	44.53905	68.6444	38.263	26.21764	20.2495	38.63235	0.80945	0.051227	0.099187	ZFPL1	chr11	+	64851695	64855870	1369
ENSG00000(	1030.613	965.8388	899.8402	2085.426	2152.89	2889.207	-1.2949	2.39E-19	2.36E-18	RPS6KA4	chr11	+	64126620	64139687	3121
ENSG00000(	1116.584	1286.179	1184.834	1012.75	1058.497	1056.225	0.1974	0.10163	0.17783	LRP5	chr11	+	68080077	68216743	5159
ENSG00000(	713.6606	800.8513	661.0263	283.1506	273.3683	305.7709	1.331	4.64E-19	4.50E-18	TPCN2	chr11	+	68816365	68858072	4376
ENSG00000(	0	0	0	5.243529	1.840864	0	-1.8401	0.17492	0.27673	FGF19	chr11	-	69513000	69519410	2447
ENSG00000(	1525.721	1506.564	1882.803	2113.891	2052.563	2016.28	-0.33113	0.007472	0.017888	CMPK1	chr1	+	47799469	47844511	2930
ENSG00000(	12.4295	24.08575	9.235896	39.701	54.30549	26.30288	-1.3403	0.008248	0.019527	BEND5	chr1	-	49193195	49242641	1716
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	ELAVL4	chr1	+	50513686	50669458	3966
ENSG00000(	189.5499	198.7075	209.7868	274.1617	328.5942	258.097	-0.52308	0.005039	0.012479	SELRC1	chr1	-	53152508	53164038	1620
ENSG00000(	695.0164	785.1956	882.6878	603.0058	661.7906	578.6633	0.35623	0.012525	0.028482	ZYG11B	chr1	+	53192126	53293014	8093
ENSG00000(	2.071584	6.021439	1.319414	1.498151	0	0	1.6885	0.18772	0.29247	SLC1A7	chr1	-	53552855	53608289	2637
ENSG00000(	633.9046	615.391	519.849	608.9984	465.7386	560.5801	0.11314	0.46805	0.59732	C1orf123	chr1	-	53679771	53686289	1912
ENSG00000(	343.8829	398.6192	325.8952	662.1828	813.6619	1198.425	-1.3164	1.89E-11	1.18E-10	MAGOH	chr1	-	53692564	53704282	756
ENSG00000(	0	0	7.916483	40.45008	32.21512	47.67397	-3.047	0.006661	0.016088	ACOT11	chr1	+	55007930	55104865	6369
ENSG00000(	0	0	0	0.749076	2.761296	10.68554	-2.9243	0.024282	0.051647	FAM151A	chr1	-	55074855	55089229	2005
ENSG00000(	113.9371	107.1816	100.2754	179.0291	182.2455	165.2149	-0.70507	0.001336	0.003675	PARS2	chr1	-	55222571	55230187	2347
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	C1orf177	chr1	+	55271736	55307925	1777
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	BSND	chr1	+	55464606	55476556	3472
ENSG00000(	756.1281	682.8311	1047.615	984.2853	1042.849	863.8851	-0.21777	0.18363	0.2876	USP24	chr1	-	55532032	55680786	10549
ENSG00000(	3631.486	3775.442	4075.669	798.5145	828.3888	753.7418	2.2662	9.37E-91	6.00E-89	PPAP2B	chr1	-	56960419	57110974	3292
ENSG00000(	767.5218	712.9383	621.4439	1438.225	1201.164	1369.394	-0.92813	8.68E-12	5.55E-11	NOL9	chr1	-	6581407	6614595	6649
ENSG00000(	23.82321	32.51577	32.98534	232.2134	263.2436	223.5745	-2.9888	1.36E-28	1.96E-27	PRKAA2	chr1	+	57110995	57181008	9347
ENSG00000(	714.6964	755.0884	734.9135	1126.61	1187.357	1158.971	-0.65438	5.57E-08	2.62E-07	KLHL21	chr1	-	6650784	6674667	6445
ENSG00000(	8.286335	12.04288	14.51355	18.72689	14.72691	9.041614	-0.28025	0.6607	0.76504	ZSWIM5	chr1	-	45482071	45771881	5819
ENSG00000(	358.384	322.7491	360.2	385.0248	362.6502	353.4449	-0.08053	0.60741	0.7217	GMEB1	chr1	+	28995244	29045865	6410
ENSG00000(	81.82756	39.74149	51.45714	5.243529	5.522592	4.109825	3.4064	8.81E-11	5.24E-10	SLC45A1	chr1	+	8377886	8404227	2784
ENSG00000(	2796.638	2562.724	2630.911	1046.459	1214.05	1004.441	1.2894	4.79E-27	6.43E-26	SEPN1	chr1	+	26126667	26144713	4332
ENSG00000(	1932.788	2079.805	2128.214	889.9018	744.6295	724.9731	1.3759	1.36E-27	1.87E-26	AK4	chr1	+	65613232	65697828	6998
ENSG00000(	2471.399	2308.62	2703.479	823.234	989.4644	649.3523	1.5995	1.31E-26	1.73E-25	JAK1	chr1	-	65298912	65432187	5047
ENSG00000(	132.5814	128.8588	149.0938	316.859	332.276	258.097	-1.1391	9.33E-09	4.69E-08	RAVER2	chr1	+	65210778	65298915	4398
ENSG00000(	0	8.430014	1.319414	1.498151	0	0	1.6201	0.21686	0.32794	CTRC	chr1	+	15764935	15775737	3147
ENSG00000(	512.717	475.6936	618.8051	542.3307	480.4655	492.357	0.082967	0.58878	0.7058	LZIC	chr1	-	9982173	10003465	2281

ENSG00000(	0	4.817151	0	17.22874	5.522592	14.79537	-2.5059	0.010222	0.023714	RBP7	chr1	+	10057264	10076078	861
ENSG00000(	3833.466	3657.422	3375.06	3179.826	2967.473	3318.272	0.19889	0.06817	0.12684	FBLIM1	chr1	+	16083102	16113089	3695
ENSG00000(	5.17896	3.612863	1.319414	0	0	0	2.8008	0.034577	0.070376	TMEM82	chr1	+	16068917	16074477	1520
ENSG00000(	8.286335	26.49433	3.958241	13.48336	18.40864	27.94681	-0.58559	0.37218	0.50275	SLC25A34	chr1	+	16062900	16067891	2986
ENSG00000(	35.21692	43.35436	29.0271	20.22504	18.40864	16.4393	0.93894	0.038228	0.076954	AKR7A3	chr1	-	19609052	19615744	1710
ENSG00000(	232.0174	266.1476	234.8557	73.4094	130.7013	115.0751	1.195	3.94E-07	1.71E-06	DRAXIN	chr1	+	11751786	11785914	7346
ENSG00000(	23.82321	19.2686	18.47179	355.8109	389.3427	347.6912	-4.0968	2.91E-52	8.49E-51	PDPN	chr1	+	13909960	13944452	3104
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	LRRC38	chr1	-	13801445	13840543	2209
ENSG00000(	672.2289	755.0884	564.7091	352.0655	277.05	345.2253	1.0271	5.58E-10	3.11E-09	DHRS3	chr1	-	12627939	12677737	1723
ENSG00000(	6.214751	3.612863	9.235896	0.749076	2.761296	4.109825	1.1231	0.25151	0.36905	MATN1	chr1	-	31184124	31196434	3832
ENSG00000(	5.17896	0	0	5.243529	5.522592	3.28786	-1.0567	0.35593	0.48556	LAPTM5	chr1	-	31205316	31230667	2223
ENSG00000(	4532.625	4224.641	4202.333	1669.689	2392.203	2361.505	1.0104	4.80E-13	3.36E-12	SDC3	chr1	-	31342314	31381608	6392
ENSG00000(	468.1779	507.0051	457.8366	1244.964	823.7866	951.8354	-1.0727	5.38E-11	3.25E-10	PEF1	chr1	-	32095463	32110497	1629
ENSG00000(	687.7658	773.1527	814.0783	158.0549	169.3595	176.7225	2.1666	2.71E-44	6.34E-43	SYNC	chr1	-	33145507	33169197	3413
ENSG00000(	1100.011	1156.116	1374.829	1468.937	1675.186	1346.379	-0.30634	0.0243	0.051675	RBBP4	chr1	+	33116743	33146258	2385
ENSG00000(	528.2539	568.4238	555.4732	997.0196	1552.769	1451.59	-1.2711	9.35E-15	7.27E-14	KIAA1522	chr1	+	33207486	33240571	5438
ENSG00000(	3.107376	1.204288	6.597069	0.749076	0.920432	4.109825	0.70125	0.53572	0.65998	TSSK3	chr1	+	32817122	32829913	1368
ENSG00000(	75.61281	46.96722	48.81831	78.65293	58.90765	75.62077	-0.30519	0.35036	0.47998	TMCO4	chr1	-	20008706	20126438	2974
ENSG00000(	0	0	0	5.243529	3.681728	4.93179	-2.9957	0.019038	0.041511	UBXN10	chr1	+	20512578	20522541	5571
ENSG00000(	1005.754	899.6029	887.9655	498.8843	458.3751	410.9825	1.0272	1.93E-13	1.39E-12	CAMK2N1	chr1	-	20808884	20812713	2336
ENSG00000(	571.7571	488.9408	416.9348	360.3053	281.6522	329.6079	0.60303	0.000488	0.001438	ALPL	chr1	+	21835858	21904905	2589
ENSG00000(	0	2.408575	5.277655	49.43899	64.43024	39.45432	-4.1055	7.81E-10	4.32E-09	WNT4	chr1	-	22446461	22470462	1182
ENSG00000(	46.61064	75.87013	30.34652	9.737982	9.20432	12.32947	2.2127	5.76E-06	2.20E-05	SCNN1D	chr1	+	1215816	1227409	3475
ENSG00000(	542.755	593.7138	428.8095	120.6012	121.497	154.5294	1.9717	2.43E-25	3.04E-24	MXRA8	chr1	-	1288069	1297157	2625
ENSG00000(	1164.23	1127.213	827.2724	973.7982	733.5843	884.4343	0.26641	0.095521	0.16885	C1orf86	chr1	-	2115903	2144159	3576
ENSG00000(	47.64643	85.50443	80.48424	53.18436	87.44104	105.2115	-0.20248	0.54899	0.67052	MEGF6	chr1	-	3406484	3528059	5455
ENSG00000(	1.035792	0	1.319414	2.996302	0	0.821965	-0.39956	0.76686	0.84621	CCDC27	chr1	+	3668962	3688209	2252
ENSG00000(	31.07376	14.45145	6.597069	17.97781	8.283888	6.575719	0.62824	0.35547	0.48506	DIRAS3	chr1	-	68511645	68517314	1973
ENSG00000(	0	0	1.319414	0	2.761296	0.821965	-0.69816	0.6064	NA	C1orf87	chr1	-	60452941	60539442	3012
ENSG00000(	497.1801	521.4566	544.9179	7.490755	8.283888	16.4393	5.5381	1.49E-83	8.51E-82	NFIA	chr1	+	61330931	61928465	9487
ENSG00000(	42.46747	54.19295	43.54065	97.37982	72.71413	67.40112	-0.75253	0.020104	0.043576	OMA1	chr1	-	58881056	59012474	2105
ENSG00000(	786.1661	861.0657	971.0885	605.253	760.2768	529.3454	0.465	0.003418	0.008753	MYSM1	chr1	-	59120411	59165764	7793
ENSG00000(	246.5185	293.8462	267.841	223.2245	185.9273	234.26	0.32503	0.08177	0.14812	TM2D1	chr1	-	62146719	62191095	1250
ENSG00000(	291.0575	295.0505	376.0329	1322.867	1310.695	1202.535	-1.9928	3.66E-43	8.34E-42	USP1	chr1	+	62901968	62917475	3996
ENSG00000(	1318.563	1490.908	1492.257	2728.133	2932.496	2742.897	-0.96493	1.17E-17	1.06E-16	FUBP1	chr1	-	78409740	78444794	2524
ENSG00000(	163.6551	133.6759	149.0938	220.9773	178.5638	178.3664	-0.36999	0.081375	0.14749	NEXN	chr1	+	78354198	78409580	3195
ENSG00000(	1452.18	1606.52	1675.656	202.2504	211.6994	202.2034	2.9347	1.25E-105	1.04E-103	DNAJB4	chr1	+	78444859	78483648	2988
ENSG00000(	21.75163	7.225726	14.51355	131.0882	107.6905	71.51095	-2.751	2.93E-11	1.80E-10	ELTD1	chr1	-	79355449	79472403	3527
ENSG00000(	5.17896	12.04288	11.87472	8.988907	15.64734	13.15144	-0.35896	0.59829	0.71378	LRRIQ3	chr1	-	74491699	74663871	4524
ENSG00000(	390.4935	373.3292	368.1164	557.3122	487.829	487.4252	-0.43585	0.003498	0.008936	TYW3	chr1	+	75198836	75232362	3430
ENSG00000(	3.107376	6.021439	11.87472	41.94823	30.37426	17.26126	-2.0031	0.001417	0.003871	LHX8	chr1	+	75594119	75627218	2373
ENSG00000(	391.5293	364.8992	390.5465	561.0576	430.7622	428.2437	-0.30808	0.060672	0.11474	SNX7	chr1	+	99127236	99226056	1742
ENSG00000(	8.286335	6.021439	7.916483	0	3.681728	2.465895	1.5797	0.11214	0.19266	B3GALT2	chr1	-	1.93E+08	1.93E+08	3274
ENSG00000(	175.0488	132.4716	124.0249	129.5901	83.75931	107.6774	0.42319	0.098595	0.17336	NTNG1	chr1	+	1.08E+08	1.08E+08	4703

ENSG00000(	233.0532	217.9761	310.0622	377.5341	477.7042	416.7362	-0.73929	6.43E-05	0.000215	FAM102B	chr1	+	1.09E+08	1.09E+08	8333
ENSG00000(	88.04231	49.3758	85.7619	120.6012	90.20234	100.2797	-0.47383	0.1094	0.18869	HENMT1	chr1	-	1.09E+08	1.09E+08	1874
ENSG00000(	3.107376	12.04288	9.235896	0	1.840864	1.64393	2.3115	0.025729	0.05432	AKNAD1	chr1	-	1.09E+08	1.1E+08	3053
ENSG00000(	315.9165	401.0278	348.3252	579.7845	470.3408	514.55	-0.55469	0.000627	0.001813	C1orf52	chr1	-	85715639	85725355	3388
ENSG00000(	143.9751	172.2131	163.6073	47.19176	39.57858	38.63235	1.9131	4.46E-13	3.13E-12	WDR63	chr1	+	85464830	85598821	3477
ENSG00000(	142.9393	162.5788	100.2754	65.16957	43.2603	52.60575	1.3157	5.65E-06	2.16E-05	GBP2	chr1	-	89571815	89616139	3687
ENSG00000(	159.512	187.8689	110.8308	158.0549	95.72493	150.4196	0.17866	0.49995	0.6282	ATXN7L2	chr1	+	1.1E+08	1.1E+08	4375
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	GBP4	chr1	-	89646831	89664615	6127
ENSG00000(	516.8602	431.135	515.8908	615.7401	762.1177	857.3094	-0.60772	0.000153	0.000487	ZNF326	chr1	+	90460671	90494097	2729
ENSG00000(	0	4.817151	2.638828	15.73059	10.12475	8.219649	-1.9358	0.033062	0.06761	HFM1	chr1	-	91726323	91870426	4931
ENSG00000(	5.17896	6.021439	1.319414	0	1.840864	0	1.9684	0.11035	0.19002	FAM5C	chr1	-	1.9E+08	1.9E+08	2889
ENSG00000(	2.071584	0	0	7.490755	6.443024	10.68554	-2.693	0.013823	0.031165	GFI1	chr1	-	92940319	92952433	2855
ENSG00000(	102.5434	114.4073	127.9831	18.72689	12.88605	6.575719	3.1015	1.64E-16	1.41E-15	KCNT2	chr1	-	1.96E+08	1.97E+08	5883
ENSG00000(	336.6324	313.1148	468.3919	372.2905	531.0893	384.6796	-0.20372	0.30052	0.42557	AGL	chr1	+	1E+08	1E+08	7446
ENSG00000(	406.0304	322.7491	366.797	26.21764	37.73771	27.94681	3.5581	1.11E-50	3.12E-49	VCAM1	chr1	+	1.01E+08	1.01E+08	3865
ENSG00000(	900.1032	885.1515	1050.253	435.2129	331.3555	316.4565	1.3815	3.41E-18	3.17E-17	EXTL2	chr1	-	1.01E+08	1.01E+08	3985
ENSG00000(	674.3005	706.9169	804.8424	593.2678	587.2356	474.2738	0.39952	0.007255	0.017416	SLC30A7	chr1	+	1.01E+08	1.01E+08	7898
ENSG00000(	308.666	255.309	471.0307	225.4717	339.6394	230.1502	0.37701	0.10487	0.18237	ZNF281	chr1	-	2E+08	2E+08	3132
ENSG00000(	2162.733	2314.641	2373.625	3238.254	3275.817	3321.56	-0.52127	6.12E-07	2.60E-06	ARPC5	chr1	-	1.84E+08	1.84E+08	2985
ENSG00000(	0	1.204288	1.319414	106.3687	113.2131	128.2265	-6.4167	8.85E-17	7.66E-16	CADM3	chr1	+	1.59E+08	1.59E+08	3745
ENSG00000(	0	1.204288	2.638828	19.47596	23.0108	7.397684	-3.2267	0.000494	0.001452	NLRP3	chr1	+	2.48E+08	2.48E+08	4318
ENSG00000(	997.4676	1052.547	1072.683	1322.118	1365.921	1334.049	-0.36488	0.001548	0.004202	ZNF496	chr1	-	2.47E+08	2.47E+08	9243
ENSG00000(	0	1.204288	5.277655	158.0549	243.9145	208.7791	-6.3058	5.47E-26	7.03E-25	TRIM58	chr1	+	2.48E+08	2.48E+08	3225
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	SLAMF9	chr1	-	1.6E+08	1.6E+08	1156
ENSG00000(	0	1.204288	0	0	1.840864	4.109825	-1.2058	0.37206	0.50265	KCNJ9	chr1	+	1.6E+08	1.6E+08	4170
ENSG00000(	572.7929	667.1754	513.252	670.4226	591.8378	643.5985	-0.12007	0.41642	0.54704	IGSF8	chr1	-	1.6E+08	1.6E+08	2366
ENSG00000(	471.2853	444.3822	924.9091	19.47596	56.14635	31.23467	3.9519	4.05E-14	3.03E-13	DDR2	chr1	+	1.63E+08	1.63E+08	3207
ENSG00000(	4972.837	4724.421	5001.898	6185.117	6409.888	6832.994	-0.40182	7.32E-05	0.000243	PEA15	chr1	+	1.6E+08	1.6E+08	2694
ENSG00000(	414.3168	415.4793	426.1707	555.8141	530.1688	490.7131	-0.32767	0.023158	0.049439	PEX19	chr1	-	1.6E+08	1.6E+08	3661
ENSG00000(	2150.304	2077.396	2096.548	2436.743	1898.851	1770.512	0.050205	0.70822	0.80278	NCSTN	chr1	+	1.6E+08	1.6E+08	3031
ENSG00000(	951.8928	684.0354	814.0783	842.71	1226.015	1079.24	-0.35874	0.030101	0.062368	VANGL2	chr1	+	1.6E+08	1.6E+08	5340
ENSG00000(	2121.302	1900.366	2026.62	196.2578	286.2544	247.4114	3.0454	1.04E-94	7.26E-93	OLFML2B	chr1	-	1.62E+08	1.62E+08	3160
ENSG00000(	10.35792	21.67718	6.597069	25.46857	34.05598	25.48091	-1.0835	0.050413	0.09782	FCRLB	chr1	+	1.62E+08	1.62E+08	1989
ENSG00000(	2.071584	0	2.638828	0	0	1.64393	0.80176	0.55354	0.6745	SLC9C2	chr1	-	1.73E+08	1.74E+08	4428
ENSG00000(	14.50109	4.817151	11.87472	55.43159	44.18074	36.98842	-2.0449	5.45E-05	0.000184	KLHDC9	chr1	+	1.61E+08	1.61E+08	1333
ENSG00000(	46.61064	28.90291	30.34652	83.14739	72.71413	70.68898	-1.071	0.001933	0.005165	C1orf74	chr1	-	2.1E+08	2.1E+08	1576
ENSG00000(	0	0	0	1.498151	17.48821	4.93179	-3.7054	0.002708	0.007055	LMX1A	chr1	-	1.65E+08	1.65E+08	3545
ENSG00000(	161.5835	133.6759	141.1773	340.8294	268.7661	328.786	-1.0974	2.18E-08	1.06E-07	FLVCR1	chr1	+	2.13E+08	2.13E+08	5939
ENSG00000(	181.2636	167.396	129.3026	744.5811	703.21	752.0979	-2.1886	3.00E-39	6.07E-38	ATF3	chr1	+	2.13E+08	2.13E+08	2117
ENSG00000(	168.8341	180.6432	226.9392	252.4385	364.4911	307.4149	-0.67893	0.000897	0.002536	RBM15	chr1	+	1.11E+08	1.11E+08	4244
ENSG00000(	9.322127	0	3.958241	11.98521	5.522592	4.93179	-0.63564	0.50107	0.62917	DENND2D	chr1	-	1.12E+08	1.12E+08	3207
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	AXDND1	chr1	+	1.79E+08	1.8E+08	3642
ENSG00000(	1.035792	0	0	14.23244	11.96562	13.9734	-3.9155	0.000264	0.000809	TDRD5	chr1	+	1.8E+08	1.8E+08	3678
ENSG00000(	1965.933	1895.549	1737.668	857.6915	890.9782	831.0065	1.1166	1.55E-21	1.67E-20	IER5	chr1	+	1.81E+08	1.81E+08	2340

ENSG00000(	4649.67	4463.09	4521.631	14.98151	31.29469	17.26126	7.7324	0	0	SNED1	chr2	+	2.42E+08	2.42E+08	8174
ENSG00000(	547.9339	644.2939	580.5421	909.3777	641.5411	625.5153	-0.29623	0.076405	0.13984	BPNT1	chr1	-	2.2E+08	2.2E+08	2737
ENSG00000(	19.68005	15.65574	1.319414	6.74168	17.48821	13.15144	-0.005	0.9946	0.99663	SPATA17	chr1	+	2.18E+08	2.18E+08	5818
ENSG00000(	6.214751	6.021439	2.638828	66.66772	67.19154	71.51095	-3.6146	2.99E-12	1.98E-11	C1orf115	chr1	+	2.21E+08	2.21E+08	3413
ENSG00000(	579.0077	637.0682	560.7509	698.8875	681.1197	594.2806	-0.15156	0.28082	0.40315	BROX	chr1	+	2.23E+08	2.23E+08	4124
ENSG00000(	3.107376	4.817151	2.638828	0.749076	1.840864	2.465895	0.83821	0.45416	0.58388	NBPF8	chr1	+	1.44E+08	1.44E+08	11691
ENSG00000(	56.96855	78.2787	88.40072	151.3133	101.2475	129.0485	-0.77131	0.005817	0.01422	ACP6	chr1	-	1.47E+08	1.47E+08	1788
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	WDR64	chr1	+	2.42E+08	2.42E+08	4371
ENSG00000(	6298.651	6246.64	7206.638	386.523	514.5215	461.9443	3.8501	7.07E-194	1.89E-191	KIF26B	chr1	+	2.45E+08	2.46E+08	12113
ENSG00000(	169.8699	143.3102	170.2044	313.1136	323.0716	297.5513	-0.94486	3.06E-07	1.34E-06	TFB2M	chr1	-	2.47E+08	2.47E+08	1848
ENSG00000(	383.243	329.9748	440.6842	176.7818	184.0864	130.6924	1.2244	5.16E-10	2.89E-09	CNST	chr1	+	2.47E+08	2.47E+08	5126
ENSG00000(	268.2701	325.1577	345.6864	351.3164	329.5147	356.7328	-0.14628	0.38586	0.51674	PPP1R21	chr2	+	48667737	48742525	3208
ENSG00000(	0	0	1.319414	0.749076	3.681728	0.821965	-1.111	0.40933	0.54007	KLHDC8A	chr1	-	2.05E+08	2.05E+08	3177
ENSG00000(	9.322127	2.408575	2.638828	1.498151	4.60216	6.575719	0.1766	0.85726	0.90929	PM20D1	chr1	-	2.06E+08	2.06E+08	2152
ENSG00000(	483.7148	529.8866	379.9912	229.2171	207.0972	233.438	1.0531	2.37E-09	1.26E-08	PKDCC	chr2	+	42275160	42285668	2502
ENSG00000(	11.39371	4.817151	5.277655	44.19546	19.32907	35.34449	-2.0702	0.000529	0.00155	OXER1	chr2	-	42989642	42991401	1760
ENSG00000(	10.35792	25.29004	19.79121	48.68991	61.66894	55.07165	-1.5473	0.000353	0.001061	HAAO	chr2	-	42994229	43019733	1522
ENSG00000(	380.1356	395.0064	443.323	179.0291	264.164	182.4762	0.95885	5.94E-07	2.52E-06	B3GALNT2	chr1	-	2.36E+08	2.36E+08	3034
ENSG00000(	10.35792	9.634302	7.916483	0	3.681728	1.64393	2.0682	0.031393	0.064687	C1orf147	chr1	-	2.07E+08	2.07E+08	2096
ENSG00000(	3006.904	2690.379	2805.074	2232.245	2030.473	2072.174	0.42386	0.000112	0.000361	MAPKAPK2	chr1	+	2.07E+08	2.07E+08	2961
ENSG00000(	7.250543	0	1.319414	19.47596	9.20432	4.109825	-1.6193	0.088409	0.15836	IL24	chr1	+	2.07E+08	2.07E+08	1819
ENSG00000(	2.071584	3.612863	2.638828	31.46117	15.64734	18.90519	-2.7434	0.000256	0.000785	FAIM3	chr1	-	2.07E+08	2.07E+08	1950
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	FCAMR	chr1	-	2.07E+08	2.07E+08	2846
ENSG00000(	8487.279	8273.457	9200.272	9828.62	9335.021	8799.956	-0.10715	0.29941	0.42438	CAPN2	chr1	+	2.24E+08	2.24E+08	4130
ENSG00000(	397.7441	367.3078	302.1458	604.504	437.2052	537.5651	-0.56209	0.001247	0.003444	MRPL55	chr1	-	2.28E+08	2.28E+08	1423
ENSG00000(	30.03797	28.90291	19.79121	6.74168	7.363456	8.219649	1.7378	0.002484	0.006508	C1orf145	chr1	-	2.28E+08	2.28E+08	2893
ENSG00000(	2029.116	1978.645	2451.471	1119.119	1222.334	1128.558	0.89428	1.01E-12	6.91E-12	WDR26	chr1	-	2.25E+08	2.25E+08	6872
ENSG00000(	34.18113	34.92434	52.77655	25.46857	30.37426	16.4393	0.73141	0.094496	0.16732	REL	chr2	+	61108656	61150645	3155
ENSG00000(	87.00652	89.11729	137.219	55.43159	57.06678	87.95025	0.63175	0.040032	0.080077	PUS10	chr2	-	61167357	61245394	6366
ENSG00000(	295.2007	326.362	328.534	316.859	302.8221	327.142	0.003392	0.98332	0.99044	PEX13	chr2	+	61244360	61276394	1739
ENSG00000(	247.5543	262.5347	254.6469	603.7549	651.6659	588.5269	-1.266	4.18E-17	3.69E-16	KIAA1841	chr2	+	61293006	61391960	4516
ENSG00000(	52.82539	83.09585	63.33186	123.5975	149.11	179.1884	-1.1719	2.00E-05	7.14E-05	TRIM17	chr1	-	2.29E+08	2.29E+08	2652
ENSG00000(	342.8471	321.5448	335.1311	25.46857	37.73771	32.05663	3.3755	5.57E-47	1.39E-45	RFTN2	chr2	-	1.98E+08	1.99E+08	3251
ENSG00000(	68.36227	91.52587	85.7619	107.1178	88.36147	77.2647	-0.15407	0.58298	0.70056	DISC1	chr1	+	2.32E+08	2.32E+08	7059
ENSG00000(	1.035792	0	1.319414	0	0	1.64393	0.22525	0.86714	NA	AC007364.	chr2	-	1.51E+08	1.51E+08	1832
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	CAPN13	chr2	-	30945637	31043408	2683
ENSG00000(	6.214751	30.10719	25.06886	11.98521	14.72691	13.9734	0.55232	0.36844	0.49869	LRRTM1	chr2	-	80515483	80531874	4023
ENSG00000(	66.29068	75.87013	47.4989	42.69731	69.95283	50.96182	0.21718	0.52542	0.65042	MEMO1	chr2	-	32092878	32236299	1756
ENSG00000(	470.2495	490.1451	444.6424	716.1162	639.7002	766.8933	-0.59373	2.99E-05	0.000105	DPY30	chr2	-	32092878	32264881	1519
ENSG00000(	131.5456	149.3317	174.1626	262.9255	201.5746	175.9005	-0.49423	0.027765	0.058082	TYW5	chr2	-	2.01E+08	2.01E+08	6525
ENSG00000(	104.615	136.0845	117.4278	283.8996	178.5638	221.9305	-0.93139	6.83E-05	0.000228	C2orf47	chr2	+	2.01E+08	2.01E+08	1495
ENSG00000(	0	0	0	3.745378	1.840864	1.64393	-2.0159	0.13434	0.22333	KCNF1	chr2	+	11052063	11054350	2288
ENSG00000(	285.8786	349.2434	284.9934	109.365	85.60018	88.77221	1.684	4.28E-16	3.61E-15	PQLC3	chr2	+	11295324	11319000	1830
ENSG00000(	755.0923	843.0014	971.0885	1093.65	886.376	1017.593	-0.2238	0.11708	0.19985	ARL5A	chr2	-	1.53E+08	1.53E+08	5326

ENSG0000(	761.307	722.5726	796.9259	764.0571	848.6383	724.1511	-0.03469	0.79305	0.8648	FAM84A	chr2	+	14772810	14790933	6355
ENSG0000(	12.4295	12.04288	15.83297	1.498151	0	0	3.7954	0.000158	0.0005	KCNJ3	chr2	+	1.56E+08	1.56E+08	5021
ENSG0000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	NEUROD1	chr2	-	1.83E+08	1.83E+08	2852
ENSG0000(	140.8677	99.95588	137.219	92.88537	74.55499	127.4046	0.35389	0.19601	0.30268	CLHC1	chr2	-	55401927	55459699	2248
ENSG0000(	24.85901	7.225726	13.19414	10.48706	9.20432	13.15144	0.4439	0.49683	0.62535	PRORSD1P	chr2	+	55509455	55511658	2154
ENSG0000(	47.64643	33.72006	40.90183	58.42789	81.91845	73.97684	-0.79095	0.019501	0.042419	FRZB	chr2	-	1.84E+08	1.84E+08	3162
ENSG0000(	44.53905	61.41867	36.94359	67.4168	71.7937	54.24968	-0.42785	0.20954	0.31918	DUSP19	chr2	+	1.84E+08	1.84E+08	5176
ENSG0000(	890.781	874.3129	703.2475	358.0581	280.7318	286.0438	1.4106	1.73E-18	1.64E-17	CCDC104	chr2	+	55746740	55773015	2048
ENSG0000(	132.5814	125.2459	160.9685	335.5858	265.0844	313.1686	-1.1235	1.96E-08	9.61E-08	NUP35	chr2	+	1.84E+08	1.84E+08	2828
ENSG0000(	80.79177	107.1816	75.20659	345.3238	267.8457	265.4947	-1.7281	1.62E-14	1.24E-13	CCDC138	chr2	+	1.09E+08	1.09E+08	2383
ENSG0000(	0	6.021439	0	8.988907	31.29469	9.863579	-2.6369	0.004374	0.01096	C2orf48	chr2	+	10281509	10351851	1897
ENSG0000(	0	1.204288	0	0	0	4.109825	-0.75943	0.57378	NA	ZSWIM2	chr2	-	1.88E+08	1.88E+08	2091
ENSG0000(	359.4198	343.222	314.0205	85.39461	126.0992	119.1849	1.6161	2.63E-15	2.12E-14	FBXO41	chr2	-	73481810	73511559	7336
ENSG0000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	ALMS1P	chr2	+	73872046	73912703	1601
ENSG0000(	1622.05	1564.37	1366.913	825.4813	682.9605	592.6367	1.1124	2.51E-14	1.90E-13	ACTG2	chr2	+	74119441	74146992	2064
ENSG0000(	241.3395	248.0833	269.1604	315.3608	322.1512	283.5779	-0.27999	0.10151	0.17766	C2orf44	chr2	-	24252210	24272445	3817
ENSG0000(	502.3591	461.2422	608.2498	907.8796	844.9566	775.1129	-0.68503	4.06E-06	1.58E-05	SMC6	chr2	-	17845079	17981509	5233
ENSG0000(	431.9252	464.8551	453.8783	14.23244	20.2495	13.15144	4.7944	4.57E-77	2.31E-75	VSNL1	chr2	+	17720393	17838285	2725
ENSG0000(	200.9436	151.7403	125.3443	65.91865	79.15715	81.37453	1.0739	3.66E-05	0.000127	CCDC74A	chr2	+	1.32E+08	1.32E+08	2809
ENSG0000(	2964.436	2873.43	2675.771	4274.225	3504.085	3624.865	-0.42078	0.000332	0.001004	H3F3A	chr1	+	2.26E+08	2.26E+08	1863
ENSG0000(	163.6551	168.6003	118.7472	159.5531	157.3939	177.5444	-0.12879	0.56146	0.6815	ADCK3	chr1	+	2.27E+08	2.27E+08	5523
ENSG0000(	3.107376	0	9.235896	5.992604	8.283888	3.28786	-0.44144	0.65626	0.76117	SLC16A14	chr2	-	2.31E+08	2.31E+08	4390
ENSG0000(	314.8807	280.599	294.2293	160.3022	143.5874	131.5144	1.0256	5.45E-08	2.56E-07	EN1	chr2	-	1.2E+08	1.2E+08	2457
ENSG0000(	106.6866	152.9445	105.5531	92.13629	67.19154	67.40112	0.67701	0.014558	0.032612	ZNF2	chr2	+	95831177	95850065	3888
ENSG0000(	2006.329	2160.492	2264.114	874.9202	960.0106	812.9233	1.2777	5.24E-26	6.74E-25	SGCB	chr4	-	52886872	52904648	4431
ENSG0000(	510.6454	534.7037	555.4732	407.4971	551.3388	436.4634	0.19853	0.21079	0.3207	SPATA18	chr4	+	52917497	52963458	4396
ENSG0000(	21.75163	15.65574	5.277655	50.18806	34.05598	29.59074	-1.3416	0.010508	0.024308	NOSTRIN	chr2	+	1.7E+08	1.7E+08	2537
ENSG0000(	0	0	0	1.498151	1.840864	4.93179	-2.195	0.10101	0.17689	PCDP1	chr2	+	1.2E+08	1.2E+08	3294
ENSG0000(	0	0	0	41.94823	38.65814	45.20807	-6.215	2.80E-09	1.48E-08	CCDC140	chr2	+	2.23E+08	2.23E+08	1699
ENSG0000(	11.39371	10.83859	10.55531	53.18436	44.18074	69.86702	-2.2786	8.62E-07	3.60E-06	SGPP2	chr2	+	2.23E+08	2.23E+08	3336
ENSG0000(	1.035792	0	0	0	0.920432	1.64393	-0.43567	0.74499	NA	INHBB	chr2	+	1.21E+08	1.21E+08	3204
ENSG0000(	0	0	0	1.498151	1.840864	2.465895	-1.7134	0.20614	NA	XIRP2	chr2	+	1.68E+08	1.68E+08	12675
ENSG0000(	217.5163	264.9433	226.9392	100.3761	110.4518	110.1433	1.1379	4.08E-08	1.95E-07	BBS5	chr2	+	1.7E+08	1.7E+08	3475
ENSG0000(	697.088	643.0896	884.0072	965.5584	851.3996	782.5106	-0.22574	0.14123	0.23244	SMARCAD1	chr4	+	95128762	95212443	5017
ENSG0000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	HPGDS	chr4	-	95219686	95264027	1636
ENSG0000(	2415.467	2195.417	2923.821	3098.926	3231.637	2600.697	-0.24499	0.07088	0.13118	PDLIM5	chr4	+	95373037	95589377	6083
ENSG0000(	592.473	640.6811	649.1516	304.8737	610.2464	514.55	0.39602	0.051996	0.10047	OTUD7B	chr1	-	1.5E+08	1.5E+08	6352
ENSG0000(	2.071584	0	1.319414	0	2.761296	1.64393	-0.21042	0.87378	0.92068	STPG2	chr4	-	98105244	99064391	4203
ENSG0000(	812.0609	844.2057	967.1303	668.9245	894.6599	743.0563	0.18528	0.20956	0.31919	RPRD2	chr1	+	1.5E+08	1.5E+08	7605
ENSG0000(	7.250543	4.817151	6.597069	7.490755	8.283888	7.397684	-0.27893	0.7255	0.81586	ANKRD23	chr2	-	97490263	97523671	2597
ENSG0000(	18.64425	28.90291	15.83297	3.745378	0.920432	0	3.3278	4.58E-05	0.000157	CTSS	chr1	-	1.51E+08	1.51E+08	4107
ENSG0000(	1280.239	1188.632	1192.75	9145.463	7585.28	8077.449	-2.755	6.97E-129	8.15E-127	MSX1	chr4	+	4861393	4865663	1939
ENSG0000(	186.4425	254.1047	230.8974	292.1395	222.7445	278.6461	-0.24357	0.21899	0.33054	PACRGL	chr4	+	20697905	20754530	2073
ENSG0000(	13.46529	12.04288	1.319414	50.93714	32.21512	43.56414	-2.1129	0.000155	0.000493	BNIPL	chr1	+	1.51E+08	1.51E+08	2336

ENSG00000(	9.322127	7.225726	0	0	0	1.64393	2.3196	0.058648	0.11152	C1QTNF7	chr4	+	15341442	15447790	4516
ENSG00000(	2.071584	0	2.638828	0	1.840864	1.64393	0.2791	0.83206	0.8925	TNFAIP8L2	chr1	+	1.51E+08	1.51E+08	1178
ENSG00000(	182.2994	219.1804	219.0227	140.8262	167.5186	189.0519	0.31631	0.12904	0.21592	LYSMD1	chr1	-	1.51E+08	1.51E+08	2479
ENSG00000(	417.4241	472.0808	352.2835	591.7697	432.603	557.2922	-0.3478	0.044005	0.086974	SCNM1	chr1	+	1.51E+08	1.51E+08	2016
ENSG00000(	789.2734	820.1199	650.471	970.8019	861.5243	1006.907	-0.32774	0.019197	0.041818	VPS72	chr1	-	1.51E+08	1.51E+08	4267
ENSG00000(	686.73	718.9598	628.041	1223.24	1008.793	1056.225	-0.69149	3.01E-07	1.32E-06	ERCC3	chr2	-	1.28E+08	1.28E+08	4018
ENSG00000(	818.2756	812.8942	708.5252	992.5251	890.0577	882.7903	-0.24007	0.067676	0.12614	RNF149	chr2	-	1.02E+08	1.02E+08	2458
ENSG00000(	646.3341	578.0581	684.7758	992.5251	1110.961	1020.88	-0.70889	7.89E-08	3.65E-07	IWS1	chr2	-	1.28E+08	1.28E+08	2958
ENSG00000(	186.4425	196.2989	155.6908	420.9805	400.3879	457.8345	-1.2411	1.59E-12	1.07E-11	BOLA3	chr2	-	74362525	74375121	2982
ENSG00000(	1398.319	1395.769	1667.739	1114.624	916.7503	766.8933	0.67004	9.39E-06	3.50E-05	CDC42EP3	chr2	-	37869032	37965611	5700
ENSG00000(	6998.846	6701.861	6116.802	15448.93	10209.43	13374.19	-0.97526	4.17E-12	2.73E-11	S100A11	chr1	-	1.52E+08	1.52E+08	594
ENSG00000(	0	0	0	12.73428	11.04518	14.79537	-4.5518	6.70E-05	0.000224	IVL	chr1	+	1.53E+08	1.53E+08	2153
ENSG00000(	466.1064	451.6079	468.3919	504.1278	515.4419	446.327	-0.08032	0.58049	0.69858	DHX57	chr2	-	39024871	39103075	5518
ENSG00000(	0	0	0	26.21764	11.96562	15.61733	-5.0183	6.60E-06	2.50E-05	SPRR2D	chr1	-	1.53E+08	1.53E+08	800
ENSG00000(	0	0	0	0.749076	0.920432	1.64393	-1.0185	0.44577	NA	ARHGAP25	chr2	+	68906733	69053965	2979
ENSG00000(	0	0	0	9.737982	4.60216	6.575719	-3.6201	0.003096	0.007975	S100A9	chr1	+	1.53E+08	1.53E+08	577
ENSG00000(	0	1.204288	0	46.44268	23.93123	19.72716	-5.0095	3.26E-07	1.43E-06	TGFA	chr2	-	70674412	70781325	4310
ENSG00000(	213.3731	227.6104	262.5633	674.168	634.1776	626.3373	-1.4578	8.26E-21	8.65E-20	CCNYL1	chr2	+	2.09E+08	2.09E+08	3767
ENSG00000(	14.50109	7.225726	7.916483	77.15478	76.39586	64.11326	-2.7729	4.56E-10	2.56E-09	FZD5	chr2	-	2.09E+08	2.09E+08	6708
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CRYGC	chr2	-	2.09E+08	2.09E+08	629
ENSG00000(	825.5261	815.3028	869.4937	1223.989	1127.529	1063.623	-0.44372	0.000357	0.001074	DCAF16	chr4	-	17802278	17812381	4548
ENSG00000(	0	0	1.319414	2.247227	0	0	-0.3289	0.80275	NA	C1orf189	chr1	-	1.54E+08	1.54E+08	387
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	NPPC	chr2	-	2.33E+08	2.33E+08	1051
ENSG00000(	410.1736	446.7907	535.682	302.6265	224.5854	272.8924	0.79247	8.23E-06	3.09E-05	GNPDA2	chr4	-	44703885	44728612	5382
ENSG00000(	0	3.612863	3.958241	50.93714	31.29469	28.76877	-3.639	2.89E-07	1.27E-06	ALPP	chr2	+	2.33E+08	2.33E+08	2971
ENSG00000(	1.035792	0	1.319414	5.243529	0	0	-0.6462	0.63176	0.7417	GABRG1	chr4	-	46037786	46126098	6785
ENSG00000(	0	0	1.319414	4.494453	12.88605	5.753754	-3.0464	0.008656	0.020417	ALPPL2	chr2	+	2.33E+08	2.33E+08	2493
ENSG00000(	26.93059	21.67718	56.73479	0	0	0	6.3376	2.94E-09	1.55E-08	GABRB1	chr4	+	46995740	47428461	2143
ENSG00000(	276.5564	280.599	337.7699	738.5885	716.0961	603.3223	-1.1996	4.32E-14	3.23E-13	PAQR3	chr4	-	79808281	79860592	9811
ENSG00000(	11.39371	28.90291	11.87472	157.3059	166.5982	161.9271	-3.1716	4.39E-20	4.46E-19	NIPAL1	chr4	+	47916159	48042188	5298
ENSG00000(	1319.599	1251.255	1436.842	610.4966	600.1217	514.55	1.2128	3.33E-20	3.40E-19	ANTXR2	chr4	-	80822303	81046608	8273
ENSG00000(	125.3308	192.686	141.1773	216.4828	195.1316	206.3132	-0.42807	0.050385	0.097774	HELQ	chr4	-	84328496	84377009	3579
ENSG00000(	174.013	193.8903	126.6637	274.1617	292.6974	291.7975	-0.78794	9.37E-05	0.000307	MRPS18C	chr4	+	84377085	84390888	2482
ENSG00000(	1519.507	1658.304	1934.261	1092.901	1182.755	938.6839	0.66725	1.25E-06	5.15E-06	CGGBP1	chr3	-	88101094	88199035	5298
ENSG00000(	262.0554	278.1905	250.6886	77.90386	94.8045	69.04505	1.7026	2.34E-15	1.89E-14	FAM175A	chr4	-	84382092	84444501	2869
ENSG00000(	255.8406	299.8676	376.0329	26.96672	47.86246	32.05663	3.1044	5.93E-33	9.93E-32	GPR155	chr2	-	1.75E+08	1.75E+08	6730
ENSG00000(	716.768	604.5524	569.9868	365.5489	401.3084	542.4968	0.52969	0.002427	0.006371	PMVK	chr1	-	1.55E+08	1.55E+08	1280
ENSG00000(	1667.625	1560.757	1442.119	344.5748	422.4783	414.2703	1.9801	3.62E-48	9.46E-47	PBXIP1	chr1	-	1.55E+08	1.55E+08	3212
ENSG00000(	32.10955	21.67718	21.11062	103.3724	75.47542	53.42772	-1.5908	4.35E-05	0.000149	CLDN1	chr3	-	1.9E+08	1.9E+08	3481
ENSG00000(	495.1085	562.4024	628.041	785.7803	817.3436	911.5591	-0.5773	5.92E-05	0.000199	PYGO2	chr1	-	1.55E+08	1.55E+08	3146
ENSG00000(	700.1953	690.0569	893.2431	716.8653	924.1137	701.1361	-0.03676	0.81683	0.88128	HIPK1	chr1	+	1.14E+08	1.15E+08	8157
ENSG00000(	0	0	0	0	5.522592	3.28786	-2.1349	0.11377	0.19496	LENEP	chr1	+	1.55E+08	1.55E+08	649
ENSG00000(	3.107376	2.408575	2.638828	3.745378	0.920432	4.109825	-0.09015	0.93443	0.96052	DCST2	chr1	-	1.55E+08	1.55E+08	2494
ENSG00000(	6.214751	1.204288	3.958241	3.745378	4.60216	9.863579	-0.56997	0.54753	0.66926	DCST1	chr1	+	1.55E+08	1.55E+08	2279

ENSG00000(	311380.8	299402.8	386034.1	132.5864	235.6306	239.1918	10.641	0	0	COL6A3	chr2	-	2.38E+08	2.38E+08	10749
ENSG00000(	63.18331	37.33292	52.77655	380.5304	468.4999	392.8992	-2.9886	3.85E-39	7.78E-38	C1orf106	chr1	+	2.01E+08	2.01E+08	4298
ENSG00000(	29.00217	25.29004	22.43003	1.498151	0.920432	0	4.3687	2.31E-07	1.02E-06	AC017048.	chr2	-	1.77E+08	1.78E+08	1407
ENSG00000(	519.9675	479.3065	608.2498	495.888	388.4223	327.964	0.40352	0.023714	0.050539	YY1AP1	chr1	-	1.56E+08	1.56E+08	2927
ENSG00000(	19.68005	9.634302	31.66593	181.2763	177.6434	135.6242	-2.9831	5.10E-18	4.71E-17	KBTBD8	chr3	+	67048727	67061634	4684
ENSG00000(	0	4.817151	0	1.498151	7.363456	1.64393	-0.80085	0.51196	0.63899	FAM19A4	chr3	-	68780917	68981761	2292
ENSG00000(	436.0684	425.1136	474.989	379.0322	399.4675	277.0022	0.33869	0.051887	0.1003	EOGT	chr3	-	69024365	69063112	4731
ENSG00000(	1.035792	0	1.319414	2.247227	3.681728	6.575719	-1.7404	0.14574	0.23839	LMOD3	chr3	-	69156023	69172183	4086
ENSG00000(	906.3179	846.6143	647.8322	940.8389	783.2876	861.4192	-0.10561	0.4881	0.61718	APOA1BP	chr1	+	1.57E+08	1.57E+08	1125
ENSG00000(	1621.014	1605.316	1563.505	405.9989	381.9793	355.9108	2.0613	2.05E-61	7.44E-60	NBPF10	chr1	+	1.45E+08	1.45E+08	10697
ENSG00000(	433.9968	367.3078	460.4754	334.8368	374.6158	286.8658	0.33996	0.046239	0.090686	POGLUT1	chr3	+	1.19E+08	1.19E+08	3598
ENSG00000(	0	0	0	68.91495	45.10117	56.71558	-6.6139	1.39E-10	8.15E-10	SLC22A15	chr1	+	1.17E+08	1.17E+08	4720
ENSG00000(	41.43168	36.12863	30.34652	0	0	0	6.4174	1.22E-09	6.61E-09	CCKAR	chr4	-	26483022	26492084	1720
ENSG00000(	36.25272	51.78437	32.98534	0	0.920432	0.821965	5.3809	2.14E-10	1.24E-09	IGFN1	chr1	+	2.01E+08	2.01E+08	11810
ENSG00000(	4111.058	3834.452	4040.045	7746.19	7612.893	6913.547	-0.89262	6.84E-18	6.26E-17	ATP1A1	chr1	+	1.17E+08	1.17E+08	3763
ENSG00000(	15.53688	13.24716	17.15238	72.66033	90.20234	83.01846	-2.3702	1.04E-09	5.71E-09	SLC15A2	chr3	+	1.22E+08	1.22E+08	5673
ENSG00000(	83.89914	87.913	79.16483	67.4168	59.82808	34.52253	0.62405	0.054049	0.10401	EIF4E3	chr3	-	71728440	71803924	6205
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	PROK2	chr3	-	71820807	71834357	1549
ENSG00000(	848.3136	909.2372	1110.946	894.3962	873.49	763.6054	0.17851	0.21246	0.32254	LRRC58	chr3	-	1.2E+08	1.2E+08	7903
ENSG00000(	23492.8	23353.55	24166.38	14029.44	14403.84	12287.55	0.80115	1.06E-14	8.23E-14	FSTL1	chr3	-	1.2E+08	1.2E+08	5943
ENSG00000(	21.75163	37.33292	30.34652	62.92235	45.10117	47.67397	-0.79114	0.044621	0.087962	LMOD1	chr1	-	2.02E+08	2.02E+08	3970
ENSG00000(	0	7.225726	0	76.40571	71.7937	54.24968	-3.8511	0.000283	0.000863	ELF3	chr1	+	2.02E+08	2.02E+08	4994
ENSG00000(	1046.15	973.0645	1155.806	1677.929	1362.239	1282.265	-0.44473	0.00137	0.003759	TMEM183A	chr1	+	2.03E+08	2.03E+08	3019
ENSG00000(	1.035792	13.24716	11.87472	50.93714	70.87326	41.09825	-2.558	3.07E-06	1.21E-05	TMEM169	chr2	+	2.17E+08	2.17E+08	3460
ENSG00000(	785.1303	767.1313	778.4541	200.0032	226.4263	427.4218	1.4392	7.43E-11	4.44E-10	IGFBP7	chr4	-	57896939	57976551	1427
ENSG00000(	352.1692	446.7907	278.3963	82.39831	60.74851	75.62077	2.2806	1.39E-23	1.63E-22	TRIM46	chr1	+	1.55E+08	1.55E+08	3318
ENSG00000(	951.8928	840.5928	832.5501	805.2562	658.1089	676.4771	0.29403	0.034482	0.07022	KRTCAP2	chr1	-	1.55E+08	1.55E+08	3264
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CXCR1	chr2	-	2.19E+08	2.19E+08	2488
ENSG00000(	6381.514	5845.613	5756.602	10315.52	7322.957	7576.873	-0.48642	0.000344	0.001037	ARPC2	chr2	+	2.19E+08	2.19E+08	2226
ENSG00000(	3.107376	7.225726	6.597069	18.72689	8.283888	22.19305	-1.4382	0.047053	0.092075	TSACC	chr1	+	1.56E+08	1.56E+08	751
ENSG00000(	7213.255	6757.258	6491.516	10095.29	8666.788	8933.937	-0.43599	5.31E-05	0.00018	CCT3	chr1	-	1.56E+08	1.56E+08	2150
ENSG00000(	98.40023	111.9988	101.5949	163.2985	126.0992	148.7757	-0.48885	0.038422	0.077297	TMEM79	chr1	+	1.56E+08	1.56E+08	2442
ENSG00000(	8534.925	8887.643	6813.453	4911.688	3818.872	3938.856	0.9334	5.87E-12	3.80E-11	SSR2	chr1	-	1.56E+08	1.56E+08	5166
ENSG00000(	402.9231	455.2208	390.5465	672.6698	483.2268	482.4934	-0.39141	0.022467	0.048117	RNF25	chr2	-	2.2E+08	2.2E+08	1914
ENSG00000(	698.1237	826.1414	721.7193	525.102	455.6138	457.8345	0.63982	7.91E-06	2.97E-05	STK36	chr2	+	2.2E+08	2.2E+08	4933
ENSG00000(	1.035792	0	0	85.39461	75.47542	98.63579	-6.495	2.15E-13	1.54E-12	ADORA1	chr1	+	2.03E+08	2.03E+08	3407
ENSG00000(	1269.881	1328.329	1448.716	2194.791	2695.025	2243.142	-0.81614	8.11E-11	4.83E-10	SRGAP2	chr1	+	2.07E+08	2.07E+08	5967
ENSG00000(	145.0109	146.9231	162.2879	10.48706	16.56778	24.65895	3.0938	7.05E-21	7.39E-20	NEK10	chr3	-	27151576	27410951	4250
ENSG00000(	6.214751	6.021439	5.277655	0.749076	0	0	3.0761	0.010537	0.024372	CCDC141	chr2	-	1.8E+08	1.8E+08	9127
ENSG00000(	0	0	2.638828	0	2.761296	0.821965	-0.2421	0.85821	0.90984	FEV	chr2	-	2.2E+08	2.2E+08	1879
ENSG00000(	42.46747	28.90291	40.90183	10.48706	4.60216	7.397684	2.2114	3.50E-05	0.000121	CRYBA2	chr2	-	2.2E+08	2.2E+08	893
ENSG00000(	0	8.430014	3.958241	0.749076	0	0	2.4051	0.063638	0.11952	IHH	chr2	-	2.2E+08	2.2E+08	2019
ENSG00000(	196.8005	158.966	208.4674	716.1162	777.765	676.4771	-1.9366	1.87E-32	3.07E-31	KIAA1524	chr3	-	1.08E+08	1.08E+08	4075
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	EOMES	chr3	-	27757440	27764206	3386

ENSG00000(	274.4849	295.0505	273.1187	471.9176	389.3427	312.3467	-0.47656	0.010012	0.023282	CWC22	chr2	-	1.81E+08	1.81E+08	3280
ENSG00000(	391.5293	388.9849	403.7406	280.1543	239.3123	274.5363	0.57316	0.000396	0.001183	AZI2	chr3	-	28356494	28390618	4706
ENSG00000(	1827.137	1679.981	2126.895	829.9757	720.6983	595.9246	1.3872	6.53E-21	6.86E-20	TGFBR2	chr3	+	30647994	30735634	4621
ENSG00000(	600.7593	539.5209	515.8908	409.7443	362.6502	443.0391	0.44535	0.003419	0.008754	ANKZF1	chr2	+	2.2E+08	2.2E+08	3245
ENSG00000(	290.0217	298.6634	321.937	56.18067	40.49901	76.44274	2.3713	1.32E-23	1.55E-22	HDAC11	chr3	+	13521224	13547916	2960
ENSG00000(	6594.887	6310.468	5156.269	66.66772	55.22592	55.89361	6.6385	0	0	FBLN2	chr3	+	13573824	13679922	4318
ENSG00000(	151.2256	149.3317	158.3297	116.1067	81.91845	91.23811	0.65664	0.006031	0.014703	GLB1L	chr2	-	2.2E+08	2.2E+08	2745
ENSG00000(	3695.706	3494.843	4405.523	5329.673	6000.296	4835.62	-0.4784	0.000159	0.000505	STT3B	chr3	+	31574130	31679112	4246
ENSG00000(	153.2972	154.1488	158.3297	303.3756	297.2995	347.6912	-1.0217	3.23E-08	1.56E-07	CHCHD4	chr3	-	14153580	14166370	1600
ENSG00000(	0	0	0	6.74168	6.443024	13.15144	-3.9643	0.000899	0.002539	DPPA2	chr3	-	1.09E+08	1.09E+08	1383
ENSG00000(	0	2.408575	1.319414	54.68252	80.07758	85.48435	-5.4038	2.78E-13	1.98E-12	NFASC	chr1	+	2.05E+08	2.05E+08	10654
ENSG00000(	208.1942	201.116	274.4381	615.7401	543.0549	484.9593	-1.2636	1.26E-12	8.61E-12	SGOL2	chr2	+	2.01E+08	2.01E+08	4214
ENSG00000(	240.3037	177.0303	207.148	105.6197	89.2819	54.24968	1.313	5.57E-07	2.37E-06	SERPINI1	chr3	+	1.67E+08	1.68E+08	1907
ENSG00000(	362.5272	358.8777	542.2791	761.0608	895.5803	638.6667	-0.85907	3.44E-06	1.35E-05	CLASP2	chr3	-	33537737	33759848	7282
ENSG00000(	1002.647	1073.02	845.7442	1127.359	786.0489	910.7371	0.048352	0.75694	0.83921	SUCLG1	chr2	-	84650647	84687169	1765
ENSG00000(	93.22127	60.21439	72.56776	1026.234	827.4684	853.1996	-3.5564	1.37E-77	7.09E-76	NUAK2	chr1	-	2.05E+08	2.05E+08	3405
ENSG00000(	637.012	633.4553	762.6212	853.197	870.7287	687.9846	-0.24669	0.096035	0.16965	PRKCI	chr3	+	1.7E+08	1.7E+08	4950
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	PYHIN1	chr1	+	1.59E+08	1.59E+08	2083
ENSG00000(	1925.537	1818.474	2008.148	444.2018	353.4459	294.2634	2.3883	2.75E-56	8.80E-55	IFI16	chr1	+	1.59E+08	1.59E+08	4138
ENSG00000(	0	0	0	12.73428	19.32907	8.219649	-4.5926	5.88E-05	0.000198	AIM2	chr1	-	1.59E+08	1.59E+08	1529
ENSG00000(	39.36009	40.94578	42.22124	1.498151	0	11.50751	3.0153	5.70E-06	2.18E-05	EFHB	chr3	-	19920964	19988517	2823
ENSG00000(	182.2994	219.1804	215.0644	100.3761	113.2131	77.2647	1.0762	2.71E-06	1.07E-05	EIF5A2	chr3	-	1.71E+08	1.71E+08	5593
ENSG00000(	0	0	0	0.749076	1.840864	0	-0.68825	0.58858	NA	SLC2A2	chr3	-	1.71E+08	1.71E+08	3210
ENSG00000(	1200.483	1219.943	1000.116	1406.764	863.3652	1154.039	-0.0019	0.99089	0.99468	RPL22L1	chr3	-	1.71E+08	1.71E+08	2190
ENSG00000(	7.250543	6.021439	0	0	0.920432	2.465895	1.4501	0.22778	0.34098	FABP1	chr2	-	88422510	88427635	2084
ENSG00000(	74.57702	108.3859	118.7472	179.7781	202.495	184.1201	-0.90776	0.000134	0.00043	PPM1L	chr3	+	1.6E+08	1.61E+08	10934
ENSG00000(	51.7896	19.2686	44.86007	43.44638	31.29469	32.8786	0.10508	0.80856	0.87566	ICA1L	chr2	-	2.04E+08	2.04E+08	5173
ENSG00000(	2380.25	2196.621	2355.154	1173.801	1435.874	1309.39	0.82181	7.42E-12	4.76E-11	SNHG16	chr17	+	74553848	74561430	3607
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	CTLA4	chr2	+	2.05E+08	2.05E+08	1977
ENSG00000(	1255.38	1415.038	1453.994	650.9467	774.0833	659.2159	0.98259	8.45E-14	6.19E-13	RYBP	chr3	-	72423744	72496069	4744
ENSG00000(	1004.718	976.6773	1139.974	1227.735	1142.256	989.6458	-0.10663	0.42491	0.55538	PPP4R2	chr3	+	73045936	73118350	4984
ENSG00000(	2.071584	0	0	2.247227	0	0	-0.04193	0.97501	NA	CD200R1	chr3	-	1.13E+08	1.13E+08	3679
ENSG00000(	224.7668	283.0076	258.6051	331.8405	391.1836	361.6646	-0.49999	0.003954	0.010003	GTPBP8	chr3	+	1.13E+08	1.13E+08	1787
ENSG00000(	864.8862	726.1855	792.9677	656.1902	540.2936	577.8413	0.42468	0.002776	0.007214	C3orf17	chr3	-	1.13E+08	1.13E+08	4992
ENSG00000(	186.4425	174.6217	176.8014	226.2208	220.9037	219.4646	-0.3074	0.10222	0.17857	SPICE1	chr3	-	1.13E+08	1.13E+08	5417
ENSG00000(	74.57702	65.03154	62.01245	37.45378	40.49901	32.05663	0.86398	0.010272	0.023815	KIAA1407	chr3	-	1.14E+08	1.14E+08	3976
ENSG00000(	493.0369	464.8551	488.1831	42.69731	53.38506	32.8786	3.4724	5.32E-61	1.91E-59	CADPS	chr3	-	62384022	62861054	5471
ENSG00000(	50.7538	37.33292	27.70769	16.47966	20.2495	39.45432	0.5926	0.20362	0.31176	NKX6-1	chr4	-	85413140	85419603	2628
ENSG00000(	29.00217	30.10719	58.05421	877.1675	817.3436	703.602	-4.3477	9.63E-82	5.38E-80	CDS1	chr4	+	85504132	85572491	4461
ENSG00000(	1016.112	982.6988	1453.994	709.3745	740.9478	635.3789	0.72373	7.08E-06	2.67E-05	WDFY3	chr4	-	85590704	85887544	14255
ENSG00000(	311.7734	273.3733	335.1311	331.0914	361.7298	419.2021	-0.27213	0.11339	0.1945	COX18	chr4	-	73921797	73935472	3128
ENSG00000(	1666.589	1559.553	2227.17	1024.735	1214.05	814.5672	0.83347	5.70E-07	2.42E-06	PTPN13	chr4	+	87515468	87736324	8573
ENSG00000(	0	0	0	41.94823	31.29469	29.59074	-5.9382	2.08E-08	1.02E-07	SYNPR	chr3	+	63213991	63602597	2709
ENSG00000(	94.25706	85.50443	0	3.745378	10.12475	27.94681	1.4806	0.23071	0.34409	ALB	chr4	+	74262831	74287129	2263

ENSG00000(	3.107376	4.817151	5.277655	5.992604	0	4.93179	0.20521	0.84366	0.90039	C3orf49	chr3	+	63805038	63834312	1292
ENSG00000(	33.14534	72.25726	34.30476	62.92235	60.74851	52.60575	-0.33088	0.37842	0.50912	C4orf36	chr4	-	87797358	87857354	2306
ENSG00000(	525.1465	650.3154	490.8219	1243.465	952.6471	970.7406	-0.92368	4.95E-09	2.56E-08	THOC7	chr3	-	63819546	63849579	990
ENSG00000(	273.4491	356.4692	379.9912	301.8774	350.6846	309.0588	0.068449	0.70171	0.79736	ATXN7	chr3	+	63850233	63989138	7285
ENSG00000(	1092.76	1074.225	1134.696	2418.016	2032.314	2002.307	-0.9652	3.38E-15	2.70E-14	PSMD6	chr3	-	63996225	64009658	4583
ENSG00000(	845.2062	898.3986	854.9801	531.0946	397.6266	402.7628	0.96002	2.29E-10	1.32E-09	PRICKLE2	chr3	-	64079543	64431152	8305
ENSG00000(	605.9383	669.584	736.2329	628.4744	818.264	558.9361	0.004335	0.97887	0.98772	ADAMTS9	chr3	-	64501333	64673676	7464
ENSG00000(	163.6551	132.4716	158.3297	76.40571	81.91845	55.07165	1.0825	2.67E-05	9.40E-05	PPM1K	chr4	-	89183315	89205921	2962
ENSG00000(	0	0	0	2.996302	0.920432	0	-1.1048	0.40628	NA	FAM194A	chr3	-	1.5E+08	1.5E+08	2052
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	CLRN1	chr3	-	1.51E+08	1.51E+08	2359
ENSG00000(	1179.767	1180.202	1253.443	2259.961	2108.71	1776.266	-0.76474	1.44E-09	7.79E-09	GMPS	chr3	+	1.56E+08	1.56E+08	5393
ENSG00000(	1116.584	1266.911	1344.483	807.5034	872.5695	695.3823	0.64814	2.30E-06	9.18E-06	TIPARP	chr3	+	1.56E+08	1.56E+08	4181
ENSG00000(	845.2062	952.5916	1058.17	976.0454	902.9438	773.469	0.10507	0.46102	0.59046	CCNL1	chr3	-	1.57E+08	1.57E+08	4799
ENSG00000(	2242.489	2391.715	2088.632	40.45008	51.54419	54.24968	5.5083	2.30E-240	1.10E-237	PTX3	chr3	+	1.57E+08	1.57E+08	1940
ENSG00000(	5.17896	14.45145	17.15238	11.23613	4.60216	9.863579	0.45756	0.52594	0.65083	HESX1	chr3	-	57231944	57260549	876
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	DCLK3	chr3	-	36753913	36781352	5344
ENSG00000(	494.0727	451.6079	608.2498	583.5299	728.9821	541.6749	-0.25428	0.12821	0.21482	SLMAP	chr3	+	57741177	57914895	6749
ENSG00000(	13946.94	13886.64	10518.37	8290.019	8260.877	8396.372	0.61925	5.16E-07	2.21E-06	RPL9	chr4	-	39455744	39460568	2153
ENSG00000(	142.9393	127.6545	157.0102	44.19546	30.37426	44.38611	1.8193	1.07E-10	6.32E-10	SMIM14	chr4	-	39552541	39640710	1892
ENSG00000(	22.78742	20.47289	18.47179	11.98521	11.96562	12.32947	0.73599	0.18523	0.28968	RPP14	chr3	+	58291974	58305816	3379
ENSG00000(	64.2191	63.82725	52.77655	29.96302	36.81728	32.05663	0.86138	0.014594	0.032683	ABHD6	chr3	+	58223233	58281420	2482
ENSG00000(	21.75163	28.90291	22.43003	26.96672	22.09037	30.4127	-0.12027	0.79496	0.86608	C3orf67	chr3	-	58703092	59035810	4108
ENSG00000(	39.36009	8.430014	21.11062	347.5711	321.2308	287.6877	-3.7166	5.21E-33	8.76E-32	RBM47	chr4	-	40425272	40632892	4951
ENSG00000(	924.9622	951.3873	1116.224	1638.228	1794.842	1444.192	-0.70368	1.42E-07	6.42E-07	APBB2	chr4	-	40812044	41218731	8972
ENSG00000(	38.3243	36.12863	14.51355	394.7628	396.7062	503.8645	-3.8032	5.13E-47	1.29E-45	IL17RE	chr3	+	9944296	9958086	2808
ENSG00000(	345.9545	358.8777	314.0205	133.3354	130.7013	158.6392	1.2637	1.01E-11	6.41E-11	IL17RC	chr3	+	9958758	9975314	2621
ENSG00000(	431.9252	391.3935	345.6864	303.3756	279.8113	348.5131	0.32729	0.053927	0.1038	CRELD1	chr3	+	9975506	9987097	2696
ENSG00000(	182.2994	146.9231	147.7743	30.7121	38.65814	36.16646	2.1597	4.10E-15	3.25E-14	PRRT3	chr3	-	9987226	9994078	3761
ENSG00000(	2.071584	1.204288	0	1.498151	2.761296	0.821965	-0.38463	0.76593	0.84553	FANCD2OS	chr3	-	10123001	10149915	1055
ENSG00000(	1633.444	1651.078	1432.883	208.243	186.8477	207.1352	2.961	1.90E-103	1.54E-101	PCOLCE2	chr3	-	1.43E+08	1.43E+08	2021
ENSG00000(	1029.577	918.8715	1103.03	1734.859	1658.618	1360.352	-0.63828	2.71E-06	1.07E-05	U2SURP	chr3	+	1.43E+08	1.43E+08	7420
ENSG00000(	471.2853	423.9093	493.4608	701.8838	664.5519	689.6286	-0.56526	4.77E-05	0.000163	MTMR14	chr3	+	9691117	9744077	2494
ENSG00000(	401.8873	393.8021	506.6549	310.8664	296.3791	263.8507	0.576	0.000699	0.002011	TTC14	chr3	+	1.8E+08	1.8E+08	7052
ENSG00000(	14.50109	19.2686	13.19414	2.247227	3.681728	0.821965	2.5367	0.001574	0.004266	CXCL3	chr4	-	74902306	74904524	1641
ENSG00000(	24.85901	14.45145	7.916483	38.95193	54.30549	30.4127	-1.3174	0.00842	0.019903	CXCL5	chr4	-	74861359	74864496	2538
ENSG00000(	51.7896	28.90291	51.45714	133.3354	129.7809	141.378	-1.5931	6.22E-08	2.91E-07	MTHFD2L	chr4	+	74979891	75168816	3181
ENSG00000(	217.5163	187.8689	215.0644	78.65293	44.18074	41.09825	1.8935	3.20E-12	2.12E-11	CXCL1	chr4	+	74735110	74736959	1097
ENSG00000(	195.7647	199.9118	250.6886	331.8405	287.1748	277.0022	-0.47254	0.011584	0.02653	RCHY1	chr4	-	76404247	76439974	4686
ENSG00000(	0	0	0	0	3.681728	2.465895	-1.6477	0.22446	0.33686	PLSCR2	chr3	-	1.46E+08	1.46E+08	1441
ENSG00000(	1.035792	0	1.319414	0	0.920432	0	0.55201	0.67753	NA	CCDC158	chr4	-	77234154	77343021	3663
ENSG00000(	338.704	339.6091	424.8512	859.1897	738.1865	677.2991	-1.043	5.20E-11	3.14E-10	GYG1	chr3	+	1.49E+08	1.49E+08	2052
ENSG00000(	159.512	167.396	265.2022	184.2726	269.6866	188.23	-0.11828	0.62299	0.73477	HPS3	chr3	+	1.49E+08	1.49E+08	4665
ENSG00000(	27.96638	38.53721	44.86007	391.0174	242.0736	238.3698	-2.9485	1.91E-25	2.40E-24	TM4SF18	chr3	-	1.49E+08	1.49E+08	3852
ENSG00000(	489.9296	419.0921	593.7362	1139.344	1221.413	939.5059	-1.132	1.35E-12	9.16E-12	TOPBP1	chr3	-	1.33E+08	1.33E+08	5378

ENSG0000(	1123.834	1201.879	1273.234	1397.775	1453.362	1313.5	-0.21075	0.076423	0.13986	RYK	chr3	-	1.34E+08	1.34E+08	5270
ENSG0000(	254.8048	225.2018	335.1311	261.4274	259.5618	190.6959	0.19271	0.35497	0.48465	SNRK	chr3	+	43328004	43466256	5183
ENSG0000(	27.96638	18.06432	17.15238	4.494453	4.60216	7.397684	1.825	0.004807	0.011945	UCN	chr2	-	27530268	27531313	795
ENSG0000(	422.6031	388.9849	362.8388	307.121	304.663	405.2287	0.20778	0.23072	0.34409	ZNF513	chr2	-	27600098	27603657	2139
ENSG0000(	478.5359	458.8336	567.3479	533.3418	527.4075	447.9709	-0.00503	0.97401	0.98483	SLC4A1AP	chr2	+	27886338	27917840	2959
ENSG0000(	53.86118	79.48299	54.09597	9.737982	13.80648	19.72716	2.0646	1.36E-06	5.56E-06	PLB1	chr2	+	28680012	28866654	5115
ENSG0000(	9.322127	13.24716	13.19414	5.992604	12.88605	13.15144	0.14991	0.82307	0.88585	SPDYA	chr2	+	29005383	29073477	2081
ENSG0000(	870.0652	780.3784	882.6878	1074.174	918.5911	941.9718	-0.21235	0.10457	0.18189	KIAA1143	chr3	-	44779153	44803154	5120
ENSG0000(	154.333	143.3102	157.0102	283.8996	326.7534	285.2218	-0.97303	2.18E-07	9.67E-07	KIF15	chr3	+	44803209	44914868	4842
ENSG0000(	4.143168	2.408575	11.87472	1.498151	0	4.93179	1.2112	0.25421	0.37226	TGM4	chr3	+	44916100	44956482	3388
ENSG0000(	949.8212	891.1729	964.4915	1636.73	1664.141	1463.098	-0.76238	2.31E-10	1.33E-09	WDR43	chr2	+	29117509	29171088	3533
ENSG0000(	1720.45	1738.991	1808.916	1240.469	1146.858	1225.55	0.54277	1.30E-06	5.33E-06	ZDHHC3	chr3	-	44956749	45017677	3226
ENSG0000(	21.75163	13.24716	9.235896	1414.255	1440.476	1069.376	-6.3621	2.00E-117	2.04E-115	CDCP1	chr3	-	45123770	45187914	6006
ENSG0000(	136.7245	124.0416	166.2461	0	0	0	8.2275	4.13E-17	3.64E-16	CLEC3B	chr3	+	45043040	45077563	936
ENSG0000(	2.071584	0	0	272.6635	381.0588	292.6195	-7.7855	2.07E-26	2.70E-25	SLC6A20	chr3	-	45796942	45838027	5423
ENSG0000(	273.4491	350.4477	347.0058	368.5452	222.7445	235.9039	0.22584	0.28908	0.41273	LZTFL1	chr3	-	45864808	45957534	4073
ENSG0000(	540.6834	572.0367	634.638	269.6672	471.2612	375.638	0.64449	0.000682	0.001964	FYCO1	chr3	-	45959396	46037316	8504
ENSG0000(	0	0	0	64.4205	57.98722	63.2913	-6.7312	4.98E-11	3.01E-10	CCR1	chr3	-	46243200	46249887	2731
ENSG0000(	0	0	0	1.498151	1.840864	3.28786	-1.8914	0.16147	0.25903	RTP3	chr3	+	46538981	46542439	1321
ENSG0000(	9.322127	21.67718	15.83297	22.47227	36.81728	39.45432	-1.0427	0.042079	0.083666	LRRC2	chr3	-	46556913	46621589	5100
ENSG0000(	531.3612	520.2523	412.9765	648.6994	591.8378	661.6818	-0.37454	0.012951	0.029339	ELP6	chr3	-	47537130	47555251	1401
ENSG0000(	294.1649	346.8349	267.841	116.8558	126.0992	106.0335	1.3748	5.75E-12	3.73E-11	DTX3L	chr3	+	1.22E+08	1.22E+08	5868
ENSG0000(	622.5109	670.7883	840.4666	576.0391	498.8741	500.5766	0.43392	0.005115	0.012649	ZNF148	chr3	-	1.25E+08	1.25E+08	9651
ENSG0000(	2.071584	0	0	3.745378	0	0	-0.39189	0.77243	NA	NMNAT3	chr3	-	1.39E+08	1.39E+08	2454
ENSG0000(	523.0749	457.6293	397.1435	820.2377	794.3328	864.7071	-0.84267	7.98E-09	4.03E-08	SMIM12	chr1	-	35178338	35325417	3454
ENSG0000(	402.9231	457.6293	465.7531	226.9699	214.4607	228.5062	0.97999	1.56E-09	8.40E-09	ZMYM6	chr1	-	35447134	35497569	6241
ENSG0000(	753.0207	771.9484	730.9552	605.253	526.4871	577.0194	0.39918	0.002769	0.007198	TPRA1	chr3	-	1.27E+08	1.27E+08	1933
ENSG0000(	1650.017	1596.886	1575.38	1078.669	1092.553	997.0434	0.60524	1.27E-07	5.77E-07	YEATS2	chr3	+	1.83E+08	1.84E+08	6506
ENSG0000(	0	0	0	0.749076	5.522592	9.041614	-3.0557	0.017431	0.038378	GRIK3	chr1	-	37261128	37499730	9101
ENSG0000(	67.32647	80.68728	62.01245	96.63075	48.7829	105.2115	-0.25445	0.44038	0.5701	ZC3H12A	chr1	+	37940153	37949980	2684
ENSG0000(	614.2246	643.0896	709.8446	740.0866	685.7218	590.1708	-0.03649	0.80016	0.86983	MEAF6	chr1	-	37958176	37980375	2147
ENSG0000(	293.1291	274.5776	262.5633	229.9662	305.5834	263.0288	0.058896	0.74571	0.83076	SNIP1	chr1	-	38002142	38019903	2471
ENSG0000(	158.4762	201.116	192.6344	50.93714	58.90765	69.04505	1.6122	8.45E-11	5.03E-10	DNALI1	chr1	+	38022520	38032458	3539
ENSG0000(	1125.906	1026.053	787.69	1349.085	1199.323	1345.557	-0.40319	0.005782	0.014142	POLR2H	chr3	+	1.84E+08	1.84E+08	1802
ENSG0000(	20.71584	24.08575	15.83297	67.4168	34.97642	55.89361	-1.3481	0.001842	0.004941	KLF15	chr3	-	1.26E+08	1.26E+08	2574
ENSG0000(	3.107376	6.021439	0	0.749076	4.60216	0.821965	0.44173	0.70977	0.80391	CCDC37	chr3	+	1.26E+08	1.26E+08	2089
ENSG0000(	42.46747	14.45145	23.74945	2.996302	7.363456	4.93179	2.2737	0.000469	0.001383	CAMK2N2	chr3	-	1.84E+08	1.84E+08	1362
ENSG0000(	3.107376	0	3.958241	0	4.60216	1.64393	0.13769	0.91166	0.94576	LIPH	chr3	-	1.85E+08	1.85E+08	4026
ENSG0000(	300.3797	296.2548	278.3963	412.7406	403.1492	350.1571	-0.41196	0.011278	0.025917	TMEM41A	chr3	-	1.85E+08	1.85E+08	4921
ENSG0000(	7140.749	6925.859	6896.576	5161.88	5074.342	5038.645	0.45616	2.16E-06	8.66E-06	RPN1	chr3	-	1.28E+08	1.28E+08	2310
ENSG0000(	664.9784	612.9824	621.4439	741.5848	769.4811	701.958	-0.21912	0.094548	0.16739	SENP2	chr3	+	1.85E+08	1.85E+08	5717
ENSG0000(	0	0	1.319414	2.247227	0.920432	4.109825	-1.4955	0.25748	0.37607	HEYL	chr1	-	40089825	40105617	3661
ENSG0000(	696.0522	768.3356	631.9992	457.6852	459.2956	412.6264	0.65559	5.38E-06	2.06E-05	IFT122	chr3	+	1.29E+08	1.29E+08	4532
ENSG0000(	14.50109	19.2686	19.79121	2.996302	16.56778	18.08323	0.48303	0.45935	0.58894	C3orf65	chr3	+	1.85E+08	1.85E+08	1924

ENSG00000(	197.8363	207.1375	182.0791	1012.75	785.1285	808.8135	-2.1425	2.13E-39	4.35E-38	RFC4	chr3	-	1.87E+08	1.87E+08	1448
ENSG00000(	64.2191	74.66584	51.45714	233.7116	258.6414	294.2634	-2.0277	5.02E-18	4.64E-17	RPL39L	chr3	-	1.87E+08	1.87E+08	756
ENSG00000(	2020.83	1888.323	1663.781	1883.176	1798.524	2109.162	-0.05472	0.65819	0.7629	BAP1	chr3	-	52435029	52444366	3937
ENSG00000(	11442.39	10567.62	9729.357	21582.36	17644.68	17797.18	-0.84364	8.58E-13	5.90E-12	TKT	chr3	-	53258723	53290068	7286
ENSG00000(	368.7419	431.135	386.5882	350.5674	391.1836	401.1189	0.053839	0.73174	0.82061	PRKCD	chr3	+	53190025	53226733	2810
ENSG00000(	477.5001	494.9623	391.8659	761.8098	645.2228	660.8598	-0.59724	8.20E-05	0.00027	RFT1	chr3	-	53122499	53164478	5108
ENSG00000(	14.50109	31.31148	23.74945	149.066	141.7465	141.378	-2.6109	1.00E-15	8.26E-15	SFMBT1	chr3	-	52937588	53080766	4548
ENSG00000(	1571.296	1690.82	1465.869	2924.391	2314.886	2398.494	-0.69052	6.71E-08	3.13E-07	GNL3	chr3	+	52715172	52728508	2118
ENSG00000(	968.4654	1027.257	1296.984	1243.465	1527.917	1232.947	-0.28213	0.05488	0.10542	PBRM1	chr3	-	52579368	52719933	7523
ENSG00000(	209.23	316.7277	199.2315	193.2615	289.0156	267.1386	-0.04556	0.83989	0.8975	UVSSA	chr4	+	1341054	1381837	4819
ENSG00000(	986.0739	1086.268	1244.207	793.271	975.6579	841.6921	0.34409	0.014089	0.031699	FAM208A	chr3	-	56654161	56717265	7119
ENSG00000(	392.5651	379.3506	428.8095	130.3391	141.7465	141.378	1.532	2.40E-18	2.25E-17	ARHGEF3	chr3	-	56761446	57113357	3992
ENSG00000(	613.1888	657.5411	683.4563	1992.541	1473.612	1575.707	-1.3649	1.13E-21	1.23E-20	SLBP	chr4	-	1694527	1714282	1977
ENSG00000(	3483.368	3393.683	2815.629	2942.369	2518.302	2776.597	0.23442	0.05571	0.10671	LRPAP1	chr4	-	3508103	3534286	7819
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	ZDHHC19	chr3	-	1.96E+08	1.96E+08	1813
ENSG00000(	141.9035	93.93444	106.8725	83.14739	71.7937	68.22309	0.61485	0.024678	0.052355	SLC51A	chr3	+	1.96E+08	1.96E+08	1463
ENSG00000(	1600.298	1530.65	1815.513	619.4855	1288.605	1083.35	0.72252	0.000237	0.000732	UBXN7	chr3	-	1.96E+08	1.96E+08	10568
ENSG00000(	362.5272	368.512	389.2271	408.2462	450.0912	453.7246	-0.22749	0.13133	0.21903	RNF168	chr3	-	1.96E+08	1.96E+08	5347
ENSG00000(	262.0554	248.0833	258.6051	431.4675	365.4115	383.0357	-0.61649	0.000184	0.000578	PIGX	chr3	+	1.96E+08	1.96E+08	3057
ENSG00000(	22.78742	13.24716	18.47179	137.8299	173.9616	211.245	-3.2013	9.61E-22	1.05E-20	MFI2	chr3	-	1.97E+08	1.97E+08	3963
ENSG00000(	3.107376	1.204288	0	5.992604	5.522592	18.08323	-2.2591	0.023955	0.051015	S100P	chr4	+	6694796	6698897	1279
ENSG00000(	0	0	1.319414	2.247227	3.681728	7.397684	-2.2762	0.067418	0.12571	ABLIM2	chr4	-	7967039	8160559	3587
ENSG00000(	38.3243	43.35436	47.4989	80.15108	82.83888	72.33291	-0.85702	0.006853	0.016526	EXO5	chr1	+	40974413	40982228	2567
ENSG00000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	CLDN19	chr1	-	43198764	43205925	3517
ENSG00000(	181.2636	173.4174	159.6491	176.0328	148.1896	197.2716	-0.01971	0.92522	0.95464	C1orf50	chr1	+	43232940	43263968	1558
ENSG00000(	149.154	157.7617	145.1355	69.66403	51.54419	46.852	1.4101	8.47E-08	3.91E-07	ERMAP	chr1	+	43282795	43310660	3949
ENSG00000(	118.0803	127.6545	113.4696	143.8225	150.0304	140.556	-0.27165	0.22216	0.33404	ZNF691	chr1	+	43312280	43318148	1935
ENSG00000(	663.9426	653.9282	608.2498	1073.425	652.5863	841.6921	-0.41385	0.015421	0.034328	AIMP1	chr4	+	1.07E+08	1.07E+08	2586
ENSG00000(	185.4068	180.6432	246.7304	107.1178	79.15715	117.541	0.99924	2.71E-05	9.53E-05	SGMS2	chr4	+	1.09E+08	1.09E+08	6149
ENSG00000(	971.5728	900.8072	1056.85	1764.073	1579.461	1380.901	-0.68852	2.62E-07	1.16E-06	METAP1	chr4	+	99916771	99983964	2791
ENSG00000(	527.2181	646.7025	902.479	572.2937	670.0745	494.8229	0.2546	0.17799	0.28039	DNAJB14	chr4	-	1.01E+08	1.01E+08	6463
ENSG00000(	1876.855	1761.873	1394.62	7206.856	4884.733	5683.887	-1.814	1.58E-32	2.60E-31	H2AFZ	chr4	-	1.01E+08	1.01E+08	1880
ENSG00000(	17.60846	6.021439	17.15238	3.745378	4.60216	0	2.0303	0.018871	0.041177	EMCN	chr4	-	1.01E+08	1.02E+08	4037
ENSG00000(	36.25272	16.86003	10.55531	5.243529	8.283888	16.4393	1.0342	0.11235	0.19298	SLC9B1	chr4	-	1.04E+08	1.04E+08	1879
ENSG00000(	274.4849	261.3304	261.2439	232.9625	193.2907	175.0785	0.40363	0.032969	0.067461	SLC9B2	chr4	-	1.04E+08	1.04E+08	3126
ENSG00000(	247.5543	192.686	199.2315	68.91495	86.52061	79.7306	1.4378	3.87E-10	2.19E-09	BDH2	chr4	-	1.04E+08	1.04E+08	2781
ENSG00000(	1778.455	1926.86	1884.123	2098.91	1879.522	2132.177	-0.12889	0.25442	0.3725	PGRMC2	chr4	-	1.29E+08	1.29E+08	3785
ENSG00000(	118.0803	102.3645	131.9414	1231.48	1569.337	1814.899	-3.6968	9.39E-96	6.73E-94	CDC25A	chr3	-	48198636	48229892	3783
ENSG00000(	148.1182	192.686	149.0938	256.9329	309.2652	341.1154	-0.88398	1.20E-05	4.40E-05	ZNF589	chr3	+	48282590	48340743	4703
ENSG00000(	5.17896	0	0	8.239831	4.60216	0.821965	-1.0038	0.39534	0.52637	FBXW12	chr3	+	48413709	48442666	2188
ENSG00000(	1568.189	1542.693	1472.466	1062.189	1355.796	1530.499	0.21512	0.13045	0.21787	PLXNB1	chr3	-	48445261	48471594	7308
ENSG00000(	251.6974	292.6419	261.2439	456.187	352.5255	498.9327	-0.69745	0.000101	0.000331	CCDC51	chr3	-	48473574	48481866	1560
ENSG00000(	193.6931	183.0517	153.052	356.56	295.4587	297.5513	-0.83566	1.07E-05	3.97E-05	ATRIP	chr3	+	48488114	48507115	2721
ENSG00000(	4841.291	4779.818	4365.94	5134.913	4367.45	4603.004	-0.01213	0.91259	0.94652	SHISA5	chr3	-	48509197	48542259	2369

ENSG00000(	486.8222	534.7037	471.0307	782.0349	819.1845	687.9846	-0.61499	1.36E-05	4.98E-05	SPRY1	chr4	+	1.24E+08	1.24E+08	2504
ENSG00000(	155.3688	163.7831	168.885	26.21764	66.2711	34.52253	1.9273	6.75E-10	3.75E-09	BSN	chr3	+	49591922	49708978	15955
ENSG00000(	1886.177	1758.26	1866.971	2856.974	2320.409	2514.391	-0.48023	5.36E-05	0.000181	APEH	chr3	+	49711435	49721396	3220
ENSG00000(	124.295	134.8802	178.1209	120.6012	112.2927	115.8971	0.31913	0.17624	0.27821	INTU	chr4	+	1.29E+08	1.29E+08	5740
ENSG00000(	574.8645	505.8008	558.112	325.8479	355.2868	388.7894	0.61401	5.12E-05	0.000174	RNF123	chr3	+	49726932	49758962	5882
ENSG00000(	153.2972	121.6331	187.3568	406.748	490.5903	351.801	-1.4273	3.53E-12	2.33E-11	HSPA4L	chr4	+	1.29E+08	1.29E+08	4128
ENSG00000(	172.9772	156.5574	208.4674	306.3719	279.8113	230.1502	-0.60067	0.00294	0.007606	MFSD8	chr4	-	1.29E+08	1.29E+08	4510
ENSG00000(	169.8699	133.6759	142.4967	321.3534	248.5166	283.5779	-0.92937	3.94E-06	1.53E-05	C4orf29	chr4	+	1.29E+08	1.29E+08	5450
ENSG00000(	2.071584	0	0	8.988907	8.283888	3.28786	-2.4283	0.032365	0.066416	CAMKV	chr3	-	49895421	49907655	3314
ENSG00000(	212.3373	178.2346	188.6762	252.4385	195.1316	208.7791	-0.1794	0.3684	0.49868	MON1A	chr3	-	49946302	49967606	2527
ENSG00000(	0	2.408575	0	8.988907	12.88605	13.9734	-3.1738	0.001891	0.005059	MST1R	chr3	-	49924435	49941299	4683
ENSG00000(	219.5879	201.116	323.2564	94.38352	294.5382	170.9687	0.39722	0.41311	0.54357	RAD54L2	chr3	+	51575160	51697610	5129
ENSG00000(	755.0923	755.0884	666.304	417.2351	395.7858	524.4136	0.70051	5.32E-06	2.04E-05	TEX264	chr3	+	51696709	51738339	3937
ENSG00000(	19.68005	4.817151	13.19414	4.494453	25.7721	15.61733	-0.24685	0.72662	0.81673	GRM2	chr3	+	51741086	51752629	6550
ENSG00000(	466.1064	401.0278	463.1142	489.1463	497.9537	498.1107	-0.15816	0.27871	0.40082	DUSP7	chr3	-	52082935	52090566	3340
ENSG00000(	138.7961	111.9988	126.6637	756.5663	613.0077	692.9164	-2.4381	1.31E-44	3.07E-43	POC1A	chr3	-	52109269	52188706	1999
ENSG00000(	396.7083	391.3935	348.3252	69.66403	63.50981	74.79881	2.4361	6.11E-35	1.09E-33	PPM1M	chr3	+	52279841	52284613	2429
ENSG00000(	0	0	0	0.749076	0	4.93179	-1.5344	0.25706	NA	AGXT2L1	chr4	-	1.1E+08	1.1E+08	2099
ENSG00000(	2623.661	2364.017	2625.633	2386.555	2958.268	2671.386	-0.0739	0.53697	0.66092	WDR82	chr3	-	52288437	52322036	4333
ENSG00000(	295.2007	216.7718	261.2439	194.0106	149.11	157.8173	0.62199	0.002454	0.006436	PITX2	chr4	-	1.12E+08	1.12E+08	3359
ENSG00000(	2925.076	2966.161	2661.258	933.3481	1117.404	1324.185	1.3385	2.27E-22	2.53E-21	C4orf3	chr4	-	1.2E+08	1.2E+08	2327
ENSG00000(	93.22127	99.95588	69.92893	1584.295	1989.974	1611.051	-4.2765	3.00E-135	3.83E-133	PRSS12	chr4	-	1.19E+08	1.19E+08	4809
ENSG00000(	0	1.204288	0	20.97412	31.29469	18.08323	-4.677	2.96E-06	1.17E-05	NDST3	chr4	+	1.19E+08	1.19E+08	5961
ENSG00000(	1045.114	1097.106	848.3831	3510.168	3193.899	3998.859	-1.8342	3.49E-42	7.68E-41	HMGB2	chr4	-	1.74E+08	1.74E+08	1889
ENSG00000(	633.9046	557.5852	420.893	247.1949	240.2328	263.0288	1.1005	6.42E-10	3.57E-09	SAP30	chr4	+	1.74E+08	1.74E+08	1108
ENSG00000(	360.4556	356.4692	302.1458	1.498151	0.920432	2.465895	7.3359	7.26E-42	1.58E-40	SCRG1	chr4	-	1.74E+08	1.74E+08	1642
ENSG00000(	1820.922	1643.853	1770.653	121.3502	96.64536	133.9803	3.8789	5.45E-148	8.16E-146	HAND2	chr4	-	1.74E+08	1.74E+08	2780
ENSG00000(	189.5499	250.4918	254.6469	1495.155	1314.377	1426.109	-2.6051	3.92E-67	1.61E-65	MAD2L1	chr4	-	1.21E+08	1.21E+08	1654
ENSG00000(	8520.424	8444.465	8760.908	10809.91	8618.005	9364.646	-0.16233	0.14859	0.24203	ANXA5	chr4	-	1.23E+08	1.23E+08	1762
ENSG00000(	0	0	0	2.247227	0	0.821965	-0.85594	0.51054	NA	TMEM155	chr4	-	1.23E+08	1.23E+08	2389
ENSG00000(	198.872	204.7289	298.1875	319.8553	254.9597	239.1918	-0.21728	0.30127	0.4264	MAP9	chr4	-	1.56E+08	1.56E+08	7333
ENSG00000(	1.035792	0	0	1515.38	1891.488	1540.362	-10.407	2.78E-42	6.16E-41	GUCY1A3	chr4	+	1.57E+08	1.57E+08	4400
ENSG00000(	165.7267	167.396	164.9267	151.3133	93.88406	120.0069	0.44034	0.062459	0.11764	FBXO8	chr4	-	1.75E+08	1.75E+08	2577
ENSG00000(	146.0467	161.3746	178.1209	279.4052	220.9037	161.9271	-0.44764	0.052661	0.10159	CEP44	chr4	+	1.75E+08	1.75E+08	4534
ENSG00000(	1.035792	10.83859	0	137.0808	126.0992	123.2947	-4.295	4.82E-06	1.86E-05	HPGD	chr4	-	1.75E+08	1.75E+08	3027
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	ASB5	chr4	-	1.77E+08	1.77E+08	3031
ENSG00000(	60.07593	46.96722	56.73479	131.0882	117.8153	120.8288	-1.1616	2.14E-05	7.64E-05	TMEM144	chr4	+	1.59E+08	1.59E+08	4872
ENSG00000(	968.4654	1085.063	1060.809	1250.956	1051.133	854.0216	-0.01995	0.8943	0.93465	FAM198B	chr4	-	1.59E+08	1.59E+08	4985
ENSG00000(	0	1.204288	0	5.243529	3.681728	4.109825	-2.2944	0.065133	0.12195	NPY1R	chr4	-	1.64E+08	1.64E+08	3029
ENSG00000(	790.3092	822.5285	931.5061	2034.489	2003.78	1675.986	-1.1656	5.18E-19	5.02E-18	NAA15	chr4	+	1.4E+08	1.4E+08	6222
ENSG00000(	11.39371	14.45145	10.55531	0.749076	3.681728	2.465895	2.1543	0.011351	0.026058	IL15	chr4	+	1.43E+08	1.43E+08	6026
ENSG00000(	16.57267	14.45145	13.19414	34.45748	51.54419	40.27628	-1.4599	0.001663	0.004489	FAM160A1	chr4	+	1.52E+08	1.53E+08	4576
ENSG00000(	536.5402	534.7037	555.4732	474.1648	461.1364	451.2587	0.2294	0.097844	0.1722	ARFIP1	chr4	+	1.54E+08	1.54E+08	3424
ENSG00000(	786.1661	826.1414	1000.116	895.1453	964.6127	710.1777	0.022817	0.88208	0.92636	KIAA0947	chr5	+	5420777	5490347	7927

ENSG00000(	371.8493	366.1035	430.1289	47.94084	40.49901	45.20807	3.1036	2.26E-48	5.98E-47	HHIP	chr4	+	1.46E+08	1.46E+08	10072
ENSG00000(	64.2191	62.62296	81.80365	169.2911	138.9852	182.4762	-1.2284	1.34E-06	5.50E-06	ANAPC10	chr4	-	1.46E+08	1.46E+08	1025
ENSG00000(	980.8949	1024.849	1031.782	2731.879	2147.368	2019.568	-1.1811	3.82E-18	3.55E-17	ABCE1	chr4	+	1.46E+08	1.46E+08	3921
ENSG00000(	600.7593	715.3469	839.1472	608.9984	691.2444	546.6067	0.22087	0.16537	0.26399	OTUD4	chr4	-	1.46E+08	1.46E+08	7069
ENSG00000(	137.7603	118.0202	117.4278	266.6709	282.5726	426.5998	-1.3747	9.68E-10	5.31E-09	LSM6	chr4	+	1.47E+08	1.47E+08	1352
ENSG00000(	1141.443	1223.556	1296.984	973.7982	1071.383	913.203	0.30693	0.014661	0.032816	TMEM184C	chr4	+	1.49E+08	1.49E+08	4178
ENSG00000(	167.7983	149.3317	166.2461	167.7929	163.8369	128.2265	0.071765	0.7412	0.82706	PRMT10	chr4	-	1.49E+08	1.49E+08	3528
ENSG00000(	360.4556	344.4263	448.6007	929.6028	921.3524	825.2528	-1.2126	5.15E-16	4.32E-15	ITGA2	chr5	+	52285156	52390609	7869
ENSG00000(	540.6834	549.1552	535.682	809.0016	697.6875	635.3789	-0.39748	0.005762	0.014104	MOCS2	chr5	-	52391509	52405893	3568
ENSG00000(	2.071584	0	3.958241	1.498151	0.920432	0	0.80653	0.53966	0.66319	SLC45A2	chr5	-	33944721	33984835	2723
ENSG00000(	2104.729	2091.848	2963.403	1317.624	1349.353	1109.653	0.91949	1.13E-09	6.18E-09	EDIL3	chr5	-	83236373	83680611	4727
ENSG00000(	214.4089	207.1375	255.9663	200.7522	231.9489	170.1467	0.16709	0.407	0.53794	TMEM161B	chr5	-	87485450	87565293	7608
ENSG00000(	6.214751	21.67718	5.277655	271.9144	271.5274	236.7259	-4.4817	2.87E-36	5.33E-35	ELOVL7	chr5	-	60047618	60140216	4165
ENSG00000(	369.7777	458.8336	372.0747	426.9731	341.4803	477.5616	-0.05453	0.75565	0.8383	NDUFAF2	chr5	+	60240956	60448853	708
ENSG00000(	9.322127	8.430014	15.83297	1.498151	0.920432	1.64393	2.6183	0.004277	0.010745	ZNF474	chr5	+	1.21E+08	1.22E+08	1964
ENSG00000(	152.2614	181.8474	230.8974	181.2763	153.7121	135.6242	0.25687	0.25781	0.37648	LMBRD2	chr5	-	36098514	36152063	8185
ENSG00000(	126.3666	186.6646	232.2168	1.498151	0	2.465895	6.6353	8.60E-28	1.19E-26	RANBP3L	chr5	-	36248536	36302216	3104
ENSG00000(	764.4144	651.5197	927.5479	707.1273	839.434	690.4505	0.066592	0.67093	0.77365	NIPBL	chr5	+	36876861	37066515	10435
ENSG00000(	0	7.225726	1.319414	31.46117	30.37426	16.4393	-2.9305	0.000134	0.000429	RNF180	chr5	+	63461671	63668696	4906
ENSG00000(	8.286335	26.49433	15.83297	43.44638	46.94203	39.45432	-1.3261	0.005563	0.013662	GPR98	chr5	+	89825161	90460038	19338
ENSG00000(	701.2311	739.4327	812.7589	904.1342	810.9006	774.291	-0.14467	0.28145	0.40399	SLC25A46	chr5	+	1.1E+08	1.1E+08	6232
ENSG00000(	1328.921	1388.544	1642.67	971.551	806.2984	712.6436	0.80439	4.10E-08	1.95E-07	STARD4	chr5	-	1.11E+08	1.11E+08	4606
ENSG00000(	207.1584	195.0946	183.3985	277.907	375.5363	309.8808	-0.71132	0.000166	0.000524	PGGT1B	chr5	-	1.15E+08	1.15E+08	2727
ENSG00000(	454.7126	503.3923	443.323	21.72319	22.09037	18.08323	4.4664	6.66E-78	3.48E-76	F2RL2	chr5	-	75911307	75919259	3429
ENSG00000(	273.4491	251.6961	240.1333	136.3317	129.7809	127.4046	0.95547	8.11E-07	3.39E-06	CCDC112	chr5	-	1.15E+08	1.15E+08	2566
ENSG00000(	140.8677	113.203	184.7179	32.95932	94.8045	78.90863	1.0741	0.001312	0.003613	ANKRD33B	chr5	+	10564442	10650308	1591
ENSG00000(	4653.813	4772.592	4604.754	900.3888	925.9546	969.0966	2.3241	1.59E-108	1.38E-106	CMBL	chr5	-	10275987	10308138	2335
ENSG00000(	5.17896	3.612863	0	2.247227	3.681728	1.64393	0.19026	0.86732	0.9166	C5orf63	chr5	-	1.26E+08	1.26E+08	5680
ENSG00000(	1816.779	1749.83	2045.091	1073.425	981.1805	853.1996	0.94572	4.10E-13	2.89E-12	PRRC1	chr5	+	1.27E+08	1.27E+08	5504
ENSG00000(	406.0304	484.1237	419.5736	1028.481	901.1029	835.9383	-1.076	1.77E-13	1.27E-12	F2RL1	chr5	+	76114758	76131140	2914
ENSG00000(	575.9003	639.4768	626.7215	510.8695	671.9154	520.3038	0.11352	0.45956	0.58904	AGGF1	chr5	+	76325076	76361059	4509
ENSG00000(	1119.691	1091.085	1139.974	600.0095	557.7818	494.8229	1.0169	9.16E-15	7.12E-14	WDR41	chr5	-	76721795	76916436	3958
ENSG00000(	688.8016	776.7656	649.1516	529.5964	418.7966	550.7165	0.49383	0.001351	0.003713	NDUFS4	chr5	+	52856463	52979168	833
ENSG00000(	1.035792	0	0	103.3724	133.4626	115.8971	-6.9057	1.57E-15	1.28E-14	SCGB3A2	chr5	+	1.47E+08	1.47E+08	672
ENSG00000(	1.035792	0	1.319414	5.992604	0.920432	1.64393	-1.2594	0.31919	0.44629	SPINK1	chr5	-	1.47E+08	1.47E+08	1188
ENSG00000(	0	0	0	6.74168	18.40864	7.397684	-4.2584	0.000283	0.000863	HTR4	chr5	-	1.48E+08	1.48E+08	3082
ENSG00000(	350.0977	355.2649	329.8534	468.9213	494.272	489.0691	-0.48601	0.00104	0.002909	GRPEL2	chr5	+	1.49E+08	1.49E+08	4109
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	CDC20B	chr5	-	54408799	54469005	3070
ENSG00000(	194.7289	220.3847	253.3274	265.9218	226.4263	265.4947	-0.1842	0.3312	0.45909	ARSK	chr5	+	94890778	94940768	3354
ENSG00000(	2210.38	2189.395	2658.619	3852.496	3660.558	3199.087	-0.60106	1.39E-06	5.69E-06	RHOBTB3	chr5	+	95049226	95160087	5537
ENSG00000(	3633.558	3617.68	3349.992	2150.596	1572.098	1745.032	0.95255	3.12E-13	2.21E-12	GPX8	chr5	+	54455946	54462899	3422
ENSG00000(	92.18548	59.0101	71.24834	69.66403	69.0324	46.852	0.26195	0.41349	0.54394	TIGD6	chr5	-	1.49E+08	1.49E+08	4006
ENSG00000(	165.7267	175.826	196.5927	200.7522	747.3908	431.5316	-1.3083	0.010257	0.023792	SERINC5	chr5	-	79407050	79551898	2767
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	ENPP6	chr4	-	1.85E+08	1.85E+08	3936

ENSG00000(	5.17896	0	0	0.749076	7.363456	3.28786	-0.78092	0.51796	0.64421	CAGE1	chr6	-	7326889	7389976	3284
ENSG00000(	824.4904	732.2069	825.953	1704.147	1213.129	1301.992	-0.8225	3.29E-08	1.58E-07	CASP3	chr4	-	1.86E+08	1.86E+08	2673
ENSG00000(	109.7939	99.95588	93.67838	171.5383	170.2799	123.2947	-0.60879	0.012156	0.027719	CCDC111	chr4	+	1.86E+08	1.86E+08	2289
ENSG00000(	446.4263	440.7693	534.3626	291.3904	323.9921	294.2634	0.64133	5.86E-05	0.000197	ERAP1	chr5	-	96096521	96143803	5488
ENSG00000(	19.68005	14.45145	9.235896	2.996302	4.60216	1.64393	2.0396	0.009398	0.021988	ERAP2	chr5	+	96211643	96255420	5705
ENSG00000(	6.214751	12.04288	7.916483	15.73059	12.88605	10.68554	-0.55379	0.41382	0.54422	CMYA5	chr5	+	78985700	79096063	12847
ENSG00000(	180.2278	167.396	166.2461	25.46857	46.0216	19.72716	2.4747	5.23E-16	4.39E-15	EGFLAM	chr5	+	38258511	38465123	4411
ENSG00000(	657.7279	686.444	854.9801	451.6926	516.3624	418.3801	0.66277	2.13E-05	7.58E-05	KIAA1430	chr4	-	1.86E+08	1.86E+08	4852
ENSG00000(	336.6324	313.1148	395.8241	183.5235	241.1532	156.9953	0.84265	2.63E-05	9.27E-05	RICTOR	chr5	-	38938021	39074510	9543
ENSG00000(	469.2137	521.4566	647.8322	911.6249	728.0617	708.5338	-0.51993	0.001415	0.003866	PAPD4	chr5	+	78907943	78982471	3523
ENSG00000(	594.5446	682.8311	596.375	2.996302	0	1.64393	8.1941	1.24E-54	3.80E-53	EBF1	chr5	-	1.58E+08	1.59E+08	5250
ENSG00000(	124.295	155.3531	162.2879	143.8225	138.0648	109.3213	0.17134	0.46231	0.59158	ANKRA2	chr5	-	72848160	72861511	2063
ENSG00000(	352.1692	384.1678	511.9325	688.4004	554.1001	567.9778	-0.53764	0.00187	0.005011	UBLCP1	chr5	+	1.59E+08	1.59E+08	2388
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	FAM170A	chr5	+	1.19E+08	1.19E+08	1336
ENSG00000(	165.7267	148.1274	262.5633	499.6334	513.6011	411.8044	-1.3025	5.29E-10	2.96E-09	UTP15	chr5	+	72861268	72877794	3687
ENSG00000(	26.93059	33.72006	23.74945	16.47966	11.96562	13.9734	0.95346	0.059139	0.11229	TLR3	chr4	+	1.87E+08	1.87E+08	3047
ENSG00000(	19.68005	34.92434	30.34652	3.745378	0.920432	3.28786	3.1476	4.16E-06	1.61E-05	KLKB1	chr4	+	1.87E+08	1.87E+08	2363
ENSG00000(	1272.988	1377.705	1258.721	1272.679	857.8426	1049.649	0.29601	0.046586	0.091282	NSA2	chr5	+	74062817	74072737	1393
ENSG00000(	286.9144	276.9862	333.8117	253.9366	289.9361	230.9721	0.21112	0.2394	0.35441	GFM2	chr5	-	74017029	74063196	3249
ENSG00000(	0	0	0	38.20285	43.2603	55.07165	-6.3178	1.36E-09	7.35E-09	TERT	chr5	-	1253262	1295184	4018
ENSG00000(	403.9588	411.8664	430.1289	438.2092	318.4695	378.9258	0.13106	0.4302	0.56016	CCDC127	chr5	-	204872	218330	1456
ENSG00000(	12.4295	9.634302	13.19414	9.737982	10.12475	9.863579	0.23066	0.72719	0.81726	FOXQ1	chr6	+	1312675	1314992	2318
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	C6orf195	chr6	-	2622147	2634837	2434
ENSG00000(	0	0	0	2.996302	0	2.465895	-1.5141	0.2635	NA	GPR111	chr6	+	47624172	47665533	5126
ENSG00000(	0	7.225726	0	0	0	0	1.9679	0.14595	0.2386	ACSL6	chr5	-	1.31E+08	1.31E+08	6539
ENSG00000(	1145.586	1099.515	1132.057	1092.152	1366.842	1163.902	-0.10035	0.43448	0.56417	8-Sep	chr5	-	1.32E+08	1.32E+08	4390
ENSG00000(	50.7538	39.74149	34.30476	83.89646	69.0324	71.51095	-0.82816	0.012196	0.027799	SHROOM1	chr5	-	1.32E+08	1.32E+08	4019
ENSG00000(	3.107376	0	1.319414	7.490755	0.920432	0.821965	-0.7484	0.5413	0.66417	GDF9	chr5	-	1.32E+08	1.32E+08	2640
ENSG00000(	329.3818	407.0492	288.9516	380.5304	225.5058	267.1386	0.22863	0.28129	0.4038	UQCRQ	chr5	+	1.32E+08	1.32E+08	874
ENSG00000(	22.78742	7.225726	18.47179	29.21395	23.0108	20.54912	-0.55653	0.31044	0.43655	LEAP2	chr5	+	1.32E+08	1.32E+08	2207
ENSG00000(	1.035792	1.204288	0	8.239831	17.48821	15.61733	-3.4117	0.000601	0.001746	GJB7	chr6	-	87992696	88038996	2281
ENSG00000(	77.68439	102.3645	88.40072	83.89646	46.0216	66.57916	0.43755	0.15548	0.25129	SLC35A1	chr6	+	88180341	88222054	1851
ENSG00000(	1.035792	2.408575	1.319414	12.73428	13.80648	6.575719	-2.4014	0.010353	0.023989	GRIK2	chr6	+	1.02E+08	1.03E+08	4921
ENSG00000(	23.82321	25.29004	30.34652	81.64923	71.7937	80.55256	-1.5381	1.14E-05	4.19E-05	MB21D1	chr6	-	74123238	74161999	3182
ENSG00000(	0	0	0	11.23613	5.522592	8.219649	-3.8917	0.001176	0.003261	FABP7	chr6	+	1.23E+08	1.23E+08	2086
ENSG00000(	0	0	0	20.97412	11.04518	13.9734	-4.7998	2.03E-05	7.27E-05	TLX3	chr5	+	1.71E+08	1.71E+08	1493
ENSG00000(	2549.084	2572.359	2403.972	2495.92	2213.639	2109.162	0.14195	0.21269	0.32283	CITED2	chr6	-	1.4E+08	1.4E+08	1905
ENSG00000(	0	0	0	1.498151	1.840864	0	-0.93652	0.47589	NA	FAM26D	chr6	+	1.17E+08	1.17E+08	1353
ENSG00000(	52.82539	59.0101	71.24834	30.7121	34.05598	31.23467	0.91295	0.010024	0.023305	CREBRF	chr5	+	1.72E+08	1.73E+08	7788
ENSG00000(	339.7397	272.169	418.2542	502.6297	482.3064	417.5582	-0.44478	0.013409	0.030292	DCBLD1	chr6	+	1.18E+08	1.18E+08	3626
ENSG00000(	1376.567	1317.491	1378.787	1703.398	1422.988	1371.037	-0.14316	0.25491	0.37311	SFXN1	chr5	+	1.75E+08	1.75E+08	4231
ENSG00000(	6.214751	21.67718	15.83297	23.97042	19.32907	21.37109	-0.55177	0.33742	0.46595	SAMD3	chr6	-	1.3E+08	1.31E+08	3690
ENSG00000(	655.6563	593.7138	733.5941	339.3312	435.3643	360.0206	0.80358	3.52E-07	1.53E-06	TMEM200A	chr6	+	1.31E+08	1.31E+08	5017
ENSG00000(	0	0	0	4.494453	1.840864	8.219649	-3.0359	0.017686	0.038878	DACT2	chr6	-	1.69E+08	1.69E+08	2942

ENSG00000(	267.2343	291.4376	267.841	205.2467	205.2563	177.5444	0.48886	0.007014	0.016887	PDSS2	chr6	-	1.07E+08	1.08E+08	3540
ENSG00000(	530.3255	502.188	662.3457	215.7338	272.4479	207.1352	1.2807	4.39E-13	3.09E-12	STXBP5	chr6	+	1.48E+08	1.48E+08	4431
ENSG00000(	157.4404	173.4174	221.6615	0.749076	2.761296	2.465895	6.2776	4.95E-31	7.78E-30	IL31RA	chr5	+	55147207	55218678	2903
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	ANKRD55	chr5	-	55395507	55529186	2500
ENSG00000(	3.107376	0	1.319414	1.498151	0	0	0.79403	0.55806	NA	RAET1E	chr6	-	1.5E+08	1.5E+08	2099
ENSG00000(	0	0	0	1.498151	0.920432	2.465895	-1.4807	0.27499	NA	TBX20	chr7	-	35242042	35293758	1871
ENSG00000(	379.0998	332.3834	336.4505	382.7776	335.0372	388.7894	-0.07782	0.62851	0.73907	DAGLB	chr7	-	6448757	6523821	2897
ENSG00000(	12.4295	16.86003	23.74945	112.3613	110.4518	110.1433	-2.6226	2.06E-13	1.48E-12	KIAA0895	chr7	-	36363830	36429734	4241
ENSG00000(	698.1237	667.1754	832.5501	669.6735	525.5667	534.2772	0.34272	0.026295	0.055406	STK17A	chr7	+	43622357	43666385	3368
ENSG00000(	1438.715	1404.199	1377.468	1821.752	1892.408	1921.754	-0.41627	0.000139	0.000444	TRA2A	chr7	-	23544399	23571660	1845
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	FAM183B	chr7	-	38724946	38726637	1595
ENSG00000(	1491.54	1286.179	1849.818	832.2229	969.2149	835.9383	0.80862	5.17E-08	2.44E-07	GALNT10	chr5	+	1.54E+08	1.54E+08	5961
ENSG00000(	190.5857	183.0517	204.5091	250.9403	303.7426	281.934	-0.53029	0.004069	0.010267	SAP30L	chr5	+	1.54E+08	1.54E+08	1486
ENSG00000(	25548.84	25652.53	18128.75	17195.78	15632.62	17492.24	0.46123	0.000654	0.001888	RPS14	chr5	-	1.5E+08	1.5E+08	3119
ENSG00000(	16.57267	4.817151	7.916483	8.239831	19.32907	13.9734	-0.44724	0.5192	0.64544	HCN1	chr5	-	45259349	45696253	5405
ENSG00000(	25.8948	20.47289	29.0271	56.18067	66.2711	55.89361	-1.2175	0.001395	0.00382	MYOZ3	chr5	+	1.5E+08	1.5E+08	3445
ENSG00000(	474.3927	386.5764	547.5567	381.2795	408.6718	328.786	0.33062	0.055332	0.10612	COG5	chr7	-	1.07E+08	1.07E+08	5418
ENSG00000(	343.8829	279.3948	354.9223	132.5864	174.8821	115.8971	1.2039	6.81E-09	3.47E-08	C7orf60	chr7	-	1.12E+08	1.13E+08	3981
ENSG00000(	83.89914	90.32158	71.24834	38.20285	34.05598	38.63235	1.1302	0.000396	0.001182	GPR85	chr7	-	1.13E+08	1.13E+08	4933
ENSG00000(	467.1421	519.048	552.8344	614.991	548.5775	544.1408	-0.1516	0.29552	0.41991	SLU7	chr5	-	1.6E+08	1.6E+08	3793
ENSG00000(	338.704	310.7062	257.2857	466.6741	323.9921	335.3617	-0.31037	0.10601	0.18399	RP9	chr7	-	33134409	33149013	1121
ENSG00000(	296.2365	293.8462	314.0205	1323.616	1089.791	1233.769	-2.0081	3.73E-46	9.18E-45	PTTG1	chr5	+	1.6E+08	1.6E+08	1070
ENSG00000(	1543.33	1596.886	1381.426	465.1759	435.3643	459.4784	1.7293	1.84E-42	4.11E-41	CAMLG	chr5	+	1.34E+08	1.34E+08	2218
ENSG00000(	6.214751	7.225726	13.19414	898.1416	975.6579	868.8169	-6.622	1.35E-90	8.56E-89	FBXL21	chr5	+	1.35E+08	1.35E+08	1742
ENSG00000(	13.46529	12.04288	11.87472	103.3724	103.0884	107.6774	-3.0042	2.85E-15	2.29E-14	BMPER	chr7	+	33944523	34195484	5031
ENSG00000(	44.53905	72.25726	64.65128	67.4168	40.49901	44.38611	0.23945	0.49969	0.62804	RELL2	chr5	+	1.41E+08	1.41E+08	2520
ENSG00000(	0	1.204288	1.319414	0	0	0.821965	0.59385	0.65509	NA	SMAD5-AS1	chr5	-	1.35E+08	1.35E+08	1816
ENSG00000(	7.250543	9.634302	6.597069	32.21025	38.65814	63.2913	-2.4101	6.70E-06	2.54E-05	KCNK5	chr6	-	39156749	39197226	3756
ENSG00000(	3.107376	4.817151	15.83297	40.45008	28.53339	36.16646	-2.0754	0.000459	0.001356	KIF6	chr6	-	39297766	39693181	9082
ENSG00000(	370.8135	415.4793	444.6424	337.8331	352.5255	246.5895	0.39112	0.029791	0.061785	ZNF12	chr7	-	6728064	6746554	5051
ENSG00000(	568.6498	515.4351	459.156	202.2504	197.8929	189.8739	1.3834	3.47E-17	3.07E-16	SLC29A4	chr7	+	5314000	5343696	2880
ENSG00000(	150.1898	127.6545	143.8161	53.18436	33.13555	27.94681	1.8537	7.15E-10	3.96E-09	STEAP1	chr7	+	89783689	89794143	1313
ENSG00000(	278.628	252.9004	362.8388	188.767	171.2004	128.2265	0.8656	5.44E-05	0.000184	CDCA7L	chr7	-	21940518	21985702	3066
ENSG00000(	0	0	0	17.22874	36.81728	21.37109	-5.488	4.30E-07	1.86E-06	SP8	chr7	-	20823906	20826505	1714
ENSG00000(	278.628	314.3191	316.6593	626.9762	639.7002	500.5766	-0.95607	3.66E-09	1.91E-08	MIOS	chr7	+	7606503	7648560	3453
ENSG00000(	353.205	340.8134	347.0058	281.6524	266.9253	210.423	0.45383	0.010087	0.023437	KIAA1324L	chr7	-	86506222	86689015	6841
ENSG00000(	149.154	179.4389	167.5656	98.87797	139.9057	115.8971	0.48251	0.036412	0.073671	USP49	chr6	-	41757634	41863099	9034
ENSG00000(	19.68005	19.2686	23.74945	14.23244	25.7721	9.041614	0.34372	0.53987	0.6633	INTS4L1	chr7	+	64601603	64694600	2550
ENSG00000(	64.2191	59.0101	59.37362	14.98151	11.96562	23.83698	1.8003	1.10E-05	4.07E-05	SYTL3	chr6	+	1.59E+08	1.59E+08	2292
ENSG00000(	3.107376	4.817151	9.235896	8.239831	8.283888	6.575719	-0.40124	0.62677	0.73786	IQUB	chr7	-	1.23E+08	1.23E+08	3428
ENSG00000(	30.03797	15.65574	38.263	432.2166	491.5107	423.3119	-3.974	1.11E-54	3.40E-53	HEY1	chr8	-	80676245	80680098	2296
ENSG00000(	65.25489	95.13873	110.8308	283.8996	481.3859	292.6195	-1.9518	2.01E-14	1.53E-13	ZNF704	chr8	-	81540686	81787016	14386
ENSG00000(	651.5131	668.3797	629.3604	1345.34	794.3328	1112.119	-0.73613	1.86E-05	6.67E-05	FABP5	chr8	+	82192598	82197012	986
ENSG00000(	3.107376	0	0	0	4.60216	2.465895	-0.6946	0.5974	0.71304	SHH	chr7	-	1.56E+08	1.56E+08	4454

ENSG00000(	2.071584	1.204288	2.638828	4.494453	3.681728	1.64393	-0.57587	0.60712	0.72145	TAGAP	chr6	-	1.59E+08	1.59E+08	3887
ENSG00000(	265678.6	259837.1	277567.7	33547.35	37209.38	32148.69	2.9601	2.01E-186	4.96E-184	COL1A2	chr7	+	94023873	94060544	5993
ENSG00000(	138.7961	101.1602	151.7326	29.21395	23.0108	22.19305	2.3581	8.04E-14	5.90E-13	FNDC1	chr6	+	1.6E+08	1.6E+08	6552
ENSG00000(	0	3.612863	0	299.6302	242.994	300.0172	-7.2892	1.20E-27	1.66E-26	CHMP4C	chr8	+	82644669	82671750	1866
ENSG00000(	125.3308	115.6116	166.2461	65.91865	96.64536	83.01846	0.72332	0.006471	0.015675	SLC13A4	chr7	-	1.35E+08	1.35E+08	7186
ENSG00000(	2374.035	2317.05	1947.455	2199.286	2246.775	2223.415	-0.00609	0.95851	0.97558	BRI3	chr7	+	97881691	97937162	819
ENSG00000(	230.9816	284.2119	282.3545	448.6963	566.9861	492.357	-0.91682	6.45E-08	3.01E-07	LMTK2	chr7	+	97736197	97838945	8946
ENSG00000(	29464.14	28854.73	26140.23	5427.801	4881.971	5185.777	2.4428	1.03E-123	1.13E-121	CTSB	chr8	-	11700033	11726957	3875
ENSG00000(	0	0	0	2.247227	0.920432	1.64393	-1.4644	0.28023	NA	SOX17	chr8	+	55370495	55373448	2342
ENSG00000(	473.3569	488.9408	654.4292	1522.122	1781.036	1380.901	-1.5315	7.49E-23	8.49E-22	DLC1	chr8	-	12940870	13373167	7447
ENSG00000(	40.39588	38.53721	40.90183	99.62705	116.8949	92.88204	-1.35	8.44E-06	3.16E-05	ADCY1	chr7	+	45613739	45762715	12503
ENSG00000(	54.89697	61.41867	55.41538	28.46487	33.13555	49.3179	0.61964	0.089634	0.16021	C8orf48	chr8	+	13424352	13425796	1445
ENSG00000(	0	0	0	0.749076	0	3.28786	-1.135	0.39451	NA	SUN3	chr7	-	48026745	48068716	1456
ENSG00000(	0	0	0	1.498151	4.60216	0.821965	-1.9199	0.15532	0.25108	C7orf57	chr7	+	48075108	48100901	2125
ENSG00000(	3.107376	3.612863	5.277655	2.247227	0	1.64393	1.2163	0.28881	0.41244	HNF4G	chr8	+	76320149	76479078	4209
ENSG00000(	481.6432	456.425	447.2813	211.2393	243.9145	254.8091	0.96274	2.74E-09	1.45E-08	PEX2	chr8	-	77892494	77913280	4386
ENSG00000(	1451.144	1356.028	1655.864	3134.132	3034.664	2794.681	-1.0046	4.70E-17	4.12E-16	RAD21	chr8	-	1.18E+08	1.18E+08	3749
ENSG00000(	99.43602	77.07441	81.80365	173.0365	193.2907	216.9987	-1.1619	6.59E-07	2.78E-06	MED30	chr8	+	1.19E+08	1.19E+08	985
ENSG00000(	16.57267	3.612863	14.51355	84.64554	69.0324	57.53754	-2.5188	5.27E-08	2.48E-07	TNFRSF11B	chr8	-	1.2E+08	1.2E+08	2402
ENSG00000(	40.39588	43.35436	32.98534	504.8769	380.1384	455.3686	-3.491	6.80E-51	1.92E-49	SBSPON	chr8	-	73976775	74036323	3801
ENSG00000(	21.75163	20.47289	26.38828	21.72319	12.88605	17.26126	0.38025	0.46157	0.59078	PHKG1	chr7	-	56148440	56160689	1717
ENSG00000(	6.214751	3.612863	5.277655	362.5526	456.5343	433.1755	-6.1982	4.97E-50	1.37E-48	EN2	chr7	+	1.55E+08	1.55E+08	3395
ENSG00000(	0	0	0	96.63075	78.23672	84.66239	-7.1655	1.27E-12	8.67E-12	KCNV1	chr8	-	1.11E+08	1.11E+08	6979
ENSG00000(	34.18113	33.72006	50.13772	102.6234	69.95283	61.64737	-0.98045	0.0053	0.013066	CSMD3	chr8	-	1.13E+08	1.14E+08	13212
ENSG00000(	1197.375	1085.063	1133.376	531.8436	520.0441	415.0923	1.2164	5.02E-18	4.64E-17	KIAA0146	chr8	+	48173167	48648868	3988
ENSG00000(	196.8005	210.7504	245.411	552.8178	372.775	404.4067	-1.0248	1.24E-07	5.63E-07	ORC5	chr7	-	1.04E+08	1.04E+08	2043
ENSG00000(	765.4502	739.4327	675.5399	1461.446	1223.254	1082.528	-0.78635	3.84E-08	1.84E-07	HEATR2	chr7	+	766338	829190	3410
ENSG00000(	156.4046	150.536	204.5091	288.3941	293.6178	241.6577	-0.68677	0.000629	0.001819	OSGIN2	chr8	+	90914087	90940116	4266
ENSG00000(	1151.801	1204.288	1234.971	1366.314	1604.313	1380.079	-0.27619	0.023574	0.050263	SUN1	chr7	+	855528	936072	4514
ENSG00000(	1520.543	1384.931	2071.48	521.3566	602.883	483.3154	1.6246	7.43E-24	8.80E-23	OXR1	chr8	+	1.07E+08	1.08E+08	4550
ENSG00000(	0	0	1.319414	11.98521	6.443024	13.15144	-3.5187	0.001479	0.004025	TMEM74	chr8	-	1.1E+08	1.1E+08	1741
ENSG00000(	33.14534	33.72006	23.74945	44.94453	48.7829	36.98842	-0.51123	0.19877	0.30619	FAM86FP	chr12	-	8385108	8395544	969
ENSG00000(	10.35792	2.408575	5.277655	5.243529	8.283888	4.93179	-0.01095	0.98992	0.99415	GPR146	chr7	+	1084212	1098897	1966
ENSG00000(	740.5912	581.671	552.8344	92.88537	102.168	95.34793	2.6817	7.60E-49	2.04E-47	GPER	chr7	+	1121844	1133451	2971
ENSG00000(	21.75163	16.86003	29.0271	8.988907	11.04518	9.041614	1.1605	0.043527	0.086161	TMEM184A	chr7	-	1585796	1600457	2843
ENSG00000(	2.071584	0	5.277655	5.992604	0.920432	0.821965	-0.07774	0.94817	0.96872	NOS3	chr7	+	1.51E+08	1.51E+08	4388
ENSG00000(	414.3168	407.0492	314.0205	130.3391	129.7809	132.3364	1.5269	5.96E-16	4.97E-15	MICALL2	chr7	-	1468101	1499138	5248
ENSG00000(	1.035792	3.612863	5.277655	50.93714	31.29469	41.09825	-3.4581	8.92E-08	4.11E-07	CA3	chr8	+	86285665	86361269	1753
ENSG00000(	3290.711	3011.924	2848.614	3164.844	4117.092	3968.447	-0.29677	0.019617	0.042644	INTS1	chr7	-	1509913	1545489	7485
ENSG00000(	338.704	275.7819	269.1604	419.4823	324.9125	350.1571	-0.30634	0.085975	0.15483	CDK5	chr7	-	1.51E+08	1.51E+08	1758
ENSG00000(	2324.317	2232.749	2053.008	1572.31	1844.546	2410.823	0.18156	0.22408	0.33654	SLC4A2	chr7	+	1.51E+08	1.51E+08	4925
ENSG00000(	1236.736	1116.375	837.8278	1089.156	805.378	974.8504	0.15321	0.34823	0.47789	FASTK	chr7	-	1.51E+08	1.51E+08	3011
ENSG00000(	912.5327	873.1086	695.3311	1060.691	924.1137	1179.52	-0.34903	0.018535	0.040514	TMUB1	chr7	-	1.51E+08	1.51E+08	1563
ENSG00000(	2.071584	10.83859	5.277655	2.247227	11.96562	5.753754	-0.1153	0.89771	0.93645	C7orf55	chr7	+	1.39E+08	1.39E+08	1210

ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	GBX1	chr7	-	1.51E+08	1.51E+08	1092
ENSG00000(	966.3938	991.1288	1001.435	1226.986	1029.963	1172.944	-0.21341	0.08736	0.1569	PHAX	chr5	+	1.26E+08	1.26E+08	4288
ENSG00000(	1444.93	1389.748	1447.397	2009.77	2039.677	2016.28	-0.50152	3.24E-06	1.27E-05	ALDH7A1	chr5	-	1.26E+08	1.26E+08	4964
ENSG00000(	1332.028	1340.372	1254.763	705.6292	1290.446	1103.899	0.34085	0.055217	0.10597	FOXK1	chr7	+	4683388	4811074	11181
ENSG00000(	1432.5	1315.082	1033.101	1083.912	1047.452	1246.921	0.16286	0.26176	0.38111	COX6C	chr8	-	1.01E+08	1.01E+08	828
ENSG00000(	67.32647	86.70872	51.45714	51.68621	44.18074	32.05663	0.67258	0.055528	0.10642	OSR2	chr8	+	99956631	99964332	1838
ENSG00000(	8636.433	8876.805	9427.211	23953.94	22208.18	20591.87	-1.3072	5.77E-36	1.07E-34	YWHAZ	chr8	-	1.02E+08	1.02E+08	5248
ENSG00000(	2123.373	2005.139	1828.708	31.46117	28.53339	31.23467	5.9975	4.88E-229	1.94E-226	BAALC	chr8	+	1.04E+08	1.04E+08	2831
ENSG00000(	2087.121	2179.761	2568.899	1023.986	1040.088	806.3476	1.2483	1.84E-19	1.82E-18	FZD6	chr8	+	1.04E+08	1.04E+08	3788
ENSG00000(	5239.035	5580.669	4698.432	620.2346	572.5087	568.7997	3.1328	1.17E-158	2.03E-156	CTHRC1	chr8	+	1.04E+08	1.04E+08	1271
ENSG00000(	1025.434	1134.439	1201.986	914.6212	639.7002	642.7766	0.60993	0.000114	0.000368	SLC25A32	chr8	-	1.04E+08	1.04E+08	2891
ENSG00000(	1268.845	1402.995	1320.733	1508.638	1286.764	1292.951	-0.03479	0.7773	0.85333	DCAF13	chr8	+	1.04E+08	1.04E+08	5300
ENSG00000(	1.035792	0	0	5.992604	6.443024	11.50751	-3.169	0.006143	0.014951	DCSTAMP	chr8	+	1.05E+08	1.05E+08	1953
ENSG00000(	1260.559	1219.943	1711.28	420.2314	613.0077	462.7662	1.4813	6.12E-18	5.62E-17	TP53INP1	chr8	-	95938200	95961639	5638
ENSG00000(	508.5738	551.5638	628.041	680.1606	611.1668	568.7997	-0.1415	0.33848	0.46708	INTS8	chr8	+	95825539	95893974	4633
ENSG00000(	1208.769	1113.966	1471.146	1044.211	1030.884	890.188	0.35386	0.011658	0.026679	KIAA1429	chr8	-	95499921	95565757	6528
ENSG00000(	7.250543	24.08575	7.916483	90.63814	104.9292	102.7456	-2.8609	8.22E-12	5.27E-11	FREM1	chr9	-	14734664	14910993	10089
ENSG00000(	728.1617	710.5298	724.3582	14.23244	3.681728	14.79537	5.9462	2.47E-104	2.04E-102	GEM	chr8	-	95261481	95274578	2208
ENSG00000(	713.6606	797.2385	946.0197	686.1532	793.4124	667.4355	0.19308	0.19154	0.29714	PDP1	chr8	+	94870035	94938294	4358
ENSG00000(	277.5922	337.2006	275.7575	140.8262	140.8261	126.5826	1.1195	6.30E-09	3.22E-08	TMEM67	chr8	+	94767072	94831462	4651
ENSG00000(	795.4882	776.7656	922.2702	682.4078	621.2916	536.7431	0.43635	0.002665	0.00695	KIAA0196	chr8	-	1.26E+08	1.26E+08	4187
ENSG00000(	270.3417	273.3733	174.1626	196.2578	137.1444	169.3248	0.51082	0.025015	0.052994	RPP25L	chr9	-	34610483	34612101	1092
ENSG00000(	860.7431	930.9144	750.7464	513.8658	526.4871	556.4703	0.66996	1.39E-06	5.67E-06	FAM219A	chr9	-	34398182	34458568	3644
ENSG00000(	0	2.408575	2.638828	1.498151	0	0	0.90396	0.50381	0.63148	C9orf24	chr9	-	34379017	34397830	1151
ENSG00000(	1211.877	1270.524	1277.193	925.8574	948.9654	858.1314	0.45908	0.000115	0.000373	SNAPC3	chr9	+	15422702	15465951	5680
ENSG00000(	44.53905	39.74149	36.94359	120.6012	157.3939	126.5826	-1.7127	2.96E-09	1.56E-08	KIAA1161	chr9	-	34366668	34376851	6398
ENSG00000(	333.525	351.652	269.1604	353.5637	325.8329	354.2669	-0.11345	0.50365	0.63148	NUDT2	chr9	+	34329504	34343709	1073
ENSG00000(	782.0229	961.0216	948.6585	221.7264	245.7553	263.0288	1.8754	1.09E-34	1.94E-33	TMEM65	chr8	-	1.25E+08	1.25E+08	3228
ENSG00000(	847.2778	822.5285	876.0908	1456.203	1451.521	1329.117	-0.73359	7.40E-10	4.10E-09	PSIP1	chr9	-	15464064	15511017	3391
ENSG00000(	56.96855	54.19295	56.73479	32.95932	21.16994	23.83698	1.0786	0.004638	0.011571	CCDC171	chr9	+	15552895	16061661	6512
ENSG00000(	865.922	804.4642	905.1179	733.345	756.5951	801.4158	0.16817	0.18741	0.29208	UBAP1	chr9	+	34179003	34252521	2898
ENSG00000(	217.5163	210.7504	238.8139	151.3133	144.5078	161.9271	0.53903	0.005832	0.014255	DIRAS2	chr9	-	93372114	93405386	4385
ENSG00000(	0	0	0	452.4416	414.1944	458.6564	-9.2411	3.77E-23	4.32E-22	SYK	chr9	+	93564069	93660831	5005
ENSG00000(	10.35792	10.83859	9.235896	8.239831	1.840864	0	1.3621	0.13918	0.22965	NIPSNAP3B	chr9	+	1.08E+08	1.08E+08	1752
ENSG00000(	92.18548	150.536	127.9831	56.92974	57.98722	50.13986	1.1514	5.61E-05	0.000189	ABCA1	chr9	-	1.08E+08	1.08E+08	10494
ENSG00000(	696.0522	846.6143	664.9845	412.7406	276.1296	279.4681	1.1816	7.13E-11	4.27E-10	NFIL3	chr9	-	94171327	94186144	2085
ENSG00000(	66.29068	83.09585	63.33186	89.88907	69.0324	62.46933	-0.05908	0.84511	0.90109	LETM2	chr8	+	38243725	38267045	2745
ENSG00000(	671.1932	600.9396	645.1933	1089.156	928.7159	1167.19	-0.73043	1.10E-07	5.04E-07	METTL2B	chr7	+	1.28E+08	1.28E+08	5743
ENSG00000(	193.6931	171.0089	114.789	446.449	299.1404	303.3051	-1.1175	1.11E-06	4.59E-06	FXN	chr9	+	71650175	71715094	2608
ENSG00000(	70.43385	48.17151	44.86007	71.16218	73.63456	83.01846	-0.46449	0.14299	0.23462	ZMAT4	chr8	-	40388109	40755352	2466
ENSG00000(	1.035792	0	0	11.23613	6.443024	7.397684	-3.2411	0.004742	0.011803	TMEM71	chr8	-	1.34E+08	1.34E+08	1993
ENSG00000(	364.5988	414.275	451.2395	1498.151	1223.254	935.3961	-1.5672	1.23E-19	1.23E-18	MAMDC2	chr9	+	72658497	72841886	3616
ENSG00000(	4.143168	0	3.958241	0	2.761296	0.821965	0.81699	0.51923	0.64545	PRSS37	chr7	-	1.42E+08	1.42E+08	1834
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	CPA6	chr8	-	68334360	68658620	1861

ENSG00000(	10.35792	13.24716	14.51355	5.243529	19.32907	8.219649	0.21022	0.75915	0.84083	C8orf34	chr8	+	69242957	69731257	3652
ENSG00000(	18.64425	12.04288	9.235896	0	3.681728	1.64393	2.5823	0.003899	0.009876	TMC1	chr9	+	75136717	75451267	3201
ENSG00000(	2.071584	2.408575	2.638828	10.48706	10.12475	10.68554	-1.8826	0.032188	0.066097	ALDH1A1	chr9	-	75515578	75695358	2107
ENSG00000(	314.8807	287.8248	308.7428	310.8664	349.7642	227.6843	0.038032	0.84209	0.89915	KDM1B	chr6	+	18155560	18224084	4574
ENSG00000(	1548.509	1511.381	1688.85	627.7253	563.3044	611.5419	1.3936	8.92E-30	1.35E-28	HGSNAT	chr8	+	42995556	43057998	5249
ENSG00000(	0	7.225726	1.319414	112.3613	165.6778	156.1733	-5.4366	4.29E-22	4.74E-21	RASEF	chr9	-	85594500	85678092	5576
ENSG00000(	0	1.204288	0	20.22504	16.56778	10.68554	-4.12	8.76E-05	0.000288	GKAP1	chr9	-	86354336	86444431	1778
ENSG00000(	23.82321	28.90291	40.90183	47.19176	38.65814	42.74218	-0.45791	0.25447	0.37255	KIF27	chr9	-	86451613	86536342	4653
ENSG00000(	16.57267	21.67718	19.79121	413.4897	424.3192	411.8044	-4.3927	1.93E-60	6.82E-59	C9orf64	chr9	-	86553226	86571901	2443
ENSG00000(	8466.563	8246.962	8830.836	11910.3	13326.93	13610.92	-0.60396	4.66E-09	2.41E-08	HNRNPK	chr9	-	86582998	86595569	2942
ENSG00000(	0	3.612863	0	0	0	0.821965	0.85103	0.52479	NA	SSMEM1	chr7	+	1.3E+08	1.3E+08	1159
ENSG00000(	9.322127	6.021439	3.958241	35.20655	24.85166	11.50751	-1.753	0.008135	0.019289	RP11-213G	chr9	+	88430881	88464426	1656
ENSG00000(	825.5261	806.8728	1215.18	457.6852	592.7582	462.7662	0.90799	3.00E-07	1.31E-06	SVEP1	chr9	-	1.13E+08	1.13E+08	12341
ENSG00000(	0	0	0	13.48336	11.04518	27.12484	-4.9483	1.00E-05	3.72E-05	TRPV6	chr7	-	1.43E+08	1.43E+08	10425
ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	C7orf34	chr7	+	1.43E+08	1.43E+08	766
ENSG00000(	409.1378	444.3822	415.6153	385.7739	438.1256	333.7178	0.13288	0.41046	0.54116	ANKS6	chr9	-	1.01E+08	1.02E+08	7164
ENSG00000(	0	0	0	24.71949	17.48821	25.48091	-5.3598	8.43E-07	3.52E-06	FBP1	chr9	-	97365415	97402531	1487
ENSG00000(	154.333	162.5788	133.2608	115.3576	115.054	92.06007	0.47926	0.039979	0.07998	TMEM246	chr9	-	1.04E+08	1.04E+08	5070
ENSG00000(	357.3482	337.2006	533.0432	323.6006	371.8545	307.4149	0.28852	0.13507	0.22421	ZHX1	chr8	-	1.24E+08	1.24E+08	5108
ENSG00000(	0	0	0	5.243529	5.522592	0.821965	-2.6659	0.042047	0.08362	CYBB	chrX	+	37639264	37672714	4324
ENSG00000(	660.8352	804.4642	831.2307	414.9879	359.8889	350.979	1.023	1.88E-11	1.17E-10	DYNLT3	chrX	-	37696010	37706890	2217
ENSG00000(	32.10955	36.12863	13.19414	30.7121	16.56778	34.52253	-0.00307	0.99511	0.9969	WBSCR27	chr7	-	73248920	73256865	941
ENSG00000(	1026.47	900.8072	821.9948	1014.248	910.3072	1101.433	-0.13715	0.31972	0.44689	MID1IP1	chrX	+	38660685	38665790	2536
ENSG00000(	0	3.612863	0	0	0	2.465895	0.26281	0.84633	0.90204	NCF1C	chr7	-	74572445	74587848	1427
ENSG00000(	23.82321	25.29004	31.66593	13.48336	9.20432	10.68554	1.2151	0.022526	0.048221	C9orf84	chr9	-	1.14E+08	1.15E+08	5060
ENSG00000(	1.035792	0	0	2.247227	0	0	-0.31629	0.80869	NA	CXorf58	chrX	+	23925918	23957624	1752
ENSG00000(	46.61064	75.87013	87.08131	146.0697	182.2455	127.4046	-1.1161	8.13E-05	0.000268	KIAA1958	chr9	+	1.15E+08	1.15E+08	11775
ENSG00000(	33.14534	10.83859	21.11062	183.5235	228.2671	243.3016	-3.2629	2.08E-24	2.52E-23	PTCHD1	chrX	+	23352133	23422489	13714
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RNF183	chr9	-	1.16E+08	1.16E+08	2312
ENSG00000(	4.143168	15.65574	0	0	0	0	1.5976	0.22029	0.332	ASB11	chrX	-	15298053	15333778	2866
ENSG00000(	37.28851	45.76293	75.20659	182.0254	225.5058	171.7907	-1.8638	3.68E-11	2.25E-10	PCDH19	chrX	-	99546642	99665271	9756
ENSG00000(	160.5477	184.256	135.8996	205.9958	255.8801	241.6577	-0.54346	0.008342	0.019732	PIGA	chrX	-	15337573	15353676	3590
ENSG00000(	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	FIGF	chrX	-	15363713	15402498	2037
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	OR1K1	chr9	+	1.26E+08	1.26E+08	1026
ENSG00000(	122.2234	175.826	134.5802	746.0792	681.1197	679.765	-2.2773	4.66E-39	9.39E-38	STRBP	chr9	-	1.26E+08	1.26E+08	6290
ENSG00000(	1.035792	1.204288	0	213.4865	231.0284	212.8889	-7.2962	8.00E-23	9.06E-22	CLDN3	chr7	-	73183328	73184600	1273
ENSG00000(	828.6335	915.2587	1005.393	781.2858	872.5695	671.5453	0.24043	0.095191	0.16835	GAPVD1	chr9	+	1.28E+08	1.28E+08	8923
ENSG00000(	672.2289	684.0354	621.4439	250.1912	239.3123	273.7143	1.3695	3.63E-20	3.70E-19	C9orf89	chr9	+	95858500	95875565	2690
ENSG00000(	1.035792	0	0	19.47596	45.10117	23.83698	-4.9934	3.99E-07	1.73E-06	WNK2	chr9	+	95947198	96082854	7792
ENSG00000(	386.3504	349.2434	605.6109	94.38352	113.2131	57.53754	2.3189	5.83E-20	5.89E-19	ATP7A	chrX	+	77166194	77305892	8483
ENSG00000(	24.85901	8.430014	5.277655	217.2319	211.6994	171.7907	-3.8319	2.63E-25	3.29E-24	ZNF367	chr9	-	99148223	99180611	3646
ENSG00000(	462.999	508.2094	587.1391	613.4929	642.4615	556.4703	-0.21884	0.14254	0.23408	NLGN4Y	chrY	+	16634518	16957530	6617
ENSG00000(	171.9415	138.4931	143.8161	95.88167	82.83888	101.1017	0.69425	0.003455	0.008836	HDX	chrX	-	83572882	83757487	6200
ENSG00000(	453.6769	375.7378	332.4923	549.0724	481.3859	584.4171	-0.47099	0.004312	0.010822	NDUFB6	chr9	-	32552997	32573160	1366

ENSG00000(	1.035792	6.021439	0	0	1.840864	1.64393	0.67934	0.59797	0.71361	AQP7	chr9	-	33384765	33402643	1668
ENSG00000(	851.4209	904.4201	893.2431	1819.505	1912.658	1881.478	-1.0818	1.67E-21	1.80E-20	NOL6	chr9	-	33461439	33473928	4741
ENSG00000(	16.57267	14.45145	3.958241	15.73059	26.69253	17.26126	-0.70771	0.2544	0.37249	AQP3	chr9	-	33441152	33447609	2911
ENSG00000(	197.8363	209.5461	186.0373	206.7449	201.5746	195.6277	-0.02483	0.89567	0.93537	TRMT10B	chr9	+	37753804	37778969	2281
ENSG00000(	8601.216	8890.052	8493.067	9878.808	10416.53	10580.33	-0.24847	0.01025	0.023778	VCP	chr9	-	35056061	35073246	4370
ENSG00000(	534.4686	510.618	501.3772	695.8912	675.5971	590.9928	-0.34227	0.014743	0.032969	PIGO	chr9	-	35088685	35096591	6655
ENSG00000(	2367.82	2289.351	1860.373	4199.318	2872.668	3242.652	-0.66013	1.01E-05	3.76E-05	STOML2	chr9	-	35099888	35103154	1278
ENSG00000(	632.8689	605.7567	810.1201	500.3825	955.4084	806.3476	-0.14184	0.48104	0.61015	BRWD3	chrX	-	79926353	80065187	11381
ENSG00000(	416.3883	397.4149	407.6989	41.94823	47.86246	38.63235	3.2338	4.25E-54	1.28E-52	SLITRK5	chr13	+	88324870	88331868	4444
ENSG00000(	362.5272	304.6848	399.7824	1544.594	1385.25	1288.841	-1.9786	3.77E-42	8.29E-41	MELK	chr9	+	36572859	36677678	2347
ENSG00000(	2.071584	0	2.638828	0.749076	6.443024	4.109825	-0.93865	0.42313	0.55364	ARMC3	chr10	+	23216953	23326518	2811
ENSG00000(	43.50326	50.58008	40.90183	26.21764	14.72691	14.79537	1.234	0.004917	0.012199	OTUD1	chr10	+	23728198	23731308	3111
ENSG00000(	591.4372	557.5852	606.9303	543.8288	591.8378	437.2853	0.15868	0.30331	0.42847	ARHGAP12	chr10	-	32094365	32217742	4914
ENSG00000(	14.50109	51.78437	38.263	267.42	315.7082	210.423	-2.9004	5.05E-20	5.11E-19	FAT3	chr11	+	92085262	92629618	19126
ENSG00000(	0	0	0	8.988907	7.363456	4.109825	-3.5829	0.003503	0.008948	CCDC67	chr11	+	93063137	93171653	2784
ENSG00000(	383.243	349.2434	521.1684	194.0106	181.3251	135.6242	1.2854	4.57E-10	2.57E-09	HECTD2	chr10	+	93170096	93274586	5368
ENSG00000(	0	1.204288	0	53.18436	21.16994	26.30288	-5.1596	1.09E-07	4.98E-07	SLC7A3	chrX	-	70145432	70150975	2236
ENSG00000(	210.2658	150.536	281.0351	194.0106	173.0412	147.1317	0.31479	0.18653	0.29112	FBXO33	chr14	-	39866873	39901704	3853
ENSG00000(	259.9838	286.6205	252.008	190.2652	216.3015	180.0103	0.44446	0.016164	0.035836	DDX26B	chrX	+	1.35E+08	1.35E+08	6791
ENSG00000(	8.286335	2.408575	5.277655	0	0	0.821965	2.8938	0.017983	0.039434	CLDN2	chrX	+	1.06E+08	1.06E+08	3150
ENSG00000(	305.5586	232.4275	304.7846	519.8584	572.5087	503.0425	-0.91637	3.38E-08	1.63E-07	LRFN5	chr14	+	42076773	42373752	4253
ENSG00000(	6.214751	3.612863	9.235896	262.1764	320.3103	222.7525	-5.287	3.01E-38	5.94E-37	ZNF488	chr10	+	48355024	48373866	3561
ENSG00000(	744.7344	871.9043	998.7962	1047.208	1070.462	1206.645	-0.34658	0.01431	0.032132	SPTSSA	chr14	-	34901995	34931562	2777
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	ANXA8	chr10	+	48255253	48279200	1971
ENSG00000(	181.2636	193.8903	278.3963	253.9366	273.3683	156.1733	-0.06656	0.78276	0.85696	WRN	chr8	+	30891317	31031285	5215
ENSG00000(	509.6096	507.0051	535.682	208.243	206.1768	204.6693	1.3214	1.43E-17	1.29E-16	8-Mar	chr10	-	45950035	46090354	5021
ENSG00000(	100.4718	98.75159	105.5531	2.247227	1.840864	0	5.8254	1.35E-20	1.40E-19	TSHR	chr14	+	81421333	81612646	4566
ENSG00000(	1030.613	1213.922	1234.971	865.1823	675.5971	646.8864	0.66594	7.02E-06	2.65E-05	CFL2	chr14	-	35179593	35184029	3131
ENSG00000(	1036.828	1079.042	1143.932	1383.543	1047.452	1225.55	-0.16645	0.21872	0.33021	SUGT1	chr13	+	53226844	53262433	1663
ENSG00000(	1153.872	1287.384	1662.461	806.0053	1018.918	775.1129	0.6558	4.09E-05	0.000141	GTF2A1	chr14	-	81641796	81687721	6306
ENSG00000(	5517.663	5313.317	6210.481	536.3381	817.3436	598.3905	3.1182	2.50E-98	1.85E-96	ZCCHC24	chr10	-	81142081	81205383	4933
ENSG00000(	496.1443	433.5436	661.0263	198.505	215.3811	198.9155	1.369	1.14E-13	8.34E-13	PGM2L1	chr11	-	74041363	74109518	8515
ENSG00000(	3.107376	10.83859	3.958241	39.701	40.49901	30.4127	-2.5042	2.22E-05	7.89E-05	PHYHIPL	chr10	+	60936350	61007534	3578
ENSG00000(	31.07376	62.62296	40.90183	338.5821	274.2887	277.0022	-2.7083	1.54E-25	1.94E-24	SLC16A9	chr10	-	61410523	61495760	4174
ENSG00000(	2928.184	3257.598	2708.756	1436.727	1679.788	1722.017	0.87696	1.28E-12	8.70E-12	INPPL1	chr11	+	71934745	71950149	4733
ENSG00000(	0	1.204288	0	0.749076	0	0	0.1572	0.90001	NA	PHOX2A	chr11	-	71950121	71956708	1699
ENSG00000(	161.5835	216.7718	146.4549	20.22504	18.40864	22.19305	3.0675	5.14E-24	6.13E-23	GJB2	chr13	-	20761609	20767037	2309
ENSG00000(	237.1963	210.7504	149.0938	46.44268	25.7721	33.70056	2.4597	1.87E-17	1.68E-16	CRYL1	chr13	-	20977806	21099996	1581
ENSG00000(	964.3223	894.7858	877.4102	1040.466	1005.112	1001.975	-0.15445	0.20162	0.30921	REEP3	chr10	+	65281123	65384883	5205
ENSG00000(	6.214751	1.204288	0	4.494453	2.761296	2.465895	-0.27283	0.81077	0.87724	HEPACAM	chr11	-	1.25E+08	1.25E+08	3602
ENSG00000(	160.5477	118.0202	116.1084	848.7026	723.4595	789.0863	-2.5634	9.02E-49	2.42E-47	SKA3	chr13	-	21727734	21750741	2919
ENSG00000(	612.153	556.3809	675.5399	858.4406	797.0941	823.6088	-0.42685	0.001595	0.004318	MICU2	chr13	-	22066836	22178353	1920
ENSG00000(	81.82756	32.51577	59.37362	451.6926	322.1512	339.4715	-2.6458	1.84E-23	2.14E-22	C11orf82	chr11	+	82611017	82669319	3533
ENSG00000(	644.2626	712.9383	819.356	541.5816	585.3947	580.3072	0.34823	0.014715	0.032912	PCF11	chr11	+	82868030	82898493	7677

ENSG00000(	134.6529	166.1917	100.2754	82.39831	92.0432	96.99186	0.56114	0.031528	0.064919	PKNOX2	chr11	+	1.25E+08	1.25E+08	4531
ENSG00000(	44.53905	42.15007	56.73479	331.8405	214.4607	226.0404	-2.4125	7.36E-20	7.41E-19	LRR1	chr14	+	50065415	50081390	1886
ENSG00000(	2887.788	2879.452	2274.669	1697.405	1836.262	2779.885	0.34799	0.040309	0.080598	RPL36AL	chr14	-	50085237	50087403	746
ENSG00000(	263.0911	297.4591	242.7721	552.8178	498.8741	464.4102	-0.91278	2.25E-08	1.10E-07	DNAAF2	chr14	-	50091892	50101948	2963
ENSG00000(	40.39588	56.60152	34.30476	155.8077	127.0196	166.0369	-1.7527	1.18E-09	6.42E-09	C10orf10	chr10	-	45466429	45474258	2120
ENSG00000(	10.35792	10.83859	15.83297	38.95193	26.69253	26.30288	-1.2728	0.015089	0.033667	C10orf25	chr10	-	45493146	45496336	3078
ENSG00000(	152.2614	137.2888	131.9414	431.4675	265.0844	277.8241	-1.2007	8.09E-08	3.74E-07	ZNF22	chr10	+	45495923	45500774	2551
ENSG00000(	510.6454	481.7151	523.8073	403.7517	361.7298	398.653	0.37915	0.00973	0.022689	KLHDC2	chr14	+	50234326	50249909	2320
ENSG00000(	53.86118	60.21439	59.37362	123.5975	102.168	64.93523	-0.73741	0.019464	0.042354	EML5	chr14	-	89078775	89259096	9570
ENSG00000(	602.8309	729.7984	732.2746	823.234	762.1177	700.3141	-0.14773	0.29712	0.42161	NEMF	chr14	-	50249997	50319921	5038
ENSG00000(	683.6227	697.2826	637.2769	661.4337	584.4743	609.898	0.12055	0.37023	0.50069	RPUSD4	chr11	-	1.26E+08	1.26E+08	2508
ENSG00000(	1352.744	1276.545	1500.173	1969.32	2533.029	2426.44	-0.7449	1.53E-08	7.57E-08	ARF6	chr14	+	50359810	50361490	1583
ENSG00000(	412.2452	404.6407	391.8659	220.2282	183.166	150.4196	1.1196	1.33E-09	7.21E-09	TTC8	chr14	+	89290497	89344335	2226
ENSG00000(	0	0	5.277655	1.498151	3.681728	4.109825	-0.61387	0.61495	0.72804	TMEM63C	chr14	+	77582911	77725838	5334
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	NGB	chr14	-	77731826	77737655	1884
ENSG00000(	13.46529	12.04288	13.19414	26.96672	8.283888	9.863579	-0.2167	0.73781	0.82434	NOXRED1	chr14	-	77860364	77889860	2023
ENSG00000(	0	0	0	1497.402	1492.941	1583.926	-10.818	6.27E-35	1.12E-33	CDX2	chr13	-	28536274	28545276	4053
ENSG00000(	0	0	0	3.745378	1.840864	6.575719	-2.7725	0.032909	0.067348	AMER2	chr13	-	25735822	25746426	10055
ENSG00000(	39.36009	37.33292	46.17948	65.91865	79.15715	50.13986	-0.65743	0.058573	0.11143	AKR1E2	chr10	+	4828821	4890254	1655
ENSG00000(	229.9458	244.4704	302.1458	325.8479	327.6738	301.6611	-0.30027	0.090457	0.1614	KBTBD6	chr13	-	41701705	41706882	5178
ENSG00000(	4.143168	0	0	16.47966	30.37426	13.15144	-3.2611	0.000221	0.000687	FAAH2	chrX	+	57313139	57515629	1983
ENSG00000(	0	0	0	0	6.443024	0	-1.5465	0.25144	0.36902	DRGX	chr10	-	50572237	50603497	2727
ENSG00000(	632.8689	632.2511	622.7633	1146.086	890.0577	1053.759	-0.70958	2.88E-07	1.26E-06	NUDT5	chr10	-	12207324	12238143	3433
ENSG00000(	209.23	148.1274	171.5238	393.2647	544.8957	470.9859	-1.4022	4.60E-13	3.23E-12	DACT1	chr14	+	59100685	59115039	3734
ENSG00000(	1.035792	0	0	4.494453	8.283888	4.109825	-2.6767	0.027205	0.057094	OXGR1	chr13	-	97637973	97646984	2285
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	UCMA	chr10	-	13263767	13276334	826
ENSG00000(	4.143168	2.408575	2.638828	52.43529	30.37426	41.09825	-3.5019	5.60E-08	2.63E-07	BEND7	chr10	-	13480484	13570974	6524
ENSG00000(	1960.754	2090.643	1823.43	2870.458	2187.867	2572.75	-0.3767	0.003362	0.008622	ATP5C1	chr10	+	7830092	7849778	1163
ENSG00000(	59.04014	90.32158	69.92893	54.68252	53.38506	70.68898	0.28791	0.36165	0.49135	PRPF18	chr10	+	13628927	13672868	1717
ENSG00000(	158.4762	152.9445	242.7721	403.7517	400.3879	438.1073	-1.1633	4.32E-09	2.24E-08	TAF3	chr10	+	7860467	8058590	4872
ENSG00000(	4.143168	4.817151	6.597069	2.996302	0	0	1.7545	0.12928	0.21626	VSTM4	chr10	-	50226490	50323554	2192
ENSG00000(	3498.905	3491.23	3199.578	4745.394	3603.491	4012.011	-0.27819	0.024809	0.052604	VDAC2	chr10	+	76969912	76991206	1581
ENSG00000(	123.2592	101.1602	87.08131	244.1986	195.1316	244.1236	-1.1213	6.46E-07	2.73E-06	COMTD1	chr10	-	76993727	76995788	1094
ENSG00000(	106.6866	128.8588	65.97069	122.8484	73.63456	92.88204	0.058735	0.8464	0.90208	SLC18A2	chr10	+	1.19E+08	1.19E+08	4125
ENSG00000(	351.1335	337.2006	420.893	321.3534	404.9901	353.4449	0.03849	0.82073	0.88422	PDZD8	chr10	-	1.19E+08	1.19E+08	6484
ENSG00000(	1569.225	1377.705	1324.691	393.2647	416.0353	514.55	1.686	1.48E-31	2.37E-30	ZNF503	chr10	-	77157588	77161664	3347
ENSG00000(	26.93059	20.47289	25.06886	253.1875	364.4911	251.5213	-3.5382	4.81E-35	8.63E-34	DACH1	chr13	-	72012098	72441330	5239
ENSG00000(	321.0955	280.599	360.2	458.4342	411.4331	399.475	-0.40017	0.01515	0.033781	FAM175B	chr10	+	1.26E+08	1.27E+08	2992
ENSG00000(	613.1888	619.0039	613.5274	722.8579	824.7071	813.7453	-0.35404	0.00729	0.017484	QSOX2	chr9	-	1.39E+08	1.39E+08	4530
ENSG00000(	662.9068	608.1653	639.9157	774.5441	624.0529	688.8066	-0.12763	0.36308	0.49286	FAM204A	chr10	-	1.2E+08	1.2E+08	5930
ENSG00000(	1436.643	1447.554	1595.171	1660.7	2245.854	1869.148	-0.36564	0.006458	0.015646	NSD1	chr5	+	1.77E+08	1.77E+08	12892
ENSG00000(	1594.084	1751.034	1750.862	3050.985	2181.424	2683.715	-0.63453	2.86E-06	1.13E-05	PRDX3	chr10	-	1.21E+08	1.21E+08	2277
ENSG00000(	305.5586	262.5347	312.7011	158.804	193.2907	153.7074	0.79817	2.91E-05	0.000102	ENOX2	chrX	-	1.3E+08	1.3E+08	4184
ENSG00000(	2522.153	2498.897	2405.291	3556.611	3208.626	3314.163	-0.44002	3.04E-05	0.000106	GHITM	chr10	+	85899196	85913001	2128

ENSG00000(	1.035792	0	0	4.494453	9.20432	3.28786	-2.6745	0.027645	0.057903	CLEC1B	chr12	-	10138241	10166023	3054
ENSG00000(	1096.904	965.8388	825.953	840.4628	901.1029	915.6689	0.1218	0.37987	0.5105	SNAPC4	chr9	-	1.39E+08	1.39E+08	5010
ENSG00000(	0	0	0	2.247227	7.363456	3.28786	-2.8544	0.027209	0.057094	TMEM52B	chr12	+	10323141	10344400	2731
ENSG00000(	1433.536	1334.351	1271.915	2095.913	1688.993	1826.406	-0.47293	0.000163	0.000516	PMPCA	chr9	+	1.39E+08	1.39E+08	3341
ENSG00000(	809.9893	871.9043	787.69	1346.089	976.5783	1080.062	-0.46179	0.001458	0.00397	SDCCAG3	chr9	-	1.39E+08	1.39E+08	2314
ENSG00000(	0	0	0	0.749076	9.20432	4.93179	-3.009	0.019544	0.0425	FRMD7	chrX	-	1.31E+08	1.31E+08	3198
ENSG00000(	9.322127	2.408575	3.958241	8.239831	6.443024	9.041614	-0.51557	0.54099	0.66393	AK8	chr9	-	1.36E+08	1.36E+08	2465
ENSG00000(	153.2972	144.5145	138.5384	78.65293	41.41944	39.45432	1.4274	1.75E-06	7.08E-06	C9orf9	chr9	+	1.36E+08	1.36E+08	2536
ENSG00000(	941.5348	1021.236	1052.892	516.1131	619.4507	533.4552	0.85181	3.06E-10	1.75E-09	TSC1	chr9	-	1.36E+08	1.36E+08	8604
ENSG00000(	359.4198	362.4906	345.6864	709.3745	520.9645	564.6899	-0.74778	3.98E-06	1.55E-05	HPRT1	chrX	+	1.34E+08	1.34E+08	1407
ENSG00000(	58.00435	71.05298	87.08131	113.1104	61.66894	79.7306	-0.24141	0.44533	0.57488	LOH12CR1	chr12	+	12510013	12619840	2052
ENSG00000(	77.68439	103.5687	64.65128	292.1395	249.4371	190.6959	-1.5598	4.18E-10	2.36E-09	FAM69B	chr9	+	1.4E+08	1.4E+08	2410
ENSG00000(	567.614	517.8437	423.5318	1137.846	1124.768	1159.793	-1.1758	6.98E-17	6.08E-16	ZMYND19	chr9	-	1.4E+08	1.4E+08	1375
ENSG00000(	3.107376	1.204288	0	17.97781	13.80648	10.68554	-2.7894	0.002163	0.005728	STOX1	chr10	+	70587298	70655188	3377
ENSG00000(	58.00435	52.98866	38.263	1.498151	11.96562	7.397684	2.7498	4.92E-07	2.11E-06	RET	chr10	+	43572475	43625799	5659
ENSG00000(	1595.12	1496.93	1985.718	4890.714	4828.586	4275.04	-1.4599	1.61E-29	2.41E-28	DDX21	chr10	+	70715884	70744829	4711
ENSG00000(	1044.078	1077.838	1085.878	1562.572	1777.354	1671.055	-0.64225	3.62E-08	1.74E-07	BMS1	chr10	+	43278249	43326856	4224
ENSG00000(	367.7061	360.082	258.6051	167.7929	154.6326	175.0785	0.98387	5.49E-07	2.34E-06	STK32C	chr10	-	1.34E+08	1.34E+08	2086
ENSG00000(	521.0033	611.7782	802.2036	325.0988	493.3516	401.9408	0.66153	0.000536	0.001568	KIAA1462	chr10	-	30301729	30404423	9265
ENSG00000(	909.4253	803.2599	639.9157	697.3893	607.4851	738.1245	0.20404	0.19231	0.29806	FUNDC2	chrX	+	1.54E+08	1.54E+08	6455
ENSG00000(	497.1801	405.845	480.2666	519.8584	458.3751	540.031	-0.13401	0.38261	0.51333	TMEM55B	chr14	-	20925878	20929771	3453
ENSG00000(	242.3753	217.9761	228.2586	434.4638	384.7406	442.2171	-0.8697	1.51E-07	6.82E-07	METTL17	chr14	+	21457929	21465189	2887
ENSG00000(	0	2.408575	1.319414	2.247227	1.840864	0.821965	-0.27704	0.82969	0.89078	SLC39A2	chr14	+	21467414	21470030	1379
ENSG00000(	88.04231	55.39724	54.09597	83.14739	57.98722	78.90863	-0.14914	0.64317	0.75059	NDRG2	chr14	-	21484922	21539031	2880
ENSG00000(	3415.006	3278.071	3297.215	764.8061	1128.45	976.4943	1.796	8.59E-38	1.67E-36	ARHGEF40	chr14	+	21538429	21558399	5919
ENSG00000(	3353.894	3270.845	2774.727	1103.388	1017.998	1035.676	1.571	1.67E-39	3.41E-38	NSMF	chr9	-	1.4E+08	1.4E+08	3646
ENSG00000(	327.3102	264.9433	250.6886	868.9276	763.0381	776.7568	-1.5066	4.79E-22	5.27E-21	ZNF219	chr14	-	21558205	21572881	3071
ENSG00000(	448.4979	458.8336	453.8783	295.8848	304.663	287.6877	0.61411	4.83E-05	0.000164	CASP7	chr10	+	1.15E+08	1.15E+08	2694
ENSG00000(	13.46529	19.2686	7.916483	10.48706	11.04518	10.68554	0.32006	0.62059	0.73278	PPP1R36	chr14	+	65016620	65056098	1686
ENSG00000(	1.035792	0	0	2.247227	0.920432	0	-0.62282	0.6445	NA	BTNL9	chr5	+	1.8E+08	1.8E+08	3500
ENSG00000(	234.089	209.5461	290.271	164.7966	233.7897	220.2866	0.24479	0.24404	0.36012	C10orf118	chr10	-	1.16E+08	1.16E+08	7245
ENSG00000(	1.035792	0	0	31.46117	29.45382	43.56414	-5.2505	4.44E-08	2.11E-07	VWA2	chr10	+	1.16E+08	1.16E+08	2946
ENSG00000(	675.3363	641.8854	675.5399	961.813	931.4772	820.321	-0.44442	0.000721	0.00207	METTL3	chr14	-	21966277	21979517	2523
ENSG00000(	492.0012	450.4036	507.9743	305.6228	473.102	412.6264	0.28439	0.1087	0.1878	SALL2	chr14	-	21989232	22005350	4925
ENSG00000(	379.0998	432.3393	431.4483	451.6926	471.2612	387.1455	-0.07662	0.62482	0.73627	TRUB1	chr10	+	1.17E+08	1.17E+08	3403
ENSG00000(	5.17896	7.225726	5.277655	2.247227	2.761296	4.109825	0.82215	0.38269	0.51334	FAM194B	chr13	-	46108657	46189874	2421
ENSG00000(	753.0207	826.1414	775.8153	251.6894	289.0156	252.3432	1.5669	3.39E-27	4.58E-26	ZFYVE1	chr14	-	73436159	73493920	4485
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	PNLIPRP2	chr10	+	1.18E+08	1.18E+08	1481
ENSG00000(	1.035792	1.204288	2.638828	97.37982	86.52061	117.541	-5.5666	6.90E-17	6.01E-16	C10orf82	chr10	-	1.18E+08	1.18E+08	1791
ENSG00000(	107.7224	120.4288	130.622	26.21764	24.85166	24.65895	2.2122	5.65E-13	3.93E-12	HSPA12A	chr10	-	1.18E+08	1.19E+08	5722
ENSG00000(	0	1.204288	0	1.498151	0	0	-0.08768	0.94524	NA	FAM35BP	chr10	+	46897592	46939143	3337
ENSG00000(	22.78742	22.88147	25.06886	16.47966	8.283888	6.575719	1.1079	0.055176	0.10591	FRAT1	chr10	+	99079022	99081672	2651
ENSG00000(	1116.584	1046.526	913.0343	812.747	570.6678	697.0263	0.56196	0.000261	0.000801	UBTD1	chr10	+	99258625	99330966	1706
ENSG00000(	1.035792	1.204288	0	5.992604	8.283888	18.90519	-3.0847	0.003006	0.007764	ANKRD2	chr10	+	99332198	99343641	1484

ENSG00000(	275.5206	217.9761	361.5194	585.028	679.2788	590.9928	-1.1144	1.21E-09	6.57E-09	E2F7	chr12	-	77415027	77459360	5740
ENSG00000(	236.1606	166.1917	306.104	327.346	431.6826	256.4531	-0.51604	0.028345	0.059138	ARHGAP42	chr11	+	1.01E+08	1.01E+08	5685
ENSG00000(	102.5434	185.4603	89.72014	222.4754	172.1208	180.0103	-0.60036	0.024741	0.052479	ISCA2	chr14	+	74960423	74963809	2626
ENSG00000(	33.14534	12.04288	31.66593	4.494453	6.443024	4.93179	2.1482	0.000804	0.002289	OTOGL	chr12	+	80603233	80772870	8083
ENSG00000(	1.035792	6.021439	5.277655	158.0549	146.3487	126.5826	-4.9949	1.29E-23	1.52E-22	GYLTL1B	chr11	+	45943172	45950647	2528
ENSG00000(	567.614	640.6811	505.3355	1045.709	914.9094	1168.834	-0.86604	4.29E-09	2.23E-08	PACSIN3	chr11	-	47199076	47207994	2009
ENSG00000(	383.243	357.6735	321.937	477.9102	400.3879	335.3617	-0.18997	0.28031	0.40256	TTC7B	chr14	-	91006932	91282823	3484
ENSG00000(	2042.582	1884.71	1560.867	494.3899	396.7062	504.6865	1.9689	3.33E-41	7.09E-40	SLC39A13	chr11	+	47428683	47438047	3553
ENSG00000(	2435.147	2242.384	2016.064	4122.912	3307.112	3915.019	-0.7593	1.34E-09	7.24E-09	PSMC3	chr11	-	47440320	47447993	1544
ENSG00000(	6.214751	13.24716	1.319414	15.73059	2.761296	18.90519	-0.75942	0.35745	0.48691	RAPSN	chr11	-	47459308	47470730	1671
ENSG00000(	10.35792	3.612863	0	14.98151	24.85166	22.19305	-1.9209	0.010162	0.023589	AGBL2	chr11	-	47681143	47736941	3577
ENSG00000(	12.4295	3.612863	11.87472	113.1104	106.7701	119.1849	-3.5074	2.57E-17	2.29E-16	TC2N	chr14	-	92246095	92333880	5146
ENSG00000(	744.7344	617.7996	913.0343	1198.521	1300.57	1022.524	-0.62854	7.15E-05	0.000238	CPSF2	chr14	+	92588281	92630755	5301
ENSG00000(	60.07593	61.41867	43.54065	2.996302	0	9.863579	3.4807	2.76E-09	1.46E-08	SMCO2	chr12	+	27619743	27655118	1272
ENSG00000(	138.7961	151.7403	147.7743	300.3793	238.3919	251.5213	-0.84828	1.87E-05	6.72E-05	MOAP1	chr14	-	93648541	93651273	2529
ENSG00000(	298.3081	373.3292	288.9516	146.0697	133.4626	202.2034	0.98879	2.44E-06	9.68E-06	IFI27L1	chr14	+	94547628	94570192	828
ENSG00000(	19.68005	25.29004	10.55531	23.97042	10.12475	18.90519	0.062472	0.91345	0.94699	IFI27	chr14	+	94571182	94583033	2430
ENSG00000(	35.21692	25.29004	35.62417	59.92604	74.55499	52.60575	-0.94026	0.010265	0.023805	CLMN	chr14	-	95654735	95786243	6289
ENSG00000(	0	2.408575	0	0.749076	5.522592	0	-0.78768	0.55617	0.67676	PDZRN4	chr12	+	41582250	41968392	3411
ENSG00000(	0	0	0	1.498151	0	2.465895	-1.1271	0.39798	NA	SLC6A5	chr11	+	20620946	20680831	7084
ENSG00000(	0	0	7.916483	2.247227	3.681728	0.821965	0.14271	0.90805	0.94343	CCDC38	chr12	-	96260826	96336752	2599
ENSG00000(	1.035792	0	0	4.494453	14.72691	3.28786	-3.0346	0.010205	0.023679	NELL1	chr11	+	20691117	21597227	3329
ENSG00000(	43.50326	40.94578	35.62417	277.158	316.6286	292.6195	-2.855	7.06E-33	1.18E-31	PTER	chr10	+	16478942	16555736	3777
ENSG00000(	0	0	5.277655	59.92604	80.07758	89.59418	-5.1505	1.02E-13	7.48E-13	C1QL3	chr10	-	16555742	16564004	2493
ENSG00000(	154.333	140.9017	174.1626	13.48336	13.80648	20.54912	3.2469	3.20E-24	3.84E-23	CACNB2	chr10	+	18429606	18830798	4464
ENSG00000(	175.0488	215.5675	159.6491	662.9319	601.0421	512.0841	-1.6827	4.61E-21	4.87E-20	PTPLA	chr10	-	17631958	17659376	1310
ENSG00000(	601.7951	594.9181	881.3684	928.8537	1016.157	712.6436	-0.35466	0.047436	0.09271	ARL5B	chr10	+	18948334	18970568	7196
ENSG00000(	49.71801	60.21439	36.94359	159.5531	129.7809	124.9387	-1.4762	2.44E-07	1.08E-06	SMCO4	chr11	-	93211638	93276674	1104
ENSG00000(	192.6573	155.3531	233.5362	182.7744	215.3811	166.8589	0.040873	0.85048	0.90483	KIAA1731	chr11	+	93394805	93463522	8055
ENSG00000(	1507.077	1714.906	1559.547	1644.97	1718.447	1550.226	-0.03932	0.73523	0.82291	TAF1D	chr11	-	93463114	93517557	4358
ENSG00000(	187.4783	249.2876	193.9538	122.8484	118.7357	110.9653	0.83287	0.000115	0.000372	ABTB2	chr11	-	34172535	34379555	4902
ENSG00000(	257.9122	234.8361	241.4527	320.6043	360.8093	257.275	-0.35116	0.058623	0.1115	R3HCC1L	chr10	+	99894387	1E+08	3418
ENSG00000(	2728.276	2784.313	3472.697	2847.236	3982.709	3604.316	-0.21519	0.13446	0.2235	AMOTL1	chr11	+	94439597	94609918	8970
ENSG00000(	28635.5	27778.1	25971.34	32.95932	40.49901	35.34449	9.5371	0	0	HTRA1	chr10	+	1.24E+08	1.24E+08	2120
ENSG00000(	670.1574	717.7555	759.9823	931.1009	775.9242	683.0528	-0.15498	0.29707	0.4216	CEP57	chr11	+	95523129	95565857	3178
ENSG00000(	20.71584	28.90291	31.66593	10.48706	21.16994	0	1.2679	0.072358	0.13348	TCP11L2	chr12	+	1.07E+08	1.07E+08	3198
ENSG00000(	1395.212	1600.498	1884.123	832.2229	994.0666	788.2644	0.89746	7.19E-10	3.98E-09	SPRED1	chr15	+	38544527	38649450	7780
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	TMCO5A	chr15	+	38214140	38259925	2894
ENSG00000(	635.9762	584.0795	575.2644	80.90016	56.14635	73.97684	3.0679	1.13E-60	4.02E-59	GPR176	chr15	-	40091233	40213093	3844
ENSG00000(	1806.421	1724.54	1938.219	665.1791	657.1884	545.7847	1.546	4.09E-33	6.90E-32	JAM3	chr11	+	1.34E+08	1.34E+08	3912
ENSG00000(	0	1.204288	0	17.97781	17.48821	14.79537	-4.2118	5.01E-05	0.00017	GLB1L3	chr11	+	1.34E+08	1.34E+08	3862
ENSG00000(	1472.896	1323.512	1390.662	405.9989	565.1452	507.9743	1.4988	4.31E-25	5.35E-24	ADAMTS15	chr11	+	1.3E+08	1.3E+08	5669
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	SVOP	chr12	-	1.09E+08	1.09E+08	3104
ENSG00000(	1189.089	1215.126	1033.101	942.337	856.0018	950.1914	0.32216	0.011347	0.026053	GPT2	chr16	+	46918290	46965209	4228

ENSG00000(	13.46529	18.06432	2.638828	4.494453	16.56778	2.465895	0.50329	0.54052	0.66379	AMN	chr14	+	1.03E+08	1.03E+08	2772
ENSG00000(	597.6519	567.2195	713.8029	374.5378	417.8761	415.9142	0.63425	2.81E-05	9.86E-05	RAB8B	chr15	+	63481668	63559981	4943
ENSG00000(	1792.956	1976.236	1886.762	2062.205	1620.881	1728.592	0.062895	0.6173	0.72978	IKBIP	chr12	-	99007183	99038891	3189
ENSG00000(	167.7983	173.4174	109.5113	317.608	327.6738	361.6646	-1.1481	2.25E-08	1.10E-07	RPUSD2	chr15	+	40861499	40866659	1875
ENSG00000(	775.8081	853.84	899.8402	453.9398	670.0745	669.9014	0.49448	0.002712	0.007061	HIF1AN	chr10	+	1.02E+08	1.02E+08	3019
ENSG00000(	12.4295	12.04288	15.83297	5.992604	6.443024	18.90519	0.3349	0.62352	0.73518	NDUFB8	chr10	-	1.02E+08	1.02E+08	1234
ENSG00000(	351.1335	309.5019	259.9245	355.0618	322.1512	375.638	-0.19062	0.27417	0.39528	ZFYVE19	chr15	+	41099284	41106767	2913
ENSG00000(	7.250543	0	0	3.745378	0.920432	1.64393	0.15897	0.89843	0.93708	PPP1R14D	chr15	-	41107650	41120907	750
ENSG00000(	12.4295	9.634302	5.277655	2979.823	3010.733	2594.943	-8.1433	2.08E-154	3.31E-152	SPINT1	chr15	+	41136216	41150405	3056
ENSG00000(	18150.18	17821.05	22845.65	1496.653	1894.249	1223.906	3.6607	3.25E-128	3.76E-126	FBN1	chr15	-	48700503	48938046	11756
ENSG00000(	1.035792	0	1.319414	2.996302	12.88605	0	-1.9196	0.1167	0.19933	AVPR1A	chr12	-	63539014	63544722	1525
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	C16orf78	chr16	+	49407734	49433342	1068
ENSG00000(	10.35792	3.612863	5.277655	33.7084	38.65814	14.79537	-2.0286	0.00142	0.003877	DEPDC4	chr12	-	1.01E+08	1.01E+08	2337
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	LRTM2	chr12	+	1929433	1945918	3986
ENSG00000(	758.1997	740.6369	745.4688	1613.509	1574.859	1452.412	-1.046	1.59E-18	1.51E-17	BRD7	chr16	-	50347398	50402845	5370
ENSG00000(	1144.55	956.2044	840.4666	802.2599	488.7494	645.2425	0.60014	0.000775	0.002214	CKB	chr14	-	1.04E+08	1.04E+08	1709
ENSG00000(	519.9675	428.7264	345.6864	727.3524	566.0657	732.3707	-0.64146	0.00025	0.000769	TRMT61A	chr14	+	1.04E+08	1.04E+08	3229
ENSG00000(	470.2495	478.1022	571.3062	397.7591	498.8741	397.0091	0.23141	0.15234	0.2473	BTRC	chr10	+	1.03E+08	1.03E+08	6134
ENSG00000(	350.0977	302.2762	290.271	333.3386	254.9597	297.5513	0.089451	0.61555	0.72863	POLL	chr10	-	1.03E+08	1.03E+08	2914
ENSG00000(	631.8331	528.6823	639.9157	792.5219	820.1049	792.3742	-0.41641	0.002277	0.00601	BAG5	chr14	-	1.04E+08	1.04E+08	4867
ENSG00000(	640.1194	727.3898	530.4043	306.3719	286.2544	344.4033	1.0148	7.15E-10	3.97E-09	DPCD	chr10	+	1.03E+08	1.03E+08	1499
ENSG00000(	988.1455	944.1616	891.9237	202.2504	191.4499	270.4265	2.0807	2.46E-38	4.87E-37	LARP6	chr15	-	71123863	71146498	2075
ENSG00000(	1246.058	1150.095	1358.996	2595.547	2335.136	2098.476	-0.903	9.82E-13	6.73E-12	API5	chr11	+	43333513	43366079	3714
ENSG00000(	0	0	0	0	4.60216	4.109825	-2.1232	0.11583	0.19807	ASPG	chr14	+	1.05E+08	1.05E+08	2157
ENSG00000(	177.1204	173.4174	146.4549	152.8114	146.3487	170.9687	0.08139	0.69961	0.79573	ZNF319	chr16	-	58028572	58034357	4221
ENSG00000(	528.2539	511.8223	461.7948	649.4485	543.9753	626.3373	-0.2759	0.058109	0.1107	HPS6	chr10	+	1.04E+08	1.04E+08	2646
ENSG00000(	24.85901	21.67718	21.11062	27.7158	28.53339	39.45432	-0.48323	0.2859	0.4092	SENP8	chr15	+	72406599	72433311	1834
ENSG00000(	1814.707	1735.379	1827.388	4146.882	4209.136	3920.773	-1.1891	4.02E-30	6.13E-29	NOLC1	chr10	+	1.04E+08	1.04E+08	3966
ENSG00000(	212.3373	192.686	217.7033	312.3645	208.9381	233.438	-0.27812	0.17436	0.27599	ALKBH3	chr11	+	43902361	43941816	1557
ENSG00000(	1708.021	1684.799	1741.626	1911.641	1503.986	1448.302	0.077371	0.5571	0.67761	COPS2	chr15	-	49398268	49447858	4061
ENSG00000(	14.50109	22.88147	32.98534	316.859	377.3771	302.4831	-3.8097	6.37E-42	1.39E-40	GABRB3	chr15	-	26788693	27184686	5934
ENSG00000(	26.93059	13.24716	17.15238	0	0	0	5.5109	6.80E-07	2.87E-06	TBATA	chr10	-	72530995	72545157	1583
ENSG00000(	1664.518	1576.413	1360.316	991.027	953.5675	895.9418	0.69497	3.91E-08	1.87E-07	SGPL1	chr10	+	72575717	72640930	5745
ENSG00000(	451.6053	439.565	558.112	325.8479	422.4783	245.7675	0.54142	0.006063	0.014775	FRS2	chr12	+	69864129	69973562	6861
ENSG00000(	3548.623	3414.156	3299.854	7546.187	6092.339	6060.347	-0.9389	2.35E-15	1.90E-14	CCT2	chr12	+	69979114	69995350	2189
ENSG00000(	375.9925	375.7378	310.0622	611.9947	601.0421	720.0413	-0.85988	3.40E-08	1.63E-07	PCBD1	chr10	-	72642037	72648541	1006
ENSG00000(	866.9578	903.2158	1142.612	1104.886	990.3848	853.1996	-0.01891	0.89993	0.9378	ARIH1	chr15	+	72766667	72879692	6047
ENSG00000(	14.50109	18.06432	22.43003	5.243529	7.363456	6.575719	1.4276	0.027263	0.0572	C16orf71	chr16	+	4784273	4799397	3705
ENSG00000(	651.5131	597.3267	678.1787	152.8114	262.3231	212.8889	1.6133	1.17E-17	1.06E-16	CLMP	chr11	-	1.23E+08	1.23E+08	2610
ENSG00000(	14.50109	0	3.958241	18.72689	3.681728	18.08323	-0.98283	0.25857	0.37728	SCN3B	chr11	-	1.23E+08	1.24E+08	6061
ENSG00000(	707.4459	696.0783	736.2329	650.9467	613.9281	595.1026	0.20113	0.12358	0.20875	COX11	chr17	-	53029263	53046146	3244
ENSG00000(	178.1562	187.8689	201.8703	265.9218	258.6414	259.7409	-0.46561	0.01054	0.024375	ZNF202	chr11	-	1.24E+08	1.24E+08	4130
ENSG00000(	53.86118	67.44011	31.66593	45.69361	52.46462	54.24968	0.010896	0.97613	0.98625	FAM227B	chr15	-	49619159	49913128	2204
ENSG00000(	245.4827	270.9647	340.4088	143.0734	123.3379	147.9537	1.0381	3.56E-07	1.55E-06	STXBP4	chr17	+	53046088	53241646	6243

ENSG00000(	184.371	230.019	224.3003	262.1764	246.6758	254.8091	-0.25954	0.16073	0.25812	CYYR1	chr21	-	27838528	27945603	3101
ENSG00000(	536.5402	556.3809	699.2893	620.2346	674.6767	631.2691	-0.10514	0.47875	0.60784	CUL5	chr11	+	1.08E+08	1.08E+08	6351
ENSG00000(	0	0	0	20.97412	2.761296	5.753754	-4.054	0.000766	0.002192	MYRFL	chr12	+	70219084	70352877	3465
ENSG00000(	1304.062	1182.611	1368.232	725.1051	791.5715	764.4274	0.75562	1.23E-09	6.69E-09	WBP1L	chr10	+	1.05E+08	1.05E+08	4104
ENSG00000(	233.0532	291.4376	274.4381	283.1506	197.8929	208.7791	0.20698	0.30284	0.42801	C10orf32	chr10	+	1.05E+08	1.05E+08	2422
ENSG00000(	5.17896	10.83859	7.916483	0	3.681728	0.821965	2.0227	0.048025	0.093728	C2	chr6	+	31865562	31913449	2850
ENSG00000(	288.9859	309.5019	204.5091	149.066	113.2131	135.6242	1.0061	4.42E-06	1.71E-05	PLEKHF1	chr19	+	30155963	30166364	2084
ENSG00000(	510.6454	482.9194	477.6278	36.7047	46.0216	68.22309	3.2666	1.00E-50	2.82E-49	TMEM100	chr17	-	53796988	53809482	1962
ENSG00000(	851.4209	776.7656	786.3706	1310.133	1016.157	1275.69	-0.57566	3.02E-05	0.000105	ANAPC16	chr10	+	73975787	73995618	3195
ENSG00000(	2085.049	1919.635	1712.599	343.0766	326.7534	295.9074	2.5596	2.37E-81	1.32E-79	SMPD1	chr11	+	6411655	6416228	2452
ENSG00000(	1561.974	1620.971	1347.121	551.3196	611.1668	594.2806	1.3646	4.87E-26	6.29E-25	APBB1	chr11	-	6416355	6440644	2642
ENSG00000(	6.214751	2.408575	1.319414	1.498151	0	4.93179	0.48358	0.67773	0.779	SYNPO2L	chr10	-	75404639	75415830	4921
ENSG00000(	118.0803	137.2888	120.0667	149.8151	132.5422	180.0103	-0.29977	0.19205	0.29776	NUDT13	chr10	+	74870217	74891586	2140
ENSG00000(	22.78742	10.83859	11.87472	9.737982	6.443024	8.219649	0.84535	0.2046	0.31308	C11orf65	chr11	-	1.08E+08	1.08E+08	2683
ENSG00000(	851.4209	764.7227	1194.069	416.486	719.7778	579.4853	0.70846	0.000371	0.001114	TRIM44	chr11	+	35684353	35829775	3182
ENSG00000(	41.43168	26.49433	26.38828	6.74168	17.48821	12.32947	1.3292	0.012732	0.028884	ILK	chr11	+	6624961	6632102	2074
ENSG00000(	1233.628	1303.039	1055.531	972.3001	800.7758	1149.107	0.29682	0.050374	0.097767	TAF10	chr11	-	6627526	6633898	5393
ENSG00000(	2925.076	2913.172	3183.745	1470.435	1268.355	1070.198	1.2406	6.34E-21	6.67E-20	TPP1	chr11	-	6634000	6640692	3536
ENSG00000(	4545.055	4526.918	4443.786	564.803	905.7051	747.9881	2.6007	2.13E-68	9.00E-67	DCHS1	chr11	-	6642556	6677085	10763
ENSG00000(	159.512	140.9017	160.9685	488.3973	434.4439	405.2287	-1.5191	1.24E-17	1.12E-16	NETO1	chr18	-	70409549	70535381	3058
ENSG00000(	103.5792	101.1602	98.95603	60.67512	57.98722	60.8254	0.75101	0.005838	0.014264	MSS51	chr10	-	75183339	75193319	2421
ENSG00000(	368.7419	346.8349	294.2293	558.0613	479.5451	584.4171	-0.67978	2.43E-05	8.60E-05	CYB5A	chr18	-	71920530	71959251	5913
ENSG00000(	136.7245	101.1602	122.7055	217.981	258.6414	212.0669	-0.92417	1.82E-05	6.55E-05	USP54	chr10	-	75257296	75385711	6247
ENSG00000(	27.96638	39.74149	65.97069	26.21764	21.16994	17.26126	1.0074	0.025706	0.054283	RAG1	chr11	+	36532259	36614706	6564
ENSG00000(	178.1562	180.6432	122.7055	180.5272	129.7809	170.1467	0.004262	0.98553	0.99136	C11orf74	chr11	+	36616051	36694823	930
ENSG00000(	17.60846	21.67718	7.916483	15.73059	23.0108	11.50751	-0.07421	0.90104	0.93855	WDR88	chr19	+	33622996	33666701	1835
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	OR10A5	chr11	+	6866883	6867936	1054
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	OR2D2	chr11	-	6912721	6913830	1110
ENSG00000(	357.3482	357.6735	379.9912	248.6931	284.4135	218.6427	0.54115	0.001645	0.004447	ATP9B	chr18	+	76829285	77138283	7353
ENSG00000(	865.922	744.2498	843.1054	439.7073	562.384	481.6714	0.7249	7.82E-07	3.28E-06	PPFIBP2	chr11	+	7534529	7678358	3557
ENSG00000(	1036.828	1041.709	1035.74	704.8801	653.5067	685.5187	0.60591	7.04E-07	2.97E-06	CYB5R2	chr11	-	7686331	7698453	7463
ENSG00000(	265.1627	290.2333	299.5069	224.7227	138.9852	146.3098	0.73621	0.000647	0.001868	SERPINB7	chr18	+	61420169	61472604	2203
ENSG00000(	287.9501	252.9004	314.0205	429.9694	535.6914	408.5166	-0.68161	8.68E-05	0.000285	KIAA0355	chr19	+	34745457	34846491	6702
ENSG00000(	170.9057	213.1589	179.4403	353.5637	259.5618	234.26	-0.58729	0.005189	0.012823	SERPINB8	chr18	+	61637159	61672278	3477
ENSG00000(	590.4014	552.7681	678.1787	352.8146	502.5559	400.2969	0.53556	0.001374	0.003769	TUB	chr11	+	8040791	8127659	6420
ENSG00000(	0	2.408575	1.319414	39.701	50.62376	46.852	-4.7364	1.00E-09	5.48E-09	RIC3	chr11	-	8127597	8190602	5272
ENSG00000(	0	0	0	32.21025	14.72691	7.397684	-4.9858	9.73E-06	3.62E-05	LMO1	chr11	-	8245851	8290263	1279
ENSG00000(	0	0	0	3.745378	4.60216	0	-2.0709	0.12551	0.2113	OR5P1P	chr11	-	7794437	7795361	925
ENSG00000(	185.4068	175.826	201.8703	154.3096	214.4607	181.6542	0.034218	0.86966	0.91821	IDH3A	chr15	+	78423840	78464291	4128
ENSG00000(	4.143168	14.45145	26.38828	76.40571	40.49901	82.19649	-2.1015	2.54E-05	8.97E-05	WDR72	chr15	-	53805938	54055075	7507
ENSG00000(	182.2994	190.2775	170.2044	17.97781	10.12475	4.93179	3.9509	2.14E-29	3.17E-28	CRABP1	chr15	+	78632666	78640572	772
ENSG00000(	3.107376	3.612863	0	0.749076	1.840864	2.465895	0.3118	0.7989	0.8689	PLD4	chr14	+	1.05E+08	1.05E+08	2007
ENSG00000(	8.286335	7.225726	5.277655	17.22874	9.20432	6.575719	-0.6097	0.41577	0.54636	ZMAT1	chrX	-	1.01E+08	1.01E+08	5754
ENSG00000(	94.25706	98.75159	149.0938	39.701	46.0216	60.00344	1.2122	8.14E-05	0.000269	XRRA1	chr11	-	74518784	74660245	5681

ENSG00000(	308.666	301.0719	278.3963	149.8151	237.4715	133.1583	0.76988	0.000551	0.001606	TRIM66	chr11	-	8633584	8693413	10083
ENSG00000(	176.0846	187.8689	278.3963	68.16587	150.0304	64.93523	1.1704	0.000115	0.000372	RNF169	chr11	+	74459913	74553458	7823
ENSG00000(	33831.04	34113.86	26261.61	14763.53	15560.82	18952.87	0.93268	2.69E-12	1.78E-11	RPL27A	chr11	+	8703958	8736306	4916
ENSG00000(	624.5825	539.5209	663.6651	440.4564	630.4959	549.0726	0.17456	0.28814	0.41172	ST5	chr11	-	8714898	8932498	4545
ENSG00000(	11.39371	13.24716	23.74945	8.239831	11.04518	7.397684	0.80218	0.21414	0.32456	CDYL2	chr16	-	80637609	80838226	2353
ENSG00000(	38.3243	33.72006	60.69303	4.494453	1.840864	3.28786	3.5607	2.60E-09	1.38E-08	TMEM130	chr7	-	98444111	98468394	3891
ENSG00000(	17.60846	7.225726	6.597069	6315.456	8064.825	5900.886	-9.1611	4.98E-210	1.62E-207	PRTG	chr15	-	55903744	56035288	11967
ENSG00000(	101.5076	80.68728	149.0938	652.4448	538.4527	497.2888	-2.3413	3.88E-28	5.47E-27	CENPN	chr16	+	81040103	81066719	2481
ENSG00000(	343.8829	386.5764	368.1164	365.5489	280.7318	395.3651	0.074393	0.67097	0.77365	AKIP1	chr11	+	8932686	8941631	1421
ENSG00000(	740.5912	810.4856	928.8673	1294.403	1226.936	1024.99	-0.51592	0.000284	0.000867	ATMIN	chr16	+	81069452	81080963	5343
ENSG00000(	38.3243	12.04288	17.15238	22.47227	24.85166	33.70056	-0.23911	0.6461	0.75315	C16orf46	chr16	-	81087102	81110872	1857
ENSG00000(	447.4621	428.7264	426.1707	1184.288	1012.475	1095.679	-1.3347	1.69E-23	1.97E-22	TMEM41B	chr11	-	9302201	9336327	3968
ENSG00000(	0	0	0	2.996302	2.761296	4.109825	-2.4776	0.060295	0.11416	DKFZP686J	chr16	-	81134480	81253975	7379
ENSG00000(	533.4328	598.531	571.3062	474.9139	451.9321	383.8576	0.37603	0.012222	0.027854	LEO1	chr15	-	52230222	52264003	2193
ENSG00000(	242.3753	289.0291	296.8681	288.3941	213.5402	247.4114	0.13993	0.45907	0.58866	ZNF143	chr11	+	9481866	9550071	2947
ENSG00000(	1059.615	1080.246	1260.04	797.0164	795.2532	745.5222	0.5383	2.84E-05	9.97E-05	TMX3	chr18	-	66340925	66382535	4927
ENSG00000(	1261.595	1256.072	1004.074	5.992604	13.80648	9.041614	6.8881	4.13E-130	4.90E-128	MFAP4	chr17	-	19286755	19290553	1932
ENSG00000(	555.1845	576.8538	631.9992	1898.907	1925.544	1742.566	-1.6558	3.11E-41	6.62E-40	WEE1	chr11	+	9595228	9615004	5187
ENSG00000(	1212.912	1077.838	1004.074	698.1384	569.7474	673.1893	0.76128	4.43E-08	2.10E-07	MAPK7	chr17	+	19281034	19286857	4533
ENSG00000(	2.071584	1.204288	0	106.3687	114.1336	136.4462	-6.1041	5.90E-18	5.42E-17	FAM86GP	chr11	-	3431582	3443726	971
ENSG00000(	0	0	0	16.47966	8.283888	4.109825	-4.0746	0.000626	0.001812	PRKCB	chr16	+	23847322	24231932	7969
ENSG00000(	733.3407	669.584	827.2724	994.0233	1110.041	896.7637	-0.42731	0.002395	0.006294	HDGFRP3	chr15	-	83784320	83876770	2422
ENSG00000(	404.9946	429.9307	422.2124	218.7301	287.1748	231.7941	0.76786	6.62E-06	2.51E-05	NDST2	chr10	-	75556272	75571589	5818
ENSG00000(	856.5999	849.0228	829.9113	7464.538	6025.148	6749.154	-2.991	1.79E-142	2.50E-140	MCM7	chr7	-	99690351	99699563	2957
ENSG00000(	0	1.204288	5.277655	9.737982	18.40864	16.4393	-2.4942	0.004779	0.011885	CCDC68	chr18	-	52568740	52626739	4132
ENSG00000(	0	0	0	1.498151	2.761296	0	-1.199	0.3707	NA	CLEC4E	chr12	-	8685901	8693559	2159
ENSG00000(	720.9112	687.6483	635.9574	578.2863	590.9173	570.4437	0.23347	0.080173	0.14563	ZNF3	chr7	-	99661656	99680171	3473
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	CLEC4D	chr12	+	8662071	8674962	1936
ENSG00000(	89.0781	97.54731	106.8725	53.93344	88.36147	58.35951	0.54518	0.064069	0.12021	ZSCAN21	chr7	+	99647390	99662661	2005
ENSG00000(	538.6118	480.5108	630.6798	772.2969	822.8662	750.454	-0.50708	0.000467	0.001377	RIMKLB	chr12	+	8834196	8935691	5830
ENSG00000(	3.107376	0	1.319414	20.97412	40.49901	35.34449	-3.9481	5.15E-07	2.21E-06	A2ML1	chr12	+	8975068	9039597	5274
ENSG00000(	6.214751	8.430014	10.55531	18.72689	17.48821	14.79537	-0.96822	0.12945	0.21647	BEAN1	chr16	+	66461200	66527432	2929
ENSG00000(	277.5922	276.9862	229.578	109.365	115.054	131.5144	1.1351	2.22E-08	1.09E-07	TK2	chr16	-	66541906	66586447	5114
ENSG00000(	5835.652	5585.486	5121.964	1987.297	1741.457	1864.216	1.5618	2.92E-45	7.05E-44	TMED3	chr15	+	79603404	79704334	1483
ENSG00000(	4.143168	0	0	4.494453	0	3.28786	-0.57062	0.6585	0.7631	SLC38A8	chr16	-	84043272	84076241	1308
ENSG00000(	298.3081	255.309	302.1458	355.0618	289.9361	378.1039	-0.25761	0.14541	0.23798	SEC11C	chr18	+	56806709	56826068	1202
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	CPLX4	chr18	-	56942388	56985881	1966
ENSG00000(	0	0	0	0.749076	3.681728	0.821965	-1.5443	0.25498	NA	GALR1	chr18	+	74962505	74980858	1050
ENSG00000(	194.7289	228.8147	250.6886	247.944	299.1404	244.9455	-0.23271	0.2208	0.33262	TMEM135	chr11	+	86748886	87034800	3938
ENSG00000(	20.71584	24.08575	18.47179	23.22134	26.69253	30.4127	-0.33112	0.48492	0.61414	IQCD	chr12	-	1.14E+08	1.14E+08	1872
ENSG00000(	1385.89	1318.695	1248.165	910.1268	882.6943	974.0284	0.51396	1.92E-05	6.87E-05	NDEL1	chr17	+	8316449	8393729	3927
ENSG00000(	171.9415	178.2346	134.5802	913.1231	639.7002	669.0794	-2.1837	3.05E-31	4.82E-30	CENPV	chr17	-	16245848	16256970	1770
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	CDH16	chr16	-	66942025	66952887	3539
ENSG00000(	24.85901	22.88147	32.98534	14.23244	11.04518	18.90519	0.83058	0.1064	0.18457	RRAD	chr16	-	66955582	66959547	1569

ENSG00000(	807.9177	705.7126	671.5816	884.6582	828.3888	1067.732	-0.34581	0.017394	0.038307	FAM96B	chr16	-	66965959	66968326	718
ENSG00000(	6.214751	6.021439	0	3.745378	3.681728	3.28786	0.17343	0.8677	0.91691	WDR16	chr17	+	9479944	9546776	2266
ENSG00000(	24615.59	24749.32	24274.57	18470.7	16661.66	15616.51	0.5363	2.07E-07	9.21E-07	HSP90B1	chr12	+	1.04E+08	1.04E+08	3032
ENSG00000(	1558.867	1554.735	1567.464	966.3075	844.9566	931.2863	0.76924	6.73E-11	4.03E-10	BLCAP	chr20	-	36130816	36156333	2205
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	SERPINB12	chr18	+	61223393	61234244	1278
ENSG00000(	3.107376	8.430014	6.597069	4.494453	4.60216	4.93179	0.31656	0.72079	0.81224	CHRFAM7A	chr15	-	30653443	30686052	2794
ENSG00000(	108.7581	134.8802	122.7055	75.65663	98.48622	119.1849	0.31792	0.2236	0.33584	SPDYE6	chr7	-	1.02E+08	1.02E+08	3145
ENSG00000(	64.2191	89.11729	68.60952	243.4496	216.3015	238.3698	-1.6441	8.34E-13	5.74E-12	ATF7IP2	chr16	+	10420291	10577495	3665
ENSG00000(	1.035792	1.204288	3.958241	23.22134	20.2495	32.05663	-3.3157	1.81E-05	6.52E-05	MMP10	chr11	-	1.03E+08	1.03E+08	1758
ENSG00000(	9.322127	7.225726	11.87472	3.745378	18.40864	6.575719	-0.00394	0.99587	0.99736	TVP23A	chr16	-	10854776	10912651	3677
ENSG00000(	4570.95	4732.851	4616.629	2413.521	2490.689	3771.997	0.67985	9.65E-06	3.59E-05	NGFRAP1	chrX	+	1.03E+08	1.03E+08	921
ENSG00000(	9.322127	8.430014	3.958241	4.494453	2.761296	6.575719	0.58	0.50201	0.63008	TMPRSS5	chr11	-	1.14E+08	1.14E+08	2232
ENSG00000(	451.6053	446.7907	397.1435	342.3275	341.4803	261.3848	0.45412	0.007289	0.017483	COG1	chr17	+	71189129	71204646	4051
ENSG00000(	17.60846	24.08575	14.51355	946.0824	1225.095	1186.917	-5.8429	1.16E-115	1.14E-113	PLEKHA7	chr11	-	16799842	17035990	4804
ENSG00000(	172.9772	197.5032	193.9538	141.5753	115.9744	128.2265	0.5424	0.010427	0.024143	ZNF606	chr19	-	58488421	58514717	4248
ENSG00000(	38.3243	49.3758	31.66593	13.48336	11.04518	13.9734	1.5794	0.000813	0.002313	ZCCHC18	chrX	+	1.03E+08	1.03E+08	1248
ENSG00000(	19581.65	20878.74	18437.49	2224.005	1862.034	1738.456	3.3313	1.18E-172	2.48E-170	B2M	chr15	+	45003675	45011075	2329
ENSG00000(	773.7366	759.9056	876.0908	1087.658	960.0106	1039.786	-0.35796	0.005557	0.013648	ZNF592	chr15	+	85291866	85349659	7861
ENSG00000(	1710.092	1770.303	1720.516	597.7623	532.9301	545.7847	1.6293	3.29E-42	7.26E-41	CASC4	chr15	+	44580927	44707956	3962
ENSG00000(	3842.788	3888.645	3158.677	1051.702	699.5283	775.9349	2.0998	8.42E-43	1.90E-41	NNMT	chr11	+	1.14E+08	1.14E+08	1867
ENSG00000(	0	0	0	0.749076	6.443024	1.64393	-2.2447	0.09353	0.16597	ACSM1	chr16	-	20634559	20710212	2147
ENSG00000(	1459.431	1380.114	1571.422	1403.768	1632.846	1435.151	-0.01957	0.87205	0.91966	AP1G1	chr16	-	71762913	71843104	6959
ENSG00000(	1304.062	1253.664	1467.188	894.3962	1026.282	892.6539	0.51561	5.37E-05	0.000182	SLFN5	chr17	+	33570055	33600674	10591
ENSG00000(	11.39371	33.72006	22.43003	38.20285	30.37426	41.09825	-0.68822	0.14721	0.24027	CATSPER2	chr15	-	43920701	43960316	5071
ENSG00000(	0	0	0	2.996302	0.920432	0	-1.1048	0.40628	NA	STRCP1	chr15	-	43991686	44010382	5328
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC004696.	chr19	+	56988619	57012035	1521
ENSG00000(	400.8515	375.7378	374.7135	29.96302	52.46462	27.94681	3.3704	3.94E-45	9.47E-44	C16orf45	chr16	+	15528152	15718885	2404
ENSG00000(	740.5912	722.5726	897.2014	334.0877	460.216	294.2634	1.1129	3.55E-10	2.01E-09	KIAA0430	chr16	-	15688243	15737023	7743
ENSG00000(	232.0174	276.9862	215.0644	573.7919	580.7926	549.0726	-1.2295	2.01E-14	1.53E-13	SAAL1	chr11	-	18091482	18127638	1582
ENSG00000(	37.28851	50.58008	43.54065	17.22874	45.10117	49.3179	0.2326	0.59044	0.70703	YPEL4	chr11	-	57412560	57417417	4000
ENSG00000(	6994.703	6821.086	5681.396	2460.713	2728.16	2945.922	1.2589	4.69E-25	5.81E-24	PPIB	chr15	-	64448011	64455404	1208
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	LDHC	chr11	+	18433854	18473605	2041
ENSG00000(	572.7929	525.0694	535.682	788.0275	601.9625	735.6586	-0.37919	0.010591	0.024476	FAM96A	chr15	-	64364758	64386217	1536
ENSG00000(	12.4295	7.225726	10.55531	3.745378	5.522592	4.93179	0.99628	0.20509	0.31364	LDHAL6A	chr11	+	18477371	18501147	2526
ENSG00000(	76.6486	103.5687	87.08131	355.8109	386.5814	323.0322	-1.9862	4.51E-22	4.97E-21	FAM111A	chr11	+	58910221	58922512	6189
ENSG00000(	373.9209	393.8021	395.8241	918.3666	844.9566	1030.744	-1.2614	4.60E-19	4.47E-18	KIAA0101	chr15	-	64657193	64679886	1511
ENSG00000(	419.4957	484.1237	402.4212	316.1099	389.3427	478.3836	0.14192	0.42932	0.5595	KIF7	chr15	-	90152020	90198682	4551
ENSG00000(	5.17896	15.65574	3.958241	0	6.443024	0	1.5967	0.13562	0.22487	LDHD	chr16	-	75145758	75150669	2067
ENSG00000(	8.286335	14.45145	7.916483	5.243529	8.283888	0.821965	0.98538	0.24027	0.35554	PLIN1	chr15	-	90207596	90222658	2953
ENSG00000(	112.9013	110.7945	157.0102	53.18436	37.73771	50.96182	1.4002	1.39E-06	5.69E-06	PEX11A	chr15	-	90220995	90234014	2740
ENSG00000(	264.1269	268.5562	253.3274	835.9683	680.1992	740.5904	-1.5171	2.25E-23	2.61E-22	TMEM170A	chr16	-	75476952	75499395	4959
ENSG00000(	4.143168	3.612863	0	2.247227	6.443024	2.465895	-0.38652	0.72619	0.81637	MESP1	chr15	-	90291892	90294541	2369
ENSG00000(	4643.455	4386.016	4177.264	21.72319	27.61296	27.94681	7.3899	0	0	ANPEP	chr15	-	90328120	90358633	3678
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	SCNN1G	chr16	+	23194036	23228204	3507

ENSG00000(	25.8948	20.47289	14.51355	439.7073	416.0353	420.0241	-4.3241	7.98E-60	2.77E-58	RBPMS2	chr15	-	65032091	65067786	2008
ENSG00000(	248.5901	254.1047	312.7011	641.9577	975.6579	733.1927	-1.5219	4.63E-17	4.06E-16	NAV2	chr11	+	19372271	20143144	11000
ENSG00000(	131.5456	186.6646	117.4278	88.39091	56.14635	71.51095	0.99706	0.000345	0.00104	ANKDD1A	chr15	+	65204101	65251042	3113
ENSG00000(	0	3.612863	1.319414	4.494453	6.443024	3.28786	-1.2113	0.27652	0.39806	GLYATL1	chr11	+	58672871	58811000	2281
ENSG00000(	164.6909	152.9445	208.4674	417.9842	501.6354	417.5582	-1.3419	3.61E-13	2.56E-12	C18orf54	chr18	+	51884287	51911588	5237
ENSG00000(	1120.727	1022.44	1279.831	1217.248	1169.869	1080.062	-0.01912	0.88325	0.92688	DCTN5	chr16	+	23652713	23681195	3430
ENSG00000(	933.2485	958.613	936.7838	585.028	406.8309	504.6865	0.91382	1.70E-09	9.13E-09	TERF2IP	chr16	+	75681684	75795051	2118
ENSG00000(	720.9112	723.7769	621.4439	4075.72	2839.533	2714.128	-2.2126	4.87E-45	1.16E-43	PLK1	chr16	+	23688977	23701688	4135
ENSG00000(	816.204	893.5815	881.3684	659.1865	626.8142	639.4887	0.4266	0.000796	0.002268	CLPX	chr15	-	65440557	65477680	4695
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	GPR182	chr12	+	57388230	57390468	1694
ENSG00000(	175.0488	197.5032	245.411	391.0174	413.274	355.9108	-0.90848	7.41E-07	3.11E-06	ZBTB39	chr12	-	57392618	57400230	6170
ENSG00000(	0	0	0	333.3386	213.5402	324.6761	-8.6969	9.60E-20	9.60E-19	TAC3	chr12	-	57403784	57422667	1237
ENSG00000(	1.035792	3.612863	0	0	0.920432	1.64393	0.515	0.69957	0.79573	MYO1A	chr12	-	57422301	57444982	3658
ENSG00000(	270.3417	251.6961	315.3399	884.6582	981.1805	802.2378	-1.6679	2.50E-27	3.41E-26	TMEM194A	chr12	-	57449426	57481846	5590
ENSG00000(	1449.073	1553.531	1237.61	910.8759	1002.35	1184.451	0.45234	0.001361	0.003738	NAB2	chr12	+	57482677	57489259	2711
ENSG00000(	1228.449	1205.492	1332.608	883.9091	820.1049	986.3579	0.48369	0.000141	0.000451	VPS39	chr15	-	42450899	42500514	4844
ENSG00000(	1869.604	1931.678	1642.67	1044.211	1279.4	1427.753	0.53652	0.000113	0.000367	STAT6	chr12	-	57489191	57525922	4034
ENSG00000(	727.1259	588.8967	785.0512	785.0312	858.7631	643.5985	-0.12207	0.43984	0.56958	PATL1	chr11	-	59404189	59436453	4072
ENSG00000(	70.43385	40.94578	50.13772	93.63444	87.44104	84.66239	-0.70237	0.023446	0.050014	XRCC6BP1	chr12	+	58335324	58351052	1245
ENSG00000(	59.04014	68.6444	87.08131	1.498151	0.920432	0.821965	5.5595	8.18E-16	6.76E-15	ELFN2	chr22	-	37764000	37823505	8360
ENSG00000(	112.9013	104.773	100.2754	2305.655	2143.686	1972.716	-4.3192	1.93E-179	4.49E-177	STX3	chr11	+	59480929	59573354	6363
ENSG00000(	456.7842	494.9623	438.0454	827.7285	624.9733	752.0979	-0.66443	1.24E-05	4.57E-05	MRPL16	chr11	-	59573608	59578345	1182
ENSG00000(	233.0532	267.3519	291.5904	692.8949	654.4271	674.8332	-1.3514	9.72E-19	9.29E-18	PIP4K2C	chr12	+	57984957	57997198	2924
ENSG00000(	250.6616	261.3304	440.6842	649.4485	645.2228	511.2622	-0.92113	7.15E-06	2.70E-05	MTMR10	chr15	-	31231144	31283810	5679
ENSG00000(	4391.758	4100.6	4368.579	8218.857	6199.109	6555.992	-0.70425	1.48E-08	7.35E-08	YWHAB	chr20	+	43514317	43537173	3109
ENSG00000(	0	0	0	78.65293	62.58938	81.37453	-6.965	7.34E-12	4.72E-11	C15orf48	chr15	+	45722727	45740959	875
ENSG00000(	19.68005	14.45145	7.916483	53.93344	65.35067	50.96182	-1.9393	1.44E-05	5.24E-05	SCG5	chr15	+	32933877	32989299	1238
ENSG00000(	6939.806	7114.932	8250.294	1101.89	1210.368	999.5093	2.7465	2.44E-115	2.39E-113	GREM1	chr15	+	33010175	33026870	4168
ENSG00000(	113.9371	174.6217	114.789	45.69361	73.63456	98.63579	0.87843	0.004421	0.011065	NYAP1	chr7	+	1E+08	1E+08	3584
ENSG00000(	2465.185	2307.415	1954.052	1072.676	909.3868	1184.451	1.0842	3.75E-15	2.99E-14	TSC22D4	chr7	-	1E+08	1E+08	2383
ENSG00000(	2.071584	0	0	16.47966	2.761296	7.397684	-2.7638	0.012489	0.028411	MS4A6E	chr11	+	60102304	60164069	711
ENSG00000(	0	0	0	3.745378	2.761296	0.821965	-2.0174	0.13428	0.22327	MS4A7	chr11	+	60145955	60163424	2871
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	MS4A14	chr11	+	60146003	60185161	2997
ENSG00000(	220.6237	187.8689	183.3985	738.5885	595.5195	479.2055	-1.6055	2.02E-17	1.81E-16	DIS3L	chr15	+	66585555	66626236	3763
ENSG00000(	138.7961	143.3102	125.3443	456.187	385.661	384.6796	-1.5818	7.04E-18	6.45E-17	CCNDBP1	chr15	+	43477316	43487396	2746
ENSG00000(	0	6.021439	3.958241	14.23244	3.681728	9.041614	-1.2579	0.18366	0.28764	EPB42	chr15	-	43398423	43513481	4553
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	TGM6	chr20	+	2361554	2413399	2292
ENSG00000(	1366.21	1396.974	1597.81	1582.797	1854.67	1611.051	-0.21101	0.090289	0.16119	SMAD3	chr15	+	67356101	67487533	6247
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	MS4A8	chr11	+	60467047	60483284	1353
ENSG00000(	3.107376	0	5.277655	0	0	0.821965	1.8765	0.15881	0.25562	CCDC178	chr18	-	30517366	31021065	3391
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	MS4A15	chr11	+	60524426	60544205	2110
ENSG00000(	4725.283	4455.865	5727.575	330.3423	644.3024	456.1905	3.3679	1.21E-75	5.92E-74	MAP1A	chr15	+	43803156	43823818	10553
ENSG00000(	248.5901	315.5234	262.5633	293.6376	273.3683	345.2253	-0.14273	0.43278	0.56268	RCCD1	chr15	+	91498100	91506349	3157
ENSG00000(	82.86335	87.913	60.69303	227.719	262.3231	184.9421	-1.5261	3.55E-10	2.02E-09	AKTIP	chr16	-	53525291	53538323	2133

ENSG00000(	606.9741	481.7151	556.7926	1307.886	1286.764	1101.433	-1.1634	1.49E-16	1.27E-15	MAPRE2	chr18	+	32556892	32723434	4323
ENSG00000(	420.5315	343.222	419.5736	0	2.761296	0	8.2319	1.74E-36	3.24E-35	EVA1C	chr21	+	33784314	33887707	2492
ENSG00000(	1898.607	1735.379	1717.877	4201.565	3620.979	3850.084	-1.1228	2.30E-23	2.66E-22	MARS	chr12	+	57869228	57911352	3592
ENSG00000(	1265.738	1183.815	984.2827	789.5256	1169.869	937.04	0.24639	0.12188	0.20652	MBD6	chr12	+	57914493	57923931	4282
ENSG00000(	306.5944	290.2333	336.4505	220.9773	229.1876	263.8507	0.38409	0.028625	0.059658	CNPY4	chr7	+	99717236	99723134	1502
ENSG00000(	11342.96	12333.11	10379.83	9304.267	7877.057	8305.956	0.41736	0.000229	0.00071	PDIA3	chr15	+	44038590	44065477	3727
ENSG00000(	1097.939	1160.933	1373.51	2407.529	2664.651	2400.96	-1.0395	8.31E-17	7.21E-16	NUDT21	chr16	-	56463045	56486111	4436
ENSG00000(	2.071584	6.021439	3.958241	1.498151	0	0	2.0262	0.10154	0.17769	NAT16	chr7	-	1.01E+08	1.01E+08	2935
ENSG00000(	6.214751	0	0	23.97042	28.53339	21.37109	-3.1168	9.77E-05	0.000319	NKX3-1	chr8	-	23536206	23540440	3271
ENSG00000(	0	0	2.638828	0.749076	0	3.28786	-0.35447	0.79328	0.86489	SGSM1	chr22	+	25202236	25323545	6643
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-93B1	chr20	-	61272071	61274656	1933
ENSG00000(	71.46964	75.87013	65.97069	46.44268	38.65814	29.59074	0.87976	0.009073	0.021307	DUSP18	chr22	-	31048038	31063877	2920
ENSG00000(	210.2658	183.0517	196.5927	165.5457	186.8477	188.23	0.12715	0.51724	0.64351	TEF	chr22	+	41763337	41795330	4394
ENSG00000(	3.107376	1.204288	0	0	1.840864	0.821965	0.43741	0.74354	0.82919	MEI1	chr22	+	42095503	42195460	4020
ENSG00000(	545.8623	557.5852	546.2373	528.8473	405.9105	402.7628	0.30023	0.056162	0.10747	PBX3	chr9	+	1.29E+08	1.29E+08	2902
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	GNGT2	chr17	-	47280153	47287936	918
ENSG00000(	1606.513	1428.285	1244.207	2713.152	2255.979	2355.751	-0.773	4.37E-09	2.27E-08	PHB	chr17	-	47481414	47492246	1832
ENSG00000(	1114.512	1122.396	848.3831	2627.757	2172.22	2416.577	-1.2218	1.17E-18	1.11E-17	SNRPD1	chr18	+	19192228	19210344	1768
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	TTC16	chr9	+	1.3E+08	1.3E+08	5139
ENSG00000(	317.9881	322.7491	333.8117	38.95193	34.05598	64.11326	2.8037	3.64E-31	5.74E-30	SAMD14	chr17	-	48187404	48207246	4425
ENSG00000(	209.23	152.9445	93.67838	33.7084	14.72691	12.32947	2.838	1.31E-13	9.53E-13	PIP5KL1	chr9	-	1.31E+08	1.31E+08	2198
ENSG00000(	51.7896	28.90291	36.94359	19.47596	8.283888	5.753754	1.7284	0.001243	0.003433	TMEM92	chr17	+	48348767	48358844	2765
ENSG00000(	937.3917	815.3028	897.2014	319.8553	404.9901	352.623	1.2965	9.34E-19	8.94E-18	FAM102A	chr9	-	1.31E+08	1.31E+08	4316
ENSG00000(	397.7441	362.4906	329.8534	441.9546	548.5775	590.1708	-0.53167	0.001335	0.003672	ACSF2	chr17	+	48503519	48552206	2251
ENSG00000(	3454.366	3302.157	3301.173	946.8315	1139.495	1376.791	1.5346	7.56E-29	1.10E-27	GOLGA2	chr9	-	1.31E+08	1.31E+08	4260
ENSG00000(	676.3721	566.0152	515.8908	724.3561	546.7366	707.7118	-0.16911	0.29614	0.42056	TRUB2	chr9	-	1.31E+08	1.31E+08	1777
ENSG00000(	801.7029	823.7328	672.901	823.234	670.9949	870.4608	-0.04079	0.78341	0.85734	COQ4	chr9	+	1.31E+08	1.31E+08	3127
ENSG00000(	461.9632	366.1035	411.6571	805.2562	722.5391	797.306	-0.90357	6.72E-10	3.73E-09	SLC27A4	chr9	+	1.31E+08	1.31E+08	2781
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	LINC00483	chr17	-	48838390	48844918	2763
ENSG00000(	1544.366	1428.285	1170.32	1774.56	1301.491	1474.605	-0.13472	0.36362	0.4934	URM1	chr9	+	1.31E+08	1.31E+08	3045
ENSG00000(	3502.012	3415.36	2851.253	376.0359	311.106	402.7628	3.1546	1.30E-116	1.30E-114	CERCAM	chr9	+	1.31E+08	1.31E+08	5197
ENSG00000(	402.9231	366.1035	415.6153	827.7285	682.0401	720.0413	-0.91068	5.87E-10	3.27E-09	DOLPP1	chr9	+	1.32E+08	1.32E+08	2177
ENSG00000(	105.6508	89.11729	89.72014	120.6012	111.3723	153.7074	-0.43332	0.086516	0.15559	ENDOG	chr9	+	1.32E+08	1.32E+08	1172
ENSG00000(	293.1291	266.1476	217.7033	95.13259	141.7465	126.5826	1.0944	7.25E-07	3.05E-06	PRRX2	chr9	+	1.32E+08	1.32E+08	1233
ENSG00000(	245.4827	237.2447	207.148	799.2636	880.8534	781.6886	-1.8267	9.47E-34	1.63E-32	C15orf39	chr15	+	75487984	75504510	4517
ENSG00000(	69.39806	61.41867	84.44248	143.8225	182.2455	207.1352	-1.2989	3.85E-07	1.67E-06	ISLR2	chr15	+	74392652	74430881	4817
ENSG00000(	294.1649	304.6848	287.6322	352.0655	338.719	333.7178	-0.20809	0.19289	0.29873	SP2	chr17	+	45973516	46006323	3112
ENSG00000(	5.17896	0	0	2.996302	8.283888	5.753754	-1.2874	0.24872	0.36587	PRR15L	chr17	-	46029333	46035244	1519
ENSG00000(	285.8786	251.6961	270.4798	249.4422	246.6758	249.8773	0.11554	0.50287	0.63082	COQ7	chr16	+	19078921	19091417	2657
ENSG00000(	33.14534	31.31148	22.43003	415.7369	451.9321	457.8345	-3.8866	1.08E-58	3.64E-57	GPRC5B	chr16	-	19868616	19897489	4610
ENSG00000(	1738.059	1629.401	1909.192	1999.283	2020.348	2044.227	-0.20058	0.076702	0.1402	CRK	chr17	-	1323983	1366456	3880
ENSG00000(	759.2355	692.4654	827.2724	1125.861	1243.504	1154.861	-0.62772	1.02E-06	4.24E-06	FBXO22	chr15	+	76196200	76227609	3483
ENSG00000(	1655.195	1861.829	1717.877	191.7633	300.9813	283.5779	2.7468	3.04E-65	1.20E-63	TBC1D2B	chr15	-	78276378	78370066	6086
ENSG00000(	0	3.612863	1.319414	0	0	0	1.6005	0.2346	NA	NOD2	chr16	+	50727514	50766988	4486

ENSG00000(	5.17896	4.817151	0	0	0	0	2.652	0.048214	0.094019	SNX20	chr16	-	50700211	50715264	3304
ENSG00000(	43.50326	36.12863	32.98534	52.43529	49.70333	35.34449	-0.27787	0.46397	0.59321	KATNAL2	chr18	+	44497455	44627658	1877
ENSG00000(	271.3775	298.6634	316.6593	250.1912	255.8801	243.3016	0.24034	0.15991	0.25713	HDHD2	chr18	-	44633774	44676891	3229
ENSG00000(	8.286335	9.634302	10.55531	1.498151	2.761296	3.28786	1.6936	0.052576	0.10146	C17orf78	chr17	+	35732928	35749662	1862
ENSG00000(	435.0326	492.5537	513.252	508.6223	450.0912	498.9327	-0.01882	0.8991	0.93741	ZNF91	chr19	-	23487793	23578362	5489
ENSG00000(	9476.46	9806.515	7562.88	720.6107	610.2464	624.6933	3.7697	6.59E-185	1.58E-182	IGF2	chr11	-	2150342	2170833	5585
ENSG00000(	389.4578	285.4162	303.4652	366.2979	312.0264	255.6311	0.068079	0.72449	0.8151	RNF214	chr11	+	1.17E+08	1.17E+08	2846
ENSG00000(	1003.682	1051.343	1207.264	1111.628	1426.67	1195.137	-0.19429	0.16015	0.25745	CDK12	chr17	+	37617764	37721160	7734
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	DPEP2	chr16	-	68021297	68034489	2248
ENSG00000(	141.9035	209.5461	139.8579	274.1617	221.8241	244.9455	-0.59055	0.00627	0.015229	DUS2L	chr16	+	68021649	68113223	2310
ENSG00000(	317.9881	340.8134	316.6593	511.6186	474.9429	496.4668	-0.60303	5.63E-05	0.00019	POP5	chr12	-	1.21E+08	1.21E+08	913
ENSG00000(	338.704	343.222	345.6864	136.3317	221.8241	236.7259	0.78628	0.000187	0.000587	ENGASE	chr17	+	77071021	77084681	4626
ENSG00000(	3.107376	1.204288	2.638828	8.988907	11.96562	12.32947	-1.9752	0.0244	0.05186	RBFOX3	chr17	-	77085427	77613550	3072
ENSG00000(	433.9968	403.4364	406.3794	701.1347	528.328	657.5719	-0.59981	0.000118	0.00038	ATP5L	chr11	+	1.18E+08	1.18E+08	1582
ENSG00000(	3166.416	2978.204	3148.121	1020.99	1777.354	1449.124	1.1262	4.56E-12	2.98E-11	TBC1D16	chr17	-	77906142	78009647	10936
ENSG00000(	105.6508	79.48299	85.7619	73.4094	90.20234	129.0485	-0.10647	0.7142	0.80707	ENTHD2	chr17	-	79202077	79212891	3642
ENSG00000(	6.214751	21.67718	15.83297	433.7147	635.0981	433.9975	-5.0636	6.64E-58	2.20E-56	MYO5B	chr18	-	47349183	47721463	9505
ENSG00000(	9.322127	14.45145	14.51355	30.7121	25.7721	69.86702	-1.664	0.00165	0.004459	ART5	chr11	-	3659733	3663546	1504
ENSG00000(	657.7279	633.4553	563.3897	1185.787	710.5735	796.484	-0.53601	0.002874	0.007445	ACAA2	chr18	-	47309869	47340330	2018
ENSG00000(	1469.789	1311.469	1568.783	1118.37	1214.05	1192.671	0.3028	0.013164	0.029774	STIM1	chr11	+	3875757	4114439	4038
ENSG00000(	785.1303	704.5083	893.2431	2390.3	2398.646	1957.098	-1.4982	4.40E-28	6.18E-27	RRM1	chr11	+	4115937	4160106	3166
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	OR51E2	chr11	-	4701401	4719084	2781
ENSG00000(	148.1182	181.8474	197.9121	220.9773	180.4047	176.7225	-0.135	0.52271	0.6481	TRIM68	chr11	-	4619902	4629489	3352
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	OR51I1	chr11	-	5461800	5462744	945
ENSG00000(	61.11172	60.21439	29.0271	51.68621	49.70333	67.40112	-0.1567	0.66961	0.77259	FN3K	chr17	+	80693451	80709073	2515
ENSG00000(	148.1182	173.4174	168.885	10.48706	15.64734	10.68554	3.69	8.23E-29	1.20E-27	PRRT2	chr16	+	29823177	29827201	3000
ENSG00000(	16.57267	12.04288	17.15238	7.490755	14.72691	9.041614	0.52664	0.40455	0.53542	ZNF23	chr16	-	71481500	71496998	3242
ENSG00000(	886.6379	939.3444	901.1596	1531.11	1485.577	1501.73	-0.72738	2.36E-10	1.36E-09	IRGQ	chr19	-	44088521	44100287	9685
ENSG00000(	488.8938	407.0492	463.1142	211.2393	236.551	205.4912	1.0546	2.37E-10	1.36E-09	ZNF226	chr19	+	44669226	44682534	5972
ENSG00000(	141.9035	105.9773	131.9414	55.43159	96.64536	67.40112	0.78897	0.005219	0.012891	ZNF229	chr19	-	44921685	44952766	5387
ENSG00000(	114.9729	131.2674	145.1355	143.8225	173.0412	143.8439	-0.23528	0.29604	0.42047	ZNF180	chr19	-	44979854	45004576	3270
ENSG00000(	288.9859	287.8248	240.1333	1115.373	791.5715	917.3128	-1.7817	6.71E-27	8.96E-26	PPP2R3B	chrX	-	294698	347690	5802
ENSG00000(	320.0597	315.5234	269.1604	301.8774	298.22	305.7709	-0.00016	0.99924	0.99937	ZNF668	chr16	-	31072164	31085641	2865
ENSG00000(	671.1932	722.5726	614.8468	394.7628	647.9841	674.8332	0.2262	0.2258	0.33851	ZNF646	chr16	+	31085743	31095517	8118
ENSG00000(	79.75598	105.9773	64.65128	14.98151	11.96562	36.98842	1.9192	4.59E-06	1.77E-05	VKORC1	chr16	-	31102163	31107301	1077
ENSG00000(	0	0	1.319414	6.74168	11.96562	5.753754	-3.1432	0.006119	0.0149	GNG8	chr19	-	47137333	47137942	216
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	LPO	chr17	+	56295909	56345879	3371
ENSG00000(	1.035792	1.204288	0	0.749076	5.522592	4.93179	-1.5941	0.19442	0.30065	CA4	chr17	+	58227297	58248260	1154
ENSG00000(	389.4578	296.2548	283.674	396.261	406.8309	295.9074	-0.17723	0.3512	0.48093	SMG8	chr17	+	57286761	57292608	3477
ENSG00000(	24152.6	24533.75	22709.75	24312.75	23141.5	22073.87	0.03821	0.69786	0.79445	TPM4	chr19	+	16177831	16213813	2672
ENSG00000(	239.2679	222.7932	237.4945	425.4749	404.0696	356.7328	-0.75899	6.20E-06	2.36E-05	RAB8A	chr19	+	16222439	16245044	2827
ENSG00000(	2740.705	2637.39	2260.156	3757.363	2163.015	2570.284	-0.15219	0.36946	0.49987	GPX4	chr19	+	1103936	1106787	1159
ENSG00000(	2511.795	2466.381	2208.699	2156.589	2880.032	2719.882	-0.10916	0.40569	0.53658	MIDN	chr19	+	1248552	1259142	3790
ENSG00000(	8.286335	2.408575	1.319414	0.749076	1.840864	5.753754	0.44143	0.68465	0.78423	JSRP1	chr19	-	2252252	2269758	1137

ENSG00000(	22.78742	12.04288	10.55531	5.992604	5.522592	11.50751	0.9202	0.17941	0.28215	FAM129C	chr19	+	17634110	17664648	5115
ENSG00000(	75.61281	51.78437	69.92893	142.3244	162.9165	166.8589	-1.2438	1.38E-06	5.63E-06	KLHL26	chr19	+	18747775	18781309	3192
ENSG00000(	1871.676	1793.184	1911.831	3371.589	3910.916	3626.509	-0.9663	2.24E-18	2.10E-17	GATAD2A	chr19	+	19496639	19619740	5776
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	NOS2P2	chr17	-	18400886	18404348	340
ENSG00000(	2256.991	2032.838	1965.927	1752.837	1747.9	1989.155	0.18848	0.10968	0.18908	MVD	chr16	-	88718343	88729569	2352
ENSG00000(	334.5608	362.4906	324.5758	2098.91	1984.451	1948.057	-2.556	3.05E-92	2.01E-90	CDT1	chr16	+	88869621	88875666	3240
ENSG00000(	776.8439	741.8412	700.6087	811.9979	670.0745	793.1961	-0.03595	0.79278	0.86454	TRAPPC2L	chr16	+	88922628	88929094	3102
ENSG00000(	3562.088	3469.553	3574.292	2330.374	4281.85	3420.196	0.080241	0.633	0.74274	ANKRD11	chr16	-	89334038	89556969	9301
ENSG00000(	140.8677	130.0631	159.6491	217.2319	231.0284	222.7525	-0.6378	0.001438	0.003923	C16orf55	chr16	+	89724210	89737680	3339
ENSG00000(	7.250543	9.634302	2.638828	6.74168	25.7721	10.68554	-1.0292	0.1748	0.27664	SGK494	chr17	-	26934982	26941218	2975
ENSG00000(	70.43385	72.25726	59.37362	110.8632	142.667	183.2982	-1.0972	7.01E-05	0.000233	PROCA1	chr17	-	27030215	27038872	3168
ENSG00000(	38164.79	37269.09	25629.61	25380.93	19600.6	22250.59	0.58627	8.73E-05	0.000287	RPL13	chr16	+	89627065	89630950	2385
ENSG00000(	36.25272	36.12863	36.94359	158.0549	148.1896	129.8705	-1.9747	3.59E-12	2.36E-11	ZNF641	chr12	-	48733791	48745197	4872
ENSG00000(	756.1281	688.8526	686.0952	560.3085	675.5971	603.3223	0.21356	0.12397	0.20925	CACNB3	chr12	+	49207577	49222724	4029
ENSG00000(	52.82539	30.10719	60.69303	108.616	126.0992	120.0069	-1.2882	2.52E-05	8.90E-05	DHRS13	chr17	-	27224799	27230089	2037
ENSG00000(	681.5511	651.5197	461.7948	541.5816	467.5795	504.6865	0.24606	0.14193	0.23345	TP53I13	chr17	+	27893070	27900175	2468
ENSG00000(	3898.721	3782.668	4233.999	1235.226	4534.968	3640.483	0.3282	0.51705	0.64348	MLL2	chr12	-	49412758	49453557	19419
ENSG00000(	51.7896	45.76293	21.11062	67.4168	50.62376	66.57916	-0.61612	0.10598	0.18395	CORO6	chr17	-	27941774	27949925	4069
ENSG00000(	2.071584	13.24716	3.958241	11.23613	24.85166	17.26126	-1.3579	0.062918	0.11843	RHEBL1	chr12	-	49458468	49463808	1261
ENSG00000(	12094.94	12330.7	11465.71	6984.38	4751.27	4788.768	1.1157	6.48E-15	5.08E-14	TUBA1A	chr12	-	49578579	49583107	1915
ENSG00000(	2393.715	2230.341	2087.313	8045.82	5483.013	5193.996	-1.4753	6.64E-22	7.27E-21	TUBA1C	chr12	+	49582519	49667114	1800
ENSG00000(	75.61281	60.21439	80.48424	50.93714	55.22592	37.81039	0.57961	0.074576	0.13697	ZNF610	chr19	+	52839498	52871031	2723
ENSG00000(	5.17896	4.817151	9.235896	29.96302	24.85166	33.70056	-2.1062	0.00041	0.001222	ZNF528	chr19	+	52901102	52921665	4809
ENSG00000(	128.4382	101.1602	98.95603	82.39831	163.8369	112.6092	-0.11887	0.67574	0.77747	ZNF701	chr19	+	53059075	53090427	5538
ENSG00000(	367.7061	373.3292	287.6322	549.8215	420.6374	511.2622	-0.52355	0.002297	0.006056	SERTAD3	chr19	-	40946751	40950612	1734
ENSG00000(	2250.776	2272.491	2013.425	837.4665	1177.233	1297.883	0.97826	1.79E-10	1.04E-09	NCKAP5L	chr12	-	50184929	50222533	4900
ENSG00000(	30.03797	36.12863	26.38828	26.96672	33.13555	35.34449	-0.04029	0.92387	0.95388	RAB4B	chr19	+	41284121	41302847	1982
ENSG00000(	2.071584	1.204288	0	4.494453	6.443024	6.575719	-1.8559	0.091138	0.16247	GPD1	chr12	+	50497602	50505102	3082
ENSG00000(	541.7192	567.2195	444.6424	843.4591	785.1285	739.7684	-0.60538	3.15E-05	0.00011	C19orf55	chr19	+	36249044	36261930	3607
ENSG00000(	2.071584	4.817151	6.597069	945.3333	780.5263	858.9533	-7.4364	1.32E-68	5.57E-67	CYP2S1	chr19	+	41698954	41713444	2782
ENSG00000(	693.9806	640.6811	558.112	3233.759	2717.115	3021.543	-2.2383	1.76E-67	7.27E-66	AXL	chr19	+	41725108	41767671	4737
ENSG00000(	50.7538	55.39724	34.30476	65.16957	49.70333	64.93523	-0.34794	0.31461	0.44129	NFKBID	chr19	-	36378555	36393185	1834
ENSG00000(	26.93059	28.90291	19.79121	44.19546	34.97642	39.45432	-0.63097	0.13355	0.22223	TMC4	chr19	-	54663846	54676944	2412
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	ANKRD33	chr12	+	52281744	52285448	3319
ENSG00000(	100.4718	95.13873	67.2901	26.96672	36.81728	48.49593	1.2139	0.00036	0.001081	TTYH1	chr19	+	54926393	54948080	3679
ENSG00000(	4652.777	4970.095	3406.726	2782.816	3050.312	3963.515	0.41029	0.009539	0.022294	LENG8	chr19	+	54960065	54973217	5790
ENSG00000(	1270.917	1218.739	918.312	109.365	133.4626	134.8022	3.1646	2.21E-76	1.10E-74	CDC42EP5	chr19	-	54976210	54984411	864
ENSG00000(	4.143168	14.45145	5.277655	2.247227	0	3.28786	1.7391	0.082755	0.14974	TMEM145	chr19	+	42817477	42829214	2011
ENSG00000(	521.0033	478.1022	443.323	542.3307	567.9065	526.8795	-0.18038	0.2086	0.31806	ZNF526	chr19	+	42724423	42732353	4023
ENSG00000(	203.0152	183.0517	189.9956	423.2277	401.3084	404.4067	-1.088	8.00E-11	4.77E-10	TRAPPC9	chr8	-	1.41E+08	1.41E+08	29517
ENSG00000(	1.035792	0	0	5.992604	5.522592	2.465895	-2.4178	0.051579	0.099776	NLRP7	chr19	-	55434877	55477680	3826
ENSG00000(	1945.217	1923.247	2010.787	1750.59	1572.098	1389.121	0.31837	0.009191	0.021556	ZNF146	chr19	+	36705504	36729676	3780
ENSG00000(	172.9772	214.3632	186.0373	80.90016	102.168	83.84042	1.0972	1.63E-06	6.60E-06	ZNF283	chr19	+	44331444	44353307	2851
ENSG00000(	0	1.204288	2.638828	121.3502	99.40666	192.3398	-6.2741	8.31E-19	7.98E-18	PPP1R14A	chr19	-	38741877	38747231	949

ENSG00000(	1.035792	4.817151	0	3400.054	3077.925	3266.489	-10.191	3.94E-81	2.17E-79	SPINT2	chr19	+	38734675	38783254	3807
ENSG00000(	1.035792	0	0	1.498151	0	5.753754	-1.4742	0.27262	0.3934	C19orf33	chr19	+	38794801	38795649	520
ENSG00000(	1431.464	1240.416	955.2556	910.8759	738.1865	895.9418	0.51005	0.001308	0.003602	YIF1B	chr19	-	38795753	38807913	1917
ENSG00000(	0	0	1.319414	5.243529	0	0	-0.96444	0.4771	0.60629	DNAAF3	chr19	-	55670031	55678090	2228
ENSG00000(	12.4295	19.2686	17.15238	17.22874	6.443024	13.15144	0.37207	0.5471	0.66891	PSCA	chr8	+	1.44E+08	1.44E+08	1020
ENSG00000(	13.46529	18.06432	5.277655	23.97042	23.93123	29.59074	-1.0154	0.071192	0.1317	ATCAY	chr19	+	3879862	3928077	5070
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	LY6D	chr8	-	1.44E+08	1.44E+08	1423
ENSG00000(	1430.429	1240.416	1145.251	2391.798	1988.133	2343.422	-0.8145	4.35E-10	2.45E-09	DAPK3	chr19	-	3958451	3971121	2257
ENSG00000(	185945.4	177761.3	142703.8	60402.46	64066.67	69065.6	1.385	1.53E-30	2.37E-29	EEF2	chr19	-	3976054	3985467	3164
ENSG00000(	0	0	0	9.737982	1.840864	9.041614	-3.5533	0.004121	0.010386	TMIGD2	chr19	-	4292229	4302428	1262
ENSG00000(	339.7397	228.8147	283.674	1340.845	1627.324	1712.153	-2.4455	2.34E-51	6.69E-50	CHAF1A	chr19	+	4402659	4445015	3339
ENSG00000(	2657.842	2459.156	2006.828	1068.182	1042.849	1023.346	1.1823	7.43E-20	7.47E-19	UBXN6	chr19	-	4444996	4457819	4598
ENSG00000(	2337.782	2183.374	2022.661	2197.039	2470.439	2886.741	-0.20619	0.10927	0.18851	HDGFRP2	chr19	+	4472284	4502223	3115
ENSG00000(	31.07376	39.74149	30.34652	29.21395	8.283888	13.15144	0.94698	0.068928	0.12805	PLIN4	chr19	-	4502204	4517716	6341
ENSG00000(	131.5456	118.0202	104.2337	7.490755	11.04518	1.64393	4.0443	3.22E-21	3.43E-20	SEMA6B	chr19	-	4542600	4559820	3986
ENSG00000(	883.5305	910.4415	724.3582	1029.23	969.2149	983.07	-0.24212	0.070092	0.12986	ZNF444	chr19	+	56643968	56672262	5565
ENSG00000(	3195.418	3162.46	2632.23	2516.894	2466.758	2513.569	0.26189	0.023416	0.049954	NXN	chr17	-	702553	883010	3036
ENSG00000(	539.6476	507.0051	546.2373	653.1939	563.3044	500.5766	-0.10862	0.47056	0.59966	FAM57A	chr17	+	635652	646206	2406
ENSG00000(	820.3472	810.4856	736.2329	1522.871	1441.397	1408.848	-0.88316	2.53E-13	1.81E-12	GLOD4	chr17	-	660337	685581	2737
ENSG00000(	409.1378	310.7062	332.4923	399.2573	342.4007	434.8194	-0.15893	0.36055	0.49016	MFSD3	chr8	+	1.46E+08	1.46E+08	1548
ENSG00000(	20.71584	52.98866	38.263	10.48706	8.283888	13.15144	1.7308	0.000997	0.002795	GPT	chr8	+	1.46E+08	1.46E+08	1885
ENSG00000(	400.8515	450.4036	307.4234	230.7153	232.8693	364.1305	0.48324	0.022799	0.048716	KIFC2	chr8	+	1.46E+08	1.46E+08	3646
ENSG00000(	394.6367	386.5764	395.8241	216.4828	186.8477	193.1618	0.97541	5.53E-09	2.84E-08	SLC43A2	chr17	-	1477673	1532180	3254
ENSG00000(	30.03797	32.51577	14.51355	45.69361	43.2603	64.93523	-0.96418	0.022331	0.04786	RILP	chr17	-	1549444	1553371	1771
ENSG00000(	12.4295	6.021439	1.319414	11.98521	1.840864	2.465895	0.24318	0.79757	0.86812	SERPINF2	chr17	+	1646130	1658562	2284
ENSG00000(	502.3591	425.1136	389.2271	262.1764	381.0588	464.4102	0.25047	0.21506	0.32577	WDR81	chr17	+	1619817	1641893	6733
ENSG00000(	59.04014	78.2787	64.65128	134.8336	92.96363	97.81383	-0.68559	0.016629	0.036774	SRR	chr17	+	2206677	2228554	2728
ENSG00000(	807.9177	894.7858	878.7296	1126.61	1246.265	1130.202	-0.43981	0.000374	0.001121	TSR1	chr17	-	2225951	2240801	5034
ENSG00000(	26.93059	14.45145	13.19414	2.996302	8.283888	13.15144	1.0966	0.10539	0.18308	TRPV3	chr17	-	3413796	3461289	5050
ENSG00000(	316.9523	245.6747	215.0644	92.13629	79.15715	61.64737	1.7268	4.45E-13	3.12E-12	HSD11B1L	chr19	+	5680615	5688533	1884
ENSG00000(	510.6454	437.1564	440.6842	192.5124	147.2691	182.4762	1.4032	2.00E-15	1.62E-14	CYB5D2	chr17	+	4046462	4090605	1910
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	GGT6	chr17	-	4460222	4464113	2534
ENSG00000(	1517.435	1512.585	1190.111	3148.365	2512.779	3002.638	-1.0346	3.01E-14	2.27E-13	C19orf48	chr19	-	51300961	51308186	1844
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	KLK1	chr19	-	51322404	51327043	1854
ENSG00000(	0	0	0	0.749076	0.920432	0.821965	-0.73223	0.57364	NA	KLK6	chr19	-	51461887	51472929	1708
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	KLK13	chr19	-	51559463	51568371	1614
ENSG00000(	11.39371	20.47289	9.235896	14.23244	19.32907	6.575719	0.036749	0.95489	0.97324	AC018755.	chr19	-	52095036	52097633	1701
ENSG00000(	476.4643	480.5108	393.1853	483.1537	465.7386	473.4518	-0.07357	0.62477	0.73627	ZNF83	chr19	-	53097313	53193749	4442
ENSG00000(	25.8948	51.78437	42.22124	88.39091	98.48622	87.95025	-1.1865	0.000347	0.001045	KRT80	chr12	-	52562780	52585784	3894
ENSG00000(	0	0	0	4.494453	0	0	-1.1446	0.38559	NA	KRT1	chr12	-	53068520	53074191	2451
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	ACER1	chr19	-	6306153	6333640	1445
ENSG00000(	1249.165	1201.879	940.742	3434.511	2346.181	2349.998	-1.2563	1.20E-14	9.29E-14	OTUB1	chr11	+	63753325	63769283	2493
ENSG00000(	265.1627	256.5133	160.9685	397.7591	357.1276	448.7928	-0.81002	6.19E-05	0.000207	RCOR2	chr11	-	63678693	63684316	2604
ENSG00000(	1601.334	1472.844	1095.113	134.8336	118.7357	138.9121	3.395	3.91E-89	2.43E-87	ANGPTL4	chr19	+	8428173	8439257	1879

ENSG00000(	1792.956	1931.678	1382.746	1512.384	852.32	1017.593	0.5913	0.001466	0.003991	CD320	chr19	-	8367011	8373240	1729
ENSG00000(	913.5685	857.4529	845.7442	331.8405	372.775	302.4831	1.3753	5.12E-22	5.62E-21	SPRYD3	chr12	-	53458388	53473204	2644
ENSG00000(	2603.981	2491.671	1919.747	102.6234	59.82808	78.90863	4.8308	6.56E-158	1.11E-155	IGFBP6	chr12	+	53491220	53496129	1177
ENSG00000(	3.107376	2.408575	3.958241	0	0	0.821965	2.1634	0.094809	0.16773	SOAT2	chr12	+	53497302	53518322	2044
ENSG00000(	2.071584	0	0	14.98151	15.64734	28.76877	-3.9373	3.49E-05	0.000121	ZNF558	chr19	-	8920380	8943004	3498
ENSG00000(	2405.109	2488.058	1932.941	2045.725	1946.714	2321.229	0.11268	0.38985	0.52048	NDUFV1	chr11	+	67374323	67380006	1748
ENSG00000(	773.7366	632.2511	569.9868	1153.576	783.2876	795.662	-0.46508	0.00787	0.018748	CDK2AP2	chr11	-	67273968	67276120	1692
ENSG00000(	106.6866	139.6974	93.67838	74.90755	50.62376	62.46933	0.84199	0.003464	0.008856	NUDT8	chr11	-	67395409	67397401	1465
ENSG00000(	25.8948	9.634302	17.15238	5.243529	5.522592	7.397684	1.439	0.034401	0.070091	TBX10	chr11	-	67398774	67407031	1548
ENSG00000(	1989.756	1976.236	1657.184	1465.192	1103.598	1214.042	0.57021	3.78E-05	0.00013	PRDX2	chr19	-	12907634	12912694	1717
ENSG00000(	71.46964	59.0101	76.526	217.2319	213.5402	201.3814	-1.5996	5.59E-12	3.63E-11	ZNF232	chr17	-	5008836	5026411	2384
ENSG00000(	198.872	177.0303	153.052	409.7443	404.0696	443.8611	-1.2404	2.18E-12	1.46E-11	MIS12	chr17	+	5389605	5394134	2505
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	CD300C	chr17	-	72537247	72542282	1517
ENSG00000(	3.107376	0	0	244.9477	298.22	243.3016	-7.2	9.60E-27	1.27E-25	HID1	chr17	-	72946838	72969261	3271
ENSG00000(	253.769	233.6318	230.8974	548.3233	452.8525	515.372	-1.0738	4.09E-11	2.49E-10	ICT1	chr17	+	73008765	73017356	890
ENSG00000(	502.3591	496.1665	480.2666	292.8885	297.2995	438.1073	0.52197	0.003767	0.00957	ATP5H	chr17	-	73034958	73043080	2191
ENSG00000(	11.39371	14.45145	7.916483	92.13629	74.55499	84.66239	-2.8196	1.18E-11	7.46E-11	TMEM88	chr17	+	7758383	7759417	875
ENSG00000(	1.035792	2.408575	0	0	2.761296	1.64393	-0.19923	0.88039	0.92525	EVPL	chr17	-	74000583	74023533	6614
ENSG00000(	2148.232	1863.033	2039.814	2088.423	2084.778	2009.704	-0.03078	0.78258	0.85688	SRP68	chr17	-	74035184	74068734	2649
ENSG00000(	430.8894	444.3822	430.1289	183.5235	130.7013	118.3629	1.5819	3.95E-16	3.33E-15	MGAT5B	chr17	+	74864538	74946475	4492
ENSG00000(	0	0	0	11.23613	14.72691	5.753754	-4.2363	0.000301	0.000914	TMC8	chr17	+	76126851	76139049	4411
ENSG00000(	597.6519	557.5852	513.252	2754.351	2109.63	2408.357	-2.1176	1.76E-54	5.38E-53	TK1	chr17	-	76170160	76183314	1681
ENSG00000(	225.8026	285.4162	242.7721	430.7184	332.276	439.7512	-0.67285	0.000219	0.000681	TMEM68	chr8	-	56608983	56685966	2588
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	CYP7A1	chr8	-	59402737	59412795	2950
ENSG00000(	65.25489	90.32158	91.03955	65.91865	70.87326	53.42772	0.3668	0.22164	0.3333	RP11-25K1	chr8	+	60031599	60033905	1106
ENSG00000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	GSDMA	chr17	+	38119226	38134019	2164
ENSG00000(	172.9772	158.966	199.2315	326.5969	259.5618	253.9872	-0.66078	0.000827	0.00235	TMEM99	chr17	+	38975358	38992522	2058
ENSG00000(	41.43168	31.31148	27.70769	39.701	25.7721	35.34449	-0.00297	0.99434	0.99641	GHDC	chr17	-	40340817	40346531	2650
ENSG00000(	859.7073	969.4516	804.8424	572.2937	568.827	562.224	0.62757	2.78E-06	1.10E-05	ITFG3	chr16	+	284545	319942	3213
ENSG00000(	10.35792	4.817151	10.55531	0	0.920432	1.64393	2.7171	0.00904	0.021233	PRR25	chr16	+	855443	863861	1209
ENSG00000(	859.7073	874.3129	757.3435	935.5954	887.2964	897.5857	-0.12608	0.32082	0.44795	ZNF598	chr16	-	2047655	2059824	4457
ENSG00000(	31.07376	37.33292	32.98534	13.48336	18.40864	23.01502	0.86019	0.064011	0.12013	RAB26	chr16	+	2190804	2204166	1922
ENSG00000(	1347.565	1185.019	837.8278	1267.436	995.9074	947.7256	0.070393	0.68354	0.78346	MLST8	chr16	+	2254249	2259417	2116
ENSG00000(	469.2137	427.5221	365.4776	621.7327	532.9301	669.0794	-0.52767	0.000884	0.0025	E4F1	chr16	+	2273567	2285743	5931
ENSG00000(	4.143168	8.430014	9.235896	11.98521	17.48821	14.79537	-0.96234	0.16128	0.25883	DNASE1L2	chr16	+	2285817	2288712	2194
ENSG00000(	365.6345	339.6091	284.9934	794.7692	614.8486	873.7487	-1.199	2.07E-12	1.39E-11	ECI1	chr16	-	2289396	2302301	1541
ENSG00000(	22.78742	22.88147	10.55531	22.47227	16.56778	19.72716	-0.05519	0.91854	0.9507	CASKIN1	chr16	-	2227184	2246526	5756
ENSG00000(	13.46529	18.06432	15.83297	146.0697	141.7465	110.1433	-3.0242	8.25E-18	7.54E-17	ABCA3	chr16	-	2325882	2390747	6609
ENSG00000(	785.1303	792.4213	732.2746	1071.927	951.7267	992.1117	-0.38387	0.002284	0.006025	KCTD5	chr16	+	2732476	2759031	2482
ENSG00000(	11891.93	12110.32	12070	9475.057	12591.51	10745.55	0.1365	0.25047	0.36787	SRRM2	chr16	+	2802330	2822539	9353
ENSG00000(	10.35792	36.12863	22.43003	11.23613	33.13555	13.9734	0.23045	0.69523	0.79226	ZNF597	chr16	-	3486104	3493542	1831
ENSG00000(	36.25272	39.74149	27.70769	21.72319	23.0108	23.01502	0.60133	0.16896	0.26882	NLRC3	chr16	-	3589033	3627401	6603
ENSG00000(	77.68439	63.82725	77.84541	107.1178	91.12277	134.8022	-0.5969	0.031229	0.064382	SDHAF2	chr11	+	61197514	61215001	2033
ENSG00000(	8267.691	8504.68	8217.309	7746.19	9831.134	10055.92	-0.1447	0.22633	0.33918	DDB1	chr11	-	61066923	61110068	4506

ENSG00000(	671.1932	546.7466	556.7926	778.2895	709.6531	756.2077	-0.3364	0.017093	0.037705	VPS37C	chr11	-	60897728	60929089	2865
ENSG00000(	817.2398	751.4755	708.5252	656.1902	554.1001	577.0194	0.34868	0.012146	0.027699	VWCE	chr11	-	61025762	61062896	3640
ENSG00000(	489.9296	433.5436	455.1978	65.91865	80.99802	67.40112	2.6768	6.79E-45	1.62E-43	RAB3IL1	chr11	-	61664773	61687741	2284
ENSG00000(	71.46964	44.55865	52.77655	0.749076	1.840864	4.93179	4.2561	2.30E-12	1.53E-11	BEST1	chr11	+	61717293	61732987	5772
ENSG00000(	10370.35	10597.73	10346.84	3553.614	3834.52	3381.564	1.5378	6.59E-52	1.91E-50	FTH1	chr11	-	61727190	61735132	1229
ENSG00000(	27.96638	48.17151	39.58241	19.47596	29.45382	20.54912	0.71688	0.10395	0.18109	BSCL2	chr11	-	62457747	62477317	2038
ENSG00000(	856.5999	1089.88	827.2724	1103.388	942.5224	1120.338	-0.19083	0.18777	0.29251	POLR2G	chr11	+	62529016	62534182	1556
ENSG00000(	4154.561	3735.701	3615.194	6704.226	5678.145	6656.272	-0.72516	2.59E-10	1.48E-09	SLC3A2	chr11	+	62623518	62656352	2397
ENSG00000(	0	0	0	29.96302	21.16994	18.08323	-5.3868	7.36E-07	3.09E-06	HRASLS5	chr11	-	63228876	63258666	3032
ENSG00000(	785.1303	761.1098	643.8739	2072.692	1748.821	2248.074	-1.4659	2.30E-26	3.00E-25	C11orf84	chr11	+	63580860	63595190	2024
ENSG00000(	107.7224	116.8159	96.31721	101.8743	81.91845	118.3629	0.085054	0.74265	0.82838	ATG16L2	chr11	+	72525353	72554719	4577
ENSG00000(	477.5001	395.0064	531.7238	787.2784	847.7179	700.3141	-0.73184	2.11E-06	8.44E-06	C2CD3	chr11	-	73723763	73882255	7289
ENSG00000(	73.54123	115.6116	83.12307	30.7121	38.65814	38.63235	1.3154	5.99E-05	0.000201	TRANK1	chr3	-	36868311	36986548	10481
ENSG00000(	36.25272	67.44011	60.69303	14.23244	35.89685	52.60575	0.65928	0.14226	0.23373	TTC21A	chr3	+	39149152	39180394	4258
ENSG00000(	26743.11	27723.91	23362.86	28389.96	20604.79	23587.11	0.10047	0.43801	0.56758	RPSA	chr3	+	39448180	39454033	2058
ENSG00000(	2.071584	0	0	26.96672	23.93123	19.72716	-4.1976	4.94E-06	1.90E-05	ENTPD3	chr3	+	40428647	40470110	2819
ENSG00000(	4891.009	5017.063	5709.103	6887.001	7767.526	6261.729	-0.42079	0.000391	0.00117	CTNNB1	chr3	+	41236328	41301587	3729
ENSG00000(	104.615	128.8588	88.40072	89.88907	80.99802	60.00344	0.47445	0.092411	0.16428	ULK4	chr3	-	41288090	42003922	4613
ENSG00000(	199.9078	166.1917	229.578	212.7375	235.6306	258.9189	-0.2472	0.21515	0.32584	FADD	chr11	+	70049269	70053496	1841
ENSG00000(	3899.757	3235.921	3002.986	143.0734	130.7013	144.6658	4.5846	2.28E-222	8.12E-220	LTBP3	chr11	-	65306276	65326401	4443
ENSG00000(	6.214751	0	1.319414	0.749076	0	2.465895	0.81458	0.52695	0.65171	NAALADL1	chr11	-	64812290	64826021	2699
ENSG00000(	412.2452	264.9433	336.4505	851.6989	599.2012	677.2991	-1.0638	1.19E-08	5.93E-08	SAC3D1	chr11	+	64808373	64812300	1566
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	BATF2	chr11	-	64755415	64764517	2569
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	SLC22A11	chr11	+	64323098	64340347	3860
ENSG00000(	4137.989	3991.01	3691.72	7167.155	6276.426	5979.795	-0.71512	2.31E-10	1.33E-09	SF1	chr11	-	64532078	64546258	3470
ENSG00000(	340.7755	302.2762	362.8388	210.4902	173.0412	199.7375	0.78064	1.46E-05	5.30E-05	MAP4K2	chr11	-	64556290	64570713	3169
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	C11orf85	chr11	-	64704989	64739557	2046
ENSG00000(	14.50109	6.021439	13.19414	9.737982	21.16994	20.54912	-0.56607	0.37232	0.50277	CCDC88B	chr11	+	64107695	64125006	5235
ENSG00000(	1734.951	1565.574	1731.071	790.2747	948.045	1050.471	0.84982	2.87E-10	1.64E-09	SCARA3	chr8	+	27491385	27534293	3510
ENSG00000(	174.013	104.773	153.052	787.2784	713.3348	658.3939	-2.3076	7.17E-35	1.28E-33	PBK	chr8	-	27667137	27695612	2118
ENSG00000(	42.46747	38.53721	15.83297	0.749076	0	1.64393	4.6839	1.87E-08	9.21E-08	SCARA5	chr8	-	27727399	27850244	4026
ENSG00000(	0	0	1.319414	0	4.60216	0	-0.82615	0.54181	NA	PNOC	chr8	+	28174503	28200872	1310
ENSG00000(	2884.68	2663.884	2484.456	2117.637	1946.714	2076.283	0.38712	0.000564	0.001644	COPS6	chr7	+	99686577	99689823	1432
ENSG00000(	1517.435	1472.844	1465.869	2515.396	2288.194	2109.984	-0.63247	4.97E-08	2.35E-07	PAFAH1B2	chr11	+	1.17E+08	1.17E+08	4195
ENSG00000(	388.422	429.9307	336.4505	342.3275	284.4135	367.4183	0.21502	0.21374	0.32405	ANKS3	chr16	-	4746513	4784379	3098
ENSG00000(	513.7528	517.8437	457.8366	662.1828	554.1001	721.6852	-0.37849	0.012564	0.028561	NUDT16L1	chr16	+	4743695	4745860	2040
ENSG00000(	308.666	303.4805	337.7699	331.0914	287.1748	295.9074	0.053281	0.74791	0.83242	KIAA1586	chr6	+	56911347	56920023	2933
ENSG00000(	579.0077	562.4024	527.7655	474.1648	424.3192	465.2321	0.29083	0.040811	0.081497	RAB4A	chr1	+	2.29E+08	2.29E+08	2966
ENSG00000(	0	0	0	2.996302	1.840864	7.397684	-2.7726	0.033043	0.067581	OR2W6P	chr6	+	27905243	27906181	939
ENSG00000(	7.250543	0	0	9.737982	8.283888	8.219649	-1.4941	0.13734	0.22723	OR2B2	chr6	-	27878963	27880174	1212
ENSG00000(	9.322127	3.612863	3.958241	2.996302	1.840864	0	1.4479	0.17893	0.2816	KCNJ4	chr22	-	38822332	38851205	2065
ENSG00000(	2561.513	2560.316	2741.742	1894.412	2308.443	2145.328	0.30848	0.008193	0.019409	SETD5	chr3	+	9439299	9520924	6866
ENSG00000(	1423.178	1311.469	1217.819	671.1717	672.8358	693.7384	0.95451	1.55E-14	1.19E-13	VASN	chr16	+	4421849	4433529	2806
ENSG00000(	5.17896	3.612863	7.916483	89.88907	131.6218	79.7306	-4.0427	1.28E-16	1.10E-15	FAM83B	chr6	+	54711569	54806820	3167

ENSG00000(	5.17896	2.408575	5.277655	4.494453	0	1.64393	0.82033	0.45939	0.58895	HIST3H3	chr1	-	2.29E+08	2.29E+08	481
ENSG00000(	36.25272	52.98866	34.30476	83.89646	67.19154	54.24968	-0.72218	0.040189	0.080378	THAP9	chr4	+	83821837	83841122	3808
ENSG00000(	2910.575	2780.7	2464.665	1919.132	1542.644	1704.755	0.65716	1.42E-07	6.39E-07	RNF187	chr1	+	2.29E+08	2.29E+08	3017
ENSG00000(	1854.068	1735.379	2158.561	1370.059	1561.053	1295.417	0.44251	0.000664	0.001914	HOOK3	chr8	+	42752075	42885682	14398
ENSG00000(	1249.165	1337.964	1388.023	1659.202	1701.879	1546.938	-0.30405	0.008507	0.020094	MAPK1IP1I	chr14	+	55518349	55532931	2501
ENSG00000(	2023.937	1772.712	1628.157	520.6075	693.0853	653.4621	1.5361	1.27E-26	1.67E-25	DDIT4	chr10	+	74033678	74035794	1748
ENSG00000(	3861.432	3750.152	4492.604	1243.465	1175.392	1024.168	1.8096	4.42E-48	1.15E-46	RBPJ	chr4	+	26165077	26436541	5549
ENSG00000(	626.6541	664.7668	740.1911	639.7105	602.883	503.8645	0.21631	0.14421	0.23628	LMBRD1	chr6	-	70385694	70507003	2209
ENSG00000(	206.1226	221.5889	221.6615	330.3423	262.3231	297.5513	-0.45544	0.011928	0.027253	ZCCHC4	chr4	+	25314407	25372005	2785
ENSG00000(	330.4176	302.2762	287.6322	295.8848	232.8693	245.7675	0.24746	0.1646	0.26297	TTC39C	chr18	+	21572737	21715574	4117
ENSG00000(	64.2191	96.34302	62.01245	51.68621	50.62376	71.51095	0.35069	0.27935	0.40157	GLYCTK	chr3	+	52321105	52329272	3622
ENSG00000(	0	1.204288	3.958241	5.243529	10.12475	4.109825	-1.5862	0.13461	0.2237	HIST1H2BI	chr6	+	26273144	26273622	479
ENSG00000(	526.1823	539.5209	469.7113	294.3867	289.0156	229.3282	0.91506	2.93E-08	1.42E-07	GNG4	chr1	-	2.36E+08	2.36E+08	5104
ENSG00000(	1017.148	1076.633	1151.848	1041.215	1161.585	997.8654	0.019829	0.87481	0.92141	UBTD2	chr5	-	1.72E+08	1.72E+08	3301
ENSG00000(	137.7603	169.8046	124.0249	109.365	92.0432	135.6242	0.3529	0.15441	0.24993	POLR2J3	chr7	-	1.02E+08	1.02E+08	2553
ENSG00000(	1353.78	1358.437	1066.086	1130.355	1122.007	1161.436	0.1469	0.26411	0.38398	NKIRAS2	chr17	+	40163400	40177659	4213
ENSG00000(	1038.899	1175.385	951.2973	1594.033	1240.742	1257.606	-0.36971	0.009295	0.021771	DNAJC7	chr17	-	40128451	40173394	2564
ENSG00000(	0	1.204288	0	0.749076	4.60216	6.575719	-2.1154	0.096609	0.17047	C14orf183	chr14	-	50550369	50559361	975
ENSG00000(	5.17896	8.430014	17.15238	5.243529	7.363456	5.753754	0.66796	0.38872	0.51932	KCNV2	chr9	+	2717502	2730037	2186
ENSG00000(	1089.653	1028.462	1246.846	1025.484	834.8318	785.7985	0.34461	0.016217	0.03593	IRF2BP2	chr1	-	2.35E+08	2.35E+08	4663
ENSG00000(	4898.26	4572.68	4245.874	2734.126	1849.148	1849.421	1.0888	4.02E-13	2.83E-12	NT5DC2	chr3	-	52558386	52569070	2047
ENSG00000(	120.1519	93.93444	104.2337	101.1252	131.6218	212.8889	-0.47751	0.094061	0.16668	SMIM4	chr3	+	52568029	52613253	1770
ENSG00000(	51.7896	36.12863	31.66593	9.737982	18.40864	38.63235	0.81781	0.1036	0.18058	HIST1H2AE	chr6	+	26217165	26217711	547
ENSG00000(	92.18548	85.50443	93.67838	189.5161	92.96363	189.8739	-0.79358	0.005619	0.013785	COA6	chr1	+	2.35E+08	2.35E+08	1013
ENSG00000(	53.86118	40.94578	81.80365	463.6778	566.9861	507.1524	-3.1102	1.18E-43	2.72E-42	KIF5C	chr2	+	1.5E+08	1.5E+08	6931
ENSG00000(	385.3146	382.9635	391.8659	257.682	180.4047	189.8739	0.87857	2.00E-06	8.03E-06	BMI1	chr10	+	22610140	22620413	3428
ENSG00000(	361.4914	338.4048	333.8117	340.0803	269.6866	289.3317	0.19974	0.23638	0.35084	THAP11	chr16	+	67876213	67878097	1885
ENSG00000(	1184.946	1181.406	1136.015	2134.116	1596.029	1676.808	-0.62526	3.82E-06	1.49E-05	MMADHC	chr2	-	1.5E+08	1.5E+08	1726
ENSG00000(	1044.078	1235.599	1081.919	1648.715	1219.572	1340.625	-0.32424	0.022433	0.048058	PDHB	chr3	-	58413357	58419584	4459
ENSG00000(	1020.255	1172.976	1186.153	116.1067	137.1444	134.8022	3.1144	2.10E-92	1.39E-90	PXK	chr3	+	58318607	58411748	2823
ENSG00000(	24.85901	61.41867	106.8725	24.71949	123.3379	69.86702	-0.16056	0.83079	0.89147	HIST1H1E	chr6	+	26156559	26157343	785
ENSG00000(	332.4892	337.2006	317.9787	109.365	162.9165	106.8554	1.3778	3.18E-11	1.95E-10	PCMTD1	chr8	-	52730140	52811735	4252
ENSG00000(	206.1226	167.396	162.2879	187.2689	155.553	143.0219	0.14177	0.51228	0.63928	KCTD6	chr3	+	58477841	58488087	2425
ENSG00000(	377.0283	360.082	282.3545	503.3788	483.2268	544.1408	-0.58188	0.000353	0.001062	MPLKIP	chr7	-	40172342	40174258	948
ENSG00000(	124.295	108.3859	83.12307	4.494453	3.681728	9.041614	4.0774	3.11E-20	3.18E-19	ACOX2	chr3	-	58490863	58523046	2426
ENSG00000(	34.18113	37.33292	47.4989	0	0	0	6.5458	4.47E-10	2.52E-09	FAM107A	chr3	-	58549844	58613337	3465
ENSG00000(	226.8384	226.4061	262.5633	127.3428	138.0648	129.8705	0.85157	1.71E-05	6.17E-05	IRF2	chr4	-	1.85E+08	1.85E+08	2303
ENSG00000(	0	0	0	1.498151	5.522592	4.109825	-2.6308	0.044617	0.08796	MOBP	chr3	+	39508689	39570970	5675
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	CX3CR1	chr3	-	39304985	39323226	3255
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	C8orf22	chr8	+	49966870	49988649	1499
ENSG00000(	0	0	0	2.247227	0	2.465895	-1.3312	0.32317	NA	XIRP1	chr3	-	39224701	39234087	6460
ENSG00000(	0	0	6.597069	0	0	0	1.83	0.17508	0.27674	INSM2	chr14	+	36003248	36006260	3013
ENSG00000(	5.17896	0	0	1.498151	2.761296	2.465895	-0.22459	0.85797	0.90972	DEGS2	chr14	-	1.01E+08	1.01E+08	1890
ENSG00000(	2.071584	0	0	2.996302	2.761296	0.821965	-0.99219	0.4491	0.57886	SCN11A	chr3	-	38887260	38992052	6500

ENSG0000(	5214.176	5421.703	5333.071	4540.147	4087.638	4089.275	0.32786	0.001437	0.00392	ARF4	chr3	-	57557090	57583947	1660
ENSG0000(	9939.459	9836.622	10594.89	8746.955	8419.191	8016.624	0.26981	0.006665	0.016092	2-Sep	chr2	+	2.42E+08	2.42E+08	3701
ENSG0000(	1185.982	1300.631	1275.873	933.3481	664.5519	664.1477	0.7304	1.50E-06	6.11E-06	FILIP1L	chr3	-	99548985	99833357	4219
ENSG0000(	45.57484	60.21439	64.65128	38.20285	8.283888	30.4127	1.1008	0.016498	0.036504	MFSD2A	chr1	+	40420802	40435638	2432
ENSG0000(	780.9871	821.3242	701.9281	1940.855	1675.186	2036.007	-1.2912	2.18E-23	2.53E-22	DTYMK	chr2	-	2.43E+08	2.43E+08	1232
ENSG0000(	204.051	181.8474	230.8974	275.6598	292.6974	240.0138	-0.38911	0.039895	0.079845	TAP1	chr6	-	32812986	32821755	2959
ENSG0000(	625.6183	628.6382	572.6256	597.0132	585.3947	653.4621	-0.00655	0.96165	0.97784	ING5	chr2	+	2.43E+08	2.43E+08	5196
ENSG0000(	1004.718	993.5374	902.479	1433.731	1197.482	1310.212	-0.44124	0.00049	0.001443	ATG4B	chr2	+	2.43E+08	2.43E+08	3294
ENSG0000(	100.4718	62.62296	97.63662	2.247227	10.12475	6.575719	3.698	3.80E-15	3.02E-14	BDKRB2	chr14	+	96671016	96710666	6845
ENSG0000(	5.17896	3.612863	1.319414	29.21395	15.64734	32.05663	-2.6773	0.000155	0.000491	MLKL	chr16	-	74705753	74734858	3882
ENSG0000(	0	0	1.319414	3.745378	0	0	-0.686	0.61079	NA	CMAHP	chr6	-	25081548	25166793	2264
ENSG0000(	465.0706	514.2309	505.3355	2164.079	2036.916	2054.09	-2.072	1.29E-66	5.24E-65	RFWD3	chr16	-	74655292	74700779	4957
ENSG0000(	0	0	0	1.498151	9.20432	9.041614	-3.4671	0.00543	0.013351	MTNR1A	chr4	-	1.87E+08	1.87E+08	1289
ENSG0000(	0	1.204288	1.319414	1.498151	3.681728	0	-0.62697	0.63735	0.74586	RHOH	chr4	+	40192673	40246281	1999
ENSG0000(	0	0	1.319414	2.996302	0	0	-0.52076	0.6968	NA	KLHL30	chr2	+	2.39E+08	2.39E+08	3726
ENSG0000(	418.4599	425.1136	364.1582	242.7005	131.6218	156.1733	1.1759	6.01E-08	2.82E-07	COG7	chr16	-	23399814	23464501	2926
ENSG0000(	249.6258	299.8676	298.1875	245.6968	250.3575	222.7525	0.2352	0.18681	0.29146	CDC40	chr6	+	1.11E+08	1.11E+08	3927
ENSG0000(	3513.406	3332.264	3328.881	7152.173	6040.795	6804.226	-0.97326	3.34E-19	3.26E-18	STIP1	chr11	+	63952744	63972015	2743
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	SCNN1B	chr16	+	23289552	23392620	2597
ENSG0000(	5.17896	12.04288	3.958241	86.14369	83.75931	118.3629	-3.6517	3.58E-15	2.86E-14	HR	chr8	-	21971928	21990897	6336
ENSG0000(	0	6.021439	2.638828	4.494453	2.761296	3.28786	-0.24255	0.82591	0.88777	TXNDC2	chr18	+	9885763	9889272	1873
ENSG0000(	2094.371	1965.398	2370.987	2122.131	2411.532	2011.348	-0.02543	0.8373	0.89603	RAB31	chr18	+	9708162	9862548	4055
ENSG0000(	563.4708	537.1123	451.2395	1140.842	924.1137	1196.781	-1.0673	1.14E-12	7.79E-12	REEP4	chr8	-	21995533	21999464	1710
ENSG0000(	46.61064	59.0101	55.41538	2.996302	11.04518	7.397684	2.8286	1.80E-08	8.87E-08	TNXB	chr6	-	32008931	32083111	13132
ENSG0000(	3.107376	0	7.916483	0	0	0	2.7683	0.0385	0.077422	LGI3	chr8	-	22004338	22014597	4420
ENSG0000(	3279.317	3386.457	2640.147	968.5547	982.1009	1049.649	1.6298	9.75E-38	1.89E-36	BMP1	chr8	+	22022249	22069839	4333
ENSG0000(	3402.576	3160.051	3005.625	4000.813	4277.247	4058.863	-0.36568	0.000555	0.001617	ATXN2L	chr16	+	28834356	28848558	4574
ENSG0000(	0	3.612863	1.319414	4.494453	0	2.465895	-0.35939	0.77623	0.85302	PHYHIP	chr8	-	22077222	22089854	3200
ENSG0000(	32.10955	18.06432	30.34652	5.243529	3.681728	5.753754	2.3134	0.000189	0.000592	CCDC110	chr4	-	1.86E+08	1.86E+08	2898
ENSG0000(	1154.908	1182.611	1038.379	644.954	661.7906	689.6286	0.75686	1.76E-09	9.47E-09	POLR3D	chr8	+	22102617	22109485	2866
ENSG0000(	517.896	463.6508	501.3772	2084.677	2139.084	2290.816	-2.1304	8.57E-69	3.65E-67	FEN1	chr11	+	61560109	61564716	2296
ENSG0000(	236.1606	226.4061	273.1187	24.71949	13.80648	19.72716	3.6031	1.03E-37	2.00E-36	SDPR	chr2	-	1.93E+08	1.93E+08	3229
ENSG0000(	2685.808	2574.767	2776.047	797.0164	1283.082	1004.441	1.3782	2.77E-19	2.72E-18	SOGA2	chr18	+	8705659	8832776	6093
ENSG0000(	3.107376	2.408575	0	64.4205	47.86246	44.38611	-4.404	1.64E-10	9.55E-10	GBX2	chr2	-	2.37E+08	2.37E+08	2123
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	HFE2	chr1	+	1.45E+08	1.45E+08	2128
ENSG0000(	49.71801	33.72006	31.66593	18.72689	22.09037	26.30288	0.76485	0.080767	0.14658	HEXIM2	chr17	+	43238067	43247407	1528
ENSG0000(	626.6541	605.7567	637.2769	832.2229	651.6659	588.5269	-0.14893	0.33792	0.46656	FNTA	chr8	+	42889337	42940931	7327
ENSG0000(	639.0836	511.8223	518.5296	1088.407	842.1953	859.7753	-0.73777	1.90E-06	7.65E-06	SERINC2	chr1	+	31882412	31907525	2807
ENSG0000(	2.071584	0	0	48.68991	50.62376	46.03004	-5.2193	4.32E-10	2.44E-09	MYL1	chr2	-	2.11E+08	2.11E+08	1065
ENSG0000(	544.8265	499.7794	573.945	349.8183	378.2976	337.8276	0.60107	5.39E-05	0.000182	TRAPPC11	chr4	+	1.85E+08	1.85E+08	4552
ENSG0000(	0	1.204288	0	0	0	1.64393	-0.12916	0.91993	NA	CHRM1	chr11	-	62676151	62689279	2964
ENSG0000(	346664	353317.5	355050.3	24506.76	31694.16	29102.49	3.6222	1.26E-222	4.57E-220	COL3A1	chr2	+	1.9E+08	1.9E+08	5543
ENSG0000(	17.60846	15.65574	21.11062	21.72319	34.97642	21.37109	-0.50132	0.32077	0.44795	GFRA2	chr8	-	21547915	21669869	4921
ENSG0000(	165.7267	237.2447	182.0791	283.8996	184.0864	233.438	-0.26332	0.23506	0.34934	ING2	chr4	+	1.84E+08	1.84E+08	1189

ENSG00000(	148.1182	131.2674	184.7179	373.7887	292.6974	287.6877	-1.0376	4.16E-07	1.80E-06	CDKN2AIP	chr4	+	1.84E+08	1.84E+08	2721
ENSG00000(	436.0684	469.6722	544.9179	604.504	629.5755	475.0957	-0.23706	0.14392	0.23586	SNRNP48	chr6	+	7590432	7612200	4173
ENSG00000(	181.2636	156.5574	147.7743	235.9588	233.7897	244.9455	-0.55174	0.004462	0.011162	TMEM223	chr11	-	62539101	62559493	1288
ENSG00000(	1017.148	1100.719	1234.971	3224.021	2845.055	2543.159	-1.3589	2.38E-25	2.98E-24	SLC20A2	chr8	-	42273993	42397069	3657
ENSG00000(	4.143168	2.408575	1.319414	0	0	0	2.42	0.071961	0.13287	DYNLRB2	chr16	+	80574631	80584657	971
ENSG00000(	978.8233	955.0002	914.3538	794.0201	662.711	703.602	0.39741	0.002398	0.006303	TMUB2	chr17	+	42264338	42269099	2418
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	ADAM29	chr4	+	1.76E+08	1.76E+08	3325
ENSG00000(	3013.119	2738.55	3280.063	1546.092	1587.745	1495.976	0.96224	4.51E-17	3.97E-16	STAT3	chr17	-	40465342	40540586	5047
ENSG00000(	229.9458	221.5889	216.3839	327.346	275.2092	287.6877	-0.41307	0.019485	0.042396	ZSWIM1	chr20	+	44509866	44513905	2769
ENSG00000(	483.7148	385.3721	486.8637	234.4606	236.551	228.5062	0.95149	1.33E-08	6.62E-08	NBPF9	chr1	+	1.45E+08	1.45E+08	3680
ENSG00000(	5668.889	5455.423	7147.264	3932.647	4227.544	3434.169	0.65451	6.50E-07	2.75E-06	ADAM9	chr8	+	38854388	38962663	3839
ENSG00000(	0	0	0	1.498151	6.443024	9.041614	-3.248	0.010192	0.023654	ADAM18	chr8	+	39442008	39587583	2388
ENSG00000(	18.64425	14.45145	25.06886	285.3978	310.1856	315.6345	-3.9352	1.54E-43	3.53E-42	GDNF	chr5	-	37812779	37839788	3810
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	DPCR1	chr6	+	30908749	30921998	5314
ENSG00000(	2482.793	2510.94	2435.638	644.205	949.8858	732.3707	1.6718	2.00E-31	3.19E-30	AXIN2	chr17	-	63524681	63557765	4259
ENSG00000(	2634.019	2562.724	2220.573	2262.208	2030.473	2423.153	0.14326	0.23771	0.35245	NDUFS5	chr1	+	39491990	39500308	548
ENSG00000(	2.071584	0	0	0	0	1.64393	0.14412	0.91322	NA	VWA3B	chr2	+	98703579	98929762	5324
ENSG00000(	39.36009	59.0101	46.17948	64.4205	82.83888	75.62077	-0.61693	0.057057	0.10897	ZNF30	chr19	+	35417807	35436074	2651
ENSG00000(	1.035792	0	3.958241	116.8558	103.0884	106.8554	-5.6801	7.91E-18	7.24E-17	UGT3A2	chr5	-	36035119	36071460	2355
ENSG00000(	15.53688	14.45145	10.55531	6243.545	6633.553	5923.901	-8.7543	1.95E-246	9.95E-244	FAM84B	chr8	-	1.28E+08	1.28E+08	5404
ENSG00000(	20.71584	15.65574	25.06886	2.247227	2.761296	6.575719	2.2325	0.001415	0.003866	LDLRAD4	chr18	+	13217497	13652754	8686
ENSG00000(	0	1.204288	0	0.749076	0	0	0.1572	0.90001	NA	KCTD19	chr16	-	67323331	67360666	4913
ENSG00000(	98.40023	124.0416	94.99779	132.5864	122.4175	116.719	-0.22657	0.35145	0.48119	SLC16A4	chr1	-	1.11E+08	1.11E+08	2632
ENSG00000(	462.999	460.0379	560.7509	7.490755	11.04518	16.4393	5.3546	1.47E-78	7.76E-77	IL7R	chr5	+	35852797	35879705	4626
ENSG00000(	790.3092	679.2183	745.4688	481.6556	399.4675	588.5269	0.58922	0.00028	0.000855	TMEM208	chr16	+	67261006	67263181	1525
ENSG00000(	229.9458	268.5562	347.0058	28.46487	63.50981	12.32947	2.8632	2.30E-06	9.18E-06	LRP1B	chr2	-	1.41E+08	1.43E+08	16535
ENSG00000(	1899.642	1867.85	2187.588	1535.605	1566.575	1370.216	0.4119	0.000673	0.00194	AHCYL1	chr1	+	1.11E+08	1.11E+08	4015
ENSG00000(	951.8928	862.27	984.2827	1161.067	1044.69	960.877	-0.17833	0.17312	0.27446	DNAJC21	chr5	+	34929698	34959069	6208
ENSG00000(	826.5619	776.7656	540.9597	416.486	349.7642	462.7662	0.80029	7.72E-06	2.90E-05	PKIG	chr20	+	43160426	43252888	1489
ENSG00000(	22.78742	16.86003	15.83297	420.9805	440.8869	410.9825	-4.457	6.54E-61	2.34E-59	NPNT	chr4	+	1.07E+08	1.07E+08	4598
ENSG00000(	0	2.408575	0	8.988907	1.840864	1.64393	-1.662	0.1779	0.28027	FAM178B	chr2	-	97541620	97684175	2877
ENSG00000(	974.6802	953.7959	891.9237	1126.61	1331.865	1573.241	-0.51339	0.000314	0.000951	SEMA4C	chr2	-	97525453	97536494	3776
ENSG00000(	145.0109	133.6759	151.7326	255.4348	277.9705	248.2334	-0.85629	9.32E-06	3.48E-05	CNNM3	chr2	+	97481982	97499648	3447
ENSG00000(	143.9751	120.4288	129.3026	46.44268	37.73771	42.74218	1.6141	5.24E-09	2.70E-08	GSTM4	chr1	+	1.1E+08	1.1E+08	3990
ENSG00000(	546.8981	555.1766	745.4688	99.62705	202.495	138.0901	2.0594	3.13E-20	3.20E-19	TET2	chr4	+	1.06E+08	1.06E+08	10166
ENSG00000(	24.85901	30.10719	31.66593	2.996302	5.522592	4.93179	2.5518	2.94E-05	0.000103	CXXC4	chr4	-	1.05E+08	1.05E+08	5565
ENSG00000(	367.7061	449.1993	443.323	235.9588	234.7102	238.3698	0.82497	6.66E-07	2.81E-06	TCTN2	chr12	+	1.24E+08	1.24E+08	2918
ENSG00000(	632.8689	664.7668	713.8029	59.92604	69.95283	73.15488	3.2964	2.12E-76	1.07E-74	SHOX2	chr3	-	1.58E+08	1.58E+08	4078
ENSG00000(	78.72018	54.19295	76.526	128.841	107.6905	129.8705	-0.79867	0.003226	0.0083	PPIP5K1	chr15	-	43825660	43882430	5697
ENSG00000(	3222.349	3102.245	3163.954	645.7031	615.769	526.8795	2.4027	3.10E-89	1.93E-87	TSPAN5	chr4	-	99391518	99579780	4062
ENSG00000(	78.72018	99.95588	105.5531	65.16957	59.82808	41.92021	0.75437	0.012774	0.028965	ABHD15	chr17	-	27887565	27894155	3592
ENSG00000(	293.1291	369.7163	298.1875	443.4527	474.9429	394.5432	-0.44849	0.007388	0.017694	ZBTB5	chr9	-	37438111	37465396	4627
ENSG00000(	107.7224	160.1703	160.9685	119.103	196.052	192.3398	-0.24221	0.34509	0.47447	CHTF8	chr16	-	69151913	69166487	2903
ENSG00000(	110.8297	168.6003	108.1919	164.7966	142.667	137.2681	-0.19807	0.41843	0.54904	ADAL	chr15	+	43622872	43646096	3593

ENSG00000(	140.8677	113.203	174.1626	313.1136	275.2092	258.097	-0.98023	3.08E-06	1.21E-05	LCMT2	chr15	-	43619974	43622803	2830
ENSG00000(	3083.552	2908.355	3778.801	746.0792	900.1825	835.9383	1.9724	5.78E-49	1.56E-47	SNTB2	chr16	+	69221032	69342955	9789
ENSG00000(	8.286335	2.408575	0	9.737982	1.840864	4.109825	-0.43325	0.67849	0.77965	IL12A	chr3	+	1.6E+08	1.6E+08	1909
ENSG00000(	352.1692	415.4793	522.4879	382.7776	479.5451	344.4033	0.094632	0.61259	0.72597	ZNF507	chr19	+	32836500	32878571	7636
ENSG00000(	574.8645	549.1552	564.7091	572.2937	625.8938	616.4737	-0.10284	0.44604	0.57565	STX18	chr4	-	4417469	4544073	3497
ENSG00000(	20.71584	19.2686	31.66593	1011.252	929.6363	920.6007	-5.2978	9.60E-114	9.13E-112	NSG1	chr4	+	4349867	4420785	4172
ENSG00000(	54.89697	57.80581	40.90183	74.15848	43.2603	60.00344	-0.20526	0.55563	0.67625	ZBTB49	chr4	+	4291924	4323513	2889
ENSG00000(	467.1421	472.0808	554.1538	800.7618	835.7523	717.5754	-0.65601	4.35E-06	1.68E-05	GFM1	chr3	+	1.58E+08	1.58E+08	3721
ENSG00000(	0	0	0	52.43529	41.41944	58.35951	-6.4646	4.38E-10	2.47E-09	HTR1E	chr6	+	87647024	87726401	2039
ENSG00000(	269.3059	293.8462	325.8952	281.6524	273.3683	193.9837	0.24443	0.21005	0.31976	FSTL5	chr4	-	1.62E+08	1.63E+08	4831
ENSG00000(	5.17896	0	0	0	6.443024	5.753754	-0.83197	0.50077	0.62891	TPTE2P5	chr13	-	41396432	41495890	746
ENSG00000(	964.3223	904.4201	922.2702	1241.218	1162.506	1187.739	-0.36296	0.002141	0.005677	DDX19A	chr16	+	70380732	70407286	5007
ENSG00000(	630.7973	552.7681	527.7655	129.5901	126.0992	126.5826	2.155	9.42E-38	1.83E-36	ATOH8	chr2	+	85978467	86015189	3099
ENSG00000(	0	0	0	56.92974	74.55499	34.52253	-6.5555	2.59E-10	1.49E-09	SOX14	chr3	+	1.37E+08	1.37E+08	818
ENSG00000(	116.0087	121.6331	131.9414	188.018	130.7013	124.9387	-0.26538	0.27577	0.39729	ANKRD49	chr11	+	94226795	94232749	3002
ENSG00000(	1.035792	1.204288	0	0	3.681728	7.397684	-1.5194	0.22898	0.34235	SFTPB	chr2	-	85884437	85895864	3664
ENSG00000(	772.7008	661.154	676.8593	1818.755	1515.951	1486.113	-1.1879	1.23E-18	1.17E-17	USP39	chr2	+	85829979	85876403	2177
ENSG00000(	634.9404	546.7466	552.8344	636.7142	570.6678	637.8448	-0.08833	0.53117	0.65585	TNIP2	chr4	-	2743375	2758103	2006
ENSG00000(	345.9545	309.5019	331.1729	336.3349	414.1944	434.8194	-0.26219	0.11744	0.20037	C2orf68	chr2	-	85833777	85839189	2837
ENSG00000(	303.487	302.2762	241.4527	323.6006	230.108	277.8241	0.026721	0.88896	0.93101	TMEM150A	chr2	-	85825671	85830319	2323
ENSG00000(	814.1324	811.6899	635.9574	731.0977	561.4635	729.9048	0.161	0.30722	0.43297	RNF181	chr2	+	85822848	85824736	844
ENSG00000(	82.86335	61.41867	104.2337	122.0993	90.20234	123.2947	-0.43327	0.12507	0.21071	VAMP5	chr2	+	85811531	85820535	689
ENSG00000(	216.4805	244.4704	172.8432	265.1727	175.8025	173.4346	0.04371	0.8472	0.90269	LRRC28	chr15	+	99791567	99930934	5971
ENSG00000(	6120.494	6520.014	7181.569	4672.733	4284.611	4415.596	0.5666	1.51E-07	6.80E-07	MAT2A	chr2	+	85766288	85772403	2819
ENSG00000(	1.035792	0	0	2.996302	0.920432	4.93179	-1.8054	0.1675	0.26679	PLA2G4F	chr15	-	42433332	42448839	3498
ENSG00000(	0	3.612863	3.958241	1.498151	7.363456	13.9734	-1.3376	0.19223	0.29798	ENHO	chr9	-	34521038	34523039	1082
ENSG00000(	560.3634	567.2195	635.9574	646.4522	1016.157	759.4956	-0.45549	0.007207	0.01731	ZNF608	chr5	-	1.24E+08	1.24E+08	5958
ENSG00000(	152.2614	111.9988	149.0938	221.7264	188.6886	210.423	-0.5833	0.006544	0.015834	SLC35G2	chr3	+	1.37E+08	1.37E+08	2837
ENSG00000(	127.4024	183.0517	131.9414	584.2789	782.3672	698.6702	-2.2128	5.53E-32	8.93E-31	INPP5D	chr2	+	2.34E+08	2.34E+08	4728
ENSG00000(	890.781	855.0443	741.5105	1422.494	1460.726	1398.162	-0.78052	3.52E-10	2.00E-09	LETM1	chr4	-	1813206	1857974	5462
ENSG00000(	1.035792	2.408575	2.638828	0	3.681728	0	0.48092	0.71129	0.80486	CTRB1	chr16	+	75252898	75258822	858
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CTRB2	chr16	-	75237994	75241083	2248
ENSG00000(	0	0	0	5.992604	0	4.109825	-2.3529	0.079399	0.14441	TRIM49	chr11	-	89530823	89541743	2163
ENSG00000(	671.1932	569.6281	531.7238	570.0465	469.4203	604.9662	0.10857	0.48975	0.61872	TMEM129	chr4	-	1717679	1723085	2810
ENSG00000(	364.5988	428.7264	343.0476	152.0623	145.4283	161.9271	1.3004	6.42E-13	4.45E-12	PPIC	chr5	-	1.22E+08	1.22E+08	1380
ENSG00000(	98.40023	110.7945	109.5113	26.21764	49.70333	19.72716	1.7164	8.76E-07	3.66E-06	SPRY3	chrX	+	1.55E+08	1.55E+08	9019
ENSG00000(	340.7755	346.8349	389.2271	377.5341	393.0245	303.3051	0.003192	0.98492	0.99109	CEP120	chr5	-	1.23E+08	1.23E+08	4900
ENSG00000(	82.86335	80.68728	79.16483	150.5642	133.4626	132.3364	-0.7723	0.001539	0.004181	STXBP6	chr14	-	25278862	25519503	4132
ENSG00000(	0	1.204288	0	4.494453	1.840864	0	-1.281	0.34197	0.47087	TM4SF20	chr2	-	2.28E+08	2.28E+08	2296
ENSG00000(	829.6693	815.3028	854.9801	1008.256	759.3564	757.8517	-0.01564	0.91495	0.94808	MFF	chr2	+	2.28E+08	2.28E+08	3524
ENSG00000(	70.43385	45.76293	31.66593	21.72319	17.48821	41.09825	0.86074	0.05563	0.10658	LGALS9	chr17	+	25956824	25976586	3114
ENSG00000(	19.68005	37.33292	18.47179	5.243529	20.2495	41.09825	0.17425	0.77391	0.85164	JMJD7-PLA	chr15	+	42120283	42140353	7227
ENSG00000(	27.96638	30.10719	15.83297	12.73428	25.7721	18.08323	0.38291	0.4626	0.59188	CPLX1	chr4	-	778745	819986	2181
ENSG00000(	417.4241	398.6192	333.8117	204.4976	149.11	152.8855	1.1755	1.05E-09	5.74E-09	PXDC1	chr6	-	3722848	3752260	2190

ENSG0000(	201.9794	234.8361	274.4381	328.0951	335.0372	350.1571	-0.51188	0.004145	0.010442	E2F6	chr2	-	11584501	11606297	3296
ENSG0000(	1014.04	1048.935	1384.065	922.8611	1069.542	775.9349	0.31471	0.04821	0.094019	FEM1B	chr15	+	68570141	68588203	7122
ENSG0000(	172.9772	217.9761	248.0498	505.626	397.6266	415.9142	-1.0458	2.43E-08	1.18E-07	COMMD8	chr4	-	47452885	47465736	1397
ENSG0000(	8.286335	9.634302	10.55531	5.243529	8.283888	13.15144	0.086005	0.90583	0.94187	ATP5I	chr4	-	666225	668127	496
ENSG0000(	1224.306	1227.169	1134.696	2092.168	1810.49	1941.481	-0.70315	2.05E-09	1.09E-08	UQCRFS1	chr19	-	29698173	29704448	1530
ENSG0000(	6.214751	15.65574	7.916483	11.98521	6.443024	10.68554	0.020831	0.97686	0.98656	MFSD7	chr4	-	675618	683230	2123
ENSG0000(	6.214751	9.634302	19.79121	3.745378	11.04518	20.54912	0.002422	0.99736	0.99833	COL4A3	chr2	+	2.28E+08	2.28E+08	8097
ENSG0000(	1027.506	887.56	993.5186	1226.237	986.7031	1086.638	-0.18188	0.17349	0.27487	MAP2K1	chr15	+	66679155	66784650	3410
ENSG0000(	5094.025	4983.343	5294.808	6934.192	8079.552	8231.979	-0.59565	4.56E-08	2.16E-07	HNRNPH1	chr5	-	1.79E+08	1.79E+08	5564
ENSG0000(	1752.56	1716.11	1947.455	2016.511	3115.662	2436.304	-0.48104	0.00135	0.00371	IRS1	chr2	-	2.28E+08	2.28E+08	5981
ENSG0000(	1219.127	1268.115	1369.552	726.6033	925.9546	831.8285	0.63343	2.04E-06	8.18E-06	MECP2	chrX	-	1.53E+08	1.53E+08	10505
ENSG0000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	VCX3A	chrX	-	6451659	6453159	995
ENSG0000(	1132.121	1039.3	1027.823	837.4665	939.7611	1039.786	0.18398	0.16151	0.25908	UPF3A	chr13	+	1.15E+08	1.15E+08	2378
ENSG0000(	0	3.612863	0	2.996302	2.761296	2.465895	-0.82272	0.51127	0.6384	ZBBX	chr3	-	1.67E+08	1.67E+08	3250
ENSG0000(	0	1.204288	0	69.66403	87.44104	94.52597	-6.4449	3.55E-13	2.51E-12	ACTBL2	chr5	-	56775846	56778636	2791
ENSG0000(	2628.84	2585.606	2360.431	496.6371	671.9154	542.4968	2.1428	3.15E-56	1.00E-54	ROR2	chr9	-	94325373	94712444	4360
ENSG0000(	0	21.67718	5.277655	0.749076	0	3.28786	2.1247	0.05595	0.10711	BRD7P3	chr6	+	1.19E+08	1.19E+08	1477
ENSG0000(	169.8699	126.4502	186.0373	136.3317	226.4263	138.0901	-0.05128	0.83978	0.89743	AR	chrX	+	66764465	66950461	10065
ENSG0000(	394.6367	376.9421	340.4088	262.9255	196.052	178.3664	0.79791	2.87E-05	0.000101	DHRSX	chrX	-	2137557	2420846	2571
ENSG0000(	7.250543	7.225726	0	44.19546	22.09037	41.09825	-2.68	3.23E-05	0.000112	C8orf46	chr8	+	67372238	67430759	3513
ENSG0000(	23.82321	45.76293	52.77655	78.65293	85.60018	68.22309	-0.92117	0.009202	0.021577	HSPBAP1	chr3	-	1.22E+08	1.23E+08	2986
ENSG0000(	1272.988	1151.299	1019.907	597.0132	682.0401	693.7384	0.80338	4.77E-09	2.47E-08	ASMTL	chrX	-	1522032	1572655	2048
ENSG0000(	31115.19	30270.98	24062.15	13644.41	12582.31	13909.29	1.0881	9.48E-20	9.48E-19	SLC25A6	chrX	-	1505045	1511617	2062
ENSG0000(	340.7755	405.845	308.7428	547.5742	458.3751	565.5119	-0.57242	0.000547	0.001597	CHST14	chr15	+	40763160	40765353	2194
ENSG0000(	2.071584	1.204288	5.277655	86.89276	130.7013	81.37453	-4.9042	4.79E-17	4.19E-16	PARM1	chr4	+	75858305	75975325	5011
ENSG0000(	534.4686	581.671	649.1516	414.9879	523.7258	401.9408	0.39568	0.013071	0.029589	CSNK1G1	chr15	-	64457716	64648442	8107
ENSG0000(	782.0229	732.2069	738.8717	526.6001	521.8849	418.3801	0.61783	2.06E-05	7.35E-05	FAM110B	chr8	+	58907068	59116838	3438
ENSG0000(	97.36444	105.9773	105.5531	14.98151	18.40864	9.863579	2.7904	1.03E-14	7.97E-14	ARMC4	chr10	-	28064115	28287977	3572
ENSG0000(	13.46529	18.06432	9.235896	519.8584	655.3476	596.7465	-5.3659	6.89E-75	3.30E-73	AFAP1L2	chr10	-	1.16E+08	1.16E+08	3964
ENSG0000(	208.1942	215.5675	168.885	217.2319	196.9724	183.2982	-0.01031	0.95879	0.97578	ZNF354A	chr5	-	1.78E+08	1.78E+08	2484
ENSG0000(	419.4957	544.338	391.8659	1044.96	683.881	1040.608	-1.0265	2.39E-08	1.17E-07	ATF5	chr19	+	50431959	50437192	2069
ENSG0000(	807.9177	768.3356	789.0094	1396.277	1148.699	1141.709	-0.63914	1.27E-06	5.22E-06	UBE2V2	chr8	+	48920960	48977268	4373
ENSG0000(	264.1269	210.7504	282.3545	291.3904	272.4479	251.5213	-0.10697	0.56318	0.68291	ZBTB43	chr9	+	1.3E+08	1.3E+08	5965
ENSG0000(	255.8406	213.1589	230.8974	11.98521	8.283888	20.54912	4.0362	2.44E-38	4.83E-37	CPT1C	chr19	+	50194155	50216988	2950
ENSG0000(	30.03797	59.0101	50.13772	84.64554	91.12277	76.44274	-0.85213	0.010057	0.023378	PCSK9	chr1	+	55505221	55530525	3891
ENSG0000(	2391.644	2146.041	2305.016	3069.712	2538.551	2364.793	-0.22021	0.081344	0.14745	XPO6	chr16	-	28109300	28223241	4422
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	GSG1L	chr16	-	27798850	28074830	4976
ENSG0000(	538.6118	614.1867	564.7091	60.67512	87.44104	54.24968	3.0758	6.32E-54	1.89E-52	MN1	chr22	-	28144265	28197486	7556
ENSG0000(	536.5402	473.2851	498.7384	967.8056	703.21	705.2459	-0.65353	4.60E-05	0.000157	APEX2	chrX	+	55026790	55035490	3245
ENSG0000(	489.9296	529.8866	366.797	484.6519	402.2288	453.7246	0.04928	0.77317	0.85094	NSMCE1	chr16	-	27236312	27280115	1853
ENSG0000(	59.04014	74.66584	76.526	225.4717	172.1208	172.6126	-1.4337	8.10E-09	4.09E-08	CCDC126	chr7	+	23636998	23684327	2473
ENSG0000(	0	8.430014	0	0	0	0	2.183	0.10757	0.18626	IL13	chr5	+	1.32E+08	1.32E+08	1562
ENSG0000(	5.17896	10.83859	10.55531	20.97412	10.12475	15.61733	-0.77854	0.24222	0.35789	61E3.4	chr16	-	29495010	29517320	2676
ENSG0000(	399.8157	360.082	394.5047	657.6883	673.7562	609.898	-0.74736	1.70E-07	7.61E-07	RAB3B	chr1	-	52373628	52456436	12844

ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	OR6F1	chr1	-	2.48E+08	2.48E+08	1061
ENSG00000(	1770.168	1816.066	1632.115	1501.896	1780.115	2104.23	-0.04515	0.74243	0.82828	CD2BP2	chr16	-	30362087	30366682	3421
ENSG00000(	155.3688	146.9231	133.2608	124.3465	127.94	117.541	0.23665	0.28591	0.4092	RGS14	chr5	+	1.77E+08	1.77E+08	2415
ENSG00000(	2076.763	2183.374	1859.054	1662.948	1655.857	1730.236	0.27714	0.015446	0.034382	TBC1D10B	chr16	-	30368423	30381585	4614
ENSG00000(	4833.005	4588.336	3781.44	3433.762	3061.357	3300.189	0.43001	0.000401	0.001196	LMAN2	chr5	-	1.77E+08	1.77E+08	1800
ENSG00000(	0	0	0	0.749076	1.840864	1.64393	-1.2986	0.33698	NA	GCSAML	chr1	+	2.48E+08	2.48E+08	4130
ENSG00000(	133.6172	99.95588	117.4278	13.48336	30.37426	50.13986	1.8697	6.53E-07	2.76E-06	RAB24	chr5	-	1.77E+08	1.77E+08	1820
ENSG00000(	1435.608	1217.535	1037.059	2229.998	2297.398	2392.74	-0.9035	1.30E-11	8.22E-11	PRELID1	chr5	+	1.77E+08	1.77E+08	1261
ENSG00000(	337.6682	349.2434	329.8534	251.6894	240.2328	286.0438	0.38444	0.02186	0.046976	THBS3	chr1	-	1.55E+08	1.55E+08	4208
ENSG00000(	139.8319	132.4716	167.5656	179.0291	217.222	195.6277	-0.42658	0.042766	0.084867	CA5B	chrX	+	15706953	15805747	6050
ENSG00000(	270.3417	251.6961	255.9663	279.4052	185.0068	263.0288	0.094579	0.63392	0.74346	SLC50A1	chr1	+	1.55E+08	1.55E+08	1300
ENSG00000(	29.00217	16.86003	21.11062	346.822	294.5382	404.4067	-3.908	9.98E-45	2.36E-43	EFNA1	chr1	+	1.55E+08	1.55E+08	1926
ENSG00000(	0	2.408575	0	0.749076	0	0	0.55104	0.6711	NA	CXCL10	chr4	-	76942273	76944650	1173
ENSG00000(	84.93494	72.25726	52.77655	163.2985	163.8369	120.0069	-1.0721	7.99E-05	0.000264	NPIPL3	chr16	-	21413558	21459888	3501
ENSG00000(	12.4295	12.04288	17.15238	65.16957	34.97642	53.42772	-1.8376	7.26E-05	0.000241	SH3TC2	chr5	-	1.48E+08	1.48E+08	7324
ENSG00000(	0	0	0	2.247227	2.761296	0.821965	-1.7061	0.20822	NA	CXCL11	chr4	-	76954835	76962568	1606
ENSG00000(	132.5814	172.2131	141.1773	141.5753	143.5874	174.2566	-0.04372	0.84478	0.90093	ZRSR2	chrX	+	15808595	15841383	1491
ENSG00000(	882.4947	830.9585	965.8109	935.5954	945.2837	798.1279	-0.00023	0.99863	0.99905	NMD3	chr3	+	1.61E+08	1.61E+08	3061
ENSG00000(	3.107376	8.430014	11.87472	40.45008	16.56778	32.8786	-1.8641	0.002492	0.006527	ADRB2	chr5	+	1.48E+08	1.48E+08	2041
ENSG00000(	47.64643	91.52587	68.60952	227.719	220.9037	220.2866	-1.6791	2.70E-11	1.66E-10	B3GALNT1	chr3	-	1.61E+08	1.61E+08	3606
ENSG00000(	329.3818	322.7491	298.1875	296.6339	254.9597	271.2484	0.20686	0.21812	0.3295	GPRIN1	chr5	-	1.76E+08	1.76E+08	4211
ENSG00000(	1.035792	8.430014	1.319414	4.494453	0	0	0.86464	0.48489	0.61413	HSPB3	chr5	+	53751445	53752207	763
ENSG00000(	111.8655	83.09585	135.8996	40.45008	45.10117	39.45432	1.3863	5.24E-06	2.01E-05	KCNAB1	chr3	+	1.56E+08	1.56E+08	4086
ENSG00000(	432.961	451.6079	365.4776	785.0312	590.9173	663.3257	-0.70335	1.11E-05	4.08E-05	MRPL1	chr4	+	78783674	78873944	1490
ENSG00000(	2.071584	1.204288	0	2.996302	1.840864	0.821965	-0.50237	0.695	0.79211	SHE	chr1	-	1.54E+08	1.54E+08	6855
ENSG00000(	3.107376	0	0	83.89646	97.56579	95.34793	-5.7536	1.79E-15	1.45E-14	NR0B1	chrX	-	30322323	30327715	2021
ENSG00000(	525.1465	480.5108	459.156	874.9202	763.9586	799.7719	-0.73264	1.15E-07	5.24E-07	PGM2	chr4	+	37828255	37864558	3264
ENSG00000(	0	0	0	0.749076	4.60216	1.64393	-1.9321	0.1526	0.24764	STK32A	chr5	+	1.47E+08	1.47E+08	5393
ENSG00000(	11.39371	8.430014	7.916483	0	2.761296	0.821965	2.5059	0.012107	0.027621	IL1RAPL1	chrX	+	28605516	29974840	3667
ENSG00000(	5.17896	1.204288	2.638828	1.498151	5.522592	2.465895	-0.03435	0.97468	0.9853	C22orf15	chr22	+	24105208	24108048	2021
ENSG00000(	72.50543	97.54731	88.40072	20.22504	22.09037	13.9734	2.1591	2.85E-09	1.50E-08	KIAA1024	chr15	+	79724858	79764632	6732
ENSG00000(	459.8916	460.0379	620.1245	463.6778	432.603	354.2669	0.29719	0.087107	0.15658	SLC33A1	chr3	-	1.56E+08	1.56E+08	3725
ENSG00000(	172.9772	166.1917	160.9685	114.6086	146.3487	117.541	0.40262	0.067122	0.12518	SNUPN	chr15	-	75890424	75918810	1931
ENSG00000(	146.0467	185.4603	172.8432	104.1215	80.99802	76.44274	0.93529	0.000109	0.000354	CRADD	chr12	+	94071151	94288616	1470
ENSG00000(	953.9643	923.6887	1083.239	844.2081	1100.837	906.6273	0.054352	0.70103	0.79683	SIN3A	chr15	-	75661720	75748183	6737
ENSG00000(	142.9393	151.7403	172.8432	251.6894	282.5726	222.7525	-0.69326	0.000527	0.001543	ARL13B	chr3	+	93698983	93774512	3906
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RNASE2	chr14	+	21423611	21424595	755
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	ELSPBP1	chr19	+	48497908	48528410	1052
ENSG00000(	1307.169	1259.685	1567.464	2271.946	2217.321	1969.428	-0.6429	4.48E-07	1.93E-06	PTK2	chr8	-	1.42E+08	1.42E+08	4955
ENSG00000(	0	0	0	0	0	5.753754	-1.4203	0.28986	NA	RSPH10B2	chr7	+	6793740	6838996	3220
ENSG00000(	2.071584	0	1.319414	20.97412	17.48821	23.83698	-3.6276	3.34E-05	0.000116	PTAFR	chr1	-	28473677	28520447	4491
ENSG00000(	984.0023	994.7417	986.9215	789.5256	660.8702	749.632	0.429	0.000863	0.002445	PTPN9	chr15	-	75759462	75871630	3943
ENSG00000(	0	0	0	8.239831	4.60216	12.32947	-3.8915	0.001201	0.003326	RNASE6	chr14	+	21249210	21250626	1061
ENSG00000(	1.035792	1.204288	1.319414	5.992604	1.840864	5.753754	-1.4977	0.18543	0.28985	NPR1	chr1	+	1.54E+08	1.54E+08	4236

ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	KCNK9	chr8	-	1.41E+08	1.41E+08	3276
ENSG00000(	59.04014	46.96722	46.17948	8.239831	1.840864	1.64393	3.4824	1.36E-09	7.36E-09	IL8	chr4	+	74606223	74609433	1705
ENSG00000(	13.46529	24.08575	27.70769	16.47966	16.56778	18.08323	0.32863	0.53608	0.66026	SCN9A	chr2	-	1.67E+08	1.67E+08	9787
ENSG00000(	5.17896	0	1.319414	5.243529	7.363456	9.041614	-1.4052	0.164	0.26233	RASSF6	chr4	-	74437267	74486348	5994
ENSG00000(	8.286335	10.83859	3.958241	7.490755	8.283888	12.32947	-0.25235	0.73768	0.82424	COL22A1	chr8	-	1.4E+08	1.4E+08	6346
ENSG00000(	3770.283	3726.066	3963.519	3489.943	2989.563	2977.979	0.27628	0.013199	0.02984	SDC2	chr8	+	97505579	97624000	3751
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CD52	chr1	+	26644448	26647014	581
ENSG00000(	602.8309	620.2082	629.3604	664.43	643.382	494.0009	0.039495	0.7951	0.86619	MMGT1	chrX	-	1.35E+08	1.35E+08	3738
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	SPRR1B	chr1	+	1.53E+08	1.53E+08	620
ENSG00000(	1855.103	1866.646	1848.499	1434.48	1334.626	1418.711	0.41063	0.000176	0.000555	TM2D2	chr8	-	38846327	38854343	3435
ENSG00000(	5.17896	4.817151	3.958241	14.23244	24.85166	20.54912	-1.9377	0.005013	0.012413	HTRA4	chr8	+	38831683	38846181	2095
ENSG00000(	1256.416	1383.727	1132.057	111.6123	92.0432	86.30632	3.685	9.31E-115	9.00E-113	PLEKHA2	chr8	+	38758753	38831428	5638
ENSG00000(	7242.257	7041.47	8778.06	5937.173	6373.071	5158.652	0.39978	0.001388	0.003804	CLIC4	chr1	+	25071848	25170815	4346
ENSG00000(	1.035792	0	2.638828	0	2.761296	2.465895	-0.32294	0.80514	0.87369	SLC38A11	chr2	-	1.66E+08	1.66E+08	3737
ENSG00000(	1.035792	1.204288	3.958241	5.243529	1.840864	10.68554	-1.2662	0.22689	0.33987	GPR183	chr13	-	99946784	99959659	1700
ENSG00000(	961.2149	981.4945	828.5919	205.9958	242.994	342.7594	1.8005	2.04E-23	2.37E-22	CCDC8	chr19	-	46913629	46916841	3213
ENSG00000(	208.1942	205.9332	248.0498	221.7264	238.3919	223.5745	-0.04733	0.79899	0.8689	METTL15	chr11	+	28129795	28355054	4416
ENSG00000(	0	0	0	23.22134	19.32907	27.94681	-5.4173	5.90E-07	2.51E-06	MUC15	chr11	-	26580580	26593780	3252
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	CXorf48	chrX	-	1.34E+08	1.34E+08	1728
ENSG00000(	1332.028	1305.448	1622.879	503.3788	709.6531	462.7662	1.342	7.10E-16	5.89E-15	ZEB2	chr2	-	1.45E+08	1.45E+08	6280
ENSG00000(	2.071584	0	0	0	0	1.64393	0.14412	0.91322	NA	GJB1	chrX	+	70435044	70445366	1904
ENSG00000(	1817.815	1735.379	1748.223	2235.241	2283.592	2368.903	-0.37683	0.000409	0.001219	PCBP1	chr2	+	70314585	70316332	1748
ENSG00000(	2403.037	2451.93	1837.943	2972.332	2312.125	3326.492	-0.36219	0.017287	0.038099	HINT1	chr5	-	1.3E+08	1.31E+08	1081
ENSG00000(	58.00435	71.05298	89.72014	132.5864	100.3271	114.2531	-0.66752	0.016196	0.035893	DTWD2	chr5	-	1.18E+08	1.18E+08	4365
ENSG00000(	3.107376	1.204288	1.319414	5.243529	1.840864	1.64393	-0.47546	0.68016	0.78088	CLIC3	chr9	-	1.4E+08	1.4E+08	1017
ENSG00000(	799.6314	811.6899	530.4043	685.4041	589.0765	854.8435	0.009296	0.95953	0.97632	INO80E	chr16	+	30006615	30017114	4469
ENSG00000(	42.46747	38.53721	54.09597	746.8283	760.2768	554.8263	-3.9127	8.97E-71	3.95E-69	BNC1	chr15	-	83924655	83953466	4610
ENSG00000(	162.6193	192.686	193.9538	242.7005	164.7573	205.4912	-0.16166	0.44826	0.57794	DFFB	chr1	+	3773845	3801993	3152
ENSG00000(	334.5608	354.0606	302.1458	335.5858	292.6974	316.4565	0.068298	0.67886	0.77985	NFU1	chr2	-	69622882	69664760	1467
ENSG00000(	3132.235	3239.534	3543.945	807.5034	786.9694	687.1627	2.1152	2.02E-70	8.85E-69	ANTXR1	chr2	+	69240310	69476459	5859
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	GKN1	chr2	+	69201705	69208106	814
ENSG00000(	170.9057	168.6003	204.5091	420.2314	521.8849	384.6796	-1.2814	6.04E-12	3.91E-11	CKAP2L	chr2	-	1.13E+08	1.14E+08	4737
ENSG00000(	249.6258	227.6104	221.6615	238.206	242.0736	235.082	-0.03178	0.85853	0.91009	C15orf40	chr15	-	83657193	83680393	1881
ENSG00000(	34.18113	44.55865	43.54065	68.91495	39.57858	50.13986	-0.37639	0.31097	0.43718	FAM103A1	chr15	+	83654959	83659809	1568
ENSG00000(	55.93276	48.17151	58.05421	50.18806	75.47542	27.12484	0.087906	0.82103	0.88423	APLF	chr2	+	68694693	68858004	3906
ENSG00000(	15.53688	10.83859	7.916483	23.22134	9.20432	14.79537	-0.43085	0.50063	0.62888	BOLA2B	chr16	-	30204255	30205627	1012
ENSG00000(	26.93059	26.49433	40.90183	50.18806	46.94203	36.98842	-0.50372	0.20647	0.3155	RGPD8	chr2	-	1.13E+08	1.13E+08	5576
ENSG00000(	374.9567	466.0593	344.367	1296.65	2081.097	2180.673	-2.2183	4.39E-33	7.40E-32	HIC2	chr22	+	21771693	21805752	6940
ENSG00000(	538.6118	452.8122	653.1098	982.038	1066.781	909.0932	-0.84511	4.29E-08	2.04E-07	LUZP1	chr1	-	23410516	23504301	8898
ENSG00000(	298.3081	310.7062	217.7033	191.7633	183.166	207.1352	0.50545	0.010345	0.023974	HEXDC	chr17	+	80376194	80400521	2285
ENSG00000(	0	0	0	1.498151	1.840864	3.28786	-1.8914	0.16147	0.25903	DRD5	chr4	+	9783258	9785632	2375
ENSG00000(	240.3037	248.0833	310.0622	1710.139	1587.745	1357.064	-2.539	8.14E-63	3.02E-61	BUB1	chr2	-	1.11E+08	1.11E+08	3532
ENSG00000(	16.57267	15.65574	25.06886	11.98521	12.88605	15.61733	0.47322	0.40182	0.53298	SPNS1	chr16	+	28985542	28995869	2253
ENSG00000(	297.2723	343.222	205.8285	545.327	555.0205	720.0413	-1.097	1.53E-08	7.58E-08	LRRC45	chr17	+	79981178	79989027	2701

ENSG00000(	33.14534	34.92434	30.34652	53.18436	56.14635	63.2913	-0.7945	0.027087	0.05689	CHRNA5	chr15	+	78857862	78887611	3623
ENSG00000(	799.6314	611.7782	618.8051	889.1527	973.8171	1337.337	-0.65255	0.000142	0.000453	STRA13	chr17	-	79976578	79981983	894
ENSG00000(	394.6367	311.9105	307.4234	432.2166	385.661	452.0807	-0.32151	0.05513	0.10583	AGPAT2	chr9	-	1.4E+08	1.4E+08	1512
ENSG00000(	417.4241	431.135	316.6593	465.1759	448.2504	520.3038	-0.29626	0.074405	0.13669	ASPSCR1	chr17	+	79934683	79975282	5503
ENSG00000(	13304.75	12793.15	13092.54	9529.739	13326.93	11977.67	0.16973	0.17919	0.28191	FASN	chr17	-	80036214	80056208	8560
ENSG00000(	3776.497	3928.387	3632.346	6068.261	4916.027	5193.174	-0.51211	8.26E-06	3.10E-05	CNBP	chr3	-	1.29E+08	1.29E+08	1664
ENSG00000(	626.6541	611.7782	547.5567	170.0401	255.8801	269.6045	1.3572	2.16E-13	1.55E-12	MT1E	chr16	+	56659387	56661024	729
ENSG00000(	680.5153	686.444	550.1955	1868.194	1478.214	1771.334	-1.4117	2.50E-23	2.89E-22	DUS1L	chr17	-	80015382	80023763	4456
ENSG00000(	1792.956	1561.961	1510.729	2952.856	2056.245	2373.835	-0.59978	3.01E-05	0.000105	GPS1	chr17	+	80008567	80015346	4076
ENSG00000(	782.0229	749.067	601.6527	412.7406	293.6178	363.3085	0.99098	4.43E-09	2.30E-08	RFNG	chr17	-	80005778	80009707	3107
ENSG00000(	875.2442	889.9686	569.9868	673.4189	536.6119	668.2575	0.31352	0.075869	0.13899	DCXR	chr17	-	79993012	79995608	1251
ENSG00000(	223.7311	243.2661	186.0373	83.14739	57.98722	87.95025	1.4964	4.31E-10	2.43E-09	ZNF32	chr10	-	44139307	44144304	1201
ENSG00000(	326.2744	287.8248	304.7846	181.2763	124.2583	135.6242	1.0499	1.95E-07	8.71E-07	LDB2	chr4	-	16503164	16900432	2718
ENSG00000(	1196.34	1180.202	889.2849	567.7993	603.8034	606.6101	0.87582	1.95E-09	1.04E-08	RAC3	chr17	+	79989500	79992080	1090
ENSG00000(	65.25489	66.23582	88.40072	101.1252	93.88406	158.6392	-0.68194	0.020681	0.044675	NRG4	chr15	-	76228310	76352136	3406
ENSG00000(	1201.519	1303.039	1455.313	1146.835	1012.475	935.3961	0.35367	0.007879	0.01876	LIMS1	chr2	+	1.09E+08	1.09E+08	4392
ENSG00000(	45.57484	39.74149	29.0271	95.13259	90.20234	115.0751	-1.366	1.72E-05	6.20E-05	C15orf27	chr15	+	76352178	76521462	2520
ENSG00000(	107.7224	95.13873	109.5113	8.988907	12.88605	9.863579	3.244	6.30E-18	5.79E-17	NLGN1	chr3	+	1.73E+08	1.74E+08	8242
ENSG00000(	127.4024	137.2888	160.9685	147.5679	148.1896	136.4462	-0.02478	0.91039	0.94496	TAPT1	chr4	-	16162128	16229033	4591
ENSG00000(	2174.127	2392.92	2370.987	3038.25	2761.296	2578.504	-0.27203	0.017183	0.037884	UGP2	chr2	+	64068074	64118696	4397
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	TAS2R1	chr5	-	9629109	9630463	1355
ENSG00000(	13.46529	10.83859	10.55531	182.0254	105.8497	151.2415	-3.5725	1.18E-20	1.22E-19	LINGO1	chr15	-	77905369	78113242	3055
ENSG00000(	3077.338	3161.255	3079.512	5010.566	5451.719	5683.065	-0.79178	3.07E-14	2.31E-13	HNRNPF	chr10	-	43881065	43904614	2755
ENSG00000(	137.7603	125.2459	154.3714	112.3613	104.9292	72.33291	0.52108	0.041028	0.081876	BTD	chr3	+	15642848	15687329	2138
ENSG00000(	570.7213	682.8311	659.7069	274.9107	274.2887	222.7525	1.3041	3.96E-16	3.34E-15	CSGALNAC1	chr10	+	43633934	43680756	3730
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	TACR3	chr4	-	1.05E+08	1.05E+08	5190
ENSG00000(	1651.052	1581.23	2138.77	4201.565	5436.992	4414.774	-1.3842	4.05E-22	4.48E-21	PCDH7	chr4	+	30722037	31148422	6763
ENSG00000(	3805.499	3700.776	5095.576	895.8944	1142.256	797.306	2.1452	1.14E-42	2.55E-41	ROBO1	chr3	-	78646390	79816965	7510
ENSG00000(	3.107376	6.021439	6.597069	2.996302	11.04518	8.219649	-0.44644	0.60464	0.7196	ONECUT1	chr15	-	53049186	53083273	2092
ENSG00000(	479.5717	382.9635	464.4337	288.3941	293.6178	338.6495	0.52592	0.001495	0.004065	AVEN	chr15	-	34158428	34331377	1605
ENSG00000(	0	0	3.958241	22.47227	75.47542	37.81039	-4.6397	1.16E-08	5.79E-08	P2RY1	chr3	+	1.53E+08	1.53E+08	3106
ENSG00000(	0	2.408575	1.319414	56.18067	73.63456	50.13986	-5.1199	1.09E-11	6.93E-11	CTNND2	chr5	-	10971952	11904155	5481
ENSG00000(	472.3211	444.3822	449.9201	181.2763	321.2308	318.9224	0.7328	0.000358	0.001077	TRIM56	chr7	+	1.01E+08	1.01E+08	3613
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	MUC17	chr7	+	1.01E+08	1.01E+08	14241
ENSG00000(	4.143168	3.612863	1.319414	9.737982	0.920432	9.041614	-0.93305	0.34796	0.47764	WNT10B	chr12	-	49359123	49365546	2274
ENSG00000(	10.35792	13.24716	6.597069	4.494453	11.96562	27.12484	-0.48242	0.50157	0.62965	CALML6	chr1	+	1846266	1848735	1882
ENSG00000(	11.39371	16.86003	17.15238	13.48336	6.443024	0.821965	1.02	0.17963	0.28242	REPS2	chrX	+	16964814	17171395	7945
ENSG00000(	0	0	0	27.7158	19.32907	13.15144	-5.18	2.62E-06	1.04E-05	MUC3A	chr7	+	1.01E+08	1.01E+08	4238
ENSG00000(	1411.784	1490.908	1364.274	1287.661	1125.688	1251.853	0.21856	0.066339	0.12392	SYAP1	chrX	+	16737755	16783459	6129
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	ITGAM	chr16	+	31271311	31344213	4718
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	PYDC1	chr16	-	31227283	31228680	813
ENSG00000(	288.9859	281.8033	320.6175	170.0401	200.6542	184.9421	0.67947	0.00018	0.000565	TPST1	chr7	+	65670186	65885530	2116
ENSG00000(	1.035792	2.408575	2.638828	0	0	0	2.0265	0.13497	0.22409	TM4SF4	chr3	+	1.49E+08	1.49E+08	2101
ENSG00000(	1449.073	1747.421	1417.05	1715.383	1557.371	1816.542	-0.14151	0.2696	0.38994	TOR1AIP2	chr1	-	1.8E+08	1.8E+08	7905

ENSG00000(	1800.206	1888.323	1946.135	287.645	139.9057	161.9271	3.2343	5.38E-60	1.88E-58	TM4SF1	chr3	-	1.49E+08	1.49E+08	3115
ENSG00000(	430.8894	378.1463	439.3648	426.9731	481.3859	459.4784	-0.13076	0.38729	0.5181	OTUD3	chr1	+	20209006	20239438	6397
ENSG00000(	10.35792	2.408575	3.958241	4.494453	11.04518	8.219649	-0.42516	0.61781	0.73021	OTUD7A	chr15	-	31775329	32162992	3431
ENSG00000(	525.1465	625.0253	442.0036	850.2007	700.4487	793.1961	-0.55574	0.000426	0.001264	GUSB	chr7	-	65425671	65447301	2555
ENSG00000(	645.2984	639.4768	629.3604	624.729	837.5931	750.454	-0.20734	0.15621	0.25222	BRD3	chr9	-	1.37E+08	1.37E+08	5652
ENSG00000(	1172.516	1213.922	1229.694	950.5769	1406.42	1126.092	0.05464	0.71175	0.80522	KLF13	chr15	+	31619058	31727868	6825
ENSG00000(	4.143168	0	10.55531	2.247227	1.840864	0.821965	1.2147	0.28217	0.40484	FRMPD4	chrX	+	12156585	12742642	8465
ENSG00000(	109.7939	79.48299	110.8308	51.68621	34.97642	24.65895	1.4035	3.45E-05	0.00012	ZFPM2	chr8	+	1.06E+08	1.07E+08	4700
ENSG00000(	183.3352	211.9546	151.7326	178.28	121.497	137.2681	0.32001	0.166	0.26473	ZNF764	chr16	-	30565085	30569819	2970
ENSG00000(	66.29068	62.62296	52.77655	68.16587	58.90765	57.53754	-0.02087	0.94675	0.9678	ZNF747	chr16	-	30537244	30546668	3936
ENSG00000(	732.3049	779.1742	630.6798	1051.702	962.7719	999.5093	-0.49081	0.00023	0.000711	ZNF768	chr16	-	30535325	30538142	2312
ENSG00000(	22.78742	26.49433	7.916483	6.74168	12.88605	10.68554	0.87691	0.16744	0.26677	TAS1R3	chr1	+	1266694	1270686	3433
ENSG00000(	230.9816	211.9546	193.9538	60.67512	77.31629	59.18147	1.6843	5.06E-13	3.54E-12	TMEM42	chr3	+	44903361	44907162	3071
ENSG00000(	598.6877	617.7996	738.8717	340.8294	416.9557	298.3733	0.88551	1.12E-07	5.10E-07	MAP3K2	chr2	-	1.28E+08	1.28E+08	10992
ENSG00000(	191.6215	166.1917	151.7326	224.7227	222.7445	216.1768	-0.37601	0.055274	0.10604	PUSL1	chr1	+	1243947	1247057	1783
ENSG00000(	1946.253	1859.42	1355.038	2126.625	1441.397	1613.517	-0.00561	0.97301	0.98436	SF3B5	chr6	-	1.44E+08	1.44E+08	737
ENSG00000(	90.1139	114.4073	110.8308	191.7633	178.5638	170.9687	-0.77805	0.000519	0.001523	ZNF35	chr3	+	44690219	44702283	2661
ENSG00000(	8.286335	1.204288	2.638828	6.74168	6.443024	2.465895	-0.29049	0.76598	0.84553	TIGD4	chr4	-	1.54E+08	1.54E+08	2472
ENSG00000(	532.397	446.7907	529.0849	480.1574	556.8614	712.6436	-0.21281	0.21205	0.32207	IFFO2	chr1	-	19230775	19283180	6188
ENSG00000(	4232.246	4453.456	3781.44	229.9662	335.0372	337.8276	3.7789	1.07E-142	1.50E-140	NLGN2	chr17	+	7308193	7323179	4642
ENSG00000(	0	0	0	3.745378	9.20432	8.219649	-3.625	0.003062	0.007896	MYO7B	chr2	+	1.28E+08	1.28E+08	6718
ENSG00000(	10791.92	10346.04	9710.885	1335.602	2107.789	1901.205	2.5223	9.06E-66	3.61E-64	CHD3	chr17	+	7788124	7816078	7356
ENSG00000(	95.29286	98.75159	114.789	195.5087	177.6434	153.7074	-0.76846	0.000802	0.002285	TMEM154	chr4	-	1.54E+08	1.54E+08	10698
ENSG00000(	7.250543	7.225726	3.958241	2.996302	5.522592	0	0.94274	0.35126	0.48095	MYRIP	chr3	+	39850405	40301812	5077
ENSG00000(	2510.76	2524.187	3599.361	2914.653	3077.925	2391.918	0.041798	0.78451	0.85827	ALCAM	chr3	+	1.05E+08	1.05E+08	4701
ENSG00000(	6030.38	5736.022	6849.077	5943.165	7759.242	6516.538	-0.11891	0.34521	0.47459	YWHAG	chr7	-	75956116	75988348	3745
ENSG00000(	1588.905	1494.521	1290.387	2186.552	1697.277	1666.945	-0.34262	0.014795	0.033083	UBE2E3	chr2	+	1.82E+08	1.82E+08	1570
ENSG00000(	838.9914	841.7971	719.0805	721.3598	761.1973	807.9915	0.068191	0.60939	0.72335	CNTROB	chr17	+	7835419	7853236	3769
ENSG00000(	1277.131	1264.502	1056.85	1148.333	929.6363	1012.661	0.21904	0.10699	0.18545	TRAPPC1	chr17	-	7833663	7835441	811
ENSG00000(	12.4295	9.634302	2.638828	0	0	0	4.2014	0.000557	0.001623	ZPLD1	chr3	+	1.02E+08	1.02E+08	3619
ENSG00000(	101.5076	89.11729	67.2901	11.23613	12.88605	19.72716	2.5076	1.02E-10	6.01E-10	KCNAB3	chr17	-	7825177	7833121	2458
ENSG00000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	GPR37L1	chr1	+	2.02E+08	2.02E+08	2508
ENSG00000(	189.5499	164.9874	180.7597	194.7596	173.9616	138.0901	0.078385	0.71485	0.8076	SIMC1	chr5	+	1.76E+08	1.76E+08	3572
ENSG00000(	456.7842	445.5865	481.586	605.253	502.5559	568.7997	-0.27728	0.05798	0.11049	TMEM192	chr4	-	1.66E+08	1.66E+08	4542
ENSG00000(	158.4762	190.2775	145.1355	431.4675	250.3575	342.7594	-1.0471	2.22E-06	8.88E-06	RP11-423H	chr5	+	1.77E+08	1.77E+08	1570
ENSG00000(	0	7.225726	0	0.749076	1.840864	2.465895	0.35062	0.78177	0.85632	NSG2	chr5	+	1.73E+08	1.74E+08	2452
ENSG00000(	38.3243	59.0101	48.81831	37.45378	34.97642	45.20807	0.30288	0.41208	0.54269	AC018720.	chr7	+	75123401	75133628	2667
ENSG00000(	1.035792	0	0	0	0	1.64393	-0.12526	0.92174	NA	SERPINA6	chr14	-	94770585	94789731	1609
ENSG00000(	47.64643	44.55865	116.1084	33.7084	61.66894	50.13986	0.50257	0.2107	0.32061	ZNF778	chr16	+	89284118	89295363	2915
ENSG00000(	87.00652	95.13873	125.3443	406.748	381.0588	342.7594	-1.8749	3.01E-20	3.08E-19	NIPA1	chr15	-	23043277	23100005	7613
ENSG00000(	3.107376	1.204288	6.597069	2.996302	3.681728	16.4393	-0.93816	0.32627	0.45396	FOXD4	chr9	-	116237	118417	2181
ENSG00000(	1592.012	1630.606	1588.574	1576.804	1501.225	1539.54	0.059005	0.58873	0.70579	UBE2E1	chr3	+	23847394	23932807	1511
ENSG00000(	6304.865	6173.179	6434.781	8182.152	10227.84	10868.84	-0.62917	2.19E-07	9.72E-07	HNRNPA3	chr2	+	1.78E+08	1.78E+08	5688
ENSG00000(	1129.013	1123.6	1134.696	578.2863	977.4988	690.4505	0.59169	0.000508	0.001492	SIK2	chr11	+	1.11E+08	1.12E+08	9678

ENSG00000(	78.72018	74.66584	129.3026	5.243529	42.33987	16.4393	2.0878	1.43E-05	5.21E-05	RNF150	chr4	-	1.42E+08	1.42E+08	4535
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CCDC144A	chr17	+	16592851	16707767	8912
ENSG00000(	23.82321	14.45145	6.597069	7.490755	10.12475	9.041614	0.71794	0.28813	0.41172	RP11-262H	chr9	+	66553273	66555928	2541
ENSG00000(	14.50109	14.45145	6.597069	0	1.840864	0	3.5268	0.000617	0.001788	HOXD4	chr2	+	1.77E+08	1.77E+08	1464
ENSG00000(	107.7224	104.773	109.5113	98.1289	101.2475	157.8173	-0.14844	0.57482	0.69339	CHRNB1	chr17	+	7348380	7361026	2557
ENSG00000(	3.107376	0	5.277655	0	0	0	2.3663	0.080152	0.14563	HOXD12	chr2	+	1.77E+08	1.77E+08	1805
ENSG00000(	299.3439	283.0076	303.4652	476.412	472.1816	406.8726	-0.61164	0.000115	0.000372	USP38	chr4	+	1.44E+08	1.44E+08	7009
ENSG00000(	50.7538	67.44011	51.45714	179.0291	150.9508	129.8705	-1.4262	1.37E-07	6.19E-07	SLC16A5	chr17	+	73083822	73102257	2051
ENSG00000(	147.0825	203.5246	219.0227	196.2578	195.1316	145.4878	0.081229	0.71835	0.81024	NANP	chr20	-	25593571	25604811	3964
ENSG00000(	0	2.408575	3.958241	8.239831	7.363456	9.863579	-1.7342	0.074026	0.13608	ANKK1	chr11	+	1.13E+08	1.13E+08	2543
ENSG00000(	17.60846	6.021439	2.638828	131.0882	117.8153	106.0335	-3.5954	1.53E-16	1.31E-15	ADRA1B	chr5	+	1.59E+08	1.59E+08	1738
ENSG00000(	139.8319	107.1816	137.219	75.65663	60.74851	84.66239	0.78811	0.002852	0.007395	ADPRM	chr17	+	10600911	10614550	1277
ENSG00000(	169.8699	207.1375	286.3128	248.6931	259.5618	226.8623	-0.15174	0.47511	0.60436	PWWP2A	chr5	-	1.59E+08	1.6E+08	3991
ENSG00000(	2.071584	0	0	0	6.443024	0	-0.83368	0.53758	0.66147	USP50	chr15	-	50792759	50838905	1386
ENSG00000(	1158.015	1158.525	1386.704	1145.337	1194.721	937.04	0.17541	0.20755	0.31682	USP47	chr11	+	11862970	11980870	7775
ENSG00000(	2600.873	2595.24	2790.56	2462.211	2093.062	1765.581	0.3363	0.011355	0.026063	PDCD6IP	chr3	+	33839844	33911194	6161
ENSG00000(	0	0	0	5.992604	0	3.28786	-2.2293	0.097833	0.1722	MRGPRX1	chr11	-	18955360	18961054	1197
ENSG00000(	211.3015	195.0946	160.9685	265.9218	235.6306	289.3317	-0.47429	0.014902	0.033307	ZNF212	chr7	+	1.49E+08	1.49E+08	2810
ENSG00000(	12.4295	1.204288	10.55531	1.498151	0.920432	0	2.6077	0.016568	0.036649	MRAP	chr21	+	33664124	33687095	1000
ENSG00000(	103.5792	83.09585	79.16483	197.0069	214.4607	162.7491	-1.097	3.71E-06	1.45E-05	FAM161A	chr2	-	62051989	62081278	4027
ENSG00000(	1124.87	1033.279	1067.406	856.9424	872.5695	1069.376	0.20448	0.12645	0.21252	ZNF282	chr7	+	1.49E+08	1.49E+08	3721
ENSG00000(	1751.524	1746.217	1770.653	2341.61	1828.898	1858.463	-0.19458	0.12629	0.21236	GLB1	chr3	-	33038100	33138722	2616
ENSG00000(	97.36444	95.13873	113.4696	211.9884	153.7121	171.7907	-0.8109	0.000538	0.001572	C14orf142	chr14	-	93669239	93673439	1154
ENSG00000(	132.5814	107.1816	109.5113	65.91865	46.0216	55.07165	1.0509	0.000181	0.000568	FAXDC2	chr5	-	1.54E+08	1.54E+08	3817
ENSG00000(	6544.133	6463.412	5690.632	4895.958	3625.582	3546.779	0.62995	3.80E-06	1.48E-05	CRTAP	chr3	+	33155471	33185153	2518
ENSG00000(	1.035792	1.204288	2.638828	0	0	0	1.7123	0.20641	NA	CNGB3	chr8	-	87566205	87755903	4347
ENSG00000(	0	0	1.319414	5.992604	9.20432	21.37109	-3.6941	0.000758	0.00217	SLN	chr11	-	1.08E+08	1.08E+08	906
ENSG00000(	444.3547	457.6293	424.8512	701.1347	564.2248	655.928	-0.53308	0.000296	0.000901	ELP5	chr17	+	7154735	7163259	2209
ENSG00000(	200.9436	211.9546	237.4945	78.65293	50.62376	82.19649	1.6013	4.36E-11	2.65E-10	CMTM8	chr3	+	32280171	32411817	1174
ENSG00000(	32.10955	32.51577	23.74945	9.737982	12.88605	11.50751	1.3279	0.010283	0.023838	GABARAP	chr17	-	7143333	7146089	1634
ENSG00000(	390.4935	439.565	372.0747	335.5858	267.8457	318.9224	0.37948	0.023088	0.049298	STX8	chr17	-	9153789	9479908	1245
ENSG00000(	428.8178	388.9849	521.1684	2222.507	1931.987	1983.401	-2.1928	7.51E-56	2.37E-54	CDK1	chr10	+	62538089	62554610	1948
ENSG00000(	2219.702	2103.891	2477.859	985.7834	1191.039	1570.775	0.85705	4.81E-08	2.28E-07	UBB	chr17	+	16284112	16286059	1225
ENSG00000(	383.243	508.2094	453.8783	748.3265	725.3004	720.0413	-0.70507	1.96E-06	7.87E-06	NFRKB	chr11	-	1.3E+08	1.3E+08	5093
ENSG00000(	20.71584	16.86003	14.51355	3.745378	2.761296	3.28786	2.2196	0.002214	0.005853	FABP4	chr8	-	82390654	82395498	941
ENSG00000(	3.107376	0	0	28.46487	16.56778	13.9734	-3.5484	9.38E-05	0.000307	FRMPD2	chr10	-	49364601	49482941	4997
ENSG00000(	195.7647	167.396	220.3421	217.2319	271.5274	186.586	-0.20907	0.32238	0.44965	PRDM10	chr11	-	1.3E+08	1.3E+08	6322
ENSG00000(	89.0781	95.13873	92.35896	1687.667	1813.251	1436.795	-4.1438	2.41E-140	3.25E-138	B3GNT2	chr2	+	62423248	62451866	2763
ENSG00000(	108.7581	119.2245	112.1502	47.19176	53.38506	49.3179	1.1711	2.06E-05	7.35E-05	FOS	chr14	+	75745477	75748933	2158
ENSG00000(	7596.498	7253.425	7956.065	4046.506	4038.856	3679.937	0.95345	2.81E-20	2.88E-19	TMED10	chr14	-	75598173	75643334	4127
ENSG00000(	0	0	0	0.749076	0	3.28786	-1.135	0.39451	NA	OR2A20P	chr7	-	1.44E+08	1.44E+08	2913
ENSG00000(	128.4382	173.4174	163.6073	260.6783	206.1768	224.3964	-0.57173	0.00641	0.015541	SETMAR	chr3	+	4344988	4359251	2443
ENSG00000(	793.4166	785.1956	861.5772	167.7929	204.3359	159.4612	2.1935	9.89E-45	2.34E-43	SMAD1	chr4	+	1.46E+08	1.46E+08	3293
ENSG00000(	0	0	1.319414	39.701	42.33987	52.60575	-5.5877	2.00E-09	1.07E-08	EMX2	chr10	+	1.19E+08	1.19E+08	2896

ENSG00000(	0	0	0	1.498151	2.761296	6.575719	-2.5851	0.049261	0.095829	CST1	chr20	-	23728190	23731905	760
ENSG00000(	0	0	1.319414	2.247227	0.920432	1.64393	-1.054	0.43427	0.56402	SP7	chr12	-	53720362	53739099	3148
ENSG00000(	307.6302	267.3519	216.3839	38.95193	38.65814	28.76877	2.8722	9.82E-30	1.48E-28	FAM115C	chr7	+	1.43E+08	1.43E+08	5568
ENSG00000(	58.00435	31.31148	55.41538	17.22874	37.73771	30.4127	0.75017	0.080694	0.14646	SEMA3E	chr7	-	82993222	83278326	6476
ENSG00000(	32.10955	13.24716	10.55531	45.69361	17.48821	47.67397	-0.93422	0.082636	0.14955	LRRN2	chr1	-	2.05E+08	2.05E+08	5036
ENSG00000(	304.5228	286.6205	432.7677	792.5219	926.875	706.0679	-1.2412	2.96E-12	1.96E-11	SLC30A1	chr1	-	2.12E+08	2.12E+08	5474
ENSG00000(	100.4718	79.48299	83.12307	105.6197	151.8713	117.541	-0.50096	0.056213	0.10755	DCLK2	chr4	+	1.51E+08	1.51E+08	4265
ENSG00000(	30.03797	63.82725	97.63662	307.121	330.4351	229.3282	-2.1663	5.45E-13	3.80E-12	ZNF804A	chr2	+	1.85E+08	1.86E+08	4690
ENSG00000(	2.071584	3.612863	2.638828	0	3.681728	0	0.82852	0.51067	0.63792	CTA-313A1	chr7	-	1.02E+08	1.02E+08	331
ENSG00000(	6.214751	1.204288	14.51355	461.4305	469.4203	523.5917	-5.9781	1.00E-58	3.37E-57	GPRC5C	chr17	+	72420990	72447792	2988
ENSG00000(	72.50543	62.62296	59.37362	64.4205	45.10117	78.90863	0.044883	0.89028	0.93185	TMEM182	chr2	+	1.03E+08	1.03E+08	3593
ENSG00000(	0	0	0	0.749076	4.60216	3.28786	-2.2366	0.094412	0.1672	VSTM2A	chr7	+	54610018	54638773	3401
ENSG00000(	244.4469	237.2447	196.5927	108484.1	92232.81	102732.5	-8.7818	0	0	KRT8	chr12	-	53290977	53343738	2862
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	KRT78	chr12	-	53231588	53242876	2554
ENSG00000(	120.1519	138.4931	97.63662	141.5753	131.6218	123.2947	-0.15157	0.52452	0.64958	ADORA2B	chr17	+	15848231	15879060	1875
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	SDR9C7	chr12	-	57316938	57328189	1765
ENSG00000(	262.0554	274.5776	179.4403	247.944	181.3251	244.1236	0.088998	0.67982	0.78064	MGMT	chr10	+	1.31E+08	1.32E+08	1759
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	METTL7B	chr12	+	56075330	56078395	1506
ENSG00000(	0	2.408575	0	1.498151	0.920432	4.109825	-0.90395	0.48995	0.61894	KRT86	chr12	+	52643084	52702947	2091
ENSG00000(	1898.607	1887.119	1752.182	1479.424	1550.928	1679.274	0.2337	0.040971	0.081781	HARS	chr5	-	1.4E+08	1.4E+08	3494
ENSG00000(	225.8026	202.3203	278.3963	235.2097	230.108	197.2716	0.090115	0.64641	0.75329	NFXL1	chr4	-	47849257	47916653	3865
ENSG00000(	170.9057	175.826	230.8974	316.859	376.4567	313.1686	-0.79982	2.93E-05	0.000103	DENND5B	chr12	-	31535157	31744031	9470
ENSG00000(	4.143168	3.612863	0	2.996302	0	7.397684	-0.30718	0.79356	0.86507	CD14	chr5	-	1.4E+08	1.4E+08	1886
ENSG00000(	515.8244	504.5966	498.7384	128.841	109.5314	122.4728	2.0635	5.80E-34	1.01E-32	DNAJC18	chr5	-	1.39E+08	1.39E+08	5103
ENSG00000(	89.0781	78.2787	67.2901	32.95932	39.57858	50.96182	0.91676	0.005368	0.013215	SPATA24	chr5	-	1.39E+08	1.39E+08	909
ENSG00000(	942.5706	979.0859	1322.053	763.308	894.6599	720.0413	0.44574	0.004407	0.011036	RALGAPB	chr20	+	37101459	37207504	8661
ENSG00000(	406.0304	404.6407	306.104	919.1157	847.7179	983.07	-1.2936	2.71E-17	2.42E-16	WIBG	chr12	-	56295197	56326402	1226
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	MZB1	chr5	-	1.39E+08	1.39E+08	1887
ENSG00000(	11.39371	14.45145	14.51355	11.23613	4.60216	5.753754	0.82393	0.23829	0.35323	SLC23A1	chr5	-	1.39E+08	1.39E+08	2303
ENSG00000(	823.4546	735.8198	821.9948	53.18436	61.66894	60.8254	3.7482	6.20E-100	4.73E-98	NPAS2	chr2	+	1.01E+08	1.02E+08	7983
ENSG00000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	KRT72	chr12	-	52979373	52995322	2015
ENSG00000(	1.035792	0	0	21.72319	11.04518	12.32947	-4.0671	0.00013	0.000416	KISS1	chr1	-	2.04E+08	2.04E+08	709
ENSG00000(	1.035792	4.817151	6.597069	18.72689	59.82808	37.81039	-3.0489	4.65E-06	1.79E-05	LONRF2	chr2	-	1.01E+08	1.01E+08	13912
ENSG00000(	698.1237	641.8854	567.3479	362.5526	393.9449	471.8079	0.63425	6.10E-05	0.000205	NUDT9	chr4	+	88343734	88380606	2458
ENSG00000(	4.143168	1.204288	0	0	3.681728	7.397684	-0.72927	0.5472	0.66898	HSD17B13	chr4	-	88224941	88244058	2397
ENSG00000(	1719.415	1624.584	1438.161	4113.923	3253.727	3608.426	-1.1956	3.71E-21	3.94E-20	PA2G4	chr12	+	56498103	56507691	2577
ENSG00000(	645.2984	768.3356	922.2702	1050.204	1194.721	979.7822	-0.46516	0.002303	0.00607	ELOVL6	chr4	-	1.11E+08	1.11E+08	6454
ENSG00000(	1600.298	1663.121	1492.257	1285.414	1733.173	1514.059	0.069946	0.60132	0.71656	PFKFB3	chr10	+	6186881	6277495	4483
ENSG00000(	0	4.817151	5.277655	26.96672	12.88605	9.041614	-2.0734	0.012788	0.028993	TMC7	chr16	+	18995256	19075264	4499
ENSG00000(	1462.538	1354.824	1543.714	5783.612	4275.407	4376.963	-1.7229	4.68E-37	8.88E-36	ARL6IP1	chr16	-	18802991	18813000	2407
ENSG00000(	31.07376	52.98866	35.62417	420.9805	380.1384	318.1004	-3.2041	1.86E-38	3.69E-37	SERPINB9	chr6	-	2887500	2903514	4118
ENSG00000(	286.9144	245.6747	234.8557	425.4749	340.5598	347.6912	-0.53374	0.002611	0.006819	SMAGP	chr12	-	51638342	51664674	2350
ENSG00000(	11.39371	0	9.235896	2.247227	13.80648	9.863579	-0.27399	0.76262	0.84327	IRX1	chr5	+	3596168	3601517	1858
ENSG00000(	1888.249	1932.882	2287.863	1584.295	1608.915	1366.106	0.42073	0.000915	0.00258	CDH2	chr18	-	25530930	25757410	4332

ENSG00000(	123.2592	150.536	138.5384	208.9921	198.8133	221.1086	-0.60791	0.003045	0.007856	IRX2	chr5	-	2745959	2752969	2630
ENSG00000(	372.8851	481.7151	515.8908	712.3708	573.4291	583.5951	-0.44928	0.006734	0.016251	EMB	chr5	-	49692026	49739082	4281
ENSG00000(	582.1151	533.4995	469.7113	7.490755	30.37426	27.12484	4.4553	3.72E-19	3.62E-18	SIX2	chr2	-	45232300	45236569	2205
ENSG00000(	5.17896	12.04288	7.916483	155.0586	194.2112	142.1999	-4.2089	9.32E-26	1.19E-24	DLGAP1	chr18	-	3496030	4455335	6683
ENSG00000(	2923.005	2902.333	2652.022	683.1569	919.5116	873.7487	1.7723	2.87E-40	5.98E-39	STAT2	chr12	-	56735381	56753939	3278
ENSG00000(	237.1963	262.5347	273.1187	555.065	439.0461	501.3986	-0.95162	9.60E-09	4.81E-08	NUDCD2	chr5	-	1.63E+08	1.63E+08	1043
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	LINC00266	chr6	-	131910	144885	727
ENSG00000(	780.9871	739.4327	691.3728	600.0095	659.0293	623.8714	0.23306	0.078815	0.14347	IRF2BP1	chr19	-	46386866	46389376	2511
ENSG00000(	2792.495	2373.651	3033.332	4799.327	4780.724	4524.095	-0.78118	3.97E-11	2.41E-10	HSPA4	chr5	+	1.32E+08	1.32E+08	4825
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	FOXA3	chr19	+	46367247	46377055	1989
ENSG00000(	3.107376	8.430014	3.958241	0	2.761296	5.753754	0.70699	0.50383	0.63148	SLC26A5	chr7	-	1.03E+08	1.03E+08	2689
ENSG00000(	192.6573	180.6432	171.5238	341.5785	174.8821	213.7109	-0.42081	0.081247	0.14738	COMMD5	chr8	-	1.46E+08	1.46E+08	1573
ENSG00000(	513.7528	578.0581	670.2622	12.73428	29.45382	13.9734	4.9525	4.30E-81	2.36E-79	SGCD	chr5	+	1.55E+08	1.56E+08	9755
ENSG00000(	26.93059	22.88147	43.54065	5.992604	5.522592	13.9734	1.7782	0.001953	0.005213	DPY19L2P2	chr7	-	1.03E+08	1.03E+08	4078
ENSG00000(	152.2614	99.95588	117.4278	62.92235	82.83888	55.07165	0.87666	0.002009	0.005352	ZNF16	chr8	-	1.46E+08	1.46E+08	2616
ENSG00000(	579.0077	511.8223	529.0849	591.7697	578.0313	608.254	-0.13325	0.33255	0.4606	ARMC10	chr7	+	1.03E+08	1.03E+08	2629
ENSG00000(	466.1064	404.6407	455.1978	825.4813	736.3456	765.2493	-0.80935	7.06E-09	3.60E-08	RNF34	chr12	+	1.22E+08	1.22E+08	2066
ENSG00000(	90.1139	61.41867	43.54065	33.7084	35.89685	62.46933	0.55803	0.14451	0.23669	ACYP2	chr2	+	54342540	54532437	1913
ENSG00000(	698.1237	653.9282	576.5838	1100.392	937.9202	1140.887	-0.7183	2.67E-07	1.18E-06	TRABD	chr22	+	50624344	50638027	2404
ENSG00000(	76.6486	77.07441	124.0249	183.5235	176.7229	193.9837	-0.99577	5.56E-05	0.000188	TMEM133	chr11	+	1.01E+08	1.01E+08	1853
ENSG00000(	558.2918	573.241	554.1538	323.6006	289.0156	327.964	0.83829	1.35E-08	6.69E-08	ATF7	chr12	-	53901640	54020199	6680
ENSG00000(	34.18113	18.06432	26.38828	4.494453	0.920432	5.753754	2.6095	0.000108	0.000351	RASA4B	chr7	-	1.02E+08	1.02E+08	3569
ENSG00000(	307.6302	338.4048	337.7699	340.8294	360.8093	337.8276	-0.07981	0.61458	0.72785	SOCS6	chr18	+	67956137	67997436	5848
ENSG00000(	37.28851	22.88147	38.263	56.18067	56.14635	50.96182	-0.71522	0.056754	0.10845	MURC	chr9	+	1.03E+08	1.03E+08	2615
ENSG00000(	0	0	0	3.745378	4.60216	7.397684	-3.1825	0.011693	0.026753	OR10A3	chr11	-	7960081	7961141	1061
ENSG00000(	19.68005	26.49433	2.638828	95.88167	74.55499	78.90863	-2.2674	5.16E-07	2.21E-06	ZNF296	chr19	-	45574758	45579846	1744
ENSG00000(	0	0	0	10.48706	20.2495	25.48091	-5.0714	5.00E-06	1.92E-05	OR5E1P	chr11	+	7870247	7871182	927
ENSG00000(	12.4295	0	1.319414	941.588	763.9586	798.1279	-6.1793	6.19E-10	3.45E-09	HOXB9	chr17	-	46698518	46703839	2705
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	TTLL6	chr17	-	46839597	46894576	4440
ENSG00000(	277.5922	257.7176	265.2022	340.8294	587.2356	604.1442	-0.92949	7.06E-06	2.66E-05	BOP1	chr8	-	1.45E+08	1.46E+08	2336
ENSG00000(	756.1281	847.8186	901.1596	882.411	724.38	695.3823	0.11989	0.40508	0.53597	POLH	chr6	+	43543887	43586701	3540
ENSG00000(	3.107376	0	3.958241	7.490755	20.2495	15.61733	-2.3033	0.008026	0.019062	SYT9	chr11	+	7260099	7490273	3955
ENSG00000(	0	1.204288	0	34.45748	35.89685	33.70056	-5.2396	4.09E-08	1.95E-07	KCNS3	chr2	+	18059114	18542882	2397
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RBMXL2	chr11	+	7110165	7112379	2215
ENSG00000(	2137.874	2229.137	2884.239	3035.254	3506.846	2635.22	-0.33926	0.018977	0.04139	KIF5B	chr10	-	32297938	32345359	5877
ENSG00000(	100.4718	85.50443	101.5949	712.3708	792.4919	631.2691	-2.8794	1.93E-57	6.35E-56	GPR37	chr7	-	1.24E+08	1.24E+08	3021
ENSG00000(	2947.864	3111.879	3722.066	1077.92	1999.178	1588.858	1.0638	2.06E-09	1.10E-08	AKAP13	chr15	+	85923802	86292586	13215
ENSG00000(	335.5966	375.7378	321.937	952.075	928.7159	1068.554	-1.5089	2.00E-26	2.62E-25	CDCA4	chr14	-	1.05E+08	1.05E+08	2513
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	OR10A4	chr11	+	6897856	6898850	995
ENSG00000(	0	0	0	29.21395	18.40864	13.9734	-5.2122	2.19E-06	8.76E-06	SDR16C5	chr8	-	57212569	57233335	2399
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	OR10A2	chr11	+	6890924	6891976	1053
ENSG00000(	517.896	511.8223	550.1955	477.1611	508.0785	489.8911	0.098624	0.47888	0.60797	CHCHD7	chr8	+	57124245	57131357	3157
ENSG00000(	21.75163	38.53721	21.11062	45.69361	54.30549	32.05663	-0.67944	0.11468	0.19641	HTRA3	chr4	+	8271492	8308838	2541
ENSG00000(	150.1898	140.9017	168.885	286.1469	243.9145	202.2034	-0.66897	0.001418	0.003873	FOXN2	chr2	+	48541776	48606433	5408

ENSG00000(	0	0	0	2.996302	0.920432	2.465895	-1.8353	0.17499	0.27674	LMOD2	chr7	+	1.23E+08	1.23E+08	2346
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	BFSP2	chr3	+	1.33E+08	1.33E+08	1558
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	FSHR	chr2	-	49189296	49381676	2784
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	CELP	chr9	+	1.36E+08	1.36E+08	1249
ENSG00000(	608.0098	616.5953	796.9259	391.7665	577.1109	408.5166	0.55154	0.002087	0.005544	USP32	chr17	-	58256455	58499831	5171
ENSG00000(	27.96638	30.10719	14.51355	74.15848	42.33987	55.07165	-1.205	0.004002	0.010115	CEL	chr9	+	1.36E+08	1.36E+08	2384
ENSG00000(	236.1606	239.6533	329.8534	394.0137	374.6158	328.786	-0.44715	0.015594	0.034667	PPM1D	chr17	+	58677544	58741849	2996
ENSG00000(	6.214751	8.430014	5.277655	13.48336	27.61296	15.61733	-1.4042	0.035259	0.071622	GPR27	chr3	+	71803201	71805647	2447
ENSG00000(	326.2744	290.2333	279.7157	407.4971	364.4911	378.1039	-0.35733	0.027486	0.057611	AC093323.	chr4	+	6675178	6677774	2311
ENSG00000(	0	0	0	5.243529	9.20432	3.28786	-3.3507	0.007307	0.017518	PSG6	chr19	-	43406231	43423715	2321
ENSG00000(	518.9317	464.8551	498.7384	635.9651	589.0765	577.0194	-0.28071	0.044651	0.088014	KBTBD2	chr7	-	32907784	32933743	3745
ENSG00000(	409.1378	385.3721	399.7824	344.5748	380.1384	290.1536	0.23504	0.15305	0.24818	MINA	chr3	-	97663086	97691301	2923
ENSG00000(	721.947	710.5298	738.8717	1296.65	1070.462	1301.992	-0.75574	8.95E-09	4.50E-08	TRIAP1	chr12	-	1.21E+08	1.21E+08	1182
ENSG00000(	744.7344	781.5827	612.208	1581.298	1407.341	1550.226	-1.0822	6.40E-16	5.33E-15	LSM3	chr3	+	14219858	14242619	3815
ENSG00000(	584.1866	527.478	777.1347	559.5594	734.5047	469.342	0.098378	0.60067	0.71598	KIAA0232	chr4	+	6783102	6885897	7841
ENSG00000(	12.4295	20.47289	55.41538	89.13999	81.91845	76.44274	-1.47	0.000566	0.001649	MTSS1	chr8	-	1.26E+08	1.26E+08	4944
ENSG00000(	2420.646	2466.381	2386.82	1581.298	1450.601	1285.553	0.75092	2.13E-10	1.23E-09	TMEM43	chr3	+	14166440	14185179	3341
ENSG00000(	494.0727	470.8765	523.8073	411.2425	383.8201	326.3201	0.40674	0.009146	0.021459	RNF139	chr8	+	1.25E+08	1.26E+08	2637
ENSG00000(	26657.14	26886.93	21072.36	18293.17	16308.21	21170.53	0.419	0.001372	0.003765	RPS9	chr19	+	54704610	54752862	2384
ENSG00000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	PLA2G1B	chr12	-	1.21E+08	1.21E+08	565
ENSG00000(	1058.579	1095.902	913.0343	2.996302	3.681728	9.863579	7.4135	1.03E-104	8.53E-103	CYTL1	chr4	-	5016313	5021199	1003
ENSG00000(	1594.084	1576.413	1216.5	2549.104	1933.828	2010.526	-0.56372	0.000121	0.000389	TSEN34	chr19	+	54693789	54697585	2372
ENSG00000(	1.035792	0	0	1.498151	2.761296	0	-0.89883	0.50763	NA	TRH	chr3	+	1.3E+08	1.3E+08	1978
ENSG00000(	1030.613	1145.278	1129.418	273.4126	256.8005	265.4947	2.0482	9.20E-52	2.66E-50	GSTA4	chr6	-	52842751	52860176	1693
ENSG00000(	270.3417	262.5347	328.534	325.0988	314.7877	260.5629	-0.06556	0.71627	0.80882	MSANTD4	chr11	-	1.06E+08	1.06E+08	4087
ENSG00000(	580.0435	558.7895	468.3919	566.3011	524.6462	601.6783	-0.0733	0.62051	0.73278	NDUFA3	chr19	+	54606036	54612564	963
ENSG00000(	9.322127	7.225726	11.87472	6.74168	0	9.041614	0.73326	0.40371	0.53478	OSCAR	chr19	-	54597933	54606000	2055
ENSG00000(	103.5792	113.203	117.4278	916.1194	1022.6	869.6389	-3.0624	1.52E-77	7.82E-76	PAQR8	chr6	+	52226219	52272575	4738
ENSG00000(	33.14534	25.29004	23.74945	39.701	48.7829	48.49593	-0.71253	0.074736	0.13721	NUDT6	chr4	-	1.24E+08	1.24E+08	5306
ENSG00000(	352.1692	419.0921	321.937	149.8151	152.7917	183.2982	1.1646	6.21E-10	3.46E-09	TPT1-AS1	chr13	+	45915480	45965872	2869
ENSG00000(	1024.398	1011.602	1337.886	675.6661	962.7719	634.5569	0.56778	0.001012	0.002835	TANC2	chr17	+	61086917	61505060	11721
ENSG00000(	0	0	0	1.498151	2.761296	0.821965	-1.5229	0.26162	NA	PKHD1	chr6	-	51480098	51952423	16282
ENSG00000(	228.91	214.3632	213.745	191.0143	167.5186	157.8173	0.34552	0.075677	0.1387	DNAJC24	chr11	+	31391387	31453396	2745
ENSG00000(	504.4307	440.7693	435.4065	325.8479	373.6954	281.112	0.49382	0.003003	0.007757	ZNF160	chr19	-	53569859	53606689	4688
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	PGK2	chr6	-	49753366	49755053	1688
ENSG00000(	27.96638	37.33292	21.11062	124.3465	78.23672	79.7306	-1.6765	3.04E-06	1.19E-05	ZNF415	chr19	-	53611132	53636330	2630
ENSG00000(	1792.956	1552.327	1279.831	974.5473	860.6039	944.4377	0.73322	2.50E-07	1.10E-06	PRKCDBP	chr11	-	6340176	6341877	1174
ENSG00000(	4.143168	3.612863	1.319414	0	0.920432	1.64393	1.2959	0.29466	0.41906	DCDC1	chr11	-	30851916	31391357	5352
ENSG00000(	471.2853	517.8437	597.6944	174.5346	201.5746	204.6693	1.4442	1.45E-17	1.30E-16	HAS2	chr8	-	1.23E+08	1.23E+08	4190
ENSG00000(	751.9849	814.0985	1110.946	447.9472	462.0569	409.3385	1.0157	5.86E-10	3.27E-09	PDGFD	chr11	-	1.04E+08	1.04E+08	4052
ENSG00000(	5.17896	1.204288	5.277655	7.490755	0	6.575719	-0.22967	0.82724	0.88863	PLAC1	chrX	-	1.34E+08	1.34E+08	1138
ENSG00000(	0	7.225726	7.916483	1.498151	0.920432	8.219649	0.39209	0.71647	0.80897	DDI1	chr11	+	1.04E+08	1.04E+08	2615
ENSG00000(	584.1866	617.7996	522.4879	63.67142	66.2711	50.13986	3.2449	1.38E-64	5.37E-63	S1PR1	chr1	+	1.02E+08	1.02E+08	2909
ENSG00000(	80.79177	109.5902	146.4549	469.6704	688.4831	498.9327	-2.2906	7.37E-25	9.05E-24	HS6ST2	chrX	-	1.32E+08	1.32E+08	4441

ENSG00000(	281.7354	276.9862	377.3523	172.2874	196.9724	152.0635	0.83893	2.73E-05	9.60E-05	PYGO1	chr15	-	55831088	55881145	8488
ENSG00000(	3.107376	2.408575	14.51355	1.498151	1.840864	4.109825	1.1802	0.2377	0.35245	LRRC8E	chr19	+	7953390	7966901	3595
ENSG00000(	204.051	225.2018	242.7721	274.9107	256.8005	234.26	-0.1904	0.29877	0.42373	PKIA	chr8	+	79428374	79517502	4163
ENSG00000(	108.7581	114.4073	75.20659	146.8188	177.6434	144.6658	-0.6418	0.00941	0.022014	XKR6	chr8	-	10753555	11058875	3382
ENSG00000(	129.474	140.9017	98.95603	59.17697	61.66894	62.46933	1.0033	0.000201	0.000627	TSNARE1	chr8	-	1.43E+08	1.43E+08	2100
ENSG00000(	0	0	1.319414	0	0	1.64393	-0.1317	0.91874	NA	FPR2	chr19	+	52255279	52273779	2621
ENSG00000(	0	0	0	1.498151	0	5.753754	-1.8682	0.16834	0.26796	FPR1	chr19	-	52248425	52307363	1965
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	PATE1	chr11	+	1.26E+08	1.26E+08	1527
ENSG00000(	0	0	0	1.498151	5.522592	0	-1.8128	0.18144	0.28461	OR13H1	chrX	+	1.31E+08	1.31E+08	1081
ENSG00000(	743.6986	762.3141	885.3266	967.8056	577.1109	655.106	0.11792	0.51215	0.63919	FEZ2	chr2	-	36778570	36873230	4495
ENSG00000(	3.107376	10.83859	2.638828	637.4633	453.773	530.9893	-6.4648	4.04E-57	1.32E-55	SOX7	chr8	-	10581278	10697357	3216
ENSG00000(	1384.854	1260.889	1196.708	1364.067	1121.086	1209.932	0.056405	0.65987	0.76435	C11orf24	chr11	-	68028803	68039469	2063
ENSG00000(	25.8948	20.47289	10.55531	20.22504	8.283888	18.08323	0.27698	0.63808	0.74635	FAM86JP	chr3	+	1.26E+08	1.26E+08	2012
ENSG00000(	77.68439	101.1602	116.1084	18.72689	13.80648	15.61733	2.5576	1.45E-12	9.80E-12	ALK	chr2	-	29415640	30144432	6220
ENSG00000(	84.93494	92.73015	73.88717	145.3207	129.7809	115.8971	-0.62979	0.012527	0.028484	CCBL1	chr9	-	1.32E+08	1.32E+08	2490
ENSG00000(	89.0781	84.30014	139.8579	196.2578	198.8133	153.7074	-0.80757	0.001341	0.003686	MTM1	chrX	+	1.5E+08	1.5E+08	3593
ENSG00000(	105.6508	116.8159	137.219	188.018	179.4842	204.6693	-0.66967	0.002085	0.005539	TRMT61B	chr2	-	29072687	29093167	1836
ENSG00000(	53.86118	54.19295	75.20659	27.7158	27.61296	26.30288	1.1411	0.00193	0.005156	INSR	chr19	-	7112266	7294045	8954
ENSG00000(	597.6519	622.6168	798.2453	712.3708	667.3132	662.5037	-0.01877	0.89959	0.9378	MFN1	chr3	+	1.79E+08	1.79E+08	5224
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	HSFX1	chrX	+	1.49E+08	1.49E+08	1963
ENSG00000(	3.107376	3.612863	0	17.97781	7.363456	5.753754	-1.874	0.04608	0.090459	NRTN	chr19	+	5823813	5828335	1109
ENSG00000(	26.93059	18.06432	35.62417	22.47227	18.40864	16.4393	0.46963	0.34384	0.47307	KCNMB3	chr3	-	1.79E+08	1.79E+08	2055
ENSG00000(	2.071584	0	0	0	1.840864	0.821965	-0.14076	0.91727	NA	KCNG3	chr2	-	42669157	42721237	3824
ENSG00000(	45.57484	61.41867	31.66593	714.6181	672.8358	660.8598	-3.8542	1.50E-74	7.09E-73	ATP6V0E2	chr7	+	1.5E+08	1.5E+08	2722
ENSG00000(	457.82	408.2535	438.0454	160.3022	162.9165	149.5976	1.4588	5.76E-18	5.31E-17	PRKCE	chr2	+	45878484	46415129	5650
ENSG00000(	714.6964	626.2296	697.9699	943.8352	722.5391	757.8517	-0.24963	0.08961	0.16018	JAGN1	chr3	+	9932238	9936033	1693
ENSG00000(	2162.733	1983.462	1857.735	1886.172	1597.87	1740.1	0.20044	0.095623	0.169	TADA3	chr3	-	9821544	9834695	2554
ENSG00000(	629.7615	700.8955	872.1325	300.3793	357.1276	266.3166	1.2484	3.06E-13	2.18E-12	SOCS5	chr2	+	46926091	46990268	4771
ENSG00000(	179.192	216.7718	213.745	478.6593	366.3319	413.4484	-1.0444	7.69E-09	3.90E-08	C1GALT1C1	chrX	-	1.2E+08	1.2E+08	1613
ENSG00000(	1116.584	1026.053	794.2871	596.2641	463.8977	540.031	0.8732	4.50E-08	2.14E-07	C9orf16	chr9	+	1.31E+08	1.31E+08	1570
ENSG00000(	197.8363	172.2131	166.2461	177.5309	174.8821	175.0785	0.025961	0.89668	0.93588	MORN4	chr10	-	99374310	99393344	2323
ENSG00000(	341.8113	327.5663	253.3274	1080.916	1027.202	1032.388	-1.7584	2.97E-32	4.83E-31	ZNF672	chr1	+	2.49E+08	2.49E+08	2989
ENSG00000(	510.6454	520.2523	333.8117	614.991	475.8633	674.8332	-0.36851	0.052433	0.10123	ZNF692	chr1	-	2.49E+08	2.49E+08	2704
ENSG00000(	170.9057	179.4389	176.8014	154.3096	138.0648	174.2566	0.1734	0.40417	0.53513	NAIF1	chr9	-	1.31E+08	1.31E+08	3399
ENSG00000(	25.8948	39.74149	31.66593	33.7084	20.2495	35.34449	0.11289	0.79727	0.86791	RBKS	chr2	-	28004231	28113965	2151
ENSG00000(	11.39371	27.69862	22.43003	2.247227	10.12475	4.93179	1.7163	0.01313	0.029707	GRIK1	chr21	-	30909254	31312351	3624
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	MUC7	chr4	+	71296209	71348714	2540
ENSG00000(	370.8135	392.5978	292.9099	401.5045	330.4351	336.1837	-0.0153	0.93032	0.95814	TMEM126A	chr11	+	85359011	85367591	739
ENSG00000(	377.0283	416.6836	368.1164	695.1421	520.9645	641.1326	-0.67545	2.13E-05	7.58E-05	TMEM126B	chr11	+	85339629	85347580	1388
ENSG00000(	1277.131	1304.244	1153.168	923.6102	715.1757	693.7384	0.67658	2.30E-06	9.18E-06	TRIM8	chr10	+	1.04E+08	1.04E+08	2742
ENSG00000(	1088.617	909.2372	1224.416	1928.12	1704.64	1593.79	-0.69656	5.80E-07	2.47E-06	NETO2	chr16	-	47111614	47177908	7481
ENSG00000(	3.107376	9.634302	14.51355	5.243529	6.443024	4.109825	0.69378	0.40015	0.53131	CLDN20	chr6	+	1.56E+08	1.56E+08	1209
ENSG00000(	52.82539	69.84869	63.33186	614.2419	1061.258	1110.475	-3.8799	4.83E-63	1.81E-61	CDC42BPG	chr11	-	64590859	64612041	5742
ENSG00000(	1393.14	1223.556	825.953	1194.776	899.2621	1103.077	0.10706	0.54429	0.66652	SCAND1	chr20	-	34541539	34547394	1727

ENSG00000(	2326.389	2354.382	1866.971	139.3281	143.5874	170.1467	3.8422	3.13E-146	4.57E-144	JUNB	chr19	+	12902310	12904124	1815
ENSG00000(	0	3.612863	0	76.40571	59.82808	90.41614	-5.4491	1.68E-13	1.21E-12	C10orf35	chr10	+	71390007	71393352	1062
ENSG00000(	62.14751	61.41867	89.72014	41.19916	53.38506	78.08667	0.29733	0.38325	0.51389	TMEM37	chr2	+	1.2E+08	1.2E+08	1688
ENSG00000(	1.035792	3.612863	0	0	0	0.821965	1.1852	0.38234	NA	UGT2B7	chr4	+	69917081	69978705	1887
ENSG00000(	0	0	0	2.996302	4.60216	4.93179	-2.8359	0.028065	0.058606	LRG1	chr19	-	4536421	4540486	3036
ENSG00000(	304.5228	274.5776	265.2022	788.7766	708.7326	729.0829	-1.3932	3.30E-21	3.51E-20	SHCBP1	chr16	-	46614466	46655538	3461
ENSG00000(	1.035792	0	1.319414	91.38722	103.0884	84.66239	-6.117	6.49E-15	5.09E-14	SOSTDC1	chr7	-	16501106	16570205	2411
ENSG00000(	1452.18	1023.645	1646.628	104.8706	224.5854	178.3664	2.9685	1.64E-16	1.41E-15	NPTX1	chr17	-	78440948	78451643	5122
ENSG00000(	526.1823	535.908	488.1831	943.8352	973.8171	892.6539	-0.8554	5.82E-11	3.50E-10	FAM98B	chr15	+	38746328	38779911	4388
ENSG00000(	1151.801	1197.062	1150.529	488.3973	1083.348	1001.153	0.43702	0.19783	0.305	BAHCC1	chr17	+	79373540	79433357	10341
ENSG00000(	0	1.204288	1.319414	14.98151	24.85166	22.19305	-3.9709	1.89E-05	6.76E-05	ZNF439	chr19	+	11959541	11994565	2622
ENSG00000(	244.4469	272.169	269.1604	322.8516	275.2092	285.2218	-0.1703	0.32489	0.45239	ZNF440	chr19	+	11925099	11946016	4189
ENSG00000(	3229.599	3123.922	2568.899	826.9794	917.6707	828.5406	1.7908	2.27E-45	5.49E-44	GAA	chr17	+	78075355	78093678	3626
ENSG00000(	1616.871	1537.875	1669.058	2023.253	2080.176	1860.929	-0.30569	0.006623	0.016006	CANT1	chr17	-	76987799	77005949	3534
ENSG00000(	1.035792	0	0	2.996302	0	8.219649	-1.9987	0.12642	0.21252	KCNK3	chr2	+	26915619	26956288	6162
ENSG00000(	847.2778	904.4201	821.9948	1215.75	936.9998	963.3429	-0.27579	0.049394	0.096056	ZDHHC16	chr10	+	99205927	99217127	1959
ENSG00000(	274.4849	238.449	296.8681	328.0951	284.4135	247.4114	-0.0876	0.63595	0.74479	CHST11	chr12	+	1.05E+08	1.05E+08	5709
ENSG00000(	403.9588	411.8664	316.6593	676.4152	485.0677	492.357	-0.54345	0.00238	0.006259	EXOSC1	chr10	-	99195899	99205774	2113
ENSG00000(	7775.69	7678.538	6417.629	7478.021	6294.834	6143.366	0.13491	0.26966	0.38997	PGAM1	chr10	+	99185917	99193198	1830
ENSG00000(	121.1877	90.32158	125.3443	1361.819	1937.509	1402.272	-3.7848	8.74E-95	6.11E-93	CHD7	chr8	+	61591337	61779465	10446
ENSG00000(	60.07593	54.19295	50.13772	358.8072	316.6286	278.6461	-2.5146	2.26E-28	3.23E-27	ESCO2	chr8	+	27629466	27670157	3922
ENSG00000(	1239.843	1176.589	1048.934	19686.45	15744.91	16497.66	-3.8967	8.54E-223	3.18E-220	KRT19	chr17	-	39679869	39684560	1390
ENSG00000(	1.035792	1.204288	2.638828	33.7084	34.97642	30.4127	-3.9766	1.81E-07	8.09E-07	KRT15	chr17	-	39669995	39678781	5237
ENSG00000(	20.71584	25.29004	18.47179	0.749076	0	0	4.9911	6.47E-07	2.74E-06	LURAP1	chr1	+	46669006	46686933	1854
ENSG00000(	210.2658	169.8046	226.9392	1155.074	1474.532	1350.488	-2.704	5.70E-65	2.22E-63	CLCN5	chrX	+	49687225	49863892	10108
ENSG00000(	31.07376	21.67718	27.70769	11.23613	28.53339	37.81039	0.057354	0.91052	0.94504	TPPP	chr5	-	660883	693510	5116
ENSG00000(	11.39371	6.021439	22.43003	0	1.840864	0.821965	3.3148	0.000647	0.001868	KCND3	chr1	-	1.12E+08	1.13E+08	7396
ENSG00000(	113.9371	40.94578	54.09597	23.22134	23.0108	11.50751	1.8096	6.09E-05	0.000204	APLN	chrX	-	1.29E+08	1.29E+08	3220
ENSG00000(	0	0	0	43.44638	32.21512	43.56414	-6.1396	5.05E-09	2.61E-08	KRT9	chr17	-	39722096	39728310	2287
ENSG00000(	504.4307	549.1552	543.5985	2.247227	2.761296	2.465895	7.4999	2.61E-59	8.94E-58	PDE7B	chr6	+	1.36E+08	1.37E+08	5390
ENSG00000(	433.9968	343.222	294.2293	596.2641	497.0333	637.0228	-0.68594	9.89E-05	0.000323	MRPL36	chr5	-	1798500	1801480	793
ENSG00000(	1182.874	1203.083	913.0343	659.1865	615.769	627.9812	0.79229	2.51E-08	1.22E-07	ZNF581	chr19	+	56146825	56156988	1324
ENSG00000(	38.3243	18.06432	63.33186	59.17697	61.66894	50.96182	-0.51496	0.20903	0.31863	NAT1	chr8	+	18027986	18081198	2332
ENSG00000(	2.071584	9.634302	1.319414	0	1.840864	0	1.9848	0.10905	0.18821	KRT20	chr17	-	39032193	39041479	1737
ENSG00000(	0	0	0	29.21395	32.21512	36.16646	-5.8697	3.17E-08	1.53E-07	KSR2	chr12	-	1.18E+08	1.18E+08	17008
ENSG00000(	215.4447	239.6533	167.5656	164.7966	99.40666	118.3629	0.69494	0.004091	0.010317	ZNF524	chr19	+	56111388	56114504	1260
ENSG00000(	1027.506	930.9144	1101.711	346.0729	485.0677	372.3501	1.3437	8.33E-18	7.60E-17	MCC	chr5	-	1.12E+08	1.13E+08	29630
ENSG00000(	129.474	133.6759	180.7597	101.8743	137.1444	103.5676	0.36995	0.13269	0.22104	ZBTB26	chr9	-	1.26E+08	1.26E+08	4443
ENSG00000(	0	2.408575	0	1.498151	5.522592	0	-0.9145	0.49089	0.61997	CDK5R2	chr2	+	2.2E+08	2.2E+08	2500
ENSG00000(	738.5196	727.3898	814.0783	119.8521	103.0884	108.4994	2.7693	5.59E-66	2.23E-64	DSEL	chr18	-	65173819	65184217	9531
ENSG00000(	569.6855	468.4679	492.1413	688.4004	606.5647	691.2725	-0.37427	0.010134	0.023533	POLR1C	chr6	+	43477440	43497323	1882
ENSG00000(	1770.168	1699.25	1905.234	1284.665	1586.825	1560.089	0.27801	0.027169	0.057022	ASXL1	chr20	+	30946155	31027122	7031
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	OR1L6	chr9	+	1.26E+08	1.26E+08	1044
ENSG00000(	49.71801	37.33292	26.38828	155.8077	173.0412	172.6126	-2.1047	1.99E-13	1.43E-12	DLK2	chr6	-	43418090	43424370	2038

ENSG00000(	494.0727	507.0051	493.4608	671.9208	574.3496	596.7465	-0.30232	0.031669	0.06517	ZNF562	chr19	-	9759330	9785776	5706
ENSG00000(	494.0727	426.3179	589.778	288.3941	405.9105	289.3317	0.61659	0.000907	0.00256	ZNF318	chr6	-	43299513	43337181	8006
ENSG00000(	736.448	628.6382	825.953	1172.303	1013.396	927.1764	-0.50602	0.000615	0.001783	ZNF561	chr19	-	9715356	9732075	4693
ENSG00000(	7.250543	2.408575	5.277655	1.498151	0	4.109825	1.1184	0.30587	0.43137	MAP1LC3B	chr12	+	1.17E+08	1.17E+08	832
ENSG00000(	1547.473	1470.435	1537.117	839.7137	1076.905	1158.149	0.56615	4.45E-05	0.000152	WIPF2	chr17	+	38375556	38440388	7474
ENSG00000(	23.82321	18.06432	23.74945	20.22504	12.88605	13.9734	0.45554	0.39134	0.52206	HOPX	chr4	-	57514155	57548065	3203
ENSG00000(	101.5076	125.2459	124.0249	223.2245	236.551	206.3132	-0.92249	1.23E-05	4.51E-05	LRRC8C	chr1	+	90098631	90398809	7218
ENSG00000(	3775.461	3665.852	3375.06	4553.63	3811.509	4012.833	-0.19419	0.08742	0.15698	RSL1D1	chr16	-	11929056	11945442	4134
ENSG00000(	185.4068	205.9332	167.5656	1065.935	849.5587	844.9799	-2.2952	1.95E-44	4.59E-43	LRRC8D	chr1	+	90286573	90402170	3950
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	MROH2B	chr5	-	40998119	41071444	5239
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	OR1L8	chr9	-	1.25E+08	1.25E+08	1061
ENSG00000(	516.8602	513.0266	529.0849	855.4443	775.9242	823.6088	-0.6542	6.39E-07	2.70E-06	PPID	chr4	-	1.6E+08	1.6E+08	1823
ENSG00000(	32.10955	34.92434	36.94359	3.745378	5.522592	7.397684	2.5264	7.02E-06	2.65E-05	COL24A1	chr1	-	86194916	86622626	6825
ENSG00000(	331.4534	283.0076	248.0498	191.0143	181.3251	155.3514	0.70737	0.000287	0.000877	ETFDH	chr4	+	1.6E+08	1.6E+08	3282
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RXFP1	chr4	+	1.59E+08	1.6E+08	3842
ENSG00000(	1.035792	0	2.638828	195.5087	188.6886	193.9837	-6.7711	2.59E-23	3.00E-22	LPAR3	chr1	-	85277285	85358896	3345
ENSG00000(	116.0087	139.6974	101.5949	47.94084	57.06678	44.38611	1.2476	1.07E-05	3.94E-05	PTGER4	chr5	+	40679600	40693837	3848
ENSG00000(	1859.246	1952.15	1670.378	2084.677	1795.763	2593.299	-0.23928	0.093969	0.16657	TBCA	chr5	-	76986991	77164604	2301
ENSG00000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	NEUROD2	chr17	-	37759789	37766030	6242
ENSG00000(	12.4295	14.45145	5.277655	2.996302	6.443024	7.397684	0.86204	0.26963	0.38996	MAP6	chr11	-	75297963	75380165	4329
ENSG00000(	1.035792	0	0	7.490755	0	0	-1.3984	0.30178	0.42683	OTP	chr5	-	76924538	76935513	3668
ENSG00000(	0	0	2.638828	5.992604	10.12475	4.109825	-2.3002	0.041578	0.082797	ECEL1	chr2	-	2.33E+08	2.33E+08	2965
ENSG00000(	2262.17	2101.482	2264.114	2768.583	2721.717	3107.849	-0.37489	0.000761	0.002178	BCL2L1	chr20	-	30252255	30311792	2610
ENSG00000(	6.214751	1.204288	0	0	0.920432	2.465895	0.7665	0.55153	0.67269	FGG	chr4	-	1.56E+08	1.56E+08	2031
ENSG00000(	2.071584	1.204288	0	0	1.840864	3.28786	-0.37712	0.77443	0.85192	FGA	chr4	-	1.56E+08	1.56E+08	3678
ENSG00000(	0	1.204288	0	0	0	3.28786	-0.57455	0.66797	NA	FGB	chr4	+	1.55E+08	1.55E+08	1975
ENSG00000(	1030.613	973.0645	1108.308	1343.842	1098.075	1098.967	-0.18669	0.15999	0.25723	PLRG1	chr4	-	1.55E+08	1.55E+08	3351
ENSG00000(	241.3395	234.8361	201.8703	134.8336	128.8605	120.8288	0.81502	5.76E-05	0.000194	ZNF584	chr19	+	58912871	58929694	2709
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	DSCAM	chr21	-	41382926	42219065	8552
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	NMUR1	chr2	-	2.32E+08	2.32E+08	3298
ENSG00000(	5454.48	5149.534	5363.417	3191.811	3686.33	3065.929	0.68233	8.70E-10	4.79E-09	CLSTN1	chr1	-	9789084	9884584	5221
ENSG00000(	3006.904	2975.795	2786.602	979.7908	820.1049	865.5291	1.7142	6.69E-48	1.73E-46	CXXC5	chr5	+	1.39E+08	1.39E+08	2658
ENSG00000(	287.9501	329.9748	349.6447	428.4712	468.4999	494.8229	-0.52444	0.001005	0.002817	ZNF274	chr19	+	58694396	58724928	4852
ENSG00000(	426.7463	432.3393	410.3377	259.1801	293.6178	243.3016	0.6722	3.09E-05	0.000108	PIK3CD	chr1	+	9711790	9789172	5483
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	PTCRA	chr6	+	42883727	42893573	1080
ENSG00000(	172.9772	143.3102	160.9685	420.2314	411.4331	358.3767	-1.3108	3.89E-13	2.74E-12	SLC25A33	chr1	+	9599541	9642831	1448
ENSG00000(	2133.731	2064.149	2570.218	6358.153	8312.421	7266.992	-1.6929	6.58E-38	1.28E-36	ENC1	chr5	-	73923234	73937249	5517
ENSG00000(	245.4827	213.1589	179.4403	716.1162	754.7542	975.6724	-1.9267	1.08E-27	1.50E-26	SPSB1	chr1	+	9352939	9429591	3120
ENSG00000(	5.17896	2.408575	6.597069	1538.601	1486.498	1455.7	-8.1134	2.19E-90	1.39E-88	P2RY6	chr11	+	72975550	73009662	2398
ENSG00000(	1074.116	1100.719	1263.998	876.4184	1112.802	804.7037	0.29891	0.042787	0.084891	BPTF	chr17	+	65821640	65980494	11292
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	S100Z	chr5	+	76145826	76217475	1468
ENSG00000(	126.3666	119.2245	147.7743	146.8188	202.495	153.7074	-0.35173	0.12596	0.21195	ZIK1	chr19	+	58089824	58105145	4181
ENSG00000(	5.17896	8.430014	10.55531	0.749076	1.840864	1.64393	2.1227	0.030303	0.062715	GPR82	chrX	+	41583408	41589388	3349
ENSG00000(	7.250543	8.430014	10.55531	2.996302	0.920432	3.28786	1.6075	0.075147	0.13784	RP11-443P	chr3	+	1.86E+08	1.86E+08	1789

ENSG00000(	2.071584	7.225726	3.958241	0	0	1.64393	2.1042	0.085017	0.15333	GPR34	chrX	+	41548226	41556526	1924
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	SHANK2-AS	chr11	+	70708895	70711220	1683
ENSG00000(	1211.877	1224.761	939.4226	288.3941	242.0736	281.112	2.0493	2.56E-40	5.34E-39	PLEKHG5	chr1	-	6526152	6580121	5221
ENSG00000(	1060.651	940.5487	1344.483	722.8579	880.8534	587.7049	0.608	0.000381	0.001142	ATF7IP	chr12	+	14518610	14651697	4847
ENSG00000(	8.286335	2.408575	2.638828	2.247227	1.840864	0	1.32	0.24712	0.3639	C20orf201	chr20	-	62714733	62715712	868
ENSG00000(	233.0532	257.7176	193.9538	261.4274	233.7897	232.6161	-0.08679	0.64625	0.75323	RGS19	chr20	-	62704534	62711323	1593
ENSG00000(	545.8623	510.618	414.2959	495.888	388.4223	462.7662	0.12693	0.44227	0.57197	TCEA2	chr20	+	62681189	62703700	2357
ENSG00000(	4.143168	0	1.319414	35.20655	34.05598	41.92021	-3.9147	8.19E-08	3.79E-07	ANO5	chr11	+	22214722	22304903	6651
ENSG00000(	966.3938	932.1187	890.6043	1023.237	889.1373	950.1914	-0.03745	0.76506	0.84495	HDAC3	chr5	-	1.41E+08	1.41E+08	1959
ENSG00000(	0	1.204288	3.958241	0	5.522592	0.821965	-0.20273	0.87461	0.92127	C1orf111	chr1	-	1.62E+08	1.62E+08	1189
ENSG00000(	248.5901	348.0392	319.2981	256.1838	350.6846	244.9455	0.10394	0.60422	0.71921	GPHN	chr14	+	66974125	67648520	4297
ENSG00000(	439.1758	320.3405	440.6842	65.91865	48.7829	50.96182	2.8327	2.02E-37	3.88E-36	VAT1L	chr16	+	77822427	78014004	3825
ENSG00000(	89.0781	74.66584	46.17948	211.2393	226.4263	218.6427	-1.6191	1.23E-10	7.25E-10	TMEM51	chr1	+	15479028	15546976	1942
ENSG00000(	325.2387	319.1362	273.1187	742.3339	641.5411	851.5557	-1.279	1.79E-15	1.45E-14	CAMTA1	chr1	+	6845384	7829766	8444
ENSG00000(	2.071584	0	2.638828	1.498151	0.920432	7.397684	-0.77812	0.51657	0.64303	LGALS4	chr19	-	39292311	39304004	1535
ENSG00000(	30.03797	36.12863	39.58241	86.14369	76.39586	85.48435	-1.2183	0.000197	0.000616	LRRC34	chr3	-	1.7E+08	1.7E+08	3787
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	PAH	chr12	-	1.03E+08	1.03E+08	4122
ENSG00000(	137.7603	160.1703	163.6073	312.3645	302.8221	279.4681	-0.95319	4.06E-07	1.75E-06	SPATA5L1	chr15	+	45694529	45713617	2570
ENSG00000(	1.035792	2.408575	2.638828	110.8632	75.47542	57.53754	-5.0067	2.13E-14	1.62E-13	GATM	chr15	-	45653322	45694525	3911
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	SYCE1	chr10	-	1.35E+08	1.35E+08	2479
ENSG00000(	2.071584	4.817151	3.958241	0	0	0	2.9169	0.026577	0.05594	RASGRP4	chr19	-	38899695	38916945	3313
ENSG00000(	13.46529	13.24716	10.55531	14.23244	15.64734	12.32947	-0.16531	0.78624	0.85964	NHLH1	chr1	+	1.6E+08	1.6E+08	2563
ENSG00000(	52.82539	52.98866	34.30476	78.65293	80.07758	67.40112	-0.67406	0.038224	0.076953	SLFNL1	chr1	-	41481269	41488909	4310
ENSG00000(	34.18113	36.12863	55.41538	69.66403	101.2475	83.84042	-1.0089	0.002589	0.006762	BCL2	chr18	-	60790579	60987361	7461
ENSG00000(	189.5499	166.1917	180.7597	801.5108	547.657	568.7997	-1.8294	1.33E-22	1.49E-21	RHNO1	chr12	+	2985424	2998626	1870
ENSG00000(	509.6096	468.4679	477.6278	2193.293	1910.817	2065.598	-2.0786	4.33E-63	1.63E-61	CTPS1	chr1	+	41445007	41478235	3199
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	UTF1	chr10	+	1.35E+08	1.35E+08	1157
ENSG00000(	0	0	0	2.996302	3.681728	5.753754	-2.8216	0.029083	0.060514	KNDC1	chr10	+	1.35E+08	1.35E+08	6793
ENSG00000(	36.25272	38.53721	43.54065	120.6012	107.6905	103.5676	-1.4743	7.45E-07	3.13E-06	METTL18	chr1	-	1.7E+08	1.7E+08	1521
ENSG00000(	20.71584	3.612863	5.277655	5.243529	5.522592	9.041614	0.53974	0.50746	0.63498	TTC40	chr10	-	1.35E+08	1.35E+08	8278
ENSG00000(	528.2539	553.9724	511.9325	3.745378	0	3.28786	7.502	4.69E-59	1.59E-57	COL8A2	chr1	-	36560837	36590821	4670
ENSG00000(	124.295	125.2459	142.4967	471.9176	463.8977	607.4321	-1.97	5.40E-26	6.95E-25	PWWP2B	chr10	+	1.34E+08	1.34E+08	2651
ENSG00000(	20.71584	14.45145	14.51355	11.98521	6.443024	10.68554	0.72564	0.2457	0.36217	ZNF540	chr19	+	38042308	38104998	3147
ENSG00000(	5.17896	7.225726	5.277655	1.498151	0	0.821965	2.2435	0.043416	0.085969	ANGPTL7	chr1	+	11249398	11256038	2238
ENSG00000(	246.5185	233.6318	203.1897	403.7517	499.7946	383.8576	-0.90654	3.62E-07	1.58E-06	FBXL14	chr12	-	1675159	1703331	2111
ENSG00000(	751.9849	651.5197	666.304	1397.026	1042.849	918.9568	-0.69586	1.72E-05	6.21E-05	EXOSC10	chr1	-	11126675	11159938	3334
ENSG00000(	39.36009	32.51577	85.7619	34.45748	36.81728	21.37109	0.74019	0.090277	0.16118	ZNF570	chr19	+	37958487	37976260	2247
ENSG00000(	2.071584	0	1.319414	3.745378	1.840864	0.821965	-0.61313	0.62875	0.73916	NINJ2	chr12	-	673462	772945	1252
ENSG00000(	510.6454	504.5966	579.2227	207.4939	207.0972	213.7109	1.3381	2.11E-17	1.89E-16	MLLT3	chr9	-	20341663	20622542	6772
ENSG00000(	4.143168	0	0	5.243529	2.761296	0	-0.59276	0.64617	0.75319	FAM90A1	chr12	-	8373856	8380214	2513
ENSG00000(	686.73	602.1439	672.901	6322.947	5349.551	5443.052	-3.1187	1.86E-147	2.77E-145	RRM2	chr2	+	10262455	10271545	3673
ENSG00000(	1002.647	956.2044	911.7149	937.8426	893.7395	878.6805	0.08316	0.49611	0.62471	TRAPPC12	chr2	+	3383446	3488865	3401
ENSG00000(	5734.144	5513.229	4375.176	3889.949	3885.143	5455.381	0.23921	0.1109	0.19077	RPS21	chr20	+	60962172	60963576	1002
ENSG00000(	198.872	169.8046	215.0644	53.18436	41.41944	46.852	2.0228	6.34E-16	5.28E-15	C3AR1	chr12	-	8210898	8219067	2088

ENSG00000(	258.948	289.0291	261.2439	375.2868	364.4911	409.3385	-0.5046	0.001985	0.00529	RNMTL1	chr17	+	685513	695749	1809
ENSG00000(	2316.031	2264.061	2249.6	1339.347	1225.095	1038.964	0.92036	1.65E-13	1.20E-12	PTEN	chr10	+	89622870	89731687	9027
ENSG00000(	13789.5	13752.97	10258.44	12592.71	10056.64	11437.64	0.14887	0.27042	0.39093	RPS7	chr2	+	3622795	3628509	5429
ENSG00000(	374.9567	381.7592	468.3919	688.4004	772.2424	748.81	-0.84994	1.06E-08	5.30E-08	RNASEH1	chr2	-	3592383	3606206	2120
ENSG00000(	2444.469	2437.478	2314.252	2087.674	2221.002	1978.47	0.19485	0.073579	0.13538	PRNP	chr20	+	4666882	4682236	2657
ENSG00000(	3.107376	4.817151	3.958241	0	0	0	3.0739	0.018336	0.040125	KLF17	chr1	+	44584522	44600812	3131
ENSG00000(	54.89697	34.92434	34.30476	37.45378	45.10117	34.52253	0.091816	0.8135	0.8789	ADRA1D	chr20	-	4201329	4229721	2677
ENSG00000(	203.0152	172.2131	186.0373	325.8479	229.1876	282.7559	-0.57537	0.003882	0.009837	FRMD5	chr15	-	44162962	44487450	5011
ENSG00000(	0	0	0	0.749076	1.840864	1.64393	-1.2986	0.33698	NA	AQP4	chr18	-	24432002	24445782	5274
ENSG00000(	9.322127	19.2686	13.19414	0.749076	6.443024	4.109825	1.722	0.031728	0.065267	MIR31HG	chr9	-	21455641	21559668	745
ENSG00000(	304.5228	305.8891	316.6593	1260.694	1877.681	1546.938	-2.3291	1.44E-48	3.85E-47	TLN2	chr15	+	62682725	63136830	11880
ENSG00000(	559.3276	586.4881	573.945	860.6878	675.5971	717.5754	-0.39023	0.006601	0.015961	TVP23B	chr17	+	18684308	18710027	3298
ENSG00000(	0	0	3.958241	4.494453	1.840864	4.93179	-1.1341	0.34794	0.47763	FBXW10	chr17	+	18647326	18682662	3456
ENSG00000(	609.0456	684.0354	799.5648	547.5742	772.2424	618.1176	0.11023	0.50178	0.62986	ZNF217	chr20	-	52183604	52226446	5796
ENSG00000(	63.18331	45.76293	75.20659	83.14739	73.63456	71.51095	-0.3089	0.31783	0.44475	SRGAP2C	chr1	+	1.21E+08	1.21E+08	969
ENSG00000(	1193.232	1110.353	1220.458	17.22874	11.04518	9.863579	6.4549	5.16E-148	7.77E-146	SCG2	chr2	-	2.24E+08	2.24E+08	2576
ENSG00000(	272.4133	321.5448	233.5362	417.2351	383.8201	343.5813	-0.46532	0.008988	0.021125	ATPAF2	chr17	-	17880723	17942523	1737
ENSG00000(	0	3.612863	0	0	1.840864	0.821965	0.23964	0.85959	0.91076	FOXB1	chr15	+	60296421	60353929	1672
ENSG00000(	325.2387	355.2649	296.8681	784.2821	764.879	799.7719	-1.2607	1.24E-18	1.18E-17	PPIH	chr1	+	43124096	43142429	1311
ENSG00000(	87.00652	84.30014	79.16483	65.16957	54.30549	51.78379	0.54117	0.065008	0.12173	LRRC48	chr17	+	17876127	17920203	5805
ENSG00000(	14.50109	28.90291	32.98534	37.45378	23.0108	26.30288	-0.1924	0.68889	0.78751	ZNF57	chr19	+	2900896	2918474	2003
ENSG00000(	14.50109	21.67718	14.51355	24.71949	14.72691	32.8786	-0.49657	0.354	0.48384	C20orf196	chr20	+	5731039	5844558	1154
ENSG00000(	593.5088	631.0468	804.8424	491.3936	570.6678	434.8194	0.43668	0.00794	0.01888	JMJD1C	chr10	-	64926981	65225722	8666
ENSG00000(	6.214751	10.83859	6.597069	0.749076	1.840864	1.64393	2.0994	0.032659	0.066918	LDHAL6B	chr15	+	59499042	59500705	1664
ENSG00000(	180.2278	216.7718	133.2608	56.18067	52.46462	33.70056	1.8771	4.73E-11	2.87E-10	SYNPO	chr5	+	1.5E+08	1.5E+08	7063
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	OR52P2P	chr11	-	4452553	4453507	955
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	ZNF556	chr19	+	2867333	2878515	1643
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	MAL	chr2	+	95691422	95719737	1108
ENSG00000(	95.29286	93.93444	101.5949	110.1141	107.6905	116.719	-0.20144	0.41028	0.54108	ZNF554	chr19	+	2819872	2835771	4029
ENSG00000(	225.8026	223.9975	220.3421	234.4606	233.7897	224.3964	-0.04714	0.79207	0.86418	RAB33B	chr4	+	1.4E+08	1.4E+08	4562
ENSG00000(	1985.613	1928.065	1534.478	3198.553	2677.537	3273.064	-0.74556	2.57E-08	1.25E-07	THOP1	chr19	+	2785458	2813599	2977
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	ANKRD20A	chr9	+	69381812	69425560	4137
ENSG00000(	1576.475	1527.037	1356.357	842.71	910.3072	931.2863	0.73184	2.65E-09	1.40E-08	GAP43	chr3	+	1.15E+08	1.15E+08	1901
ENSG00000(	8.286335	38.53721	6.597069	27.7158	19.32907	21.37109	-0.34108	0.58137	0.69924	EPHX4	chr1	+	92495539	92529093	1437
ENSG00000(	6227.181	6079.244	5871.391	1941.604	2188.787	2135.465	1.5347	2.52E-48	6.63E-47	LAMB2	chr3	-	49158547	49170551	5674
ENSG00000(	945.678	1071.816	1033.101	923.6102	976.5783	1061.979	0.041948	0.73983	0.82574	USP19	chr3	-	49145479	49158371	4719
ENSG00000(	4967.658	4405.284	4294.692	3268.966	3120.264	3217.993	0.50798	2.29E-06	9.15E-06	QARS	chr3	-	49133365	49142553	2763
ENSG00000(	963.2865	843.0014	848.3831	688.4004	686.6423	775.1129	0.30414	0.02185	0.046958	ORMDL3	chr17	-	38077294	38083854	2230
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	SERF1A	chr5	+	70196492	70214357	1889
ENSG00000(	78.72018	98.75159	108.1919	136.3317	151.8713	78.08667	-0.35701	0.21824	0.32961	KLF11	chr2	+	10182976	10194963	4033
ENSG00000(	46.61064	33.72006	40.90183	6.74168	3.681728	1.64393	3.1457	8.63E-08	3.98E-07	LRRC15	chr3	-	1.94E+08	1.94E+08	5883
ENSG00000(	195.7647	179.4389	171.5238	395.5119	314.7877	377.2819	-0.98698	5.93E-08	2.78E-07	SMN1	chr5	+	70220768	70249769	1550
ENSG00000(	226.8384	261.3304	314.0205	206.7449	223.665	184.1201	0.38022	0.051472	0.099602	EIF2AK3	chr2	-	88856259	88927094	4646
ENSG00000(	0	0	0	22.47227	1.840864	0.821965	-3.6863	0.00335	0.008596	TEX37	chr2	+	88824169	88829102	795

ENSG00000(	1643.802	1539.08	1306.22	1385.041	1242.583	1187.739	0.2346	0.072576	0.13375	MOB3A	chr19	-	2071037	2096672	3391
ENSG00000(	268.2701	293.8462	311.3817	253.9366	231.0284	253.1652	0.23959	0.16603	0.26473	KRCC1	chr2	-	88326724	88355248	1753
ENSG00000(	229.9458	216.7718	254.6469	414.2388	296.3791	335.3617	-0.5765	0.001998	0.005325	NME6	chr3	-	48334754	48343175	2004
ENSG00000(	1596.155	1653.487	1688.85	4191.078	4074.752	5036.179	-1.427	3.58E-33	6.06E-32	CYCS	chr7	-	25159710	25164980	4098
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	CD8B	chr2	-	87042462	87089047	1417
ENSG00000(	40.39588	28.90291	26.38828	244.9477	288.0952	209.6011	-2.9116	2.04E-26	2.67E-25	SLFN12	chr17	-	33738079	33760302	2539
ENSG00000(	13.46529	3.612863	10.55531	673.4189	555.9409	636.2008	-5.9604	7.07E-73	3.24E-71	CALB2	chr16	+	71392616	71424341	1466
ENSG00000(	2.071584	0	1.319414	2.996302	3.681728	0.821965	-0.77774	0.53331	0.65794	SLC9C1	chr3	-	1.12E+08	1.12E+08	4172
ENSG00000(	5.17896	0	0	0	0	0	1.5469	0.24589	NA	CCL11	chr17	+	32612687	32615353	1079
ENSG00000(	10.35792	8.430014	7.916483	8.239831	24.85166	12.32947	-0.70147	0.30193	0.42698	FRMD3	chr9	-	85857905	86153461	5297
ENSG00000(	913.5685	1116.375	1059.489	468.1722	525.5667	450.4368	1.0942	5.82E-15	4.58E-14	SNTB1	chr8	-	1.22E+08	1.22E+08	5164
ENSG00000(	52.82539	69.84869	134.5802	170.7892	194.2112	149.5976	-0.99748	0.000885	0.002502	MTBP	chr8	+	1.21E+08	1.22E+08	3375
ENSG00000(	135.6887	143.3102	146.4549	281.6524	162.9165	250.6993	-0.7067	0.002362	0.006217	TEFM	chr17	-	29224354	29233838	2109
ENSG00000(	413.281	426.3179	358.8805	783.533	625.8938	736.4806	-0.83736	3.77E-08	1.80E-07	MRPL13	chr8	-	1.21E+08	1.21E+08	2368
ENSG00000(	379.0998	366.1035	514.5714	2399.289	2329.613	1934.083	-2.398	1.17E-55	3.68E-54	MALT1	chr18	+	56338618	56417371	5030
ENSG00000(	35.21692	24.08575	19.79121	34.45748	53.38506	40.27628	-0.66481	0.11879	0.20212	ISG20	chr15	+	89179384	89199714	5634
ENSG00000(	69.39806	36.12863	27.70769	369.2942	301.9017	306.5929	-2.825	2.99E-25	3.72E-24	MBOAT1	chr6	-	20100935	20212670	3219
ENSG00000(	725.0543	661.154	741.5105	1492.158	1347.512	1332.405	-0.96974	8.44E-15	6.58E-14	ID4	chr6	+	19837617	19840915	2344
ENSG00000(	0	0	2.638828	0	0	2.465895	0.027772	0.98358	NA	GPR22	chr7	+	1.07E+08	1.07E+08	2936
ENSG00000(	6.214751	3.612863	9.235896	29.96302	28.53339	10.68554	-1.7458	0.009076	0.021314	CXCR6	chr3	+	45982425	45989845	2805
ENSG00000(	996.4318	953.7959	894.5625	661.4337	440.8869	553.1824	0.7772	8.36E-07	3.49E-06	CEBPB	chr20	+	48807376	48809212	1837
ENSG00000(	4.143168	2.408575	0	0	0.920432	0	1.5525	0.24889	0.36605	AZU1	chr19	+	825097	832017	1713
ENSG00000(	1659.339	1604.111	1665.1	1877.183	1746.059	1620.915	-0.08955	0.43339	0.56314	PAIP1	chr5	-	43526369	43557860	2782
ENSG00000(	0	0	2.638828	22.47227	21.16994	24.65895	-4.0996	7.67E-06	2.89E-05	CLEC7A	chr12	-	10269376	10282857	3725
ENSG00000(	29.00217	33.72006	43.54065	136.3317	104.9292	135.6242	-1.8135	3.34E-09	1.75E-08	C5orf34	chr5	-	43486803	43515247	2507
ENSG00000(	18.64425	9.634302	1.319414	70.4131	37.73771	23.83698	-2.0146	0.000837	0.002375	C1QTNF4	chr11	-	47611216	47616211	1664
ENSG00000(	47.64643	34.92434	40.90183	43.44638	38.65814	47.67397	-0.06869	0.85237	0.9059	SERHL	chr22	+	42896585	42908566	1712
ENSG00000(	451.6053	533.4995	587.1391	35.95563	23.93123	22.19305	4.215	1.06E-72	4.86E-71	NEGR1	chr1	-	71868625	72748417	5809
ENSG00000(	529.2897	567.2195	576.5838	495.1389	530.1688	435.6414	0.19483	0.18203	0.2854	ZNF131	chr5	+	43065278	43192123	3340
ENSG00000(	10.35792	18.06432	10.55531	9.737982	9.20432	6.575719	0.56861	0.40112	0.53229	MACROD2	chr20	+	13976015	16033842	4994
ENSG00000(	919.7832	899.6029	763.9406	941.588	751.9929	768.5372	0.069282	0.63002	0.74012	DPAGT1	chr11	-	1.19E+08	1.19E+08	3274
ENSG00000(	11706.52	10926.5	9981.365	8236.835	6954.784	7971.416	0.49284	1.28E-05	4.70E-05	BSG	chr19	+	571297	583493	2143
ENSG00000(	317.9881	296.2548	317.9787	385.7739	374.6158	355.0888	-0.25808	0.10168	0.1779	HINFP	chr11	+	1.19E+08	1.19E+08	3486
ENSG00000(	353.205	337.2006	497.419	191.0143	257.721	183.2982	0.90519	1.02E-05	3.79E-05	CERS6	chr2	+	1.69E+08	1.7E+08	7214
ENSG00000(	107.7224	87.913	77.84541	131.0882	134.3831	113.4312	-0.46102	0.068034	0.12664	SPTLC3	chr20	+	12989627	13147411	3830
ENSG00000(	854.5283	727.3898	759.9823	665.9282	555.9409	641.9546	0.3285	0.019296	0.042018	COPRS	chr17	-	30178883	30186356	1062
ENSG00000(	625.6183	505.8008	645.1933	495.888	482.3064	446.327	0.31753	0.0354	0.071864	TP53RK	chr20	-	45313004	45318418	3515
ENSG00000(	4.143168	10.83859	22.43003	11.23613	11.96562	8.219649	0.21665	0.75914	0.84083	B3GALT1	chr2	+	1.69E+08	1.69E+08	2168
ENSG00000(	286.9144	268.5562	233.5362	230.7153	203.4155	198.0935	0.31917	0.085282	0.15374	BPGM	chr7	+	1.34E+08	1.34E+08	2051
ENSG00000(	428.8178	526.2737	294.2293	900.3888	802.6167	1121.16	-1.1694	1.26E-09	6.85E-09	POP7	chr7	+	1E+08	1E+08	927
ENSG00000(	95.29286	78.2787	108.1919	101.1252	74.55499	79.7306	0.13627	0.62227	0.7343	ALG14	chr1	-	95448297	95538501	1033
ENSG00000(	770.6292	799.647	717.7611	406.748	435.3643	406.0507	0.87301	1.55E-10	9.07E-10	SUCLG2	chr3	-	67410884	67705038	2352
ENSG00000(	32.10955	42.15007	26.38828	18.72689	9.20432	13.9734	1.2116	0.015492	0.034471	STARD5	chr15	-	81601394	81616524	4871
ENSG00000(	560.3634	564.8109	415.6153	5.992604	18.40864	15.61733	5.2378	8.43E-74	3.92E-72	CSDC2	chr22	+	41956767	41973745	2777

ENSG00000(	1062.722	1110.353	1113.585	81.64923	82.83888	70.68898	3.7922	4.12E-127	4.75E-125	RCAN2	chr6	-	46188475	46459709	3327
ENSG00000(	1.035792	8.430014	1.319414	3.745378	5.522592	1.64393	-0.01378	0.98966	0.99397	IL16	chr15	+	81451916	81605104	8321
ENSG00000(	1.035792	9.634302	3.958241	4.494453	0	4.109825	0.59317	0.5835	0.70104	ABCG4	chr11	+	1.19E+08	1.19E+08	3849
ENSG00000(	6418.802	6011.804	5071.827	6073.505	4736.543	5419.215	0.10877	0.39832	0.52942	GNB2	chr7	+	1E+08	1E+08	1878
ENSG00000(	13.46529	28.90291	9.235896	23.22134	18.40864	26.30288	-0.37963	0.49413	0.62286	CCDC11	chr18	-	47753563	47792892	1851
ENSG00000(	195.7647	202.3203	112.1502	220.9773	151.8713	229.3282	-0.23484	0.3501	0.47987	FAM195A	chr16	+	691813	698474	1728
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	PDZD3	chr11	+	1.19E+08	1.19E+08	2996
ENSG00000(	109.7939	113.203	114.789	167.7929	119.6562	153.7074	-0.38527	0.1032	0.17999	C2CD2L	chr11	+	1.19E+08	1.19E+08	5931
ENSG00000(	377.0283	357.6735	387.9077	43.44638	41.41944	44.38611	3.0983	6.20E-49	1.67E-47	ARNT2	chr15	+	80696692	80890278	6690
ENSG00000(	2913.683	3105.858	3856.646	1499.649	1573.939	1230.481	1.1948	1.33E-17	1.21E-16	GNG12	chr1	-	68167149	68299150	4404
ENSG00000(	20.71584	14.45145	14.51355	17.97781	19.32907	11.50751	0.03138	0.95586	0.97381	PRSS27	chr16	-	2762419	2770552	3579
ENSG00000(	0	2.408575	1.319414	8.239831	12.88605	9.863579	-2.5783	0.009166	0.021502	MYOZ2	chr4	+	1.2E+08	1.2E+08	2597
ENSG00000(	87.00652	89.11729	125.3443	286.8959	445.4891	354.2669	-1.8409	6.00E-16	5.00E-15	SYNPO2	chr4	+	1.2E+08	1.2E+08	7295
ENSG00000(	14.50109	3.612863	1.319414	2.247227	4.60216	9.863579	0.212	0.82082	0.88422	DNAJB7	chr22	-	41255553	41258130	2578
ENSG00000(	229.9458	207.1375	241.4527	443.4527	368.1728	423.3119	-0.8619	4.36E-07	1.88E-06	CLP1	chr11	+	57416465	57429340	2435
ENSG00000(	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	EFCAB3	chr17	+	60447579	60493837	1691
ENSG00000(	1.035792	0	2.638828	0	5.522592	0	-0.34175	0.79785	0.8683	TTC36	chr11	+	1.18E+08	1.18E+08	1009
ENSG00000(	35.21692	63.82725	42.22124	10.48706	5.522592	13.9734	2.1469	1.55E-05	5.61E-05	RSPH9	chr6	+	43612783	43640336	2586
ENSG00000(	712.6248	785.1956	593.7362	685.4041	538.4527	881.1464	-0.00923	0.95899	0.97594	MYEOV2	chr2	-	2.41E+08	2.41E+08	922
ENSG00000(	754.0565	722.5726	704.567	785.7803	811.821	858.1314	-0.17001	0.18008	0.28294	GTPBP2	chr6	-	43573053	43596899	2933
ENSG00000(	216.4805	180.6432	187.3568	82.39831	70.87326	87.12828	1.2722	2.49E-08	1.21E-07	FGGY	chr1	+	59762310	60233347	2485
ENSG00000(	718.8396	791.217	641.2351	57.67882	36.81728	67.40112	3.7029	5.80E-74	2.70E-72	IL17D	chr13	+	21276266	21297237	1861
ENSG00000(	0	0	0	10.48706	20.2495	9.041614	-4.5711	6.56E-05	0.000219	FUT9	chr6	+	96463860	96653420	2715
ENSG00000(	306.5944	280.599	304.7846	161.0512	104.0088	112.6092	1.2282	6.87E-09	3.50E-08	TCEAL1	chrX	+	1.03E+08	1.03E+08	1201
ENSG00000(	978.8233	1081.45	1347.121	1140.093	1316.218	1063.623	-0.04756	0.74685	0.83164	ZNF24	chr18	-	32912176	32925446	7419
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	HSFY1	chrY	+	20708557	20750849	1476
ENSG00000(	182.2994	236.0404	226.9392	313.1136	313.8673	258.9189	-0.45753	0.015501	0.034481	MANEA	chr6	+	96025419	96057333	4575
ENSG00000(	20.71584	38.53721	32.98534	38.95193	24.85166	27.94681	-0.00287	0.99487	0.99678	RAB40A	chrX	-	1.03E+08	1.03E+08	3126
ENSG00000(	0	0	0	11.23613	6.443024	16.4393	-4.3489	0.000185	0.00058	C2orf54	chr2	-	2.42E+08	2.42E+08	2017
ENSG00000(	1508.113	1386.135	1917.108	497.3862	694.0057	560.5801	1.4531	1.14E-19	1.13E-18	AFF1	chr4	+	87856154	88062206	9390
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	ACOT12	chr5	-	80625824	80689998	2086
ENSG00000(	1344.458	1148.89	994.838	1143.838	880.8534	955.1232	0.22698	0.12958	0.21663	FIBP	chr11	-	65651212	65656010	1378
ENSG00000(	31.07376	45.76293	36.94359	2.996302	5.522592	0.821965	3.4176	5.70E-08	2.68E-07	CARNS1	chr11	+	67182439	67193078	5065
ENSG00000(	489.9296	414.275	419.5736	548.3233	467.5795	484.1373	-0.17903	0.24152	0.357	BANP	chr16	+	87982850	88110924	2438
ENSG00000(	2323.281	1985.87	2062.244	3659.234	3267.534	3630.619	-0.72697	2.23E-10	1.29E-09	PPP1CA	chr11	-	67165654	67188654	1677
ENSG00000(	2711.703	2294.168	2592.648	3406.047	5516.149	4871.786	-0.85707	3.82E-08	1.83E-07	HCFC1	chrX	-	1.53E+08	1.53E+08	8869
ENSG00000(	2.071584	1.204288	15.83297	7.490755	2.761296	1.64393	0.5449	0.5868	0.70401	CTSW	chr11	+	65647280	65651212	1341
ENSG00000(	4.143168	4.817151	1.319414	804.5071	702.2896	755.3858	-7.5	2.31E-60	8.10E-59	NIPAL4	chr5	+	1.57E+08	1.57E+08	3274
ENSG00000(	0	0	0	3.745378	0	1.64393	-1.4934	0.26982	NA	SNTG2	chr2	+	946554	1371385	1888
ENSG00000(	5.17896	2.408575	0	0	0.920432	1.64393	1.0408	0.41991	0.55063	FNDC9	chr5	-	1.57E+08	1.57E+08	2125
ENSG00000(	71.46964	63.82725	98.95603	173.0365	297.2995	176.7225	-1.4527	1.27E-07	5.77E-07	PDE3A	chr12	+	20522179	20837315	7576
ENSG00000(	4.143168	12.04288	9.235896	57.67882	25.7721	32.05663	-2.1035	0.000217	0.000674	RASGRP1	chr15	-	38780304	38857776	5023
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	KLHL6	chr3	-	1.83E+08	1.83E+08	6298
ENSG00000(	406.0304	435.9522	440.6842	511.6186	606.5647	608.254	-0.42745	0.003917	0.009919	CHCHD1	chr10	+	75541805	75543410	1202

ENSG00000(	745.7702	735.8198	775.8153	1307.886	1075.065	1620.915	-0.82465	7.49E-08	3.48E-07	MRPL52	chr14	+	23299088	23304246	2020
ENSG00000(	113.9371	113.203	110.8308	78.65293	94.8045	65.75719	0.49644	0.059098	0.11225	SMPDL3A	chr6	+	1.23E+08	1.23E+08	1851
ENSG00000(	0	1.204288	0	6.74168	17.48821	14.79537	-3.8211	0.000416	0.001239	RND1	chr12	-	49250928	49259681	2136
ENSG00000(	178.1562	136.0845	122.7055	288.3941	201.5746	286.0438	-0.81987	0.000259	0.000795	RAD9A	chr11	+	67159176	67165881	2119
ENSG00000(	6029.345	5903.418	4902.942	137.0808	91.12277	90.41614	5.6968	6.96E-280	4.42E-277	EFEMP2	chr11	-	65633912	65641063	2277
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	OR10AD1	chr12	-	48596081	48597170	1090
ENSG00000(	4.143168	7.225726	0	0	0.920432	6.575719	0.45326	0.70279	0.79808	AGAP5	chr10	-	75434033	75457639	2430
ENSG00000(	5.17896	12.04288	6.597069	0	5.522592	1.64393	1.4805	0.13612	0.22552	C17orf66	chr17	-	34181955	34195895	2608
ENSG00000(	4442.511	4461.886	4447.744	2269.699	4710.771	5724.986	0.070277	0.85125	0.90519	TAF15	chr17	+	34136459	34191619	2191
ENSG00000(	470.2495	463.6508	548.8761	189.5161	312.9469	216.1768	1.042	9.54E-08	4.38E-07	FAM21C	chr10	+	46222648	46288409	4636
ENSG00000(	457.82	449.1993	358.8805	292.8885	313.8673	280.29	0.51346	0.002024	0.005389	TMEM134	chr11	-	67231824	67236743	1866
ENSG00000(	3972.262	4016.3	5418.832	1266.687	1560.132	1183.629	1.7361	1.10E-31	1.77E-30	ZMAT3	chr3	-	1.79E+08	1.79E+08	9406
ENSG00000(	52.82539	48.17151	64.65128	70.4131	38.65814	74.79881	-0.15447	0.65997	0.76442	ZFAND4	chr10	-	46111043	46168228	3265
ENSG00000(	136.7245	130.0631	142.4967	662.1828	527.4075	617.2957	-2.135	9.97E-35	1.77E-33	ZNF738	chr19	+	21541732	21562104	2442
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	MS4A10	chr11	+	60552821	60568778	2296
ENSG00000(	200.9436	244.4704	266.5216	29.21395	24.85166	39.45432	2.8948	7.51E-28	1.04E-26	SLFN11	chr17	-	33677324	33700720	5030
ENSG00000(	1.035792	2.408575	1.319414	0	0.920432	0	1.2549	0.35362	NA	FAM71D	chr14	+	67656110	67695267	2136
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	CCL19	chr9	-	34689564	34691274	687
ENSG00000(	2208.308	1842.56	1861.693	2874.203	2417.975	2644.261	-0.42349	0.000603	0.00175	CORO1B	chr11	-	67205519	67211292	1954
ENSG00000(	114.9729	136.0845	117.4278	223.2245	201.5746	207.9571	-0.7768	0.000192	0.000601	FUT10	chr8	-	33228342	33330940	3825
ENSG00000(	188.5141	160.1703	188.6762	355.0618	242.0736	283.5779	-0.71038	0.000473	0.001396	LRRC20	chr10	-	72058729	72142382	3414
ENSG00000(	623.5467	616.5953	489.5025	723.607	731.7434	887.7221	-0.43508	0.004333	0.010866	MUS81	chr11	+	65624597	65635124	3420
ENSG00000(	104.615	56.60152	88.40072	6.74168	9.20432	4.93179	3.4876	1.50E-14	1.15E-13	PURG	chr8	-	30853321	30891231	2875
ENSG00000(	12.4295	7.225726	6.597069	20.22504	16.56778	24.65895	-1.1473	0.062024	0.1169	TMEM217	chr6	-	37179956	37225931	1546
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-344H	chr1	+	27306656	27307466	497
ENSG00000(	74.57702	90.32158	108.1919	68.91495	70.87326	62.46933	0.42418	0.13726	0.2272	ZNF596	chr8	+	182137	197342	2868
ENSG00000(	0	0	0	7.490755	9.20432	9.863579	-3.992	0.000778	0.00222	COL6A5	chr3	+	1.3E+08	1.3E+08	9226
ENSG00000(	17214.86	16854.01	15611.3	18714.15	16852.19	20686.39	-0.17894	0.10563	0.18346	CFL1	chr11	-	65590493	65629497	1752
ENSG00000(	296.2365	290.2333	288.9516	352.8146	421.5579	353.4449	-0.36272	0.027431	0.057505	TMCC1	chr3	-	1.29E+08	1.3E+08	5992
ENSG00000(	203.0152	189.0732	224.3003	304.8737	278.8909	194.8057	-0.33615	0.10924	0.18848	NAA16	chr13	+	41885341	41951166	4347
ENSG00000(	8.286335	6.021439	10.55531	10.48706	11.96562	13.15144	-0.48449	0.48391	0.6131	EFCAB12	chr3	-	1.29E+08	1.29E+08	5607
ENSG00000(	1004.718	934.5273	854.9801	1313.129	1176.312	1259.25	-0.42236	0.000739	0.002118	FAM192A	chr16	-	57186378	57220028	2848
ENSG00000(	76.6486	51.78437	47.4989	35.20655	44.18074	60.00344	0.33716	0.35218	0.48188	RAB43	chr3	-	1.29E+08	1.29E+08	4467
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	FADS6	chr17	-	72873428	72889708	2100
ENSG00000(	121.1877	166.1917	143.8161	331.8405	326.7534	380.5698	-1.2656	6.89E-11	4.13E-10	CBWD1	chr9	-	121041	188979	3652
ENSG00000(	60.07593	55.39724	48.81831	16.47966	21.16994	13.9734	1.6381	6.44E-05	0.000215	HOXC5	chr12	+	54379629	54429145	1805
ENSG00000(	0	0	0	6.74168	6.443024	13.9734	-4.0073	0.000766	0.002192	RAB37	chr17	+	72666717	72743474	3804
ENSG00000(	632.8689	611.7782	655.7486	1468.188	1530.678	1445.836	-1.2235	1.66E-24	2.01E-23	DCP2	chr5	+	1.12E+08	1.12E+08	8947
ENSG00000(	126.3666	150.536	127.9831	6.74168	9.20432	17.26126	3.544	6.06E-22	6.63E-21	SNX32	chr11	+	65601112	65624367	2416
ENSG00000(	5610.885	6707.883	5614.106	3364.098	3780.214	5345.238	0.52018	0.00083	0.002358	RPL38	chr17	+	72199721	72206794	2450
ENSG00000(	33.14534	40.94578	60.69303	17.97781	7.363456	1.64393	2.1894	0.000166	0.000525	CYP7B1	chr8	-	65500320	65711318	2202
ENSG00000(	0	0	0	103.3724	120.5766	117.541	-7.5183	5.15E-14	3.84E-13	OVOL1	chr11	+	65554493	65564690	3034
ENSG00000(	1017.148	963.4302	927.5479	728.1014	817.3436	766.0713	0.33165	0.008427	0.019918	RARG	chr12	-	53604354	53626764	2959
ENSG00000(	12.4295	13.24716	11.87472	14.23244	9.20432	17.26126	-0.11306	0.85575	0.90842	CES4A	chr16	+	67022492	67043661	3419

ENSG00000(	3.107376	9.634302	1.319414	0	1.840864	4.109825	0.97495	0.38591	0.51677	CES3	chr16	+	66995140	67009051	3834
ENSG00000(	241.3395	216.7718	188.6762	232.9625	262.3231	268.7825	-0.23569	0.20939	0.31902	SSH3	chr11	+	67070919	67080078	2990
ENSG00000(	1017.148	957.4087	874.7713	489.1463	527.4075	581.9512	0.83288	1.24E-09	6.75E-09	CES2	chr16	+	66968347	66978999	3927
ENSG00000(	199.9078	142.106	219.0227	110.8632	192.3703	198.0935	0.16288	0.52423	0.64933	PDP2	chr16	+	66912492	66929657	4002
ENSG00000(	1297.847	1245.234	1534.478	1243.465	1469.009	1218.152	0.052658	0.69379	0.79119	SP3	chr2	-	1.75E+08	1.75E+08	6359
ENSG00000(	292.0933	320.3405	505.3355	237.4569	294.5382	190.6959	0.62331	0.005792	0.014167	DMXL1	chr5	+	1.18E+08	1.19E+08	11072
ENSG00000(	178.1562	202.3203	180.7597	164.7966	140.8261	126.5826	0.37293	0.078511	0.14304	METAP1D	chr2	+	1.73E+08	1.73E+08	3419
ENSG00000(	833.8125	836.98	839.1472	590.2715	656.268	518.6599	0.50711	0.000242	0.000745	ZNF621	chr3	+	40566369	40616176	6378
ENSG00000(	321.0955	272.169	269.1604	179.7781	165.6778	184.9421	0.69911	0.000156	0.000495	EGFL7	chr9	+	1.4E+08	1.4E+08	2125
ENSG00000(	1730.808	1654.691	1344.483	1349.834	1195.641	1232.947	0.32378	0.013917	0.031355	NADSYN1	chr11	+	71164155	71235153	3616
ENSG00000(	2544.941	2463.973	2756.255	2306.404	1961.441	2033.541	0.30028	0.009585	0.022389	DHCR7	chr11	-	71139239	71163914	2666
ENSG00000(	0	2.408575	0	0	1.840864	0	0.16879	0.89944	NA	AP002387.	chr11	-	71093647	71134469	2162
ENSG00000(	4.143168	10.83859	5.277655	1.498151	0.920432	2.465895	1.7006	0.090711	0.1618	AQPEP	chr5	+	1.15E+08	1.15E+08	4581
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	COX6B1P3	chr22	+	40965290	40965899	260
ENSG00000(	118.0803	110.7945	120.0667	71.16218	85.60018	65.75719	0.64526	0.01298	0.029403	NBEA	chr13	+	35516424	36247159	11119
ENSG00000(	751.9849	657.5411	540.9597	610.4966	501.6354	634.5569	0.15965	0.323	0.45032	RNASEH2C	chr11	-	65482367	65488418	2794
ENSG00000(	4.143168	9.634302	1.319414	44.19546	38.65814	39.45432	-2.853	1.62E-06	6.57E-06	MYEOV	chr11	+	69061605	69182494	2468
ENSG00000(	629.7615	605.7567	526.4461	676.4152	520.0441	665.7916	-0.07951	0.60672	0.7212	ANKRD13D	chr11	+	67056018	67069956	2881
ENSG00000(	1066.866	955.0002	818.0365	86.14369	68.11197	55.89361	3.7349	1.41E-88	8.58E-87	MRGPRF	chr11	-	68771863	68780877	2295
ENSG00000(	642.191	661.154	696.6505	946.8315	805.378	813.7453	-0.35983	0.007283	0.017473	MYD88	chr3	+	38179969	38184513	3314
ENSG00000(	1378.639	1582.434	1617.601	1594.033	1892.408	1573.241	-0.14402	0.25808	0.37673	OXSR1	chr3	+	38206580	38296979	4553
ENSG00000(	25.8948	18.06432	7.916483	5.243529	2.761296	0	2.4054	0.00365	0.009291	SLC22A13	chr3	+	38307303	38319806	2555
ENSG00000(	477.5001	423.9093	455.1978	596.2641	602.883	505.5084	-0.3278	0.027126	0.056937	PHF8	chrX	-	53963109	54075391	6062
ENSG00000(	220.6237	209.5461	200.5509	260.6783	348.8437	285.2218	-0.49918	0.007803	0.018598	LCLAT1	chr2	+	30670092	30867091	5060
ENSG00000(	16.57267	16.86003	3.958241	8.988907	10.12475	4.93179	0.59899	0.4134	0.54386	ADH6	chr4	-	1E+08	1E+08	3337
ENSG00000(	275.5206	240.8575	230.8974	375.2868	253.1188	370.7062	-0.41681	0.033824	0.069034	AC068491.	chr2	-	1.12E+08	1.12E+08	1587
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	XKR3	chr22	-	17264302	17302589	1690
ENSG00000(	3.107376	3.612863	6.597069	0.749076	0	0	2.6593	0.033445	0.068332	FRG2C	chr3	+	75713481	75716371	2078
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	UNC93B3	chr3	-	75668657	75673000	687
ENSG00000(	16.57267	28.90291	27.70769	27.7158	18.40864	38.63235	-0.21496	0.65804	0.76278	AC007318.	chr2	+	65432137	65433396	1260
ENSG00000(	291.0575	296.2548	201.8703	222.4754	256.8005	249.8773	0.11716	0.55247	0.67341	KAT5	chr11	+	65479467	65487075	2296
ENSG00000(	620.4394	534.7037	539.6402	88.39091	113.2131	85.48435	2.555	1.30E-44	3.06E-43	SH3RF3	chr2	+	1.1E+08	1.1E+08	3128
ENSG00000(	1073.08	1063.386	1018.587	216.4828	228.2671	196.4496	2.2937	1.99E-60	7.00E-59	GXYLT2	chr3	+	72937224	73047289	3260
ENSG00000(	0	0	0	4.494453	0	2.465895	-1.83	0.17727	0.27944	HPSE2	chr10	-	1E+08	1.01E+08	2295
ENSG00000(	550.0055	576.8538	559.4314	638.2124	532.9301	511.2622	0.002307	0.98743	0.99245	DCAKD	chr17	-	43100708	43138473	2045
ENSG00000(	0	1.204288	0	0.749076	4.60216	4.93179	-1.93	0.13446	0.2235	ARPP21	chr3	+	35680437	35835988	3433
ENSG00000(	311.7734	388.9849	343.0476	353.5637	360.8093	337.8276	-0.01249	0.93882	0.9628	TADA2B	chr4	+	7043626	7058368	3818
ENSG00000(	45.57484	46.96722	48.81831	35.20655	42.33987	41.92021	0.23932	0.50478	0.63251	CCDC96	chr4	-	7042579	7044728	2150
ENSG00000(	1083.438	1157.32	996.1574	1569.313	1299.65	1371.859	-0.38897	0.002432	0.006381	ADRBK1	chr11	+	67033881	67054027	4493
ENSG00000(	1879.962	1726.949	1731.071	1564.819	1221.413	1278.977	0.39174	0.002455	0.006437	RELA	chr11	-	65421067	65430565	3183
ENSG00000(	222.6953	199.9118	212.4256	116.8558	135.3035	147.9537	0.66438	0.001291	0.00356	EVC2	chr4	-	5544499	5711275	4828
ENSG00000(	70.43385	62.62296	94.99779	179.0291	189.609	122.4728	-1.0993	4.80E-05	0.000164	ZNF680	chr7	-	63980262	64023484	3022
ENSG00000(	1086.546	1057.365	1361.635	548.3233	775.0037	535.9211	0.9121	4.09E-08	1.95E-07	HECTD4	chr12	-	1.13E+08	1.13E+08	15405
ENSG00000(	458.8558	452.8122	428.8095	978.2927	980.2601	909.9152	-1.0942	8.18E-17	7.10E-16	FAM222B	chr17	-	27082996	27182250	4197

ENSG00000(	1796.063	1837.743	2397.375	299.6302	380.1384	353.4449	2.5383	3.65E-63	1.38E-61	BNC2	chr9	-	16409501	16870841	12844
ENSG00000(	1.035792	4.817151	1.319414	0.749076	2.761296	4.93179	-0.1801	0.87517	0.9217	1-Dec	chr9	+	1.18E+08	1.18E+08	2656
ENSG00000(	5.17896	13.24716	5.277655	0	0	0	4.1503	0.000647	0.001869	RXFP4	chr1	+	1.56E+08	1.56E+08	1146
ENSG00000(	45.57484	34.92434	18.47179	481.6556	375.5363	412.6264	-3.6242	3.01E-45	7.24E-44	HPSE	chr4	-	84213614	84256306	4652
ENSG00000(	189.5499	150.536	117.4278	506.3751	449.1708	496.4668	-1.6512	8.31E-18	7.59E-17	COQ2	chr4	-	84182689	84206067	1641
ENSG00000(	0	0	0	5.243529	4.60216	9.863579	-3.5235	0.004262	0.010712	C10orf131	chr10	+	97667360	97698480	1241
ENSG00000(	1.035792	2.408575	2.638828	0.749076	6.443024	6.575719	-0.94134	0.38931	0.51988	HSPA6	chr1	+	1.61E+08	1.61E+08	2646
ENSG00000(	1768.097	1759.464	1680.933	1488.413	1505.827	2220.127	-0.00155	0.9919	0.99508	TRMT112	chr11	-	64083932	64085556	1106
ENSG00000(	129.474	113.203	142.4967	23.22134	8.283888	7.397684	3.2149	7.83E-17	6.80E-16	LRRN3	chr7	+	1.11E+08	1.11E+08	3725
ENSG00000(	1934.859	2020.795	2085.993	1361.07	1857.432	1593.79	0.32786	0.013174	0.029787	KDM2A	chr11	+	66886740	67025141	6511
ENSG00000(	0	0	0	5.243529	4.60216	0.821965	-2.5476	0.053447	0.10297	C10orf129	chr10	+	96953957	96988685	2307
ENSG00000(	135.6887	143.3102	104.2337	229.9662	204.3359	263.8507	-0.85735	7.64E-05	0.000253	ADCK5	chr8	+	1.46E+08	1.46E+08	2027
ENSG00000(	534.4686	533.4995	456.5172	1246.462	893.7395	1059.513	-1.0659	4.27E-12	2.80E-11	MRP63	chr13	+	21750784	21753223	2246
ENSG00000(	401.8873	327.5663	399.7824	633.7179	564.2248	478.3836	-0.56796	0.000576	0.001676	NOC3L	chr10	-	96075004	96122716	3455
ENSG00000(	1077.224	1062.182	964.4915	656.1902	761.1973	1074.308	0.31625	0.061144	0.11545	ESRRA	chr11	+	64073044	64084215	2283
ENSG00000(	258.948	273.3733	270.4798	328.0951	234.7102	234.26	0.007886	0.96725	0.98074	RHOD	chr11	+	66824289	66839484	1129
ENSG00000(	8.286335	0	1.319414	19.47596	31.29469	24.65895	-2.6515	0.000436	0.001292	ADAMTS20	chr12	-	43747669	43945724	6076
ENSG00000(	368.7419	398.6192	354.9223	361.0544	367.2524	406.8726	-0.01616	0.91741	0.94983	COMMD1	chr2	+	62115859	62374382	911
ENSG00000(	786.1661	768.3356	932.8255	445.7	722.5391	526.8795	0.55191	0.001671	0.00451	RAPH1	chr2	-	2.04E+08	2.04E+08	9808
ENSG00000(	304.5228	296.2548	291.5904	315.3608	358.9685	432.3535	-0.30831	0.077092	0.1408	MTX1	chr1	+	1.55E+08	1.55E+08	2579
ENSG00000(	73.54123	42.15007	51.45714	23.22134	38.65814	18.08323	1.0492	0.011653	0.026671	ADCY5	chr3	-	1.23E+08	1.23E+08	7311
ENSG00000(	327.3102	219.1804	310.0622	135.5827	132.5422	146.3098	1.0417	6.21E-07	2.63E-06	PARP14	chr3	+	1.22E+08	1.22E+08	8437
ENSG00000(	1.035792	0	2.638828	0	0	3.28786	0.078828	0.95347	0.97227	CYSLTR1	chrX	-	77526961	77583048	3034
ENSG00000(	1.035792	0	0	1.498151	4.60216	4.109825	-1.9921	0.12178	0.20637	PARP15	chr3	+	1.22E+08	1.22E+08	4439
ENSG00000(	415.3526	385.3721	409.0183	2353.595	1978.008	2511.925	-2.4939	9.44E-77	4.77E-75	CKS1B	chr1	+	1.55E+08	1.55E+08	1166
ENSG00000(	0	0	0	1.498151	1.840864	0	-0.93652	0.47589	NA	ABCD2	chr12	-	39943835	40013553	6238
ENSG00000(	532.397	559.9938	525.1267	298.1321	269.6866	327.142	0.85034	2.87E-08	1.39E-07	AHSA2	chr2	+	61404553	61414686	2922
ENSG00000(	42.46747	59.0101	63.33186	5.243529	7.363456	2.465895	3.3241	2.22E-10	1.28E-09	ABLIM3	chr5	+	1.49E+08	1.49E+08	4569
ENSG00000(	0	0	0	0.749076	0.920432	1.64393	-1.0185	0.44577	NA	MAB21L3	chr1	+	1.17E+08	1.17E+08	3229
ENSG00000(	1.035792	0	0	2.247227	0.920432	3.28786	-1.4278	0.28462	0.40765	RP11-683L	chr18	-	47225	73545	1931
ENSG00000(	245.4827	230.019	220.3421	598.5114	565.1452	655.928	-1.3808	1.02E-18	9.75E-18	KIAA1919	chr6	+	1.12E+08	1.12E+08	5958
ENSG00000(	283.807	307.0934	406.3794	611.2456	716.0961	625.5153	-0.96856	8.73E-09	4.40E-08	VANGL1	chr1	+	1.16E+08	1.16E+08	8691
ENSG00000(	616.2962	610.5739	547.5567	159.5531	151.8713	147.9537	1.9429	7.96E-34	1.38E-32	GLRX	chr5	-	95087023	95158709	3407
ENSG00000(	352.1692	338.4048	369.4359	886.1564	710.5735	747.9881	-1.1431	1.91E-14	1.46E-13	IQCB1	chr3	-	1.21E+08	1.22E+08	2594
ENSG00000(	3.107376	3.612863	6.597069	0.749076	0.920432	0	2.163	0.070109	0.12988	SYT12	chr11	+	66774249	66818334	6028
ENSG00000(	1739.095	1706.476	2436.957	728.1014	893.7395	816.2112	1.2665	2.04E-16	1.74E-15	GOLGB1	chr3	-	1.21E+08	1.21E+08	11198
ENSG00000(	0	3.612863	1.319414	0	0	0	1.6005	0.2346	NA	C11orf86	chr11	+	66742748	66744475	1187
ENSG00000(	0	1.204288	0	1.498151	3.681728	5.753754	-2.033	0.11103	0.19091	LIPM	chr10	+	90562487	90580303	1452
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	GPR151	chr5	-	1.46E+08	1.46E+08	3088
ENSG00000(	3.107376	1.204288	0	11.23613	4.60216	2.465895	-1.6159	0.13855	0.22885	DMRT2	chr9	+	1050354	1057552	2459
ENSG00000(	4.143168	7.225726	6.597069	17.22874	19.32907	12.32947	-1.3517	0.050619	0.098155	ZNF483	chr9	+	1.14E+08	1.14E+08	3655
ENSG00000(	8.286335	8.430014	9.235896	20.97412	13.80648	13.9734	-0.86092	0.17975	0.28259	PLAC8L1	chr5	-	1.45E+08	1.45E+08	638
ENSG00000(	0	0	0	83.89646	86.52061	67.40112	-7.0499	3.53E-12	2.33E-11	SLC2A14	chr12	-	7965108	8043744	4125
ENSG00000(	863.8504	858.6571	808.8006	576.7882	563.3044	720.0413	0.44338	0.001876	0.005026	GPR137	chr11	+	64037534	64056972	1843

ENSG00000(	5.17896	8.430014	9.235896	23.97042	12.88605	24.65895	-1.3604	0.033243	0.067955	SNCG	chr10	+	88718375	88723017	794
ENSG00000(	15.53688	10.83859	7.916483	1.498151	9.20432	8.219649	0.79901	0.30724	0.43298	MMRN2	chr10	-	88695297	88729238	4127
ENSG00000(	1159.051	1199.471	854.9801	815.7433	862.4448	1046.361	0.23832	0.12901	0.21592	MZT2A	chr2	-	1.32E+08	1.32E+08	2826
ENSG00000(	1192.196	1339.168	1757.459	619.4855	715.1757	567.1558	1.1687	2.18E-13	1.56E-12	TNKS	chr8	+	9413424	9639856	9620
ENSG00000(	265.1627	270.9647	344.367	111.6123	119.6562	90.41614	1.443	6.95E-12	4.47E-11	ZNF449	chrX	+	1.34E+08	1.34E+08	3773
ENSG00000(	196.8005	230.019	266.5216	194.0106	214.4607	138.9121	0.3372	0.12373	0.20888	ZBTB21	chr21	-	43406940	43430496	7449
ENSG00000(	414.3168	460.0379	410.3377	358.0581	320.3103	255.6311	0.45743	0.008037	0.019084	PPP1R3B	chr8	-	8993765	9009084	5548
ENSG00000(	59.04014	75.87013	65.97069	95.88167	80.07758	86.30632	-0.38398	0.17817	0.28063	FAM86B3P	chr8	+	8086117	8102387	2829
ENSG00000(	20.71584	21.67718	17.15238	33.7084	88.36147	67.40112	-1.6171	0.000241	0.000743	STOX2	chr4	+	1.85E+08	1.85E+08	10458
ENSG00000(	1844.745	1836.539	1562.186	1804.523	1967.884	2210.264	-0.18923	0.13463	0.22371	MAP3K11	chr11	-	65365226	65382853	5605
ENSG00000(	92.18548	103.5687	131.9414	271.9144	264.164	213.7109	-1.1917	7.50E-08	3.48E-07	TRIB1	chr8	+	1.26E+08	1.26E+08	3635
ENSG00000(	8.286335	9.634302	1.319414	0	0	0	3.783	0.002591	0.006767	KCNK7	chr11	-	65360326	65363467	1563
ENSG00000(	253.769	207.1375	283.674	138.579	159.2347	144.6658	0.74707	0.000239	0.000737	NDNF	chr4	-	1.22E+08	1.22E+08	2885
ENSG00000(	0	0	0	16.47966	9.20432	15.61733	-4.6444	4.43E-05	0.000152	OLR1	chr12	-	10310902	10324737	2460
ENSG00000(	11.39371	6.021439	0	0	1.840864	0.821965	2.0434	0.082338	0.14907	GLIPR1L1	chr12	+	75728419	75764340	1132
ENSG00000(	1862.354	1716.11	2005.509	6125.94	8651.14	8333.08	-2.0438	2.80E-49	7.60E-48	DAG1	chr3	+	49506146	49573048	5826
ENSG00000(	17.60846	8.430014	25.06886	60.67512	62.58938	46.03004	-1.6866	0.000152	0.000482	DAB1	chr1	-	57460451	59012406	5298
ENSG00000(	179.192	199.9118	135.8996	292.8885	219.0628	240.8357	-0.54332	0.010615	0.024522	ARV1	chr1	+	2.31E+08	2.31E+08	1335
ENSG00000(	896.9958	917.6672	808.8006	1044.211	1004.191	1061.979	-0.24464	0.047471	0.092762	NAA20	chr20	+	19997760	20014299	1604
ENSG00000(	2.071584	0	2.638828	5.243529	0	0	-0.10883	0.93436	0.96049	CCDC36	chr3	+	49235861	49295537	2843
ENSG00000(	0	6.021439	1.319414	0	0	1.64393	1.2459	0.35016	0.47987	SAA1	chr11	+	18287721	18291524	675
ENSG00000(	69.39806	89.11729	93.67838	65.91865	57.06678	47.67397	0.55128	0.069006	0.12818	MINOS1	chr1	+	19923477	19956314	3712
ENSG00000(	592.473	576.8538	568.6673	53.93344	54.30549	57.53754	3.3747	5.94E-75	2.85E-73	EHBP1L1	chr11	+	65343509	65360121	5185
ENSG00000(	103.5792	154.1488	124.0249	80.90016	64.43024	64.93523	0.84735	0.00172	0.004634	THAP2	chr12	+	72056789	72074419	5719
ENSG00000(	2.071584	1.204288	10.55531	1.498151	0.920432	1.64393	1.3498	0.23087	0.34425	TMEM196	chr7	-	19758933	19813221	4054
ENSG00000(	565.5424	539.5209	514.5714	1213.502	1198.402	1026.634	-1.0826	5.32E-16	4.45E-15	RNF26	chr11	+	1.19E+08	1.19E+08	2787
ENSG00000(	5342.615	5142.309	4286.775	4804.571	4942.72	5150.432	-0.01192	0.91768	0.95008	PPP1R14B	chr11	-	64011956	64014413	982
ENSG00000(	315.9165	329.9748	265.2022	516.8621	456.5343	471.8079	-0.66217	3.73E-05	0.000129	SSSCA1	chr11	+	65337901	65341413	1077
ENSG00000(	2834.962	2710.852	3192.981	3310.914	4555.218	4016.121	-0.44217	0.000909	0.002565	SMARCC1	chr3	-	47626762	47823596	6375
ENSG00000(	246.5185	230.019	201.8703	154.3096	196.9724	209.6011	0.27638	0.17364	0.27509	ZNF417	chr19	-	58411664	58427978	3597
ENSG00000(	1129.013	1001.967	1229.694	397.01	463.8977	361.6646	1.4554	3.41E-23	3.92E-22	PTPRM	chr18	+	7566780	8406859	6095
ENSG00000(	1421.106	1363.254	1129.418	595.5151	777.765	1201.713	0.60139	0.002444	0.00641	FKBP2	chr11	+	64008475	64011604	1002
ENSG00000(	1147.657	1172.976	984.2827	555.065	478.6246	508.7963	1.0964	8.64E-16	7.13E-15	VEGFB	chr11	+	64002010	64006259	1374
ENSG00000(	1799.171	1787.163	2306.335	435.962	667.3132	530.9893	1.8448	1.15E-29	1.73E-28	PEAK1	chr15	-	77400471	77712486	11715
ENSG00000(	5170.673	4796.678	5735.492	1728.117	1530.678	1660.369	1.6711	5.08E-48	1.32E-46	TNFRSF10D	chr8	-	22993101	23021543	3538
ENSG00000(	93.22127	87.913	54.09597	26.96672	37.73771	31.23467	1.2805	0.000293	0.000892	MST1	chr3	-	49721380	49726934	4152
ENSG00000(	77.68439	46.96722	58.05421	315.3608	542.1344	383.8576	-2.7314	1.91E-27	2.61E-26	TNFRSF10C	chr8	+	22941868	22974950	1718
ENSG00000(	865.922	895.9901	1179.556	761.0608	817.3436	655.106	0.39502	0.010414	0.024114	MOB1B	chr4	+	71768043	71888166	6963
ENSG00000(	697.088	644.2939	694.0116	786.5293	657.1884	674.0112	-0.05772	0.67469	0.77655	ZNF622	chr5	-	16451628	16465901	1699
ENSG00000(	2061.226	2089.439	2046.411	71.91125	115.054	112.6092	4.3626	6.70E-161	1.23E-158	CSPG4	chr15	-	75966663	76005189	8290
ENSG00000(	1237.771	1188.632	1194.069	351.3164	360.8093	430.7096	1.6596	2.21E-34	3.89E-33	SNX33	chr15	+	75940247	75954642	8008
ENSG00000(	928.0695	875.5172	1029.143	826.2303	758.436	709.3557	0.30273	0.022615	0.048386	NABP1	chr2	+	1.93E+08	1.93E+08	3387
ENSG00000(	145.0109	155.3531	127.9831	59.92604	69.0324	50.13986	1.2495	1.68E-06	6.80E-06	NUDT18	chr8	-	21964383	21966932	1756
ENSG00000(	12.4295	12.04288	5.277655	20.97412	34.97642	35.34449	-1.5278	0.006401	0.015526	GPR113	chr2	-	26531041	26569685	4012

ENSG00000(	2465.185	2575.971	2816.948	1636.73	2035.996	1748.319	0.53466	1.40E-05	5.11E-05	CHD2	chr15	+	93425937	93571237	9857
ENSG00000(	0	0	0	9.737982	4.60216	17.26126	-4.214	0.00035	0.001056	XCR1	chr3	-	46058516	46069234	5281
ENSG00000(	445.3905	470.8765	339.0893	312.3645	289.9361	293.4415	0.48622	0.004788	0.0119	CCDC106	chr19	+	56152428	56164527	2162
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CCR9	chr3	+	45927996	45944667	2567
ENSG00000(	186.4425	183.0517	159.6491	167.0438	211.6994	189.0519	-0.09763	0.63271	0.74258	CCDC41	chr12	-	94700225	94853764	3183
ENSG00000(	4.143168	0	10.55531	0	0	0	3.2097	0.014534	0.032563	SULT1B1	chr4	-	70592566	70653679	1429
ENSG00000(	1196.34	1205.492	1286.428	2352.097	2485.166	2017.102	-0.89248	3.03E-13	2.16E-12	NUDT4	chr12	+	93771659	93797024	4855
ENSG00000(	748.8775	652.7239	709.8446	176.0328	188.6886	180.0103	1.9497	2.22E-37	4.26E-36	PC	chr11	-	66615704	66725847	4192
ENSG00000(	42.46747	43.35436	58.05421	64.4205	57.06678	38.63235	-0.15667	0.66212	0.76643	SCAI	chr9	-	1.28E+08	1.28E+08	2586
ENSG00000(	329.3818	292.6419	335.1311	197.7559	208.9381	201.3814	0.65231	0.000172	0.000544	NMNAT1	chr1	+	10003486	10045559	3781
ENSG00000(	511.6812	508.2094	485.5443	495.1389	363.5706	446.327	0.20415	0.19934	0.30695	LRFN4	chr11	+	66624118	66627946	2431
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	BET3L	chr6	-	1.17E+08	1.17E+08	2421
ENSG00000(	4.143168	0	0	7.490755	2.761296	0.821965	-0.97584	0.42516	0.55556	APOBEC4	chr1	-	1.84E+08	1.84E+08	2648
ENSG00000(	703.3027	669.584	486.8637	851.6989	773.1629	917.3128	-0.44774	0.004737	0.011792	SLC19A1	chr21	-	46913486	46964325	3811
ENSG00000(	158.4762	183.0517	122.7055	6.74168	4.60216	5.753754	4.6394	4.58E-30	6.97E-29	HSPB7	chr1	-	16340523	16346089	2892
ENSG00000(	217.5163	233.6318	191.315	496.6371	381.0588	433.1755	-1.0243	8.15E-09	4.12E-08	RCE1	chr11	+	66610306	66614017	2719
ENSG00000(	3903.9	3791.098	3121.733	2650.229	2831.249	3999.681	0.18975	0.21851	0.32999	UQCRH	chr1	+	46769303	46782448	687
ENSG00000(	1496.719	1560.757	1666.42	2239.736	2471.36	2359.861	-0.58124	2.09E-07	9.31E-07	EIF1AX	chrX	-	20142636	20159962	4427
ENSG00000(	9.322127	16.86003	6.597069	5.992604	3.681728	12.32947	0.52337	0.49036	0.61939	SPDYE2L	chr7	+	1.02E+08	1.02E+08	1742
ENSG00000(	94.25706	114.4073	85.7619	100.3761	103.0884	107.6774	-0.07807	0.75868	0.84047	CXorf23	chrX	-	19930978	19988416	6528
ENSG00000(	1715.271	1722.131	1909.192	3839.012	3691.853	3319.094	-1.0196	3.11E-19	3.04E-18	PSMD1	chr2	+	2.32E+08	2.32E+08	3326
ENSG00000(	30.03797	14.45145	38.263	8.988907	8.283888	13.9734	1.3367	0.018858	0.041157	GPR64	chrX	-	19007427	19140755	5788
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	SPATA3	chr2	+	2.32E+08	2.32E+08	1618
ENSG00000(	166.7625	174.6217	180.7597	176.0328	205.2563	160.2832	-0.05205	0.7994	0.86922	SUSD5	chr3	-	33191537	33260707	5005
ENSG00000(	996.4318	857.4529	1381.426	1355.827	1784.718	1276.512	-0.44778	0.01088	0.025091	HEG1	chr3	-	1.25E+08	1.25E+08	9156
ENSG00000(	6.214751	3.612863	0	0	0	0.821965	2.1007	0.1105	0.1902	WFIKKN2	chr17	+	48912011	48919709	3588
ENSG00000(	81.82756	113.203	96.31721	438.2092	278.8909	329.6079	-1.8366	6.87E-16	5.71E-15	C11orf80	chr11	+	66511922	66610987	2323
ENSG00000(	4866.15	5072.46	5334.39	3628.522	3774.692	3421.84	0.49579	1.87E-06	7.52E-06	TOMM20	chr1	-	2.35E+08	2.35E+08	3387
ENSG00000(	2.071584	4.817151	7.916483	2.247227	0	0	1.9414	0.10232	0.17868	AP000769.	chr11	+	65222728	65234028	693
ENSG00000(	2.071584	0	6.597069	0.749076	7.363456	0.821965	-0.03154	0.97859	0.98755	C1orf100	chr1	+	2.45E+08	2.45E+08	841
ENSG00000(	493.0369	447.995	635.9574	1361.819	1159.744	1004.441	-1.1585	1.37E-12	9.27E-12	AGFG1	chr2	+	2.28E+08	2.28E+08	4122
ENSG00000(	590.4014	623.821	713.8029	596.2641	620.3712	590.9928	0.091602	0.50936	0.63666	STAT5B	chr17	-	40351186	40428725	5103
ENSG00000(	39.36009	25.29004	15.83297	0.749076	0	0.821965	4.7976	1.10E-07	5.04E-07	CD7	chr17	-	80272744	80275478	2021
ENSG00000(	2507.652	2468.79	2245.642	2152.094	2070.052	2377.123	0.13009	0.25307	0.37088	CNP	chr17	+	40118759	40127194	2660
ENSG00000(	562.435	504.5966	515.8908	8873.549	8111.767	7938.537	-3.9687	3.98E-268	2.28E-265	JUP	chr17	-	39775692	39943183	3497
ENSG00000(	5.17896	1.204288	7.916483	102.6234	139.9057	140.556	-4.5952	3.79E-21	4.02E-20	HAP1	chr17	-	39873994	39890896	5683
ENSG00000(	0	1.204288	0	0	1.840864	1.64393	-0.67765	0.61688	NA	TDRD12	chr19	+	33210659	33320483	3934
ENSG00000(	3.107376	0	0	3.745378	0	4.109825	-0.82285	0.52754	0.65227	CCDC13-AS	chr3	+	42774067	42788260	2049
ENSG00000(	10985.61	11166.16	9292.631	8170.916	6953.864	7578.517	0.46906	4.85E-05	0.000165	EIF1	chr17	+	39845137	39848920	2330
ENSG00000(	528.2539	490.1451	393.1853	257.682	238.3919	341.1154	0.75117	5.42E-05	0.000183	ENDOV	chr17	+	78388965	78411886	2815
ENSG00000(	1758.775	1665.53	2000.231	657.6883	1183.676	942.7938	0.95913	4.51E-08	2.14E-07	RNF213	chr17	+	78234665	78372586	21055
ENSG00000(	8.286335	0	2.638828	5.992604	6.443024	7.397684	-0.70363	0.46995	0.5991	TIGD3	chr11	+	65122238	65125084	2012
ENSG00000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	KCNH6	chr17	+	61600695	61626338	3821
ENSG00000(	7.250543	2.408575	1.319414	8.988907	1.840864	3.28786	-0.2903	0.77508	0.85249	10-Mar	chr17	-	60778675	60885705	3338

ENSG00000(	310.7376	295.0505	321.937	352.8146	276.1296	341.9374	-0.06709	0.69574	0.79272	PLK3	chr1	+	45265897	45271662	2492
ENSG00000(	643.2268	574.4452	728.3164	3383.574	3631.104	3236.076	-2.3929	1.46E-81	8.13E-80	NET1	chr10	+	5454514	5500426	3402
ENSG00000(	698.1237	757.497	874.7713	1382.044	1285.843	1223.906	-0.73974	2.46E-08	1.19E-07	DPY19L1	chr7	-	34968488	35077883	4870
ENSG00000(	6.214751	1.204288	7.916483	2.996302	5.522592	3.28786	0.32547	0.73607	0.82343	RP11-89N1	chr7	+	33765593	33768068	1058
ENSG00000(	0	0	3.958241	0.749076	0.920432	0	0.60606	0.65509	NA	AC142401.	chr15	-	89002948	89054752	598
ENSG00000(	3.107376	2.408575	1.319414	0.749076	2.761296	2.465895	0.16399	0.88888	0.93101	PHOSPHO1	chr17	-	47300724	47308128	2173
ENSG00000(	412.2452	423.9093	436.726	349.8183	256.8005	304.949	0.47736	0.004516	0.01129	ZNF791	chr19	+	12721732	12742735	4554
ENSG00000(	4.143168	6.021439	3.958241	7.490755	5.522592	7.397684	-0.47414	0.58127	0.69922	TUBB8	chr10	-	92828	120103	1968
ENSG00000(	193.6931	220.3847	315.3399	134.0845	248.5166	117.541	0.53963	0.048145	0.09393	PHC3	chr3	-	1.7E+08	1.7E+08	5030
ENSG00000(	9.322127	8.430014	15.83297	47.94084	35.89685	43.56414	-1.8723	0.00015	0.000477	GPR160	chr3	+	1.7E+08	1.7E+08	2039
ENSG00000(	360.4556	369.7163	336.4505	673.4189	871.6491	845.8019	-1.1593	4.28E-14	3.20E-13	CBX2	chr17	+	77751931	77761782	4644
ENSG00000(	584.1866	541.9295	498.7384	527.3492	709.6531	728.2609	-0.27151	0.090443	0.1614	SPTBN2	chr11	-	66452719	66496697	8128
ENSG00000(	2045.689	1782.346	2409.25	902.636	1382.489	1044.717	0.90281	2.67E-08	1.30E-07	GOLIM4	chr3	-	1.68E+08	1.68E+08	4373
ENSG00000(	535.5044	564.8109	518.5296	395.5119	400.3879	397.831	0.43856	0.002009	0.005353	RBM4B	chr11	-	66432469	66445392	2339
ENSG00000(	1001.611	1132.03	833.8695	1197.023	1056.656	1488.578	-0.33326	0.034133	0.06961	USMG5	chr10	-	1.05E+08	1.05E+08	789
ENSG00000(	159.512	162.5788	96.31721	83.89646	91.12277	67.40112	0.78396	0.004306	0.010811	HOXB2	chr17	-	46618256	46623441	2652
ENSG00000(	285.8786	290.2333	275.7575	74.90755	79.15715	97.81383	1.7482	3.79E-17	3.35E-16	C1QTNF1	chr17	+	77018896	77045870	3100
ENSG00000(	128.4382	115.6116	127.9831	65.91865	61.66894	42.74218	1.1148	5.91E-05	0.000199	3-Mar	chr5	-	1.26E+08	1.26E+08	4196
ENSG00000(	14.50109	2.408575	11.87472	20.22504	20.2495	25.48091	-1.1197	0.07586	0.13899	SWSAP1	chr19	+	11485361	11487627	1684
ENSG00000(	4.143168	0	6.597069	9.737982	9.20432	9.863579	-1.2555	0.15891	0.25569	SLCO4C1	chr5	-	1.02E+08	1.02E+08	5334
ENSG00000(	101.5076	79.48299	114.789	78.65293	71.7937	72.33291	0.40264	0.14291	0.23453	RBM4	chr11	+	66384097	66434153	2321
ENSG00000(	3.107376	13.24716	18.47179	274.9107	303.7426	360.0206	-4.7299	2.84E-42	6.28E-41	PIFO	chr1	+	1.12E+08	1.12E+08	3774
ENSG00000(	620.4394	535.908	664.9845	877.1675	724.38	621.4055	-0.28733	0.072556	0.13373	XXYLT1	chr3	-	1.95E+08	1.95E+08	2727
ENSG00000(	477.5001	487.7365	418.2542	971.551	769.4811	808.8135	-0.87916	3.17E-09	1.67E-08	UBXN2A	chr2	+	24150155	24227779	6066
ENSG00000(	1.035792	0	0	0	0	6.575719	-1.2546	0.35501	0.48466	RAX2	chr19	-	3769087	3772233	2428
ENSG00000(	3.107376	1.204288	0	3.745378	0	7.397684	-0.9587	0.43157	0.56134	LRRC63	chr13	+	46786083	46851501	2327
ENSG00000(	21.75163	16.86003	22.43003	9.737982	11.96562	13.9734	0.7418	0.18896	0.29406	TCAP	chr17	+	37820440	37822808	2123
ENSG00000(	776.8439	698.4869	646.5128	267.42	259.5618	395.3651	1.1971	2.47E-11	1.53E-10	CCS	chr11	+	66360292	66373490	1430
ENSG00000(	0	0	0	8.239831	0	3.28786	-2.5345	0.057304	0.10938	LRRC33	chr3	+	1.96E+08	1.96E+08	2564
ENSG00000(	64.2191	69.84869	50.13772	71.16218	74.55499	72.33291	-0.23681	0.43289	0.56272	CEP19	chr3	-	1.96E+08	1.96E+08	2201
ENSG00000(	138.7961	191.4817	184.7179	110.1141	124.2583	74.79881	0.7286	0.00415	0.010454	KLHL15	chrX	-	24001837	24045303	6272
ENSG00000(	223.7311	270.9647	292.9099	444.2018	437.2052	433.9975	-0.74053	8.55E-06	3.20E-05	FBXO45	chr3	+	1.96E+08	1.96E+08	5899
ENSG00000(	2.071584	4.817151	1.319414	0	0	0	2.4706	0.065789	0.12303	SPERT	chr13	+	46276446	46288694	1842
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	FAM46D	chrX	+	79591003	79700810	3106
ENSG00000(	2134.767	1978.645	1506.771	3039	2347.102	2849.752	-0.54918	0.000194	0.000606	GNG5	chr1	-	84964008	84972248	920
ENSG00000(	94.25706	85.50443	84.44248	59.17697	94.8045	121.6508	-0.05671	0.85142	0.90523	FAM3C2	chrX	+	23093875	23094884	681
ENSG00000(	408.102	366.1035	507.9743	118.3539	161.996	130.6924	1.6345	1.32E-16	1.13E-15	SLC25A30	chr13	-	45967451	45992590	6041
ENSG00000(	23.82321	16.86003	10.55531	6.74168	4.60216	10.68554	1.1427	0.087345	0.1569	C9orf131	chr9	+	35041092	35045988	3409
ENSG00000(	3.107376	8.430014	5.277655	7.490755	0	0	0.88689	0.42807	0.55834	CD34	chr1	-	2.08E+08	2.08E+08	2874
ENSG00000(	2.071584	0	1.319414	14.23244	20.2495	7.397684	-3.0363	0.001421	0.003879	CTSF	chr11	-	66330934	66336312	2035
ENSG00000(	294.1649	405.845	357.5611	188.767	230.108	233.438	0.69346	0.000227	0.000702	TBC1D3	chr17	-	36337717	36421858	5098
ENSG00000(	733.3407	663.5625	782.4124	683.906	746.4703	681.4089	0.045371	0.73551	0.82303	MSRB3	chr12	+	65672423	65882024	4417
ENSG00000(	1073.08	1050.139	915.6732	1385.79	880.8534	988.8238	-0.09933	0.5466	0.66858	MRPL45	chr17	+	36452989	36479101	1705
ENSG00000(	389.4578	368.512	517.2102	452.4416	540.2936	424.1339	-0.1525	0.38233	0.51303	LEMD3	chr12	+	65563351	65642107	4764

ENSG00000(	169.8699	156.5574	153.052	219.4791	212.6198	277.8241	-0.56188	0.005635	0.013821	C16orf91	chr16	-	1469745	1479345	1071
ENSG00000(	122.2234	118.0202	131.9414	38.95193	121.497	78.08667	0.63796	0.055406	0.10623	SOCS7	chr17	+	36508111	36556019	2051
ENSG00000(	13.46529	6.021439	7.916483	5.992604	0	4.109825	1.2342	0.17938	0.28211	TLR1	chr4	-	38792298	38858438	2847
ENSG00000(	137.7603	103.5687	151.7326	36.7047	32.21512	34.52253	1.9002	1.09E-10	6.46E-10	TLR6	chr4	-	38825336	38858438	5879
ENSG00000(	157.4404	157.7617	157.0102	108.616	115.054	133.1583	0.40191	0.069054	0.12826	FAM174A	chr5	+	99871009	99922445	1356
ENSG00000(	802.7387	799.647	915.6732	361.8035	299.1404	279.4681	1.4144	1.90E-20	1.96E-19	RGMB	chr5	+	98104354	98134347	4580
ENSG00000(	31.07376	40.94578	34.30476	16.47966	11.04518	25.48091	0.96626	0.043205	0.085609	FAM53A	chr4	-	1619642	1686029	2802
ENSG00000(	332.4892	348.0392	320.6175	185.0217	166.5982	186.586	0.89086	3.43E-07	1.49E-06	CYB561D1	chr1	+	1.1E+08	1.1E+08	5077
ENSG00000(	495.1085	373.3292	360.2	185.7707	169.3595	228.5062	1.0698	3.32E-08	1.60E-07	ZDHHC24	chr11	-	66288108	66313709	1941
ENSG00000(	14.50109	8.430014	10.55531	17.22874	27.61296	28.76877	-1.0733	0.058145	0.11075	RP11-23P1	chr15	+	42184991	42189585	2900
ENSG00000(	373.9209	392.5978	377.3523	793.271	682.0401	664.9696	-0.90203	5.42E-10	3.03E-09	TRMT10C	chr3	+	1.01E+08	1.01E+08	1819
ENSG00000(	329.3818	323.9534	237.4945	643.4559	434.4439	514.55	-0.8327	1.11E-05	4.08E-05	CTU2	chr16	+	88772871	88781794	1905
ENSG00000(	23.82321	32.51577	26.38828	27.7158	17.48821	17.26126	0.38534	0.42315	0.55364	AGAP8	chr10	-	51224681	51371321	2803
ENSG00000(	474.3927	408.2535	662.3457	510.8695	723.4595	559.7581	-0.2152	0.25993	0.3788	MGA	chr15	+	41913422	42062141	12042
ENSG00000(	64.2191	75.87013	76.526	74.15848	67.19154	55.07165	0.13612	0.65022	0.75642	C12orf66	chr12	-	64580096	64616076	2698
ENSG00000(	2.071584	4.817151	2.638828	0	0.920432	0.821965	1.6927	0.17534	0.2771	ARL13A	chrX	+	1E+08	1E+08	1535
ENSG00000(	1.035792	0	1.319414	0.749076	0	0	0.56083	0.6714	NA	SNX31	chr8	-	1.02E+08	1.02E+08	2451
ENSG00000(	1135.228	1117.579	1192.75	866.6804	977.4988	906.6273	0.3245	0.007517	0.01798	PIGG	chr4	+	492989	533985	3519
ENSG00000(	4787.43	4608.809	5211.684	6564.898	6881.15	5826.087	-0.39917	0.00033	0.000997	PRPF8	chr17	-	1553923	1588176	7445
ENSG00000(	1512.256	1483.682	1625.518	575.29	717.0165	752.0979	1.1743	5.35E-18	4.93E-17	ADCY6	chr12	-	49159975	49182820	6464
ENSG00000(	13.46529	6.021439	3.958241	4.494453	3.681728	5.753754	0.67961	0.4273	0.55748	REP15	chr12	+	27849428	27850566	1139
ENSG00000(	1607.549	1290.996	1525.242	1691.413	1605.233	1648.04	-0.16005	0.19328	0.29915	PITPNA	chr17	-	1421012	1466110	3912
ENSG00000(	1395.212	1331.942	1382.746	1972.316	1919.101	1791.884	-0.4668	2.94E-05	0.000103	DDX23	chr12	-	49223840	49246625	2832
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	ZNF80	chr3	-	1.14E+08	1.14E+08	2939
ENSG00000(	88.04231	80.68728	55.41538	136.3317	96.64536	112.6092	-0.61401	0.029639	0.061494	ZNHIT2	chr11	-	64883875	64885170	1296
ENSG00000(	1777.419	1557.144	1789.125	673.4189	965.5332	885.2562	1.0194	3.84E-12	2.53E-11	ZBTB4	chr17	-	7362685	7387582	5956
ENSG00000(	60.07593	66.23582	68.60952	66.66772	77.31629	84.66239	-0.22847	0.43748	0.56711	TNK1	chr17	+	7283853	7293093	3122
ENSG00000(	1019.219	1039.3	1370.871	338.5821	401.3084	337.0056	1.6656	1.81E-26	2.37E-25	ZHX3	chr20	-	39807088	39946312	10030
ENSG00000(	2407.18	2262.857	1839.263	2103.404	2174.981	2639.329	-0.08698	0.52634	0.65112	PHLDA3	chr1	-	2.01E+08	2.01E+08	1531
ENSG00000(	10.35792	12.04288	7.916483	0	0	0	4.565	0.000104	0.00034	DIRC1	chr2	-	1.9E+08	1.9E+08	1037
ENSG00000(	11.39371	19.2686	10.55531	3.745378	13.80648	2.465895	0.96987	0.20096	0.30847	SLC16A11	chr17	-	6944949	6947242	1803
ENSG00000(	83.89914	78.2787	89.72014	86.14369	124.2583	135.6242	-0.45202	0.096911	0.17092	SLC16A13	chr17	+	6939394	6943440	1748
ENSG00000(	544.8265	544.338	377.3523	5.992604	11.96562	4.109825	5.9901	6.93E-70	3.00E-68	GLIS1	chr1	-	53971910	54199877	2812
ENSG00000(	0	0	3.958241	0	0.920432	0	0.88424	0.51108	NA	CHRNA9	chr4	+	40337346	40357234	2276
ENSG00000(	43.50326	51.78437	60.69303	0.749076	1.840864	1.64393	4.8481	1.17E-12	7.95E-12	PODN	chr1	+	53527854	53551174	3287
ENSG00000(	55.93276	59.0101	55.41538	107.8669	91.12277	136.4462	-0.96753	0.000777	0.002218	STAG3L3	chr7	-	72440227	72476445	2137
ENSG00000(	108.7581	114.4073	122.7055	190.2652	138.0648	186.586	-0.57368	0.012922	0.029276	SNHG11	chr20	+	37075221	37079564	2652
ENSG00000(	2.071584	0	3.958241	2.247227	0	1.64393	0.39717	0.75764	0.83963	PMS2P2	chr7	-	74880905	74988262	1071
ENSG00000(	10.35792	12.04288	11.87472	25.46857	32.21512	14.79537	-1.0306	0.070781	0.13104	C11orf45	chr11	-	1.29E+08	1.29E+08	3624
ENSG00000(	82.86335	90.32158	93.67838	531.0946	505.3172	512.9061	-2.5294	7.32E-44	1.69E-42	EXO1	chr1	+	2.42E+08	2.42E+08	3473
ENSG00000(	234.089	211.9546	341.7282	258.4311	362.6502	221.9305	-0.09799	0.66757	0.77083	RALGAPA1	chr14	-	36007558	36278510	8004
ENSG00000(	480.6074	467.2636	460.4754	581.2826	569.7474	614.0078	-0.32454	0.018649	0.040745	WBSCR16	chr7	-	74441226	74490064	2345
ENSG00000(	134.6529	122.8373	130.622	292.1395	326.7534	311.5247	-1.2538	3.50E-11	2.14E-10	LIG4	chr13	-	1.09E+08	1.09E+08	4103
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	C20orf166	chr20	+	61147660	61167971	1220

ENSG0000(	164.6909	143.3102	154.3714	119.103	92.0432	99.45776	0.56813	0.014337	0.032177	GTF2IRD2B	chr7	+	74508364	74565623	3545
ENSG0000(	1.035792	2.408575	3.958241	0	1.840864	0	1.28	0.32687	0.45459	ABRA	chr8	-	1.08E+08	1.08E+08	2755
ENSG0000(	4623.775	4547.39	5319.876	5254.016	5454.48	5141.391	-0.12929	0.23187	0.34541	ATP2A2	chr12	+	1.11E+08	1.11E+08	8229
ENSG0000(	218.5521	204.7289	279.7157	807.5034	653.5067	674.8332	-1.6005	4.89E-21	5.16E-20	ZWILCH	chr15	+	66797297	66842115	3609
ENSG0000(	48218.18	48131.77	39640.47	39725.72	29328.65	30619.02	0.44712	0.000829	0.002356	RPL4	chr15	-	66790355	66816870	2767
ENSG0000(	80.79177	99.95588	101.5949	188.018	148.1896	216.9987	-0.96755	6.45E-05	0.000216	SNAPC5	chr15	-	66782644	66790151	1741
ENSG0000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	STARD6	chr18	-	51850728	51884334	1135
ENSG0000(	180.2278	210.7504	141.1773	194.7596	165.6778	168.5028	0.009536	0.96497	0.97974	C12orf76	chr12	-	1.1E+08	1.11E+08	2204
ENSG0000(	36.25272	30.10719	38.263	0	1.840864	4.109825	3.8511	3.74E-08	1.79E-07	ZCCHC12	chrX	+	1.18E+08	1.18E+08	2231
ENSG0000(	185.4068	258.9219	277.0769	230.7153	225.5058	200.5594	0.13088	0.51899	0.64523	CNTNAP2	chr7	+	1.46E+08	1.48E+08	9894
ENSG0000(	17.60846	20.47289	34.30476	17.22874	0.920432	9.863579	1.2557	0.064024	0.12014	GALNTL6	chr4	+	1.73E+08	1.74E+08	3922
ENSG0000(	11.39371	6.021439	14.51355	25.46857	18.40864	12.32947	-0.77622	0.21239	0.32248	LINGO2	chr9	-	27948076	28670283	3044
ENSG0000(	15.53688	24.08575	14.51355	5.992604	15.64734	19.72716	0.37334	0.5406	0.66379	BBS1	chr11	+	66278077	66301098	3585
ENSG0000(	199.9078	234.8361	287.6322	58.42789	99.40666	46.852	1.8052	4.01E-11	2.44E-10	DENND4A	chr15	-	65950384	66084631	7172
ENSG0000(	237.1963	225.2018	246.7304	4514.678	5697.474	5160.296	-4.4277	3.04E-239	1.43E-236	IGDCC3	chr15	-	65619465	65670378	4479
ENSG0000(	3.107376	8.430014	13.19414	24.71949	29.45382	27.94681	-1.6684	0.005451	0.013399	GCSAM	chr3	-	1.12E+08	1.12E+08	3336
ENSG0000(	67.32647	90.32158	133.2608	2.996302	24.85166	13.15144	2.758	5.74E-09	2.95E-08	ANKRD36C	chr2	-	96514587	96657541	5428
ENSG0000(	1.035792	0	0	0	3.681728	0	-0.68494	0.60991	NA	SLC26A9	chr1	-	2.06E+08	2.06E+08	4799
ENSG0000(	2.071584	4.817151	3.958241	11.98521	18.40864	10.68554	-1.7502	0.026718	0.056187	MFSD4	chr1	+	2.06E+08	2.06E+08	4095
ENSG0000(	160.5477	183.0517	145.1355	78.65293	90.20234	65.75719	1.0527	1.72E-05	6.19E-05	PELI3	chr11	+	66234216	66244808	2783
ENSG0000(	8.286335	7.225726	7.916483	1.498151	0	0	2.9958	0.006724	0.016229	TTC9B	chr19	-	40721965	40724306	2323
ENSG0000(	32.10955	42.15007	50.13772	5.992604	5.522592	12.32947	2.2844	1.24E-05	4.55E-05	MYO1H	chr12	+	1.1E+08	1.1E+08	4364
ENSG0000(	41.43168	32.51577	40.90183	51.68621	55.22592	51.78379	-0.45695	0.19832	0.3056	TMEM81	chr1	-	2.05E+08	2.05E+08	1388
ENSG0000(	655.6563	681.6268	543.5985	1418.749	1285.843	1305.28	-1.0884	4.10E-16	3.46E-15	MRPL11	chr11	-	66202546	66234209	2209
ENSG0000(	14.50109	20.47289	11.87472	49.43899	19.32907	37.81039	-1.145	0.026081	0.055004	IL20RB	chr3	+	1.37E+08	1.37E+08	2047
ENSG0000(	0	0	0	6.74168	8.283888	7.397684	-3.7351	0.002031	0.005407	GOLT1A	chr1	-	2.04E+08	2.04E+08	883
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-209A	chr6	+	27179023	27179692	670
ENSG0000(	1161.123	1097.106	1323.372	3215.781	2841.374	2817.696	-1.3073	7.33E-27	9.78E-26	AKIRIN1	chr1	+	39456895	39471731	2741
ENSG0000(	0	7.225726	6.597069	6.74168	4.60216	3.28786	-0.09016	0.92803	0.95677	NPAS4	chr11	+	66188475	66194178	3303
ENSG0000(	270.3417	286.6205	347.0058	364.0507	403.1492	342.7594	-0.29685	0.082871	0.14989	MSL2	chr3	-	1.36E+08	1.36E+08	4692
ENSG0000(	94.25706	65.03154	42.22124	38.95193	16.56778	30.4127	1.1985	0.003795	0.009632	ZNF497	chr19	-	58865723	58874214	3468
ENSG0000(	21.75163	16.86003	10.55531	0	2.761296	0.821965	3.3491	0.000176	0.000553	KLF14	chr7	-	1.3E+08	1.3E+08	1488
ENSG0000(	94.25706	74.66584	54.09597	58.42789	46.94203	34.52253	0.66522	0.054408	0.10462	TRAM1L1	chr4	-	1.18E+08	1.18E+08	2019
ENSG0000(	0	1.204288	0	5.243529	13.80648	14.79537	-3.6123	0.00108	0.003013	CMKLR1	chr12	-	1.09E+08	1.09E+08	5283
ENSG0000(	388.422	356.4692	440.6842	525.851	458.3751	397.0091	-0.22105	0.18403	0.28813	ANGEL2	chr1	-	2.13E+08	2.13E+08	4649
ENSG0000(	2.071584	0	1.319414	351.3164	345.162	285.2218	-7.5033	1.34E-29	2.00E-28	UGT8	chr4	+	1.16E+08	1.16E+08	4084
ENSG0000(	3.107376	3.612863	3.958241	2.247227	0.920432	0	1.2771	0.28262	0.40531	KY	chr3	-	1.34E+08	1.34E+08	4043
ENSG0000(	68.36227	63.82725	62.01245	101.1252	70.87326	77.2647	-0.35711	0.2275	0.34067	IQCK	chr16	+	19727778	19868907	2600
ENSG0000(	39.36009	6.021439	13.19414	406.748	319.3899	343.5813	-3.9226	1.40E-09	7.58E-09	SLCO2A1	chr3	-	1.34E+08	1.34E+08	4223
ENSG0000(	350.0977	381.7592	409.0183	403.7517	340.5598	343.5813	0.065902	0.68354	0.78346	ZNF266	chr19	-	9523272	9546254	4401
ENSG0000(	354.2408	293.8462	248.0498	483.1537	389.3427	524.4136	-0.63515	0.000532	0.001555	SLC29A2	chr11	-	66129992	66139685	2514
ENSG0000(	54.89697	52.98866	29.0271	231.4643	238.3919	240.8357	-2.3412	1.36E-19	1.35E-18	BRSK2	chr11	+	1411129	1483919	4089
ENSG0000(	0	3.612863	5.277655	0	0	0	2.4403	0.070718	0.13095	FAM47DP	chrX	-	37400330	37404515	3290
ENSG0000(	0	2.408575	0	0	0	1.64393	0.21935	0.86915	NA	GRIK1-AS1	chr21	+	31120494	31136321	818

ENSG00000(	1292.668	1234.395	1093.794	661.4337	633.2572	600.0344	0.93278	4.93E-13	3.45E-12	B3GNT1	chr11	-	66112843	66115163	2072
ENSG00000(	1782.598	1730.561	2167.797	2003.777	2124.357	1916.822	-0.08988	0.47061	0.59966	TMEM167A	chr5	-	82348665	82373682	4630
ENSG00000(	7833.694	7942.278	8987.847	1567.815	2164.856	1697.358	2.1845	7.29E-61	2.60E-59	SH3PXD2B	chr5	-	1.72E+08	1.72E+08	7777
ENSG00000(	0	6.021439	0	0	4.60216	0	0.23527	0.86053	0.91133	RP11-79L9	chr3	-	1.38E+08	1.38E+08	504
ENSG00000(	214.4089	219.1804	312.7011	921.3629	857.8426	747.1661	-1.7565	3.68E-24	4.41E-23	KIAA1551	chr12	+	32112304	32146039	6228
ENSG00000(	344.9187	362.4906	343.0476	676.4152	485.0677	455.3686	-0.62069	0.000454	0.001342	LARP7	chr4	+	1.14E+08	1.14E+08	2332
ENSG00000(	17.60846	30.10719	27.70769	350.5674	338.719	366.5964	-3.7884	1.84E-47	4.69E-46	FGFBP3	chr10	-	93666346	93669240	2545
ENSG00000(	58.00435	66.23582	81.80365	456.187	535.6914	509.6182	-2.8578	1.43E-45	3.47E-44	NR1D2	chr3	+	23986751	24022109	5258
ENSG00000(	6.214751	7.225726	0	34.45748	32.21512	24.65895	-2.5532	0.000109	0.000353	PABPC5	chrX	+	90689594	90693583	3221
ENSG00000(	1107.262	953.7959	920.9508	1558.826	1319.899	1482.003	-0.54635	2.67E-05	9.40E-05	BRMS1	chr11	-	66104804	66112596	1817
ENSG00000(	39365.27	39159.82	32371.82	22195.11	19688.96	21155.73	0.81348	6.01E-13	4.17E-12	RPL15	chr3	+	23958036	23965183	2730
ENSG00000(	48.68222	22.88147	42.22124	291.3904	257.721	323.8542	-2.9046	5.08E-28	7.11E-27	C4orf32	chr4	+	1.13E+08	1.13E+08	2726
ENSG00000(	755.0923	791.217	653.1098	1400.771	1123.847	1349.666	-0.81439	4.62E-09	2.39E-08	HRAS	chr11	-	532242	537287	1233
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	WDR49	chr3	-	1.67E+08	1.67E+08	2594
ENSG00000(	2157.555	2118.342	2341.959	2016.511	1862.034	1759.005	0.23047	0.04303	0.085314	SRP72	chr4	+	57333081	57369839	3983
ENSG00000(	5.17896	3.612863	0	2.247227	10.12475	9.863579	-1.0933	0.26852	0.38882	PCP2	chr19	-	7696497	7698634	776
ENSG00000(	2583.265	2594.036	2083.354	298.8811	265.0844	275.3582	3.1042	7.57E-115	7.35E-113	RIN1	chr11	-	66097713	66104311	4416
ENSG00000(	1.035792	0	0	5.992604	0	2.465895	-1.6639	0.21163	0.32156	C4orf26	chr4	+	76481258	76491095	1874
ENSG00000(	157.4404	134.8802	164.9267	162.5494	127.0196	110.1433	0.1904	0.4179	0.54863	THAP6	chr4	+	76439156	76475683	3549
ENSG00000(	206.1226	173.4174	250.6886	212.7375	254.9597	189.0519	-0.05956	0.77655	0.85305	CEP135	chr4	+	56815037	56899529	5562
ENSG00000(	85.97073	78.2787	114.789	134.8336	152.7917	116.719	-0.53318	0.037606	0.075852	FZD4	chr11	-	86656721	86666433	7383
ENSG00000(	7587.176	7146.243	6261.938	252.4385	234.7102	254.8091	4.8117	0	0	CD248	chr11	-	66081958	66084515	2558
ENSG00000(	0	0	0	8.988907	0.920432	9.041614	-3.3897	0.007076	0.017023	BTC	chr4	-	75669969	75719896	2816
ENSG00000(	7.250543	9.634302	22.43003	8.988907	2.761296	6.575719	0.98399	0.19372	0.29968	PDZK1	chr1	+	1.46E+08	1.46E+08	2084
ENSG00000(	400.8515	397.4149	379.9912	390.2684	413.274	320.5663	0.068556	0.67261	0.77489	DENND6A	chr3	-	57611184	57678816	4655
ENSG00000(	359.4198	439.565	432.7677	708.6255	707.8122	681.4089	-0.76799	1.16E-07	5.29E-07	PDE12	chr3	+	57542003	57547684	3886
ENSG00000(	159.512	208.3418	182.0791	423.9768	277.9705	293.4415	-0.85409	5.42E-05	0.000183	GLMN	chr1	-	92711959	92764544	1995
ENSG00000(	1.035792	7.225726	2.638828	8.988907	1.840864	2.465895	-0.25531	0.80522	0.87373	DNAH12	chr3	-	57327727	57530071	9542
ENSG00000(	2440.326	2319.458	1942.177	1337.849	1125.688	1175.41	0.8791	1.40E-11	8.84E-11	YIF1A	chr11	-	66052051	66056641	1124
ENSG00000(	234.089	237.2447	230.8974	58.42789	78.23672	62.46933	1.8104	7.92E-16	6.56E-15	CNIH2	chr11	+	66045661	66052772	1524
ENSG00000(	2.071584	2.408575	2.638828	0	0	0	2.2753	0.091747	0.16332	NLRP6	chr11	+	278365	285359	2936
ENSG00000(	125.3308	95.13873	83.12307	141.5753	119.6562	162.7491	-0.47305	0.063213	0.11891	NDUFA11	chr19	-	5891287	5904017	2406
ENSG00000(	310.7376	264.9433	306.104	338.5821	299.1404	260.5629	-0.02697	0.87949	0.9246	RSRC1	chr3	+	1.58E+08	1.58E+08	2411
ENSG00000(	3.107376	0	0	0	0	0.821965	0.7418	0.57612	NA	CATSPERD	chr19	+	5720688	5778745	2516
ENSG00000(	0	0	0	5.243529	10.12475	9.041614	-3.8521	0.001354	0.003718	C3orf55	chr3	+	1.57E+08	1.57E+08	1484
ENSG00000(	1753.596	1752.239	1402.537	1537.852	1503.986	1542.006	0.099148	0.42883	0.55896	RAB1B	chr11	+	66036004	66044963	2007
ENSG00000(	6.214751	6.021439	6.597069	1.498151	0.920432	0.821965	2.051	0.050555	0.098054	METTL15P1	chr3	-	1.56E+08	1.56E+08	1045
ENSG00000(	1284.382	1132.03	992.1992	1181.292	954.488	971.5625	0.1336	0.34964	0.47938	PTDSS2	chr11	+	448268	491393	3128
ENSG00000(	805.8461	757.497	614.8468	474.1648	483.2268	639.4887	0.44737	0.006665	0.016092	C19orf70	chr19	-	5678432	5680907	896
ENSG00000(	24.85901	30.10719	18.47179	32.95932	20.2495	27.94681	-0.14082	0.76507	0.84495	C3orf33	chr3	-	1.55E+08	1.56E+08	1931
ENSG00000(	2176.199	2079.805	1530.52	432.9657	421.5579	415.9142	2.1814	4.17E-49	1.13E-47	SEZ6L2	chr16	-	29882480	29910868	3801
ENSG00000(	291.0575	291.4376	308.7428	43.44638	70.87326	78.08667	2.2003	7.04E-21	7.39E-20	ASPHD1	chr16	+	29911696	29931185	1732
ENSG00000(	457.82	427.5221	349.6447	252.4385	202.495	258.097	0.78917	1.15E-05	4.25E-05	KCTD13	chr16	-	29916333	29938356	2528
ENSG00000(	0	0	0	1.498151	5.522592	2.465895	-2.3902	0.071608	0.13235	P2RY14	chr3	-	1.51E+08	1.51E+08	2513

ENSG00000(	4.143168	1.204288	1.319414	24.71949	20.2495	32.05663	-3.1766	2.37E-05	8.40E-05	AMZ1	chr7	+	2719156	2804759	5516
ENSG00000(	0	0	0	0.749076	2.761296	3.28786	-1.9076	0.15797	0.25445	GPR171	chr3	-	1.51E+08	1.51E+08	1786
ENSG00000(	0	0	0	2.247227	5.522592	2.465895	-2.5145	0.056285	0.10767	GPR149	chr3	-	1.54E+08	1.54E+08	2323
ENSG00000(	0	0	0	2.247227	1.840864	0.821965	-1.4859	0.2733	NA	CD164L2	chr1	-	27705666	27709870	1457
ENSG00000(	0	0	0	64.4205	91.12277	69.04505	-6.9709	7.20E-12	4.64E-11	FUT1	chr19	-	49251268	49258647	4246
ENSG00000(	904.2463	981.4945	1125.46	1331.107	1282.162	1112.119	-0.30745	0.022603	0.048369	DHX36	chr3	-	1.54E+08	1.54E+08	6733
ENSG00000(	540.6834	513.0266	621.4439	41.94823	70.87326	62.46933	3.2459	2.68E-55	8.35E-54	ZIC4	chr3	-	1.47E+08	1.47E+08	4331
ENSG00000(	62.14751	71.05298	80.48424	107.1178	59.82808	98.63579	-0.31668	0.30347	0.42856	AC026271.	chr17	+	18553508	18554855	1348
ENSG00000(	863.8504	776.7656	767.8988	549.8215	555.9409	534.2772	0.55403	2.70E-05	9.50E-05	FBXW8	chr12	+	1.17E+08	1.17E+08	4648
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CA5A	chr16	-	87921625	87970135	1094
ENSG00000(	0	0	0	2.247227	2.761296	0.821965	-1.7061	0.20822	NA	ZG16	chr16	+	29789561	29793096	1934
ENSG00000(	441.2474	511.8223	381.3106	862.186	779.6059	913.203	-0.93366	6.19E-10	3.45E-09	KLC2	chr11	+	66024765	66035331	3755
ENSG00000(	5.17896	8.430014	35.62417	12.73428	5.522592	17.26126	0.41451	0.56509	0.68462	SLC22A1	chr6	+	1.61E+08	1.61E+08	1948
ENSG00000(	3.107376	2.408575	0	0	0	0	1.7825	0.18787	NA	TEX36	chr10	-	1.27E+08	1.27E+08	922
ENSG00000(	1525.721	1322.308	1415.731	2332.621	2150.129	1985.867	-0.59988	5.86E-07	2.49E-06	CTBP2	chr10	-	1.27E+08	1.27E+08	3669
ENSG00000(	2246.633	2053.311	2310.294	175.2837	151.8713	150.4196	3.7791	2.72E-171	5.60E-169	CHST2	chr3	+	1.43E+08	1.43E+08	3526
ENSG00000(	190.5857	114.4073	183.3985	389.5193	350.6846	295.0854	-1.0761	6.37E-07	2.70E-06	ZDHHC14	chr6	+	1.58E+08	1.58E+08	7380
ENSG00000(	397.7441	340.8134	523.8073	352.0655	430.7622	305.7709	0.21203	0.27191	0.39255	ATR	chr3	-	1.42E+08	1.42E+08	8249
ENSG00000(	5844.974	5933.526	5154.95	2773.078	2926.053	3601.028	0.86283	7.22E-12	4.64E-11	C17orf76-A	chr17	+	16342136	16381992	1662
ENSG00000(	597.6519	549.1552	544.9179	2539.366	2087.54	2522.61	-2.074	4.47E-58	1.49E-56	UBE2C	chr20	+	44441215	44445596	1446
ENSG00000(	1.035792	2.408575	0	0.749076	0	2.465895	0.058063	0.96545	0.97997	DSG4	chr18	+	28956740	28994875	4526
ENSG00000(	317.9881	321.5448	306.104	94.38352	117.8153	85.48435	1.6618	1.45E-16	1.24E-15	GK5	chr3	-	1.42E+08	1.42E+08	4479
ENSG00000(	362.5272	407.0492	457.8366	295.8848	381.9793	274.5363	0.36434	0.042361	0.084127	VCPIP1	chr8	-	67540722	67579452	9942
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RTP1	chr3	+	1.87E+08	1.87E+08	2217
ENSG00000(	5.17896	4.817151	2.638828	0	0	0	3.172	0.014447	0.032394	DES	chr2	+	2.2E+08	2.2E+08	2248
ENSG00000(	69.39806	55.39724	109.5113	57.67882	92.96363	89.59418	-0.03753	0.9086	0.94374	PDIK1L	chr1	+	26437664	26452034	4279
ENSG00000(	9.322127	13.24716	7.916483	1130.355	1175.392	1250.209	-6.7736	1.25E-109	1.10E-107	SPSB4	chr3	+	1.41E+08	1.41E+08	2908
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RAG2	chr11	-	36597124	36619829	2388
ENSG00000(	262.0554	214.3632	284.9934	231.4643	290.8565	236.7259	0.005412	0.97748	0.98685	TRAF6	chr11	-	36508577	36531822	4627
ENSG00000(	287.9501	315.5234	335.1311	189.5161	192.3703	126.5826	0.87859	1.74E-05	6.28E-05	ZNF654	chr3	+	88188254	88193815	4966
ENSG00000(	166.7625	161.3746	172.8432	96.63075	80.99802	114.2531	0.77139	0.000921	0.002596	TVP23C	chr17	-	15341205	15466909	2989
ENSG00000(	427.7821	485.328	453.8783	632.9688	530.1688	561.402	-0.33569	0.02272	0.048579	MRPS22	chr3	+	1.39E+08	1.39E+08	2160
ENSG00000(	1911.036	1808.84	1711.28	1341.594	1422.067	1410.492	0.37975	0.000761	0.002179	PACS1	chr11	+	65837834	66012218	4392
ENSG00000(	7145.928	6423.671	6330.547	8604.631	8748.706	9445.199	-0.42856	4.27E-05	0.000147	MARCKSL1	chr1	-	32799433	32801980	1699
ENSG00000(	1272.988	1328.329	1227.055	959.5658	1200.243	1118.694	0.22401	0.080883	0.14675	SH3BP5L	chr1	-	2.49E+08	2.49E+08	4122
ENSG00000(	0	0	0	3.745378	1.840864	0	-1.5327	0.25777	NA	TMEM51-AS	chr1	-	15442448	15478960	2962
ENSG00000(	117.0445	114.4073	133.2608	18.72689	27.61296	27.12484	2.2859	3.41E-13	2.42E-12	YPEL2	chr17	+	57409050	57479090	5217
ENSG00000(	9.322127	4.817151	9.235896	2.996302	0.920432	5.753754	1.0988	0.22893	0.34232	CADM2	chr3	+	85008132	86123579	9488
ENSG00000(	4344.111	3832.044	4367.26	7236.07	6502.852	6841.214	-0.71325	3.51E-11	2.15E-10	PSMD2	chr3	+	1.84E+08	1.84E+08	3449
ENSG00000(	0	1.204288	0	0	3.681728	1.64393	-1.0814	0.42455	0.55513	FAM182B	chr20	-	25744102	25848861	1681
ENSG00000(	0	6.021439	11.87472	6.74168	18.40864	9.863579	-0.88149	0.30301	0.42814	PPM1E	chr17	+	56833230	57058983	2988
ENSG00000(	146.0467	148.1274	110.8308	104.8706	154.6326	145.4878	0.005228	0.98301	0.99027	FAM131A	chr3	+	1.84E+08	1.84E+08	3677
ENSG00000(	744.7344	858.6571	719.0805	1203.015	1202.084	1445.014	-0.72737	9.51E-08	4.37E-07	CSRP2	chr12	-	77252495	77272840	5078
ENSG00000(	0	0	2.638828	0	0.920432	0	0.55591	0.6721	NA	INHBC	chr12	+	57828527	57845842	1992

ENSG00000(	515.8244	478.1022	467.0725	880.9128	605.6443	702.78	-0.58186	0.000319	0.000968	PARL	chr3	-	1.84E+08	1.84E+08	1414
ENSG00000(	127.4024	131.2674	113.4696	99.62705	60.74851	67.40112	0.69719	0.010947	0.025231	DDIT3	chr12	-	57910371	57914300	1151
ENSG00000(	302.4512	266.1476	357.5611	447.9472	408.6718	410.9825	-0.45304	0.006777	0.016353	PCCA	chr13	+	1.01E+08	1.01E+08	2491
ENSG00000(	0	12.04288	1.319414	0	4.60216	1.64393	0.81689	0.49487	0.62365	HIGD2B	chr15	-	72968124	72978490	1116
ENSG00000(	3257.566	3264.824	2917.224	2748.358	2325.932	2428.084	0.33072	0.004167	0.01049	DCTN2	chr12	-	57923885	57941114	2061
ENSG00000(	2.071584	8.430014	1.319414	11.23613	1.840864	4.93179	-0.52336	0.59479	0.71076	NPPA	chr1	-	11905766	11908402	855
ENSG00000(	283.807	266.1476	266.5216	390.2684	300.9813	315.6345	-0.30188	0.085508	0.15412	ZNF408	chr11	+	46722368	46727462	2442
ENSG00000(	6580.386	6080.449	7168.375	1056.946	1226.015	1078.418	2.5563	2.61E-107	2.23E-105	CTDSP2	chr12	-	58213710	58240522	4795
ENSG00000(	1874.783	1741.4	2116.34	3328.143	3261.091	2570.284	-0.67477	4.01E-07	1.74E-06	CKAP5	chr11	-	46764598	46867847	7121
ENSG00000(	2680.629	2751.797	2303.696	2320.636	2049.802	2132.177	0.25023	0.034266	0.069842	ARHGAP1	chr11	-	46698630	46722165	3375
ENSG00000(	1493.612	1390.952	1022.546	1342.343	977.4988	988.8238	0.23926	0.15071	0.24496	MED16	chr19	-	867961	893218	3121
ENSG00000(	903.2105	853.84	862.8966	892.8981	975.6579	868.8169	-0.06238	0.61644	0.72921	ATG13	chr11	+	46638826	46696368	4728
ENSG00000(	4.143168	1.204288	2.638828	2.996302	1.840864	0	0.52726	0.66278	0.76688	GAL3ST3	chr11	-	65809423	65816651	2133
ENSG00000(	291.0575	284.2119	302.1458	17.22874	5.522592	6.575719	4.7922	2.26E-49	6.14E-48	CHST1	chr11	-	45670427	45687172	2718
ENSG00000(	1134.192	1262.094	1048.934	350.5674	275.2092	292.6195	1.9	6.69E-38	1.31E-36	GOLGA8A	chr15	-	34671269	34880704	6478
ENSG00000(	1.035792	0	0	0	0	3.28786	-0.59917	0.65385	NA	VWA3A	chr16	+	22103859	22168287	4659
ENSG00000(	956.0359	903.2158	938.1032	987.2816	938.8406	1055.403	-0.09185	0.45329	0.58308	TP53I11	chr11	-	44907454	44972840	3703
ENSG00000(	40.39588	46.96722	39.58241	46.44268	40.49901	36.16646	0.042079	0.90917	0.94409	APITD1	chr1	+	10490159	10512210	1469
ENSG00000(	311.7734	296.2548	294.2293	503.3788	406.8309	452.9027	-0.59358	0.000218	0.000676	DOLK	chr9	-	1.32E+08	1.32E+08	2090
ENSG00000(	15.53688	4.817151	5.277655	149.066	103.0884	104.3895	-3.6524	4.16E-17	3.67E-16	PHYHD1	chr9	+	1.32E+08	1.32E+08	2133
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	CATSPER1	chr11	-	65784223	65793988	2619
ENSG00000(	42.46747	21.67718	14.51355	77.90386	84.67974	61.64737	-1.457	0.000287	0.000875	CCNE2	chr8	-	95891998	95908906	3330
ENSG00000(	1018.183	1201.879	942.0614	236.7079	234.7102	328.786	1.9748	3.57E-32	5.80E-31	AGXT2L2	chr5	-	1.78E+08	1.78E+08	2780
ENSG00000(	0	0	0	2.996302	3.681728	9.863579	-3.2333	0.010409	0.024107	CST6	chr11	+	65779312	65780976	759
ENSG00000(	7.250543	0	1.319414	106.3687	115.054	96.99186	-4.8666	4.24E-18	3.93E-17	GRAMD2	chr15	-	72452148	72490126	3281
ENSG00000(	53.86118	71.05298	50.13772	221.7264	209.8585	206.3132	-1.8505	2.31E-14	1.75E-13	ZNF519	chr18	-	14057456	14132489	6497
ENSG00000(	259.9838	244.4704	204.5091	242.7005	310.1856	329.6079	-0.3108	0.1062	0.18425	LSM1	chr8	-	38020839	38034248	1568
ENSG00000(	2052.94	2082.213	1779.889	2983.568	2741.967	3168.675	-0.58707	5.91E-07	2.51E-06	BANF1	chr11	+	65769550	65771620	1155
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	APOF	chr12	-	56754353	56756607	1715
ENSG00000(	4.143168	13.24716	25.06886	19.47596	44.18074	26.30288	-1.0461	0.077653	0.14168	CHRNA7	chr15	+	32322691	32464722	5669
ENSG00000(	617.332	641.8854	642.5545	651.6957	508.0785	564.6899	0.13932	0.3365	0.46489	TMEM9B	chr11	-	8968841	8986558	2083
ENSG00000(	72.50543	103.5687	75.20659	41.19916	22.09037	36.98842	1.2949	0.000215	0.000667	NRIP3	chr11	-	9002123	9025596	3809
ENSG00000(	466.1064	481.7151	445.9619	689.8986	547.657	532.6333	-0.34443	0.025718	0.054303	PTPN2	chr18	-	12785477	12929642	3390
ENSG00000(	10.35792	15.65574	17.15238	14.23244	3.681728	16.4393	0.29321	0.66203	0.76639	SCUBE2	chr11	-	9041071	9159661	4683
ENSG00000(	395.6725	417.8878	386.5882	575.29	471.2612	483.3154	-0.34991	0.022369	0.047933	EIF1AD	chr11	-	65764016	65769647	2887
ENSG00000(	1282.31	1260.889	1410.453	1562.572	1504.906	1328.295	-0.1531	0.21082	0.32071	SMAD2	chr18	-	45357922	45457515	12075
ENSG00000(	7110.711	6853.601	5457.095	6635.311	5115.761	5120.841	0.20254	0.1432	0.2349	EIF3F	chr11	+	7991798	8023409	7540
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	OR10A6	chr11	-	7949180	7950209	1030
ENSG00000(	201.9794	216.7718	207.148	6.74168	32.21512	17.26126	3.4469	1.50E-23	1.75E-22	ZNF25	chr10	-	38238500	38265561	4139
ENSG00000(	1931.752	1825.7	2016.064	343.0766	447.33	415.9142	2.255	7.03E-63	2.62E-61	ARL10	chr5	+	1.76E+08	1.76E+08	10845
ENSG00000(	913.5685	798.4428	700.6087	2229.249	1925.544	2384.52	-1.4335	2.47E-25	3.09E-24	CLTB	chr5	-	1.76E+08	1.76E+08	1489
ENSG00000(	7.250543	2.408575	17.15238	3.745378	4.60216	0.821965	1.3312	0.15305	0.24818	PCSK1	chr5	-	95726119	95769847	5086
ENSG00000(	0	0	0	301.1284	400.3879	318.9224	-8.9031	5.24E-21	5.52E-20	LPL	chr8	+	19759228	19824769	3846
ENSG00000(	6.214751	6.021439	11.87472	7.490755	9.20432	5.753754	0.086964	0.91034	0.94496	RFESD	chr5	+	94982458	94993786	2788

ENSG00000(	701.2311	782.787	915.6732	896.6434	917.6707	937.862	-0.19876	0.14764	0.24077	CCDC14	chr3	-	1.24E+08	1.24E+08	7917
ENSG00000(	26.93059	40.94578	13.19414	1.498151	4.60216	17.26126	1.6722	0.016501	0.036508	TBC1D10C	chr11	+	67171386	67177560	4480
ENSG00000(	1885.141	1895.549	1626.837	1429.985	1687.152	2068.886	0.060688	0.6747	0.77655	SART1	chr11	+	65729160	65747299	3293
ENSG00000(	488.8938	527.478	443.323	838.2155	673.7562	657.5719	-0.57005	0.00019	0.000594	PPP2R2D	chr10	+	1.34E+08	1.34E+08	5133
ENSG00000(	350.0977	390.1892	439.3648	119.103	116.8949	90.41614	1.8424	4.21E-21	4.46E-20	MCTP1	chr5	-	94039446	94620279	5396
ENSG00000(	35.21692	21.67718	26.38828	5.992604	20.2495	19.72716	0.83326	0.13117	0.21882	POLD4	chr11	-	67118248	67124443	1793
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	OR52W1	chr11	+	6220376	6221489	1114
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	LRRC25	chr19	-	18501954	18508427	2415
ENSG00000(	0	0	0	78.65293	104.9292	71.51095	-7.1348	1.78E-12	1.20E-11	DPP10	chr2	+	1.15E+08	1.17E+08	6278
ENSG00000(	79.75598	62.62296	68.60952	63.67142	38.65814	50.96182	0.45139	0.16858	0.26833	CLCF1	chr11	-	67131639	67141648	1844
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	TSGA10IP	chr11	+	65712916	65727434	1925
ENSG00000(	5.17896	13.24716	5.277655	7.490755	0.920432	2.465895	0.95244	0.30276	0.42792	UBQLNL	chr11	-	5535623	5537935	2313
ENSG00000(	2.071584	0	11.87472	25.46857	15.64734	18.08323	-1.9318	0.013708	0.030924	LIPT2	chr11	-	74202757	74204778	1018
ENSG00000(	5.17896	9.634302	18.47179	12.73428	21.16994	9.863579	-0.38149	0.56981	0.68881	KCNE3	chr11	-	74165886	74178774	3143
ENSG00000(	30.03797	27.69862	47.4989	69.66403	74.55499	56.71558	-0.92364	0.010506	0.024306	ALG10B	chr12	+	38710380	38717784	3111
ENSG00000(	2993.439	2779.496	2476.54	2107.899	1941.191	2660.7	0.29746	0.030828	0.063656	DRAP1	chr11	+	65686728	65689032	989
ENSG00000(	0	6.021439	1.319414	9.737982	3.681728	4.109825	-1.0373	0.32711	0.45476	LONRF3	chrX	+	1.18E+08	1.18E+08	3973
ENSG00000(	21.75163	30.10719	11.87472	33.7084	32.21512	38.63235	-0.68637	0.14297	0.2346	UCP3	chr11	-	73711326	73720480	2623
ENSG00000(	114.9729	103.5687	118.7472	1121.366	858.7631	895.9418	-3.0803	3.41E-70	1.48E-68	UCP2	chr11	-	73685712	73694352	2113
ENSG00000(	1071.009	900.8072	800.8842	626.9762	452.8525	429.8877	0.87331	3.40E-07	1.49E-06	C11orf68	chr11	-	65684279	65686588	1619
ENSG00000(	337.6682	313.1148	320.6175	425.4749	337.7985	403.5848	-0.26419	0.10811	0.18693	PAAF1	chr11	+	73587744	73638790	2020
ENSG00000(	423.6389	392.5978	360.2	431.4675	345.162	369.8842	0.037199	0.81932	0.88331	MRPL48	chr11	+	73498361	73576178	1922
ENSG00000(	1983.541	2118.342	2196.824	2548.355	1989.054	1868.326	-0.02486	0.85368	0.9068	RAB6A	chr11	-	73386938	73472182	3134
ENSG00000(	0	0	0	59.92604	98.48622	67.40112	-6.9703	7.80E-12	5.01E-11	P2RY2	chr11	+	72929343	72947397	2660
ENSG00000(	518.9317	505.8008	435.4065	1736.357	1216.811	1269.114	-1.526	9.25E-22	1.01E-20	FOSL1	chr11	-	65659520	65668044	1669
ENSG00000(	151.2256	140.9017	163.6073	185.0217	169.3595	145.4878	-0.13396	0.53165	0.65631	ERCC4	chr16	+	14014014	14046202	6758
ENSG00000(	1684.198	1766.69	1669.058	86.14369	92.0432	103.5676	4.1726	3.86E-179	8.89E-177	C7orf10	chr7	+	40174575	40900362	1719
ENSG00000(	1306.134	1334.351	924.9091	834.4702	712.4144	833.4724	0.58145	0.000188	0.000589	CCDC85B	chr11	+	65657875	65659105	1231
ENSG00000(	2.071584	0	2.638828	0	0	0	1.5584	0.24658	NA	RP11-276H	chr16	-	12180603	12184159	1974
ENSG00000(	306.5944	273.3733	288.9516	653.1939	430.7622	544.9627	-0.90337	4.50E-07	1.94E-06	TMEM70	chr8	+	74884672	74895018	2018
ENSG00000(	82.86335	73.46155	94.99779	87.64184	92.0432	84.66239	-0.07339	0.78537	0.85885	LINC00476	chr9	-	98521513	98638259	2825
ENSG00000(	618.3678	544.338	459.156	675.6661	602.883	654.2841	-0.25057	0.097843	0.1722	RPS6KB2	chr11	+	67195931	67202872	5528
ENSG00000(	47.64643	80.68728	60.69303	547.5742	398.5471	526.0575	-2.948	4.68E-39	9.42E-38	RMI2	chr16	+	11343476	11445619	1865
ENSG00000(	874.2084	852.6357	930.1867	1288.41	1496.622	1454.056	-0.67252	5.29E-08	2.49E-07	TOM1L2	chr17	-	17746828	17875736	5592
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	TEX26	chr13	+	31506840	31549639	1478
ENSG00000(	44.53905	27.69862	54.09597	44.19546	46.0216	52.60575	-0.17549	0.64105	0.74879	ZNF77	chr19	-	2933216	2944969	2002
ENSG00000(	5.17896	3.612863	10.55531	15.73059	15.64734	4.93179	-0.83924	0.27652	0.39806	GPR156	chr3	-	1.2E+08	1.2E+08	4442
ENSG00000(	99.43602	95.13873	81.80365	145.3207	126.0992	195.6277	-0.74852	0.003282	0.008431	LINC00116	chr2	-	1.11E+08	1.11E+08	2051
ENSG00000(	2.071584	4.817151	5.277655	205.2467	157.3939	191.5178	-5.361	2.08E-28	2.98E-27	C1orf172	chr1	-	27276053	27286897	1793
ENSG00000(	143.9751	136.0845	125.3443	131.8373	114.1336	122.4728	0.13742	0.54377	0.66614	B3GNTL1	chr17	-	80900031	81009686	3324
ENSG00000(	1.035792	0	0	0	2.761296	0.821965	-0.71844	0.59551	NA	RBMXL3	chrX	+	1.14E+08	1.14E+08	3469
ENSG00000(	773.7366	835.7757	730.9552	442.7036	680.1992	567.1558	0.46974	0.004281	0.010753	MLXIP	chr12	+	1.23E+08	1.23E+08	5799
ENSG00000(	5.17896	6.021439	13.19414	0	0	0	4.1941	0.000538	0.001572	C11orf44	chr11	+	1.31E+08	1.31E+08	3547
ENSG00000(	13.46529	9.634302	6.597069	11.98521	9.20432	16.4393	-0.31028	0.64458	0.75173	BAK1P1	chr20	-	31276723	31278816	2094

ENSG00000(	43.50326	39.74149	34.30476	47.19176	58.90765	55.07165	-0.44163	0.213	0.32324	RWDD4P2	chr7	-	39894093	39894655	563
ENSG00000(	1945.217	1754.647	1860.373	196.2578	322.1512	210.423	2.9244	1.06E-67	4.44E-66	NR2F1	chr5	+	92919043	92930321	3732
ENSG00000(	0	0	1.319414	0	3.681728	0	-0.65657	0.62582	NA	C15orf54	chr15	+	39542885	39547046	3078
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	EIF3KP1	chr5	+	1.02E+08	1.02E+08	656
ENSG00000(	1735.987	1584.843	1315.456	2479.44	2452.951	2985.377	-0.76935	1.50E-08	7.43E-08	AURKAIP1	chr1	-	1309110	1310875	1072
ENSG00000(	133.6172	81.89156	118.7472	47.94084	31.29469	57.53754	1.2681	7.59E-05	0.000251	TTLL11	chr9	-	1.25E+08	1.25E+08	3250
ENSG00000(	21.75163	26.49433	29.0271	23.22134	28.53339	47.67397	-0.35647	0.43781	0.56742	TOMM5	chr9	-	37582643	37592639	3071
ENSG00000(	7.250543	6.021439	5.277655	0.749076	0	0.821965	2.6739	0.018105	0.039667	AC112229.	chr2	-	1.11E+08	1.11E+08	2443
ENSG00000(	0	1.204288	0	0.749076	2.761296	0	-0.67728	0.61696	NA	RP11-121N	chr11	+	1.3E+08	1.3E+08	669
ENSG00000(	331.4534	352.8563	328.534	478.6593	399.4675	396.1871	-0.33112	0.038509	0.077432	SLC35E3	chr12	+	69139886	69187744	5014
ENSG00000(	0	0	0	2.996302	5.522592	6.575719	-3.1137	0.014104	0.031731	PRIMA1	chr14	-	94184644	94254827	3711
ENSG00000(	73.54123	49.3758	34.30476	53.18436	45.10117	36.98842	0.2201	0.56109	0.68128	ZNF169	chr9	+	97021593	97063736	2716
ENSG00000(	1208.769	1257.276	1270.595	2249.474	2032.314	2257.938	-0.80661	8.84E-13	6.08E-12	RUVBL1	chr3	-	1.28E+08	1.28E+08	4062
ENSG00000(	14.50109	14.45145	2.638828	809.7507	809.0597	881.9684	-6.1745	6.32E-91	4.09E-89	SFN	chr1	+	27189633	27190947	1315
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	OR52B3P	chr11	+	4399512	4400457	942
ENSG00000(	131.5456	105.9773	97.63662	185.0217	158.3143	200.5594	-0.68989	0.002642	0.006893	MSRA	chr8	+	9911778	10286401	1706
ENSG00000(	0	2.408575	1.319414	0.749076	2.761296	2.465895	-0.46861	0.71215	0.80544	CCDC168	chr13	-	1.03E+08	1.03E+08	7359
ENSG00000(	1197.375	1138.052	915.6732	833.7211	786.9694	858.1314	0.39117	0.004532	0.011324	CTDNEP1	chr17	-	7146910	7155810	1724
ENSG00000(	288.9859	234.8361	222.9809	1128.857	1198.402	1373.503	-2.2976	8.48E-51	2.39E-49	ETV4	chr17	-	41605212	41656988	2429
ENSG00000(	340.7755	372.1249	284.9934	221.7264	181.3251	259.7409	0.58699	0.002449	0.006423	SWI5	chr9	+	1.31E+08	1.31E+08	1048
ENSG00000(	638.0478	606.961	529.0849	712.3708	736.3456	720.8632	-0.28797	0.035	0.071145	BAIAP2	chr17	+	79008948	79091232	3689
ENSG00000(	0	0	0	29.96302	26.69253	29.59074	-5.7022	9.49E-08	4.37E-07	CALCB	chr11	+	14926543	15103888	2258
ENSG00000(	41.43168	49.3758	47.4989	53.18436	80.99802	81.37453	-0.62998	0.059225	0.11241	AC004840.	chr7	+	2477398	2487485	2067
ENSG00000(	7.250543	12.04288	7.916483	17.97781	11.96562	17.26126	-0.75295	0.24296	0.35881	CREG2	chr2	-	1.02E+08	1.02E+08	3187
ENSG00000(	155.3688	109.5902	176.8014	4.494453	12.88605	1.64393	4.4563	1.65E-24	2.00E-23	HOXD8	chr2	+	1.77E+08	1.77E+08	2583
ENSG00000(	2.071584	2.408575	3.958241	3.745378	2.761296	2.465895	-0.08341	0.93811	0.96242	RPL7AP66	chr18	-	36914836	36915639	804
ENSG00000(	85.97073	97.54731	126.6637	205.9958	252.1984	139.734	-0.94139	0.000325	0.000984	ZDHHC21	chr9	-	14615530	14693469	4699
ENSG00000(	9.322127	1.204288	3.958241	1.498151	0.920432	0	1.917	0.10245	0.17887	TSPEAR	chr21	-	45917775	46131495	3967
ENSG00000(	95.29286	102.3645	89.72014	298.8811	300.0608	268.7825	-1.5844	6.17E-15	4.85E-14	PLEKHF2	chr8	+	96146032	96168912	2881
ENSG00000(	1000.575	1113.966	719.0805	104.8706	107.6905	138.0901	3.0005	3.49E-56	1.11E-54	CTD-2369P	chr19	-	10332111	10333870	1760
ENSG00000(	793.4166	749.067	815.3977	2119.884	2104.108	1641.464	-1.3116	2.65E-22	2.95E-21	A2M	chr12	-	9220260	9268825	4844
ENSG00000(	548.9697	558.7895	451.2395	89.88907	50.62376	100.2797	2.6709	9.50E-34	1.64E-32	ARL4D	chr17	+	41476327	41478505	1612
ENSG00000(	101.5076	92.73015	56.73479	58.42789	56.14635	50.13986	0.6044	0.056751	0.10845	AC127496.	chr17	+	78977135	78978932	1798
ENSG00000(	14.50109	9.634302	17.15238	1.498151	1.840864	13.15144	1.1904	0.14181	0.23334	DOK7	chr4	+	3465033	3503200	2562
ENSG00000(	3.107376	7.225726	1.319414	6504.972	6033.432	5250.712	-10.278	1.14E-130	1.38E-128	LRRN1	chr3	+	3841121	3889387	3823
ENSG00000(	928.0695	975.4731	903.7984	781.2858	938.8406	981.4261	0.055949	0.67721	0.77852	UBE2O	chr17	-	74385532	74449288	5436
ENSG00000(	146.0467	98.75159	75.20659	30.7121	48.7829	32.8786	1.4969	1.05E-05	3.87E-05	ORAI3	chr16	+	30960387	30967782	2206
ENSG00000(	1.035792	3.612863	0	0	0	0	1.5346	0.25314	NA	KLHL38	chr8	-	1.25E+08	1.25E+08	1982
ENSG00000(	4.143168	0	5.277655	0.749076	0	0	2.0623	0.11889	0.20224	RP11-544L	chr6	+	1.14E+08	1.14E+08	2255
ENSG00000(	1095.868	1048.935	1277.193	721.3598	1054.815	858.1314	0.37673	0.014941	0.033373	UNC119B	chr12	+	1.21E+08	1.21E+08	4404
ENSG00000(	60.07593	56.60152	56.73479	42.69731	27.61296	36.16646	0.68705	0.054354	0.10453	DENND2C	chr1	-	1.15E+08	1.15E+08	6163
ENSG00000(	1.035792	0	2.638828	0	0.920432	0.821965	0.5719	0.67274	NA	PLEKHD1	chr14	+	69951409	69995215	3999
ENSG00000(	0	0	1.319414	2.247227	0	1.64393	-0.7954	0.55767	NA	ASCL3	chr11	-	8959119	8964580	650
ENSG00000(	3645.988	3553.853	3219.37	9972.443	8467.974	8266.501	-1.3554	5.68E-32	9.17E-31	TUBB6	chr18	+	12307668	12344319	2163

ENSG00000(	388.422	408.2535	486.8637	247.944	277.05	238.3698	0.746	9.82E-06	3.65E-05	LYSMD3	chr5	-	89811428	89825401	4259
ENSG00000(	1094.832	1086.268	949.9779	848.7026	762.1177	669.0794	0.45673	0.000949	0.002671	B3GALT6	chr1	+	1167629	1170421	2793
ENSG00000(	24.85901	48.17151	55.41538	83.89646	37.73771	77.2647	-0.62975	0.11558	0.19774	ZNF613	chr19	+	52430400	52452012	2710
ENSG00000(	1.035792	4.817151	1.319414	8.239831	8.283888	3.28786	-1.2337	0.21554	0.32624	C11orf16	chr11	-	8941623	8954553	1908
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	CHDC2	chrX	+	36053913	36163187	1958
ENSG00000(	1345.494	1333.147	919.6314	23.97042	36.81728	49.3179	5.0041	1.92E-111	1.73E-109	NUPR1	chr16	-	28548606	28550495	914
ENSG00000(	286.9144	295.0505	278.3963	61.42419	60.74851	46.852	2.3326	1.69E-26	2.22E-25	JAKMIP2	chr5	-	1.47E+08	1.47E+08	6001
ENSG00000(	6.214751	4.817151	3.958241	3.745378	12.88605	13.15144	-0.87457	0.28716	0.41072	RPL23P2	chr21	-	30369934	30370354	421
ENSG00000(	133.6172	126.4502	129.3026	71.91125	84.67974	68.22309	0.78816	0.001647	0.004452	MBLAC2	chr5	-	89754020	89770585	4280
ENSG00000(	588.3298	562.4024	455.1978	475.663	378.2976	497.2888	0.24863	0.13356	0.22225	TPRN	chr9	-	1.4E+08	1.4E+08	3350
ENSG00000(	7.250543	2.408575	5.277655	5.992604	3.681728	1.64393	0.34113	0.72499	0.81553	KCNE1L	chrX	-	1.09E+08	1.09E+08	1465
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	ZNF683	chr1	-	26688125	26701013	1712
ENSG00000(	1766.025	1699.25	1711.28	2588.056	2250.456	2006.416	-0.40229	0.001185	0.003282	SLC35A4	chr5	+	1.4E+08	1.4E+08	3617
ENSG00000(	0	0	0	631.4707	876.2513	902.5175	-9.9886	3.05E-28	4.32E-27	AIM1L	chr1	-	26648350	26680621	2523
ENSG00000(	1336.172	1347.598	1314.136	982.038	1210.368	1296.239	0.19666	0.13922	0.22969	IP6K1	chr3	-	49761727	49823975	4456
ENSG00000(	856.5999	785.1956	661.0263	1301.144	1096.235	1312.678	-0.68509	1.27E-06	5.21E-06	SSNA1	chr9	+	1.4E+08	1.4E+08	1170
ENSG00000(	556.2203	504.5966	589.778	735.5922	810.9006	779.2227	-0.49344	0.000286	0.000872	CSTF3	chr11	-	33098734	33183917	2797
ENSG00000(	1109.333	988.7202	1296.984	1471.184	1629.165	1282.265	-0.36769	0.009413	0.022019	YES1	chr18	-	721588	812547	4639
ENSG00000(	188.5141	190.2775	120.0667	197.7559	164.7573	235.082	-0.25587	0.27431	0.39542	CHMP6	chr17	+	78965398	78983317	1664
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AQP7P4	chr9	+	67032331	67048373	1042
ENSG00000(	258.948	262.5347	207.148	216.4828	157.3939	174.2566	0.40776	0.046734	0.091506	DLEU1	chr13	+	50656307	51297372	2440
ENSG00000(	23.82321	31.31148	22.43003	17.22874	21.16994	33.70056	0.10311	0.83143	0.89203	UFSP1	chr7	-	1E+08	1E+08	994
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	AL445665.	chr9	+	69650263	69660358	966
ENSG00000(	937.3917	902.0115	1070.045	532.5927	511.7602	497.2888	0.91315	9.04E-12	5.76E-11	TMEM39A	chr3	-	1.19E+08	1.19E+08	4393
ENSG00000(	287.9501	263.739	304.7846	235.2097	265.0844	210.423	0.26855	0.1367	0.22635	TCP11L1	chr11	+	33060963	33127489	3390
ENSG00000(	8.286335	7.225726	6.597069	3.745378	1.840864	5.753754	0.84366	0.33812	0.46672	GPX2	chr14	-	65405870	65409531	1134
ENSG00000(	695.0164	650.3154	567.3479	514.6149	715.1757	734.0147	-0.03593	0.82718	0.88863	CCDC57	chr17	-	80059336	80170706	5379
ENSG00000(	4.143168	1.204288	0	0.749076	0	0	1.3769	0.30991	0.43609	HSF5	chr17	-	56497528	56565745	4094
ENSG00000(	4.143168	0	2.638828	17.97781	8.283888	12.32947	-2.1769	0.014129	0.031772	FOXG1	chr14	+	29235050	29238870	2754
ENSG00000(	901.139	787.6042	699.2893	1683.922	1353.035	1621.737	-0.96044	9.67E-12	6.16E-11	SPHK1	chr17	+	74372665	74383941	2502
ENSG00000(	4013.694	4742.485	3522.835	802.2599	731.7434	682.2309	2.4637	2.07E-75	1.01E-73	BNIP3	chr10	-	1.34E+08	1.34E+08	1607
ENSG00000(	245.4827	205.9332	230.8974	136.3317	136.2239	132.3364	0.74973	0.000164	0.00052	MYPOP	chr19	-	46393278	46405862	1890
ENSG00000(	0	2.408575	0	8.239831	1.840864	0.821965	-1.4797	0.24008	0.35527	CIDEA	chr18	+	12254318	12277594	1808
ENSG00000(	0	0	0	19.47596	19.32907	22.19305	-5.2167	1.90E-06	7.66E-06	LRRTM4	chr2	-	76974845	77820445	3616
ENSG00000(	122.2234	142.106	151.7326	411.9916	468.4999	378.9258	-1.5934	1.14E-17	1.04E-16	ATAD5	chr17	+	29158988	29222887	6869
ENSG00000(	76.6486	134.8802	113.4696	202.2504	88.36147	167.6808	-0.49592	0.10439	0.18167	SMIM19	chr8	+	42396298	42408151	1466
ENSG00000(	89.0781	118.0202	69.92893	35.20655	15.64734	32.8786	1.6855	4.92E-06	1.89E-05	ZNF404	chr19	-	44376515	44405537	1851
ENSG00000(	98.40023	96.34302	124.0249	295.1358	240.2328	188.23	-1.1779	5.25E-07	2.25E-06	RTTN	chr18	-	67671029	67873181	7326
ENSG00000(	3.107376	4.817151	0	18.72689	3.681728	4.109825	-1.4576	0.13913	0.22959	C10orf111	chr10	-	15137384	15139318	1714
ENSG00000(	3.107376	2.408575	3.958241	16.47966	11.96562	20.54912	-2.1635	0.005059	0.012526	ACBD7	chr10	-	15119522	15130775	1322
ENSG00000(	1057.544	909.2372	728.3164	1135.599	1098.075	1176.232	-0.33676	0.021491	0.046262	ANAPC2	chr9	-	1.4E+08	1.4E+08	2632
ENSG00000(	315.9165	283.0076	324.5758	430.7184	368.1728	491.535	-0.48167	0.004547	0.011359	ZBTB8OS	chr1	-	33065773	33116504	1601
ENSG00000(	0	12.04288	1.319414	3.745378	0	5.753754	0.36259	0.754	0.83729	CYCSP34	chr13	-	41437735	41438038	304
ENSG00000(	78.72018	97.54731	88.40072	143.0734	158.3143	175.0785	-0.84324	0.000416	0.001238	SLC35G1	chr10	+	95653730	95715819	3490

ENSG00000(	67.32647	67.44011	81.80365	42.69731	56.14635	50.13986	0.53289	0.09113	0.16247	SLC25A53	chrX	-	1.03E+08	1.03E+08	6224
ENSG00000(	3.107376	2.408575	3.958241	0	2.761296	0.821965	1.0415	0.38817	0.51894	IDSP1	chrX	+	1.49E+08	1.49E+08	376
ENSG00000(	14.50109	8.430014	39.58241	57.67882	51.54419	58.35951	-1.3963	0.003144	0.008096	ZNF135	chr19	+	58570607	58597677	3349
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	FOXR1	chr11	+	1.19E+08	1.19E+08	1159
ENSG00000(	118.0803	150.536	164.9267	136.3317	101.2475	121.6508	0.26307	0.27459	0.39579	COX8A	chr11	+	63742079	63744015	507
ENSG00000(	1.035792	0	0	0.749076	0.920432	0	-0.14603	0.91115	NA	RPL37AP8	chr11	-	1.12E+08	1.12E+08	276
ENSG00000(	12.4295	10.83859	3.958241	0.749076	2.761296	1.64393	2.0784	0.028879	0.060133	AC110781.	chr7	+	1878222	1889567	4481
ENSG00000(	4.143168	6.021439	0	5.243529	11.04518	4.109825	-0.83017	0.39355	0.5244	TAC4	chr17	-	47915671	47925379	675
ENSG00000(	254.8048	250.4918	340.4088	100.3761	126.0992	126.5826	1.2524	3.94E-09	2.05E-08	ZSCAN2	chr15	+	85144217	85171027	3813
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	PFN1P10	chr1	-	21786249	21786575	327
ENSG00000(	0	3.612863	0	0	0	4.93179	-0.24727	0.85483	0.90765	PRR18	chr6	-	1.67E+08	1.67E+08	2704
ENSG00000(	32.10955	16.86003	14.51355	5.992604	7.363456	5.753754	1.6417	0.010396	0.024081	B3GNT4	chr12	+	1.23E+08	1.23E+08	2938
ENSG00000(	122.2234	128.8588	108.1919	173.0365	127.94	170.9687	-0.39133	0.092658	0.16463	CDC26	chr9	-	1.16E+08	1.16E+08	872
ENSG00000(	41.43168	10.83859	14.51355	4.494453	0	10.68554	1.9376	0.01303	0.029504	HSD11B2	chr16	+	67464555	67471456	1900
ENSG00000(	204.051	233.6318	187.3568	406.748	436.2848	450.4368	-1.044	7.99E-10	4.41E-09	CRLF3	chr17	-	29096406	29151794	2957
ENSG00000(	1674.876	1566.778	1519.965	2793.303	2127.118	2257.116	-0.59071	5.73E-06	2.19E-05	RNPEP	chr1	+	2.02E+08	2.02E+08	2427
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CEACAM20	chr19	-	45005729	45033811	2120
ENSG00000(	392.5651	299.8676	335.1311	484.6519	470.3408	436.4634	-0.43398	0.007354	0.017626	EID2	chr19	-	40028890	40030870	1981
ENSG00000(	27.96638	8.430014	17.15238	38.20285	35.89685	22.19305	-0.80301	0.12338	0.20854	DMRTA1	chr9	+	22446840	22452472	2302
ENSG00000(	52.82539	25.29004	25.06886	29.96302	23.0108	18.08323	0.52825	0.26533	0.38522	EID2B	chr19	-	40021630	40023494	1865
ENSG00000(	0	0	2.638828	2.247227	0	3.28786	-0.65039	0.62676	0.73786	GJC3	chr7	-	99520892	99527243	1116
ENSG00000(	49.71801	42.15007	80.48424	358.0581	333.1964	295.0854	-2.5074	5.42E-25	6.69E-24	RIMS2	chr8	+	1.05E+08	1.05E+08	8002
ENSG00000(	898.0316	757.497	861.5772	1369.31	1074.144	1084.994	-0.48618	0.00062	0.001796	KCMF1	chr2	+	85198216	85282560	3533
ENSG00000(	139.8319	192.686	142.4967	127.3428	110.4518	143.0219	0.31461	0.17927	0.28197	DNAJC30	chr7	-	73096601	73097783	1183
ENSG00000(	123.2592	97.54731	96.31721	158.0549	154.6326	175.9005	-0.61512	0.007617	0.018195	SPRYD4	chr12	+	56862301	56864763	2101
ENSG00000(	186.4425	207.1375	199.2315	3.745378	7.363456	20.54912	4.1518	5.32E-29	7.78E-28	VPS37D	chr7	+	73082155	73086442	1624
ENSG00000(	3.107376	1.204288	0	4.494453	8.283888	4.109825	-1.5174	0.16296	0.26102	CLEC14A	chr14	-	38723308	38725574	2267
ENSG00000(	500.2875	509.4137	525.1267	38.20285	86.52061	74.79881	2.9316	7.13E-37	1.35E-35	SYNE3	chr14	-	95883831	95942173	5493
ENSG00000(	758.1997	836.98	610.8886	838.9646	758.436	860.5973	-0.15489	0.29339	0.41767	CLK2	chr1	-	1.55E+08	1.55E+08	2702
ENSG00000(	620.4394	623.821	621.4439	790.2747	646.1433	753.7418	-0.23158	0.092943	0.16507	LPCAT4	chr15	-	34651106	34659479	1975
ENSG00000(	40.39588	38.53721	27.70769	42.69731	34.97642	32.8786	-0.04762	0.90498	0.94128	SLCO3A1	chr15	+	92396925	92715665	5115
ENSG00000(	72.50543	67.44011	55.41538	22.47227	28.53339	23.83698	1.3651	0.00019	0.000594	ZNF575	chr19	+	44029649	44040282	2285
ENSG00000(	372.8851	307.0934	277.0769	183.5235	168.4391	166.0369	0.88317	3.03E-06	1.19E-05	WDR25	chr14	+	1.01E+08	1.01E+08	2123
ENSG00000(	196.8005	221.5889	145.1355	208.9921	175.8025	202.2034	-0.05715	0.78968	0.86243	CCDC101	chr16	+	28565236	28603111	1153
ENSG00000(	1.035792	2.408575	5.277655	480.1574	431.6826	434.8194	-7.059	8.04E-44	1.86E-42	PLA2G16	chr11	-	63340667	63384355	2594
ENSG00000(	317.9881	325.1577	354.9223	45.69361	52.46462	30.4127	2.9377	1.45E-36	2.71E-35	DIRAS1	chr19	-	2714565	2721416	3424
ENSG00000(	1.035792	6.021439	1.319414	1.498151	0	1.64393	0.96942	0.43546	0.5651	OR10AC1P	chr7	-	1.43E+08	1.43E+08	669
ENSG00000(	201.9794	234.8361	193.9538	310.1173	311.106	421.668	-0.7217	0.000179	0.000563	PHLDB3	chr19	-	43979106	44009087	2591
ENSG00000(	64.2191	40.94578	51.45714	570.0465	697.6875	618.9396	-3.5594	3.61E-65	1.42E-63	PRR15	chr7	+	29603427	29606911	1678
ENSG00000(	26.93059	21.67718	26.38828	12.73428	31.29469	27.12484	0.080746	0.87162	0.91935	GNG7	chr19	-	2511217	2702707	4208
ENSG00000(	291.0575	363.6949	357.5611	166.2948	262.3231	191.5178	0.70461	0.000566	0.001649	KIAA2018	chr3	-	1.13E+08	1.13E+08	13708
ENSG00000(	10.35792	24.08575	21.11062	14.23244	6.443024	9.863579	0.79836	0.20248	0.3103	CNTD1	chr17	+	40950810	40963605	2657
ENSG00000(	176.0846	128.8588	125.3443	125.0956	122.4175	138.0901	0.16105	0.49206	0.62111	CTD-2368P	chr19	+	58513429	58522600	6438
ENSG00000(	1107.262	1026.053	1001.435	39.701	56.14635	41.09825	4.5067	7.36E-135	9.35E-133	KBTBD11	chr8	+	1922044	1955102	6710

ENSG00000(	452.6411	503.3923	596.375	109.365	234.7102	138.9121	1.6759	6.98E-13	4.83E-12	B3GNT5	chr3	+	1.83E+08	1.83E+08	4123
ENSG00000(	3700.884	3502.069	3503.044	8896.77	11717.1	13144.04	-1.6525	9.05E-34	1.56E-32	LMNB2	chr19	-	2427636	2456994	4671
ENSG00000(	702.2669	702.0997	704.567	486.15	404.0696	421.668	0.68181	1.40E-06	5.73E-06	RMDN1	chr8	-	87480486	87526586	3063
ENSG00000(	800.6671	893.5815	981.6439	1207.51	1356.717	1073.486	-0.4426	0.001396	0.003822	MEX3C	chr18	-	48700920	48744674	3850
ENSG00000(	191.6215	191.4817	192.6344	771.5478	1033.645	907.4493	-2.2275	5.32E-43	1.20E-41	RNF152	chr18	-	59475296	59561480	9501
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	NANOGP1	chr12	+	8045172	8051499	915
ENSG00000(	475.4285	523.8652	486.8637	909.3777	803.5371	901.6955	-0.8138	1.74E-09	9.36E-09	MYO1D	chr17	-	30819540	31204195	5563
ENSG00000(	14.50109	9.634302	10.55531	4.494453	0	3.28786	1.8748	0.032374	0.066428	C20orf197	chr20	+	58630980	58648008	2732
ENSG00000(	73.54123	81.89156	91.03955	4.494453	10.12475	5.753754	3.5185	2.39E-15	1.93E-14	FOXL1	chr16	+	86609974	86615303	3189
ENSG00000(	0	0	0	8.239831	0	0	-1.8813	0.16543	0.26405	TGIF2LY	chrY	+	3447082	3448082	905
ENSG00000(	15.53688	25.29004	29.0271	17.97781	21.16994	10.68554	0.46229	0.38944	0.52001	LRRC37A	chr17	+	44370099	44415160	5177
ENSG00000(	372.8851	372.1249	319.2981	5.992604	3.681728	0.821965	6.4666	4.11E-53	1.21E-51	FOXC2	chr16	+	86600857	86602539	1683
ENSG00000(	628.7257	584.0795	713.8029	175.2837	114.1336	129.8705	2.1846	5.36E-32	8.66E-31	BDNF	chr11	-	27676440	27743605	4766
ENSG00000(	241.3395	287.8248	209.7868	270.4163	197.8929	235.082	0.069739	0.72806	0.81784	SCAND2P	chr15	+	85174682	85185695	3961
ENSG00000(	13.46529	2.408575	25.06886	44.94453	33.13555	32.8786	-1.3849	0.014546	0.032589	CCDC121	chr2	-	27848506	27851879	2342
ENSG00000(	423.6389	399.8235	383.9494	414.2388	536.6119	481.6714	-0.24365	0.12342	0.20854	ACSF3	chr16	+	89154783	89222254	7020
ENSG00000(	6.214751	0	1.319414	0	3.681728	0	0.68003	0.60384	0.71887	OR10AB1P	chr11	+	7749632	7750935	1020
ENSG00000(	609.0456	591.3053	477.6278	1634.483	1208.527	1555.158	-1.3847	1.47E-19	1.45E-18	BOK	chr2	+	2.42E+08	2.43E+08	2650
ENSG00000(	21.75163	21.67718	30.34652	2.996302	10.12475	2.465895	2.1222	0.001304	0.003593	ZNF843	chr16	-	31445569	31454346	2161
ENSG00000(	41.43168	27.69862	15.83297	100.3761	83.75931	102.7456	-1.7064	2.21E-06	8.84E-06	TTTY14	chrY	-	21034387	21239302	1495
ENSG00000(	107.7224	98.75159	116.1084	97.37982	71.7937	82.19649	0.35278	0.17887	0.28157	C8orf59	chr8	-	86126311	86132650	853
ENSG00000(	5.17896	8.430014	9.235896	2.996302	12.88605	11.50751	-0.23688	0.76333	0.84366	PFN4	chr2	-	24338241	24346347	974
ENSG00000(	166.7625	118.0202	147.7743	289.8922	291.7769	306.5929	-1.03	1.88E-07	8.40E-07	CDK5R1	chr17	+	30813637	30818274	4325
ENSG00000(	3.107376	2.408575	3.958241	12.73428	4.60216	5.753754	-1.1265	0.21877	0.33027	C15orf56	chr15	-	40542865	40545170	2129
ENSG00000(	4.143168	3.612863	3.958241	3.745378	3.681728	1.64393	0.30737	0.76311	0.84362	ZNF285B	chr19	+	44971858	44977444	1767
ENSG00000(	0	0	0	197.0069	243.9145	225.2184	-8.3669	5.72E-18	5.28E-17	TCERG1L	chr10	-	1.33E+08	1.33E+08	4394
ENSG00000(	111.8655	115.6116	133.2608	41.94823	74.55499	66.57916	0.97113	0.000776	0.002218	NCKAP5	chr2	-	1.33E+08	1.34E+08	7592
ENSG00000(	676.3721	802.0556	782.4124	620.9836	539.3732	634.5569	0.33039	0.019389	0.042206	RUFY1	chr5	+	1.79E+08	1.79E+08	2771
ENSG00000(	5968.233	5583.078	5491.4	3983.584	4117.092	3970.913	0.49705	7.18E-07	3.02E-06	BASP1	chr5	+	17217669	17276943	1878
ENSG00000(	73.54123	75.87013	71.24834	63.67142	56.14635	52.60575	0.35051	0.24231	0.358	LRRC37A3	chr17	-	62850430	62915598	5665
ENSG00000(	3.107376	7.225726	2.638828	0	4.60216	3.28786	0.58681	0.59052	0.7071	AC009951.	chr2	-	1.45E+08	1.45E+08	2966
ENSG00000(	37.28851	48.17151	34.30476	11.98521	10.12475	9.863579	1.8401	0.000138	0.00044	FKBP9L	chr7	-	55748767	55780945	2451
ENSG00000(	132.5814	99.95588	141.1773	318.3571	318.4695	297.5513	-1.3152	5.09E-11	3.08E-10	VSIG10	chr12	-	1.19E+08	1.19E+08	4946
ENSG00000(	2.071584	0	0	0	0	1.64393	0.14412	0.91322	NA	MIR7-3HG	chr19	+	4769117	4772545	879
ENSG00000(	129.474	125.2459	117.4278	42.69731	31.29469	32.05663	1.7858	8.88E-10	4.89E-09	IRX5	chr16	+	54964774	54968397	2401
ENSG00000(	865.922	979.0859	663.6651	1107.134	1143.177	1195.959	-0.45564	0.00226	0.005967	METRNL	chr17	+	81037567	81052864	1900
ENSG00000(	1069.973	1121.192	1567.464	784.2821	856.9222	709.3557	0.67406	2.17E-05	7.73E-05	FAM91A1	chr8	+	1.25E+08	1.25E+08	5511
ENSG00000(	0	9.634302	3.958241	0	0	0.821965	2.4991	0.051743	0.10005	CTC-298B1	chr5	-	1.08E+08	1.08E+08	1146
ENSG00000(	958.1075	820.1199	880.049	1451.708	1170.789	1105.543	-0.48656	0.000573	0.001668	WSB2	chr12	-	1.18E+08	1.19E+08	2646
ENSG00000(	0	0	1.319414	3.745378	3.681728	4.109825	-2.1046	0.094445	0.16725	GRIN1	chr9	+	1.4E+08	1.4E+08	5142
ENSG00000(	1749.453	1749.83	2017.384	2003.777	2761.296	2594.121	-0.41466	0.002697	0.007029	SOX11	chr2	+	5832799	5841516	8718
ENSG00000(	514.7886	544.338	467.0725	2289.175	1914.499	1812.433	-1.9734	2.23E-47	5.67E-46	TYMS	chr18	+	657604	673578	1662
ENSG00000(	16.57267	7.225726	10.55531	32.95932	24.85166	20.54912	-1.1262	0.045164	0.088869	PXMP2	chr12	+	1.33E+08	1.33E+08	1050
ENSG00000(	14.50109	27.69862	54.09597	17.97781	14.72691	18.90519	0.85018	0.10941	0.18869	TCEANC	chrX	+	13671225	13700083	2988

ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	OR51T1	chr11	+	4903049	4904113	1065
ENSG0000(	1306.134	1304.244	1430.245	907.8796	856.9222	950.1914	0.57181	2.02E-06	8.09E-06	PNMA1	chr14	-	74178494	74181128	2635
ENSG0000(	197.8363	211.9546	146.4549	861.4369	1005.112	944.4377	-2.3242	6.22E-45	1.48E-43	C8orf4	chr8	+	40010989	40012821	1833
ENSG0000(	36.25272	49.3758	52.77655	5.243529	15.64734	11.50751	2.0359	3.70E-05	0.000128	MAMSTR	chr19	-	49215999	49222978	1837
ENSG0000(	18.64425	9.634302	6.597069	18.72689	22.09037	18.08323	-0.69728	0.24547	0.36191	C18orf56	chr18	-	641320	658340	844
ENSG0000(	1550.58	1670.347	1638.712	1487.664	1549.087	1641.464	0.054614	0.62846	0.73907	ANKLE2	chr12	-	1.33E+08	1.33E+08	10890
ENSG0000(	2.071584	0	1.319414	0.749076	3.681728	5.753754	-1.1208	0.35568	0.48528	C8G	chr9	+	1.4E+08	1.4E+08	855
ENSG0000(	44.53905	33.72006	40.90183	11.23613	5.522592	23.01502	1.5172	0.003424	0.008765	FUT2	chr19	+	49199228	49209207	3111
ENSG0000(	1.035792	8.430014	5.277655	12.73428	12.88605	9.863579	-1.163	0.14699	0.24002	EFCAB5	chr17	+	28256218	28435470	5132
ENSG0000(	18.64425	30.10719	51.45714	59.17697	150.0304	99.45776	-1.597	7.77E-05	0.000257	GCNT4	chr5	-	74323289	74326724	3436
ENSG0000(	2.071584	7.225726	6.597069	0.749076	8.283888	0.821965	0.57772	0.57868	0.69708	TOB2P1	chr6	-	28185421	28186655	1142
ENSG0000(	7.250543	4.817151	7.916483	10.48706	6.443024	4.93179	-0.12226	0.87948	0.9246	MUC20	chr3	+	1.95E+08	1.95E+08	6193
ENSG0000(	1184.946	1095.902	913.0343	1345.34	984.8622	1071.02	-0.09019	0.55226	0.67322	THAP4	chr2	-	2.43E+08	2.43E+08	2367
ENSG0000(	659.7994	650.3154	650.471	1249.458	1207.607	1405.56	-0.97618	1.03E-14	7.98E-14	NFATC2IP	chr16	+	28962128	28978418	4569
ENSG0000(	0	0	0	8.239831	6.443024	13.9734	-4.0931	0.000539	0.001575	LY6H	chr8	-	1.44E+08	1.44E+08	1591
ENSG0000(	488.8938	556.3809	546.2373	20.97412	16.56778	22.19305	4.6908	4.15E-87	2.51E-85	FIBIN	chr11	+	27015628	27018630	3003
ENSG0000(	18.64425	19.2686	23.74945	8.988907	8.283888	4.109825	1.4385	0.021334	0.045967	FAM89B	chr11	+	65339820	65341669	1409
ENSG0000(	184.371	180.6432	193.9538	733.345	774.0833	798.9499	-2.0391	2.40E-41	5.14E-40	SHMT1	chr17	-	18231187	18266856	2756
ENSG0000(	518.9317	500.9837	329.8534	231.4643	181.3251	276.1802	0.96495	4.04E-06	1.57E-05	DPP7	chr9	-	1.4E+08	1.4E+08	1590
ENSG0000(	0	0	0	2.996302	0	0.821965	-1.0802	0.41594	NA	AP000679.	chr11	+	1.2E+08	1.2E+08	2081
ENSG0000(	2365.749	2615.713	2605.842	2041.98	2513.7	2374.657	0.13049	0.27578	0.39729	SEC24C	chr10	+	75504120	75531919	4668
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	FMR1NB	chrX	+	1.47E+08	1.47E+08	1021
ENSG0000(	263.0911	243.2661	354.9223	84.64554	290.8565	175.9005	0.62195	0.2106	0.32047	SMCR8	chr17	+	18218624	18226517	3427
ENSG0000(	672.2289	582.8753	555.4732	179.7781	214.4607	201.3814	1.6012	7.21E-23	8.18E-22	MTHFR	chr1	-	11845780	11866977	7057
ENSG0000(	7.250543	9.634302	9.235896	22.47227	10.12475	8.219649	-0.60921	0.3806	0.5113	C19orf18	chr19	-	58469805	58485902	915
ENSG0000(	1274.024	1191.041	1029.143	642.7068	608.4055	580.3072	0.93041	3.80E-12	2.50E-11	DEAF1	chr11	-	644233	706715	2500
ENSG0000(	196.8005	162.5788	290.271	101.8743	204.3359	130.6924	0.5679	0.038463	0.077374	MTX3	chr5	-	79275584	79287082	4799
ENSG0000(	388.422	409.4578	411.6571	224.7227	219.9832	296.7293	0.70228	6.63E-05	0.000221	TMEM80	chr11	+	695616	705028	2047
ENSG0000(	75.61281	55.39724	39.58241	67.4168	73.63456	73.97684	-0.31948	0.32778	0.45552	SIX5	chr19	-	46268043	46272141	2975
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	IFNW1	chr9	-	21140631	21142144	1514
ENSG0000(	554.1487	574.4452	476.3084	652.4448	590.9173	621.4055	-0.21527	0.13094	0.21849	FBXO46	chr19	-	46213887	46234162	3001
ENSG0000(	140.8677	178.2346	179.4403	355.0618	277.05	249.8773	-0.82241	7.28E-05	0.000242	ZDHHC13	chr11	+	19138646	19197969	6304
ENSG0000(	137.7603	167.396	162.2879	288.3941	255.8801	312.3467	-0.87264	6.96E-06	2.63E-05	SLC38A9	chr5	-	54921673	55069022	4032
ENSG0000(	36.25272	10.83859	25.06886	39.701	91.12277	64.93523	-1.3861	0.002135	0.005662	ACER2	chr9	+	19408925	19452018	2238
ENSG0000(	643.2268	663.5625	564.7091	693.644	659.0293	629.6251	-0.0821	0.55002	0.67142	WDR73	chr15	-	85185999	85197574	5071
ENSG0000(	711.589	790.0127	667.6234	1996.286	2399.566	2359.861	-1.6346	1.16E-36	2.18E-35	POLE	chr12	-	1.33E+08	1.33E+08	8011
ENSG0000(	123.2592	163.7831	120.0667	36.7047	39.57858	33.70056	1.8679	8.15E-11	4.85E-10	FAM109B	chr22	+	42470255	42475445	2335
ENSG0000(	7.250543	4.817151	3.958241	6.74168	11.96562	18.08323	-1.0783	0.16054	0.25792	SCN4B	chr11	-	1.18E+08	1.18E+08	4484
ENSG0000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	DSCAML1	chr11	-	1.17E+08	1.18E+08	6899
ENSG0000(	1153.872	1146.482	1064.767	1171.554	820.1049	838.4042	0.24838	0.1032	0.17999	RHOG	chr11	-	3848208	3862213	1319
ENSG0000(	210.2658	215.5675	162.2879	3483.95	3331.964	3829.535	-4.1624	1.84E-195	4.98E-193	EPS8L2	chr11	+	694438	727727	3844
ENSG0000(	0	0	5.277655	14.98151	18.40864	10.68554	-2.7039	0.003515	0.008972	ZDHHC22	chr14	-	77597613	77609077	3408
ENSG0000(	14.50109	1.204288	10.55531	0	1.840864	3.28786	1.9553	0.057464	0.10964	MRVI1-AS1	chr11	+	10562819	10621479	829
ENSG0000(	1130.049	1086.268	1519.965	1877.183	2140.004	1891.341	-0.66018	4.30E-06	1.66E-05	ANO6	chr12	+	45609770	45834187	5975

ENSG00000(	475.4285	428.7264	502.6967	297.383	441.8074	312.3467	0.41997	0.020088	0.043546	ZBTB34	chr9	+	1.3E+08	1.3E+08	6564
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP1-163G9	chr1	-	2976179	2985001	4247
ENSG00000(	2.071584	2.408575	3.958241	7.490755	8.283888	4.93179	-1.1252	0.23037	0.34376	NUDT4P1	chr1	-	1.45E+08	1.45E+08	543
ENSG00000(	324.2029	292.6419	356.2417	391.7665	338.719	329.6079	-0.12469	0.45676	0.58654	FAM210A	chr18	-	13663346	13726662	4340
ENSG00000(	2230.06	1982.258	1832.666	3731.145	2830.328	3210.595	-0.69103	1.69E-07	7.58E-07	TALDO1	chr11	+	747329	765024	1346
ENSG00000(	898.0316	885.1515	748.1076	504.8769	766.7199	738.1245	0.33339	0.047168	0.09227	ULK1	chr12	+	1.32E+08	1.32E+08	5310
ENSG00000(	7.250543	2.408575	1.319414	0	10.12475	9.041614	-0.63108	0.54567	0.66782	NAP1L4P1	chr1	-	1.17E+08	1.17E+08	1157
ENSG00000(	0	0	0	8.239831	9.20432	17.26126	-4.3765	0.000161	0.000509	RIMKLA	chr1	+	42846466	42880850	1510
ENSG00000(	0	1.204288	0	4.494453	0	0	-0.84979	0.53001	NA	CLVS1	chr8	+	61969717	62414204	3622
ENSG00000(	610.0814	635.8639	775.8153	804.5071	954.488	852.3776	-0.36912	0.010571	0.024434	RPS6KA3	chrX	-	20168029	20285523	7918
ENSG00000(	10.35792	30.10719	6.597069	22.47227	30.37426	20.54912	-0.60704	0.29917	0.42415	B3GNT8	chr19	-	41931264	41934635	1874
ENSG00000(	381.1714	413.0707	358.8805	1135.599	922.2729	1225.55	-1.5051	1.39E-23	1.63E-22	PUS1	chr12	+	1.32E+08	1.32E+08	2151
ENSG00000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	PCNPP5	chr13	-	48902220	48902700	481
ENSG00000(	896.9958	1053.752	1432.883	434.4638	551.3388	381.3917	1.3012	1.29E-12	8.78E-12	CHD9	chr16	+	53088945	53363062	13110
ENSG00000(	0	0	0	5.992604	6.443024	5.753754	-3.4152	0.005864	0.014323	SPACA4	chr19	+	49110000	49110970	971
ENSG00000(	0	0	0	4.494453	0	1.64393	-1.6577	0.22164	0.3333	OR2T33	chr1	-	2.48E+08	2.48E+08	1066
ENSG00000(	1827.137	1779.937	1472.466	1361.07	1260.071	1518.169	0.29505	0.024537	0.052095	PDDC1	chr11	-	767220	777488	4357
ENSG00000(	47.64643	55.39724	38.263	17.22874	15.64734	18.08323	1.4344	0.000768	0.002196	C10orf85	chr10	+	1.22E+08	1.22E+08	1909
ENSG00000(	78.72018	43.35436	79.16483	71.91125	62.58938	78.08667	-0.07827	0.808	0.87541	AP006621.	chr11	+	780117	780755	636
ENSG00000(	3692.598	3510.499	2902.71	1179.045	1139.495	1362.818	1.4538	4.34E-29	6.35E-28	MAN1B1	chr9	+	1.4E+08	1.4E+08	5048
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	ENSAP3	chr2	+	2.16E+08	2.16E+08	333
ENSG00000(	0	0	0	5.243529	9.20432	2.465895	-3.2664	0.009445	0.022085	KCNA3	chr1	-	1.11E+08	1.11E+08	3346
ENSG00000(	68.36227	52.98866	76.526	59.17697	53.38506	66.57916	0.13938	0.65784	0.76264	FZD8	chr10	-	35927177	35930362	3186
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	GJD4	chr10	+	35894338	35897863	1580
ENSG00000(	0	0	0	5.992604	4.60216	4.93179	-3.1715	0.011964	0.027324	KCNA2	chr1	-	1.11E+08	1.11E+08	3446
ENSG00000(	882.4947	1009.193	852.3413	1250.207	1272.957	1408.848	-0.51773	4.79E-05	0.000163	TOP3A	chr17	-	18174742	18218321	4056
ENSG00000(	443.3189	415.4793	426.1707	480.9065	507.158	589.3488	-0.29432	0.050386	0.097774	CASKIN2	chr17	-	73496342	73511664	5015
ENSG00000(	648.4057	692.4654	877.4102	281.6524	419.717	298.3733	1.1456	3.23E-10	1.84E-09	ZBTB38	chr3	+	1.41E+08	1.41E+08	7683
ENSG00000(	3.107376	3.612863	0	4.494453	9.20432	3.28786	-1.067	0.30686	0.43257	C8orf31	chr8	+	1.44E+08	1.44E+08	1875
ENSG00000(	24.85901	28.90291	21.11062	19.47596	13.80648	23.83698	0.37479	0.45238	0.58213	DLGAP1-AS	chr18	+	3593730	3598350	1966
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	LINC00469	chr17	-	71746469	71824659	708
ENSG00000(	2.071584	10.83859	3.958241	3.745378	23.93123	19.72716	-1.3481	0.093005	0.16517	AC024940.	chr12	+	31477250	31478879	1630
ENSG00000(	505.4664	382.9635	394.5047	569.2974	486.9085	558.1142	-0.32868	0.041937	0.083419	CCDC71	chr3	-	49199968	49203754	1781
ENSG00000(	97.36444	61.41867	76.526	38.20285	20.2495	20.54912	1.5375	4.80E-05	0.000164	RP11-551L	chr12	-	31264586	31359088	4427
ENSG00000(	194.7289	172.2131	141.1773	3.745378	21.16994	13.9734	3.667	1.93E-22	2.16E-21	LRRN4CL	chr11	-	62453874	62457371	2585
ENSG00000(	534.4686	579.2624	451.2395	884.6582	768.5607	787.4424	-0.63864	1.19E-05	4.37E-05	TIMM22	chr17	+	900357	905407	1690
ENSG00000(	812.0609	783.9913	657.0681	27.7158	23.0108	16.4393	5.0267	6.07E-108	5.23E-106	HIC1	chr17	+	1957448	1962980	3156
ENSG00000(	207.1584	178.2346	133.2608	41.94823	64.43024	69.04505	1.5548	1.96E-08	9.64E-08	PPFIA3	chr19	+	49622646	49654283	4733
ENSG00000(	771.665	782.787	762.6212	1180.543	1338.308	1374.325	-0.74666	1.99E-09	1.06E-08	MAGEF1	chr3	-	1.84E+08	1.84E+08	1681
ENSG00000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	UMODL1	chr21	+	43483068	43563105	5442
ENSG00000(	1.035792	6.021439	14.51355	30.7121	23.93123	26.30288	-1.8276	0.00543	0.013351	RP11-218M	chr12	+	740057	772872	2338
ENSG00000(	81.82756	103.5687	94.99779	1.498151	0	0	6.5867	3.10E-17	2.75E-16	SAMD9L	chr7	-	92759368	92777682	7134
ENSG00000(	2536.654	2833.689	2023.981	1744.597	1570.257	2036.829	0.46523	0.00138	0.003783	ZFAS1	chr20	+	47894715	47905797	1075
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	UBE2U	chr1	+	64669310	64733053	1552

ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC006001.	chr7	-	66021832	66022349	516
ENSG00000(	297.2723	262.5347	316.6593	2214.267	2179.583	2014.636	-2.8642	7.24E-106	6.07E-104	PAWR	chr12	-	79968759	80084877	9129
ENSG00000(	728.1617	727.3898	614.8468	895.1453	832.0705	800.5938	-0.28641	0.034059	0.069473	TGIF1	chr18	+	3411606	3459976	3030
ENSG00000(	185.4068	177.0303	157.0102	184.2726	174.8821	224.3964	-0.16546	0.42191	0.55238	SMCR7	chr17	+	18163848	18169866	3364
ENSG00000(	208.1942	273.3733	245.411	49.43899	50.62376	45.20807	2.3045	1.82E-22	2.04E-21	NAP1L5	chr4	-	89617066	89619386	2321
ENSG00000(	4.143168	3.612863	5.277655	2.247227	1.840864	3.28786	0.67411	0.51102	0.63822	RP4-597J3.	chr1	-	64254392	64254975	584
ENSG00000(	88.04231	77.07441	75.20659	5.243529	1.840864	1.64393	4.5457	1.70E-17	1.53E-16	NIM1	chr5	+	43192173	43280952	2929
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CD19	chr16	+	28943260	28950667	2322
ENSG00000(	4.143168	8.430014	6.597069	56.92974	85.60018	53.42772	-3.2425	2.02E-10	1.17E-09	C8orf47	chr8	+	99076539	99105838	1761
ENSG00000(	0	0	0	8.988907	0	4.93179	-2.8158	0.032439	0.066544	OR2T8	chr1	+	2.48E+08	2.48E+08	939
ENSG00000(	92.18548	119.2245	179.4403	107.1178	92.96363	83.01846	0.45342	0.10645	0.18463	NR2C2	chr3	+	14989091	15095107	3308
ENSG00000(	2.071584	0	7.916483	14.23244	6.443024	11.50751	-1.5014	0.09788	0.17225	GPR4	chr19	-	46093022	46105466	3048
ENSG00000(	8.286335	7.225726	2.638828	34.45748	37.73771	36.98842	-2.4392	2.14E-05	7.62E-05	ACOT4	chr14	+	74058410	74063200	2362
ENSG00000(	0	0	0	4.494453	3.681728	6.575719	-3.0869	0.015096	0.033677	OLIG3	chr6	-	1.38E+08	1.38E+08	2196
ENSG00000(	14121.99	13430.22	13423.72	4887.718	5477.491	5437.298	1.3728	9.63E-42	2.09E-40	PTRF	chr17	-	40554470	40575535	3828
ENSG00000(	768.5576	782.787	874.7713	1099.643	1096.235	1098.967	-0.44159	0.00034	0.001026	ARIH2	chr3	+	48956254	49023815	4933
ENSG00000(	5.17896	24.08575	23.74945	7.490755	5.522592	8.219649	1.2111	0.083039	0.15016	RBM44	chr2	+	2.39E+08	2.39E+08	5358
ENSG00000(	356.3124	398.6192	497.419	503.3788	467.5795	359.1987	-0.08897	0.62441	0.73601	ZBTB33	chrX	+	1.19E+08	1.19E+08	5211
ENSG00000(	1.035792	1.204288	6.597069	101.8743	48.7829	64.11326	-4.4052	1.83E-12	1.23E-11	ZBED2	chr3	-	1.11E+08	1.11E+08	2311
ENSG00000(	0	0	0	0	2.761296	1.64393	-1.2339	0.35779	NA	VCX2	chrX	-	8137989	8139308	811
ENSG00000(	48.68222	36.12863	18.47179	220.2282	230.108	229.3282	-2.6656	1.05E-20	1.10E-19	IRX3	chr16	-	54317216	54320675	2601
ENSG00000(	0	0	0	5.992604	2.761296	9.041614	-3.3561	0.007264	0.017434	ST8SIA3	chr18	+	55018044	55038962	11833
ENSG00000(	0	0	0	130.3391	128.8605	184.1201	-7.8435	2.09E-15	1.69E-14	RPRM	chr2	-	1.54E+08	1.54E+08	1471
ENSG00000(	1005.754	873.1086	762.6212	830.7248	779.6059	849.9117	0.10354	0.45835	0.58781	SLC25A22	chr11	-	790475	798316	2894
ENSG00000(	718.8396	729.7984	581.8615	474.1648	481.3859	570.4437	0.41188	0.006852	0.016524	RABEP2	chr16	-	28915742	28947847	2821
ENSG00000(	0	0	0	56.18067	74.55499	73.97684	-6.8526	1.91E-11	1.19E-10	NHLH2	chr1	-	1.16E+08	1.16E+08	7226
ENSG00000(	1828.173	1679.981	1356.357	685.4041	657.1884	927.1764	1.0964	6.64E-12	4.28E-11	ATOX1	chr5	-	1.51E+08	1.51E+08	4341
ENSG00000(	1232.592	1303.039	1490.938	835.2192	773.1629	712.6436	0.79186	1.81E-09	9.72E-09	TBL1XR1	chr3	-	1.77E+08	1.77E+08	7948
ENSG00000(	0	0	6.597069	44.94453	49.70333	31.23467	-4.0038	4.29E-08	2.04E-07	SAMD12	chr8	-	1.19E+08	1.2E+08	8866
ENSG00000(	7.250543	8.430014	6.597069	8.988907	1.840864	3.28786	0.56605	0.51714	0.64348	CD163	chr12	-	7623409	7656489	5312
ENSG00000(	22.78742	12.04288	3.958241	6.74168	1.840864	5.753754	1.2952	0.10885	0.18797	C18orf32	chr18	-	47008028	47013622	1128
ENSG00000(	618.3678	684.0354	488.1831	850.9498	795.2532	1063.623	-0.59472	0.000272	0.000831	PIDD	chr11	-	799179	809753	4496
ENSG00000(	83.89914	87.913	94.99779	10.48706	18.40864	9.041614	2.7685	1.12E-12	7.62E-12	ZNF491	chr19	+	11908482	11920437	2471
ENSG00000(	14446.19	14874.16	12587.21	9094.526	8594.074	12096.04	0.49141	0.000315	0.000956	RPLP2	chr11	+	809647	812880	781
ENSG00000(	70.43385	60.21439	58.05421	311.6154	358.048	321.3883	-2.3717	3.39E-28	4.79E-27	GSG2	chr17	+	3627211	3630067	2857
ENSG00000(	6163.998	6105.739	5554.732	1501.147	1431.272	1486.113	2.0092	2.03E-81	1.13E-79	JUN	chr1	-	59246465	59249785	3321
ENSG00000(	642.191	626.2296	645.1933	855.4443	761.1973	904.1614	-0.39712	0.002818	0.007315	CSTF2T	chr10	-	53455247	53459355	4109
ENSG00000(	23.82321	33.72006	18.47179	131.8373	120.5766	171.7907	-2.4409	7.56E-14	5.56E-13	PGBD5	chr1	-	2.3E+08	2.31E+08	3443
ENSG00000(	1409.713	1301.835	1198.028	614.991	687.5627	646.8864	1.003	4.31E-15	3.42E-14	GBA	chr1	-	1.55E+08	1.55E+08	2400
ENSG00000(	8.286335	6.021439	11.87472	20.22504	17.48821	19.72716	-1.079	0.081314	0.14742	CASC2	chr10	+	1.2E+08	1.2E+08	3268
ENSG00000(	794.4524	792.4213	701.9281	708.6255	761.1973	808.8135	0.007447	0.95524	0.97352	ACAD9	chr3	+	1.29E+08	1.29E+08	2454
ENSG00000(	332.4892	281.8033	275.7575	400.7554	480.4655	346.8692	-0.45955	0.009902	0.023057	IL17RA	chr22	+	17565844	17596583	8607
ENSG00000(	537.576	556.3809	402.4212	475.663	384.7406	446.327	0.19539	0.24694	0.36372	PNPLA2	chr11	+	818902	825573	2726
ENSG00000(	0	1.204288	1.319414	0	1.840864	0.821965	-0.04333	0.97449	NA	MBOAT4	chr8	-	29989340	30002202	1512

ENSG00000(	431.9252	368.512	296.8681	718.3635	499.7946	512.9061	-0.653	0.000522	0.00153	AGTRAP	chr1	+	11796141	11814859	1116
ENSG00000(	23.82321	3.612863	17.15238	2.247227	5.522592	0.821965	2.1303	0.012654	0.028735	CD163L1	chr12	-	7499281	7632493	4615
ENSG00000(	285.8786	296.2548	225.6198	11.98521	18.40864	18.08323	4.0246	3.05E-44	7.12E-43	SRRM3	chr7	+	75831216	75916605	3614
ENSG00000(	180.2278	217.9761	217.7033	238.206	171.2004	208.7791	-0.00952	0.96299	0.97852	THAP5	chr7	-	1.08E+08	1.08E+08	3306
ENSG00000(	81.82756	77.07441	68.60952	35.95563	19.32907	23.83698	1.489	3.93E-05	0.000135	EFCAB4A	chr11	+	826144	831991	2440
ENSG00000(	0	0	1.319414	1.498151	0	0	-0.08979	0.94423	NA	SUMO4	chr6	+	1.5E+08	1.5E+08	683
ENSG00000(	12.4295	15.65574	29.0271	26.21764	11.96562	15.61733	0.064662	0.91005	0.94484	DNAJC28	chr21	-	34860497	34864027	1625
ENSG00000(	47.64643	49.3758	94.99779	15.73059	16.56778	15.61733	1.9469	4.72E-06	1.82E-05	NAALADL2	chr3	+	1.74E+08	1.76E+08	4953
ENSG00000(	7757.046	7703.829	7226.429	2106.4	2326.852	2990.308	1.608	9.89E-34	1.70E-32	CD151	chr11	+	832843	839831	1803
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-16K1	chr15	+	79271231	79278268	1900
ENSG00000(	2249.74	1946.129	2187.588	1331.107	1527.917	2370.547	0.28657	0.10228	0.17863	POLR2L	chr11	-	837356	842545	892
ENSG00000(	571.7571	534.7037	534.3626	229.9662	293.6178	214.5328	1.1507	6.21E-12	4.02E-11	FAM20C	chr7	+	192969	300711	2751
ENSG00000(	381.1714	425.1136	513.252	841.2118	833.9114	725.795	-0.86331	1.84E-08	9.06E-08	PVRL3	chr3	+	1.11E+08	1.11E+08	3664
ENSG00000(	4.143168	2.408575	5.277655	3.745378	0.920432	2.465895	0.57657	0.58776	0.70502	SLC35G5	chr8	+	11188397	11189717	1321
ENSG00000(	55.93276	62.62296	56.73479	7.490755	21.16994	13.9734	2.0001	5.75E-06	2.19E-05	ANXA2R	chr5	-	43039335	43043272	2234
ENSG00000(	5.17896	4.817151	2.638828	2.247227	0	2.465895	1.0972	0.3284	0.45614	AC105206.	chr8	+	22026851	22029223	2368
ENSG00000(	1326.849	1393.361	1242.888	958.0676	1017.077	974.8504	0.42562	0.000328	0.000991	KIAA0195	chr17	+	73437240	73496171	5632
ENSG00000(	2572.907	2504.918	2471.262	4303.439	4137.342	4301.342	-0.75409	7.61E-14	5.59E-13	FLII	chr17	-	18148150	18162230	4338
ENSG00000(	3359.073	3032.396	2769.45	1385.79	1500.304	1495.154	1.0628	1.28E-19	1.28E-18	SOX12	chr20	+	306207	310865	4627
ENSG00000(	6083.206	6005.783	5656.327	7526.711	8640.095	10701.16	-0.59695	5.08E-06	1.95E-05	HNRNPA0	chr5	-	1.37E+08	1.37E+08	2965
ENSG00000(	0	6.021439	0	0	0	0.821965	1.3469	0.32084	0.44795	RP11-474P	chr9	-	1.28E+08	1.28E+08	547
ENSG00000(	191.6215	213.1589	131.9414	47.94084	56.14635	82.19649	1.5132	6.58E-08	3.07E-07	CTD-2201E	chr5	-	43014516	43067521	2388
ENSG00000(	0	0	1.319414	0	0	2.465895	-0.38078	0.77353	NA	YIPF7	chr4	-	44624086	44680573	1117
ENSG00000(	3.107376	8.430014	10.55531	0	4.60216	0	1.8279	0.093428	0.16581	FAM87B	chr1	+	752751	755214	1944
ENSG00000(	71.46964	86.70872	46.17948	82.39831	78.23672	81.37453	-0.237	0.43995	0.56964	ZCCHC3	chr20	+	277737	280965	3229
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CDKN2AIPI	chr1	-	2.27E+08	2.27E+08	302
ENSG00000(	6.214751	12.04288	11.87472	2.247227	0	5.753754	1.6386	0.075051	0.1377	RP5-1061H	chr1	-	2.29E+08	2.29E+08	868
ENSG00000(	0	0	0	14.23244	23.93123	19.72716	-5.131	3.27E-06	1.28E-05	MYOZ1	chr10	-	75391412	75401515	1541
ENSG00000(	2.071584	1.204288	0	0	0.920432	0	0.824	0.54141	NA	TMEM78	chr1	+	2.29E+08	2.29E+08	2175
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-606P	chr4	+	1.65E+08	1.65E+08	657
ENSG00000(	2.071584	0	0	2.996302	0	0.821965	-0.43782	0.74676	NA	KCNJ10	chr1	-	1.6E+08	1.6E+08	5293
ENSG00000(	229.9458	231.2232	336.4505	159.5531	153.7121	190.6959	0.65498	0.002081	0.005529	AC108142.	chr4	-	1.83E+08	1.83E+08	2260
ENSG00000(	2370.928	2396.533	1947.455	1332.605	1375.125	1469.673	0.68388	3.20E-08	1.54E-07	CHID1	chr11	-	867357	915058	3537
ENSG00000(	106.6866	97.54731	110.8308	14.98151	13.80648	14.79537	2.8034	9.68E-16	7.97E-15	PCDHB9	chr5	+	1.41E+08	1.41E+08	4217
ENSG00000(	3.107376	6.021439	5.277655	219.4791	266.0048	279.4681	-5.5914	2.33E-36	4.34E-35	ZNF620	chr3	+	40547483	40560227	3291
ENSG00000(	243.4111	293.8462	296.8681	450.9435	495.1924	371.5281	-0.65846	0.000174	0.000549	ZNF518A	chr10	+	97889472	97965044	8284
ENSG00000(	183.3352	199.9118	160.9685	98.1289	105.8497	120.0069	0.74485	0.000812	0.002312	TMEM187	chrX	+	1.53E+08	1.53E+08	1880
ENSG00000(	7.250543	8.430014	3.958241	27.7158	19.32907	33.70056	-1.9201	0.001723	0.004641	CACYBPP2	chr2	-	1.84E+08	1.84E+08	678
ENSG00000(	111.8655	81.89156	77.84541	105.6197	92.96363	103.5676	-0.14794	0.5798	0.69803	CCDC23	chr1	-	43272723	43282954	708
ENSG00000(	26.93059	13.24716	35.62417	14.98151	10.12475	6.575719	1.1886	0.043503	0.086133	ZNF619	chr3	+	40518604	40531727	4153
ENSG00000(	21.75163	36.12863	29.0271	12.73428	6.443024	8.219649	1.5787	0.004449	0.011132	C12orf68	chr12	+	48577366	48579709	2344
ENSG00000(	1551.616	1599.294	1513.368	1301.144	1153.301	1181.164	0.35847	0.002014	0.005364	AP3S1	chr5	+	1.15E+08	1.15E+08	1730
ENSG00000(	1453.216	1082.655	1300.942	1128.857	1318.059	1175.41	0.083733	0.54633	0.66836	GRB2	chr17	-	73314157	73401790	3729
ENSG00000(	78.72018	71.05298	150.4132	11.23613	34.05598	13.9734	2.2931	7.71E-08	3.57E-07	ZBTB41	chr1	-	1.97E+08	1.97E+08	3779

ENSG0000(	1340.315	1383.727	1467.188	3869.724	3015.335	3384.852	-1.2909	2.20E-25	2.76E-24	UBE2N	chr12	-	93799449	93836038	3671
ENSG0000(	283.807	274.5776	303.4652	803.009	705.0509	710.9997	-1.3617	2.56E-20	2.63E-19	ARL6IP6	chr2	+	1.54E+08	1.54E+08	2805
ENSG0000(	155.3688	131.2674	215.0644	68.16587	145.4283	78.08667	0.77611	0.00921	0.021593	ZNF354C	chr5	+	1.78E+08	1.79E+08	5411
ENSG0000(	204.051	222.7932	138.5384	164.0475	159.2347	334.5397	-0.21456	0.44168	0.57145	MAMDC4	chr9	+	1.4E+08	1.4E+08	4110
ENSG0000(	55.93276	39.74149	32.98534	51.68621	25.7721	37.81039	0.15582	0.70262	0.79797	CENPBD1	chr16	-	90036206	90038942	2737
ENSG0000(	4.143168	3.612863	2.638828	0	0	4.109825	0.96137	0.43044	0.56031	ODF3	chr11	+	196738	200261	3053
ENSG0000(	614.2246	686.444	621.4439	343.0766	338.719	369.8842	0.86721	1.62E-09	8.70E-09	BET1L	chr11	-	167784	207428	2916
ENSG0000(	13739.78	14852.48	12337.84	8365.676	6855.378	9174.772	0.74482	5.22E-09	2.69E-08	RPS27	chr1	+	1.54E+08	1.54E+08	625
ENSG0000(	2255.955	2126.772	2171.755	2721.391	2431.781	2509.459	-0.22505	0.038112	0.076753	RIC8A	chr11	+	207511	215113	3703
ENSG0000(	639.0836	628.6382	519.849	1256.949	701.3692	728.2609	-0.58481	0.003324	0.00853	IMP3	chr15	-	75931426	75941047	2028
ENSG0000(	323.1671	309.5019	315.3399	231.4643	177.6434	216.9987	0.59394	0.000996	0.002794	ASB8	chr12	-	48541571	48574996	2615
ENSG0000(	0	0	0	0.749076	0.920432	1.64393	-1.0185	0.44577	NA	LCN15	chr9	-	1.4E+08	1.4E+08	2885
ENSG0000(	14.50109	25.29004	5.277655	2.247227	4.60216	8.219649	1.4483	0.061015	0.11525	ODF3B	chr22	-	50968139	50971009	1722
ENSG0000(	113.9371	132.4716	100.2754	124.3465	99.40666	100.2797	0.095857	0.70071	0.79658	DPY19L2	chr12	-	63952693	64062719	4060
ENSG0000(	3.107376	3.612863	6.597069	1.498151	4.60216	6.575719	0.056378	0.95381	0.97248	ZNRF3-AS1	chr22	-	29420987	29427464	2170
ENSG0000(	3.107376	4.817151	1.319414	0	0	0	2.6591	0.046093	0.090462	C2orf73	chr2	+	54557171	54610879	1921
ENSG0000(	2.071584	2.408575	0	2.996302	3.681728	1.64393	-0.63451	0.59655	0.71236	GPR150	chr5	+	94955782	94957846	2065
ENSG0000(	1.035792	2.408575	1.319414	0	0	0	1.6865	0.21314	NA	TSPYL6	chr2	-	54480315	54483409	3095
ENSG0000(	107.7224	110.7945	55.41538	76.40571	50.62376	53.42772	0.59446	0.072863	0.1342	FAM211B	chr22	-	24981588	24989175	2943
ENSG0000(	734.3765	731.0026	608.2498	743.832	543.0549	659.2159	0.091078	0.55898	0.67951	DMAP1	chr1	+	44679127	44686353	4552
ENSG0000(	1607.549	1604.111	1793.083	10.48706	20.2495	12.32947	6.834	1.63E-180	3.84E-178	ADAMTSL1	chr9	+	18473892	18910948	8030
ENSG0000(	363.563	278.1905	424.8512	18.72689	20.2495	27.94681	3.9557	8.79E-50	2.41E-48	FAM26E	chr6	+	1.17E+08	1.17E+08	9784
ENSG0000(	4901.367	5017.063	3963.519	5083.227	4191.647	4463.27	0.015078	0.90503	0.94129	IMPDH2	chr3	-	49061758	49066841	1643
ENSG0000(	4.143168	2.408575	5.277655	203.7485	224.5854	258.9189	-5.6739	6.78E-33	1.13E-31	ALS2CL	chr3	-	46710487	46735194	6593
ENSG0000(	213.3731	209.5461	118.7472	110.8632	129.7809	115.0751	0.60657	0.016022	0.035549	MLF1	chr3	+	1.58E+08	1.58E+08	3048
ENSG0000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	PRSS42	chr3	-	46871032	46875585	1280
ENSG0000(	669.1216	552.7681	493.4608	552.0687	354.3663	461.1223	0.32532	0.075249	0.138	NDUFAF3	chr3	+	49057892	49060928	2012
ENSG0000(	194.7289	205.9332	292.9099	415.7369	435.3643	383.8576	-0.83242	9.87E-06	3.67E-05	C2orf69	chr2	+	2.01E+08	2.01E+08	3728
ENSG0000(	93.22127	71.05298	84.44248	39.701	23.0108	32.8786	1.3516	7.69E-05	0.000254	GRAMD1C	chr3	+	1.14E+08	1.14E+08	4177
ENSG0000(	18.64425	8.430014	5.277655	435.962	287.1748	359.1987	-4.9275	2.44E-46	6.04E-45	STAP2	chr19	-	4324040	4342783	2043
ENSG0000(	4.143168	1.204288	5.277655	2.996302	0	0	1.2507	0.31204	0.43837	ULK4P3	chr15	+	30395923	30423960	1158
ENSG0000(	6.214751	2.408575	1.319414	0	0.920432	1.64393	1.4053	0.25257	0.37033	TWF1P1	chr17	-	27530441	27531492	1050
ENSG0000(	54.89697	34.92434	31.66593	71.91125	36.81728	60.8254	-0.46692	0.22938	0.34281	TSSK6	chr19	-	19623222	19627004	2513
ENSG0000(	112.9013	151.7403	69.92893	135.5827	94.8045	144.6658	-0.16182	0.57965	0.69789	BOLA1	chr1	+	1.5E+08	1.5E+08	1096
ENSG0000(	2741.741	2489.263	3199.578	534.0909	698.6079	542.4968	2.2424	6.16E-55	1.90E-53	PDE4DIP	chr1	-	1.45E+08	1.45E+08	8824
ENSG0000(	832.7767	779.1742	783.7318	657.6883	665.4723	667.4355	0.2672	0.034509	0.070256	DDX10	chr11	+	1.09E+08	1.09E+08	6707
ENSG0000(	1.035792	4.817151	0	2.247227	0	0	0.77564	0.5628	0.68256	GOLGA8Q	chr15	+	30844183	30854704	1899
ENSG0000(	1.035792	0	0	0	0	4.109825	-0.79743	0.55418	NA	PPP1R42	chr8	-	67876334	67968839	1282
ENSG0000(	11.39371	7.225726	27.70769	17.97781	19.32907	9.041614	-0.01116	0.98603	0.99155	NDUFV2	chr18	+	9102628	9134343	942
ENSG0000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP1-232L2	chrX	-	1.01E+08	1.01E+08	1570
ENSG0000(	449.5337	485.328	294.2293	500.3825	337.7985	371.5281	0.023302	0.90995	0.94478	DALRD3	chr3	-	49052921	49059726	2987
ENSG0000(	33.14534	24.08575	34.30476	440.4564	334.1168	385.5015	-3.6324	2.21E-47	5.63E-46	ZNF114	chr19	+	48675575	48790865	2478
ENSG0000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	AC140481.	chr2	-	1.31E+08	1.31E+08	3992
ENSG0000(	356.3124	373.3292	515.8908	549.0724	669.1541	469.342	-0.43777	0.017689	0.038879	ZNF518B	chr4	-	10441498	10459034	6894

ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	AMER3	chr2	+	1.32E+08	1.32E+08	6172
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	ZNF366	chr5	-	71738479	71803554	3830
ENSG00000(	88.04231	101.1602	135.8996	103.3724	166.5982	126.5826	-0.28566	0.28843	0.41206	LCORL	chr4	-	17844839	18023499	5009
ENSG00000(	551.0413	525.0694	587.1391	365.5489	365.4115	349.3351	0.62039	1.81E-05	6.50E-05	PARD6G	chr18	-	77915115	78005429	3868
ENSG00000(	5.17896	2.408575	1.319414	6.74168	17.48821	7.397684	-1.5707	0.075172	0.13788	ZNF454	chr5	+	1.78E+08	1.78E+08	2332
ENSG00000(	1359.995	1350.007	1079.28	734.8431	994.987	1187.739	0.37672	0.025457	0.053834	SH2B1	chr16	+	28857921	28885526	6043
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP4-682C2	chr1	-	76175688	76189696	806
ENSG00000(	52.82539	55.39724	34.30476	2.996302	1.840864	0.821965	4.3379	2.85E-11	1.75E-10	ZC3H12D	chr6	-	1.5E+08	1.5E+08	3046
ENSG00000(	3.107376	13.24716	6.597069	2.996302	0	2.465895	1.6928	0.094155	0.16683	VN1R1	chr19	-	57966542	57967854	1313
ENSG00000(	973.6444	1099.515	1232.332	1361.819	1341.99	1128.558	-0.21388	0.11752	0.20041	KDELC2	chr11	-	1.08E+08	1.08E+08	4374
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CYP4F31P	chr2	+	1.32E+08	1.32E+08	2249
ENSG00000(	48236.83	48137.79	46133.3	7143.184	14000.69	13793.39	2.0191	2.03E-28	2.90E-27	PLEC	chr8	-	1.45E+08	1.45E+08	15249
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	SH2D4B	chr10	+	82297658	82406316	3983
ENSG00000(	2.071584	2.408575	7.916483	0	0	6.575719	0.66766	0.57331	0.69206	RNF212	chr4	-	1050038	1107350	2332
ENSG00000(	1.035792	4.817151	1.319414	8.239831	8.283888	9.041614	-1.5838	0.090723	0.1618	PRSS36	chr16	-	31150246	31161415	2840
ENSG00000(	113.9371	110.7945	117.4278	166.2948	149.11	153.7074	-0.45344	0.040491	0.080912	ZNF543	chr19	+	57831877	57842144	3659
ENSG00000(	32.10955	19.2686	21.11062	8.988907	12.88605	6.575719	1.2967	0.024992	0.052955	TMEM151B	chr6	+	44238203	44346694	4895
ENSG00000(	699.1595	718.9598	701.9281	583.5299	545.8162	489.8911	0.38741	0.004754	0.011827	GALNT11	chr7	+	1.52E+08	1.52E+08	3863
ENSG00000(	9.322127	6.021439	13.19414	8.988907	11.04518	3.28786	0.26491	0.729	0.81844	SLITRK1	chr13	-	84451344	84456528	5185
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AP000345.	chr22	-	23804273	23829167	1578
ENSG00000(	3172.631	3160.051	3055.762	2397.042	2718.956	2780.707	0.24952	0.022909	0.048934	WDR6	chr3	+	49044495	49053386	4401
ENSG00000(	223.7311	222.7932	246.7304	792.5219	644.3024	612.3639	-1.5598	1.94E-21	2.08E-20	GEN1	chr2	+	17935125	17966632	6367
ENSG00000(	56.96855	56.60152	51.45714	28.46487	23.0108	48.49593	0.70669	0.068874	0.12795	TMPRSS9	chr19	+	2389769	2426237	3331
ENSG00000(	25.8948	33.72006	30.34652	48.68991	27.61296	29.59074	-0.23662	0.58359	0.70112	AQP11	chr11	+	77300436	77321400	2152
ENSG00000(	394.6367	363.6949	304.7846	778.2895	543.9753	641.9546	-0.88104	3.41E-07	1.49E-06	TMEM11	chr17	-	21100593	21117937	2095
ENSG00000(	84.93494	127.6545	149.0938	148.317	105.8497	108.4994	-0.0116	0.96579	0.98014	ZNF354B	chr5	+	1.78E+08	1.78E+08	2802
ENSG00000(	2.071584	3.612863	9.235896	0	8.283888	2.465895	0.38748	0.71619	0.80876	KCNG2	chr18	+	77623668	77660184	1538
ENSG00000(	30.03797	44.55865	23.74945	0.749076	5.522592	0.821965	3.5628	4.52E-07	1.95E-06	SHISA3	chr4	+	42399856	42404504	1971
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	OR2D3	chr11	+	6942205	6943264	1060
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CALML5	chr10	-	5540658	5541533	876
ENSG00000(	152.2614	113.203	121.3861	202.9995	131.6218	136.4462	-0.28141	0.25949	0.37826	ZFAND2A	chr7	-	1191707	1200395	1084
ENSG00000(	21.75163	14.45145	23.74945	8.239831	21.16994	9.041614	0.61876	0.2997	0.4246	PLEKHM3	chr2	-	2.09E+08	2.09E+08	3689
ENSG00000(	13.46529	9.634302	10.55531	10.48706	16.56778	4.93179	0.078081	0.91041	0.94496	ZNF223	chr19	+	44555520	44572144	2418
ENSG00000(	7.250543	4.817151	3.958241	0	0	0	3.5552	0.004955	0.012283	HTR1A	chr5	-	63256183	63258334	1598
ENSG00000(	443.3189	408.2535	391.8659	307.121	335.0372	318.9224	0.37221	0.016644	0.036804	FAM220A	chr7	-	6369040	6388612	2214
ENSG00000(	18.64425	4.817151	23.74945	0	0.920432	4.93179	2.6233	0.003695	0.009401	DNAJC22	chr12	+	49740700	49751309	2628
ENSG00000(	39.36009	28.90291	27.70769	2.247227	18.40864	32.8786	0.80461	0.1904	0.29577	CTD-2373H	chr17	-	76866992	76899299	2090
ENSG00000(	89.0781	85.50443	88.40072	280.1543	394.8653	325.4981	-1.9138	3.58E-19	3.49E-18	BEND3	chr6	-	1.07E+08	1.07E+08	6644
ENSG00000(	0	3.612863	2.638828	2.996302	0	5.753754	-0.37082	0.76053	0.8417	RP11-567M	chr18	-	77398928	77439745	1111
ENSG00000(	210.2658	173.4174	178.1209	375.2868	383.8201	409.3385	-1.0492	1.86E-09	9.93E-09	NT5DC1	chr6	+	1.16E+08	1.17E+08	3118
ENSG00000(	11.39371	7.225726	1.319414	14.23244	2.761296	9.863579	-0.37178	0.66264	0.76683	RPS3AP5	chr10	+	86320199	86321019	786
ENSG00000(	4.143168	0	2.638828	2.996302	1.840864	1.64393	0.054607	0.96345	0.97878	AC006111.	chr16	+	3725411	3727060	1649
ENSG00000(	29.00217	20.47289	30.34652	23.22134	31.29469	23.83698	0.029179	0.94925	0.96942	LINC00843	chr10	+	51732523	51741813	562
ENSG00000(	58.00435	49.3758	75.20659	392.5156	405.9105	366.5964	-2.6628	3.73E-35	6.71E-34	GLDC	chr9	-	6532464	6645650	3767

ENSG00000(	348.0261	361.2863	314.0205	327.346	305.5834	521.9477	-0.17329	0.39739	0.52848	COX14	chr12	+	50505762	50559203	739
ENSG00000(	14.50109	8.430014	10.55531	17.97781	13.80648	11.50751	-0.34491	0.58469	0.70216	H3F3AP6	chr4	-	1.41E+08	1.41E+08	411
ENSG00000(	16.57267	12.04288	15.83297	16.47966	11.96562	14.79537	0.035945	0.95111	0.97069	MCMDC2	chr8	+	67782984	67834283	5096
ENSG00000(	18.64425	13.24716	21.11062	33.7084	11.04518	24.65895	-0.38074	0.49244	0.62149	CTD-2192J	chr19	-	12754089	12754733	645
ENSG00000(	220.6237	226.4061	159.6491	289.8922	282.5726	300.0172	-0.51845	0.006879	0.016587	P4HTM	chr3	+	49027319	49044587	5285
ENSG00000(	451.6053	437.1564	434.0871	190.2652	203.4155	179.1884	1.2041	1.68E-13	1.22E-12	DTX3	chr12	+	57998405	58003587	3199
ENSG00000(	56.96855	34.92434	76.526	24.71949	60.74851	46.852	0.34329	0.40158	0.5328	KLHL11	chr17	-	40009797	40021684	2383
ENSG00000(	0	0	0	9.737982	7.363456	2.465895	-3.4892	0.004904	0.012171	AMBN	chr4	+	71457973	71473005	2005
ENSG00000(	1858.211	1661.917	1234.971	1442.72	1290.446	1191.027	0.27697	0.070183	0.13	CTXN1	chr19	-	7989372	7991051	1272
ENSG00000(	291.0575	289.0291	320.6175	217.981	209.8585	179.1884	0.56568	0.001696	0.004574	SLC25A20	chr3	-	48894369	48936426	1879
ENSG00000(	7.250543	7.225726	14.51355	606.0021	618.5303	622.2274	-5.9385	8.71E-75	4.16E-73	CA8	chr8	-	61099906	61193971	3812
ENSG00000(	812.0609	843.0014	1011.99	546.8252	507.158	452.9027	0.81986	2.09E-08	1.02E-07	EPM2AIP1	chr3	-	37027357	37034795	7439
ENSG00000(	0	0	0	53.18436	102.168	57.53754	-6.8808	1.87E-11	1.17E-10	ERBB4	chr2	-	2.12E+08	2.13E+08	12132
ENSG00000(	392.5651	333.5877	341.7282	41.19916	51.54419	47.67397	2.914	1.75E-41	3.78E-40	MAF	chr16	-	79619740	79634611	6384
ENSG00000(	2108.872	2041.268	1922.386	1185.038	1135.813	1140.887	0.80961	3.96E-13	2.79E-12	CTNNBIP1	chr1	-	9908334	9970394	3000
ENSG00000(	0	4.817151	7.916483	0	0	0	2.9847	0.024423	0.051895	PSAPL1	chr4	-	7432022	7436700	4679
ENSG00000(	3.107376	6.021439	5.277655	0	0	0	3.3751	0.008359	0.019766	OTOS	chr2	-	2.41E+08	2.41E+08	642
ENSG00000(	1059.615	899.6029	730.9552	1325.864	1083.348	1151.573	-0.40202	0.008414	0.019891	GTPBP6	chrX	-	220025	230886	2016
ENSG00000(	80.79177	97.54731	118.7472	16.47966	72.71413	45.20807	1.1256	0.004995	0.012371	ERN1	chr17	-	62120353	62207504	4025
ENSG00000(	11.39371	10.83859	15.83297	14.98151	19.32907	9.041614	-0.17888	0.77371	0.85146	GPR35	chr2	+	2.42E+08	2.42E+08	2249
ENSG00000(	5.17896	3.612863	2.638828	5.243529	11.04518	0.821965	-0.47368	0.63072	0.74081	ACTG1P1	chr3	+	1.39E+08	1.39E+08	1129
ENSG00000(	0	0	1.319414	1.498151	9.20432	4.93179	-2.4656	0.044805	0.088287	RP11-455G	chr4	-	1.2E+08	1.2E+08	2097
ENSG00000(	9.322127	4.817151	3.958241	15.73059	20.2495	11.50751	-1.2684	0.072065	0.13302	AL513477.	chr1	+	2316811	2319922	3110
ENSG00000(	1.035792	0	0	0.749076	0	0.821965	-0.11768	0.9281	NA	ARMC10P1	chr3	-	94225610	94226464	855
ENSG00000(	65.25489	59.0101	105.5531	41.19916	47.86246	48.49593	0.72521	0.031115	0.064203	CSRNP3	chr2	+	1.66E+08	1.67E+08	11788
ENSG00000(	36.25272	21.67718	42.22124	66.66772	49.70333	39.45432	-0.62714	0.11747	0.20038	ZNF713	chr7	+	55955169	56009918	3550
ENSG00000(	99.43602	103.5687	65.97069	44.94453	47.86246	38.63235	1.0233	0.001249	0.003448	PARP10	chr8	-	1.45E+08	1.45E+08	3497
ENSG00000(	0	0	0	8.239831	8.283888	6.575719	-3.7807	0.001729	0.004654	DYNAP	chr18	+	52254988	52266724	2027
ENSG00000(	569.6855	608.1653	750.7464	799.2636	849.5587	711.8216	-0.29222	0.050429	0.097844	SUZ12	chr17	+	30264037	30328064	4491
ENSG00000(	106.6866	136.0845	151.7326	106.3687	77.31629	79.7306	0.57069	0.029187	0.06071	NSUN3	chr3	+	93781760	93847389	3289
ENSG00000(	27185.39	26997.72	33837.69	2964.092	3762.726	3034.694	3.1655	5.45E-130	6.40E-128	KCTD12	chr13	-	77454312	77460540	6214
ENSG00000(	263.0911	276.9862	278.3963	88.39091	108.611	83.84042	1.5367	8.71E-14	6.38E-13	DHFRL1	chr3	-	93766680	93782233	4038
ENSG00000(	47.64643	48.17151	50.13772	346.0729	273.3683	274.5363	-2.5972	2.93E-28	4.15E-27	RPP25	chr15	-	75246757	75249805	3049
ENSG00000(	4872.365	4171.653	3744.496	2956.601	2082.938	2174.919	0.8233	2.98E-08	1.44E-07	GRINA	chr8	+	1.45E+08	1.45E+08	1968
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	C5orf64	chr5	+	60933535	61047590	2970
ENSG00000(	3.107376	0	2.638828	0	0	0.821965	1.4274	0.29154	0.41564	GLULP4	chr9	+	34917172	34918293	1122
ENSG00000(	0	0	0	102.6234	84.67974	57.53754	-7.075	3.30E-12	2.18E-11	THBD	chr20	-	23026270	23030378	4109
ENSG00000(	0	1.204288	0	0	0	1.64393	-0.12916	0.91993	NA	GP5	chr3	-	1.94E+08	1.94E+08	3534
ENSG00000(	2.071584	1.204288	3.958241	0	1.840864	3.28786	0.35727	0.76976	0.84862	C13orf45	chr13	+	76445187	76457947	1154
ENSG00000(	1763.954	1798.002	1512.048	2097.412	1798.524	2212.73	-0.26696	0.036133	0.073188	COX5A	chr15	-	75212132	75230509	1268
ENSG00000(	3.107376	0	6.597069	4.494453	4.60216	4.93179	-0.44921	0.66434	0.76831	STX19	chr3	-	93733213	93747454	1158
ENSG00000(	52.82539	59.0101	63.33186	25.46857	18.40864	32.05663	1.1751	0.002183	0.005778	FAM132B	chr2	+	2.39E+08	2.39E+08	2307
ENSG00000(	690.8732	593.7138	628.041	420.9805	435.3643	441.3952	0.55907	7.38E-05	0.000245	FAM219B	chr15	-	75192328	75199462	4706
ENSG00000(	183.3352	174.6217	158.3297	537.8362	689.4036	540.8529	-1.7653	6.28E-24	7.46E-23	ZHX2	chr8	+	1.24E+08	1.24E+08	4622

ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	CPN2	chr3	-	1.94E+08	1.94E+08	3028
ENSG00000(	83.89914	65.03154	60.69303	171.5383	132.5422	230.9721	-1.3337	1.16E-06	4.77E-06	CPNE7	chr16	+	89642176	89663654	2657
ENSG00000(	0	2.408575	0	10.48706	11.04518	23.01502	-3.4745	0.000476	0.001403	C5orf46	chr5	-	1.47E+08	1.47E+08	573
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	GDPD4	chr11	-	76927603	77012732	2533
ENSG00000(	674.3005	697.2826	667.6234	355.0618	321.2308	318.1004	1.0325	3.31E-13	2.35E-12	MPI	chr15	+	75182346	75191798	3066
ENSG00000(	11.39371	1.204288	2.638828	2.247227	3.681728	4.93179	0.43231	0.66645	0.76995	ADORA2A-A	chr22	-	24825178	24891042	2568
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	H1FOO	chr3	+	1.29E+08	1.29E+08	1067
ENSG00000(	4.143168	1.204288	0	0	3.681728	5.753754	-0.55209	0.65295	0.75865	TRIM73	chr7	+	75024337	75040279	3875
ENSG00000(	107.7224	78.2787	84.44248	46.44268	47.86246	46.03004	0.93822	0.001919	0.005129	OPLAH	chr8	-	1.45E+08	1.45E+08	4033
ENSG00000(	18.64425	8.430014	3.958241	16.47966	13.80648	12.32947	-0.40681	0.54952	0.671	TMEM52	chr1	-	1849029	1850712	1118
ENSG00000(	9.322127	1.204288	2.638828	8.239831	8.283888	15.61733	-1.1167	0.18825	0.29316	TMEM139	chr7	+	1.43E+08	1.43E+08	2383
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RNF186	chr1	-	20140523	20141771	1249
ENSG00000(	46.61064	51.78437	52.77655	16.47966	34.05598	18.08323	1.1201	0.007688	0.018354	EFCAB13	chr17	+	45400656	45518678	3931
ENSG00000(	2.071584	8.430014	5.277655	2.247227	0	4.109825	1.0364	0.33426	0.46228	MSC	chr8	-	72753784	72756703	2023
ENSG00000(	96.32865	86.70872	129.3026	81.64923	75.47542	73.97684	0.42609	0.11902	0.2024	APOLD1	chr12	+	12878865	12944400	4646
ENSG00000(	0	4.817151	9.235896	244.9477	266.9253	364.9524	-5.6151	2.80E-17	2.49E-16	FAM101A	chr12	+	1.25E+08	1.25E+08	2148
ENSG00000(	164.6909	150.536	139.8579	451.6926	262.3231	350.1571	-1.2175	2.45E-08	1.19E-07	EXOSC4	chr8	+	1.45E+08	1.45E+08	1065
ENSG00000(	824.4904	794.8299	996.1574	580.5336	578.0313	507.1524	0.6482	6.47E-06	2.46E-05	DPY19L3	chr19	+	32896655	32976801	6015
ENSG00000(	1124.87	1233.191	1179.556	1293.653	935.1589	954.3013	0.15088	0.30317	0.42832	TAF7	chr5	-	1.41E+08	1.41E+08	2274
ENSG00000(	39.36009	37.33292	62.01245	44.19546	111.3723	83.01846	-0.76825	0.042758	0.084858	ZNF852	chr3	-	44540462	44552128	3535
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	FOXE1	chr9	+	1.01E+08	1.01E+08	3451
ENSG00000(	1044.078	1038.096	976.3662	2030.744	2292.796	2326.983	-1.1179	1.50E-21	1.62E-20	PFAS	chr17	+	8150936	8173809	5371
ENSG00000(	156.4046	119.2245	124.0249	108.616	98.48622	139.734	0.2048	0.40825	0.53904	HYI	chr1	-	43916824	43919660	2173
ENSG00000(	1490.505	1543.897	1139.974	1065.935	729.9026	900.0516	0.62825	0.000101	0.000329	C17orf62	chr17	-	80400465	80408705	4327
ENSG00000(	0	1.204288	6.597069	0.749076	0	0	1.772	0.187	0.29167	LGALS7B	chr19	+	39279851	39282389	532
ENSG00000(	117.0445	114.4073	80.48424	259.1801	300.0608	350.1571	-1.5276	3.89E-12	2.55E-11	ZNF552	chr19	-	58315209	58326281	2352
ENSG00000(	4.143168	7.225726	6.597069	2.247227	4.60216	1.64393	0.92796	0.33327	0.46137	LINC00086	chrX	+	1.35E+08	1.35E+08	2913
ENSG00000(	2337.782	2231.545	1976.482	1753.586	2201.673	2360.683	0.052114	0.69959	0.79573	GAK	chr4	-	843064	926161	4442
ENSG00000(	1454.252	1286.179	1265.318	598.5114	679.2788	731.5488	0.99407	7.33E-14	5.40E-13	ZBTB7A	chr19	-	4044362	4066943	5422
ENSG00000(	4839.22	4289.673	3571.653	6459.278	5150.737	5494.835	-0.42822	0.001457	0.003969	TUFM	chr16	-	28853732	28857729	2071
ENSG00000(	142.9393	139.6974	129.3026	414.9879	406.8309	330.4299	-1.4752	4.46E-15	3.54E-14	RMI1	chr9	+	86595626	86618985	3416
ENSG00000(	109.7939	108.3859	110.8308	224.7227	254.9597	216.1768	-1.0735	2.46E-07	1.09E-06	CTC1	chr17	-	8130191	8151362	4797
ENSG00000(	14.50109	8.430014	23.74945	8.239831	5.522592	4.93179	1.2141	0.08336	0.15067	AC097658.	chr4	-	1.44E+08	1.44E+08	2552
ENSG00000(	354.2408	313.1148	311.3817	258.4311	285.3339	219.4646	0.35941	0.042742	0.084834	FBXO34	chr14	+	55738021	55828636	3464
ENSG00000(	7.250543	25.29004	6.597069	3.745378	3.681728	4.93179	1.5003	0.060737	0.11484	LINC00324	chr17	-	8123960	8127361	2082
ENSG00000(	2150.304	2243.588	1740.307	2977.575	2572.607	3166.209	-0.50535	0.000133	0.000425	SEPW1	chr19	+	48281829	48287943	2503
ENSG00000(	2461.042	2183.374	1782.528	2678.694	2125.277	2650.015	-0.21288	0.13548	0.22472	EIF3K	chr19	+	39109735	39127595	1327
ENSG00000(	889.7452	900.8072	918.312	1031.477	847.7179	886.0782	-0.03057	0.81465	0.87961	MRFAP1L1	chr4	-	6709428	6711607	2127
ENSG00000(	1417.999	1346.394	1625.518	649.4485	797.0941	621.4055	1.0836	1.24E-14	9.57E-14	SNX18	chr5	+	53813589	53842415	5375
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	EXD1	chr15	-	41474923	41522941	2942
ENSG00000(	327.3102	243.2661	219.0227	1720.627	1506.747	1745.032	-2.6405	6.62E-63	2.47E-61	AURKB	chr17	-	8108056	8113918	1249
ENSG00000(	34.18113	51.78437	13.19414	23.97042	23.0108	9.041614	0.79296	0.14916	0.24287	C14orf39	chr14	-	60863187	60982261	2813
ENSG00000(	7718.721	7246.199	6835.883	7281.763	7331.241	7714.963	-0.03427	0.73649	0.82369	MRFAP1	chr4	+	6641818	6644472	2049
ENSG00000(	278.628	264.9433	321.937	360.3053	339.6394	276.1802	-0.17431	0.33	0.45781	C3orf38	chr3	+	88198893	88207118	2633

ENSG00000(	0	0	0	3.745378	1.840864	8.219649	-2.9534	0.021724	0.046705	KLHDC7A	chr1	+	18807424	18812478	5055
ENSG00000(	170.9057	134.8802	122.7055	130.3391	132.5422	162.7491	0.013608	0.95338	0.97225	TMEM107	chr17	-	8076555	8079717	2358
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	LL0XNC01-	chrX	+	1E+08	1E+08	778
ENSG00000(	5.17896	7.225726	1.319414	6.74168	8.283888	0	-0.09757	0.9246	0.95436	AP001885.	chr11	-	66963391	66964638	1248
ENSG00000(	338.704	279.3948	282.3545	1548.339	1632.846	1815.721	-2.4628	2.82E-69	1.22E-67	RRS1	chr8	+	67341263	67342966	1704
ENSG00000(	39.36009	33.72006	6.597069	7.490755	8.283888	13.15144	1.3869	0.028595	0.059615	EXOC3L1	chr16	-	67218269	67224107	2510
ENSG00000(	6.214751	7.225726	7.916483	1062.938	868.8878	913.203	-6.9436	2.59E-85	1.51E-83	TRIML2	chr4	-	1.89E+08	1.89E+08	1639
ENSG00000(	2490.044	2418.21	2374.945	3339.379	5393.732	5229.341	-0.93548	2.32E-09	1.23E-08	RCC2	chr1	-	17733256	17766220	4087
ENSG00000(	2.071584	2.408575	9.235896	0	2.761296	0	1.6924	0.16086	0.25827	IGSF22	chr11	-	18725852	18747777	4284
ENSG00000(	7.250543	2.408575	3.958241	0	1.840864	0.821965	1.7974	0.12342	0.20854	C9orf50	chr9	-	1.32E+08	1.32E+08	1620
ENSG00000(	0	0	0	20.97412	30.37426	23.01502	-5.4887	3.81E-07	1.65E-06	ZFP42	chr4	+	1.89E+08	1.89E+08	2651
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC020907.	chr19	+	35596873	35598141	1269
ENSG00000(	5.17896	9.634302	2.638828	1.498151	1.840864	1.64393	1.4943	0.14713	0.24021	CCDC89	chr11	-	85394893	85397320	2428
ENSG00000(	1.035792	0	0	0	2.761296	0	-0.44657	0.73574	NA	C9orf106	chr9	+	1.32E+08	1.32E+08	3145
ENSG00000(	1.035792	3.612863	0	2.247227	0	0	0.55949	0.67862	0.77969	FAM133A	chrX	+	92929012	92967273	3416
ENSG00000(	505.4664	468.4679	402.4212	295.1358	288.0952	364.1305	0.53807	0.00146	0.003977	DPM3	chr1	-	1.55E+08	1.55E+08	517
ENSG00000(	0	0	0	1.498151	0	3.28786	-1.3443	0.31856	NA	C12orf42	chr12	-	1.04E+08	1.04E+08	2090
ENSG00000(	1892.392	1955.763	1497.535	2509.403	1904.374	2388.63	-0.34652	0.015341	0.034173	CYC1	chr8	+	1.45E+08	1.45E+08	1832
ENSG00000(	2746.92	2616.917	2153.283	510.1204	644.3024	720.0413	1.9988	4.41E-41	9.37E-40	PER1	chr17	-	8043790	8059824	4707
ENSG00000(	0	0	0	8.239831	22.09037	19.72716	-4.8965	1.32E-05	4.84E-05	HTR1F	chr3	+	88039846	88042919	3074
ENSG00000(	0	2.408575	2.638828	3.745378	0	0.821965	0.063773	0.96087	0.9773	RP11-349N	chrX	+	1.23E+08	1.23E+08	400
ENSG00000(	340.7755	373.3292	440.6842	263.6746	372.775	304.949	0.29349	0.10848	0.18746	TMTC2	chr12	+	83080659	83528649	6211
ENSG00000(	15.53688	14.45145	27.70769	19.47596	7.363456	7.397684	0.69362	0.2677	0.38796	HES7	chr17	-	8023908	8027410	1674
ENSG00000(	1342.386	1345.189	1178.237	2552.849	1795.763	2049.981	-0.72502	3.71E-07	1.61E-06	FARSA	chr19	-	13033293	13044851	2057
ENSG00000(	527.2181	534.7037	631.9992	361.8035	428.9213	378.9258	0.53242	0.000527	0.001543	SPTY2D1	chr11	-	18627948	18656338	5754
ENSG00000(	0	0	0	2.247227	0.920432	0.821965	-1.2297	0.36205	NA	RP11-458F	chr7	+	66379568	66379930	363
ENSG00000(	6.214751	3.612863	0	0	3.681728	0	0.97804	0.44345	0.57315	C10orf67	chr10	-	23556124	23633774	2799
ENSG00000(	3108.412	2921.602	3029.374	1981.305	2430.861	2356.573	0.42017	0.000339	0.001022	SAMD4B	chr19	+	39833036	39876350	4519
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	LINC00670	chr17	+	12453099	12546171	2953
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	MTUS2-AS1	chr13	-	30050652	30061887	1114
ENSG00000(	1.035792	0	3.958241	3.745378	5.522592	4.109825	-1.13	0.31333	0.43977	ALOXE3	chr17	-	7999218	8022365	3362
ENSG00000(	837.9557	847.8186	785.0512	1056.197	1135.813	1076.774	-0.40224	0.000936	0.002634	EDC3	chr15	-	74922899	74988633	3763
ENSG00000(	360.4556	427.5221	464.4337	443.4527	425.2396	423.3119	-0.04724	0.76323	0.84364	TCAIM	chr3	+	44379611	44450943	3687
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-480N	chr6	+	43331217	43331957	741
ENSG00000(	114.9729	108.3859	79.16483	134.0845	96.64536	104.3895	-0.14439	0.58653	0.70381	FUCA1	chr1	-	24171567	24194784	2047
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	PXT1	chr6	-	36358328	36410666	2108
ENSG00000(	30.03797	32.51577	13.19414	5.992604	10.12475	9.041614	1.5222	0.010682	0.024664	GGN	chr19	-	38874905	38878722	2239
ENSG00000(	0	0	2.638828	108.616	69.95283	81.37453	-6.0013	3.63E-14	2.72E-13	TMEM125	chr1	+	43735665	43739673	1850
ENSG00000(	1872.712	1885.915	2203.421	2171.57	2799.954	2468.361	-0.31883	0.014039	0.031595	ZNF664	chr12	+	1.24E+08	1.24E+08	5108
ENSG00000(	35514.2	35335.01	31855.93	21912.71	22621.46	25534.34	0.55084	2.49E-07	1.10E-06	CALR	chr19	+	13049392	13055303	1903
ENSG00000(	8.286335	24.08575	15.83297	0	1.840864	3.28786	2.8617	0.000983	0.00276	LINC00311	chr16	+	85316564	85319569	1566
ENSG00000(	9631.829	9075.512	9063.053	4305.686	4259.759	3630.619	1.1853	1.98E-27	2.71E-26	MAGED1	chrX	+	51546103	51645453	5418
ENSG00000(	42.46747	36.12863	35.62417	19.47596	34.97642	31.23467	0.41246	0.32788	0.45558	RP11-111N	chr11	+	76092357	76125663	5363
ENSG00000(	608.0098	661.154	661.0263	435.2129	484.1472	360.0206	0.59159	0.000123	0.000396	LDLRAD3	chr11	+	35965531	36253686	3798

ENSG00000(	146.0467	128.8588	162.2879	632.9688	643.382	614.0078	-2.106	4.62E-37	8.77E-36	CDH4	chr20	+	59827482	60515673	6511
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-429E	chr20	-	60292562	60294804	2000
ENSG00000(	35.21692	34.92434	21.11062	5.243529	0.920432	3.28786	3.0317	4.38E-06	1.69E-05	SMCO3	chr12	-	14957584	14967116	2104
ENSG00000(	1427.321	1506.564	1361.635	2127.375	1544.485	1641.464	-0.30638	0.027795	0.058134	RAD23A	chr19	+	13056669	13064456	1746
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	C2orf71	chr2	-	29283842	29297127	7044
ENSG00000(	2078.834	1773.916	1534.478	2051.718	1719.367	1988.333	-0.09557	0.48421	0.61334	GADD45GI	chr19	-	13064972	13068050	743
ENSG00000(	0	0	0	0.749076	1.840864	0.821965	-1.0455	0.43461	NA	DAND5	chr19	+	13075973	13085567	1868
ENSG00000(	112.9013	138.4931	112.1502	1.498151	5.522592	0.821965	5.3674	2.71E-24	3.26E-23	TMEM151A	chr11	+	66059341	66064135	2562
ENSG00000(	42.46747	72.25726	44.86007	106.3687	138.9852	158.6392	-1.3244	1.02E-05	3.77E-05	C17orf96	chr17	-	36827961	36831187	3227
ENSG00000(	2241.454	2072.579	3000.347	2568.58	3262.931	2414.111	-0.17254	0.26701	0.38713	PTPN11	chr12	+	1.13E+08	1.13E+08	6101
ENSG00000(	16.57267	7.225726	17.15238	8.239831	6.443024	3.28786	1.092	0.13509	0.22423	CTGLF12P	chr10	-	49217898	49239743	2485
ENSG00000(	8.286335	7.225726	5.277655	119.8521	147.2691	153.7074	-4.2101	2.49E-23	2.88E-22	NSUN7	chr4	+	40751914	40812002	3698
ENSG00000(	0	0	3.958241	2.996302	6.443024	1.64393	-1.0986	0.36633	0.49632	ZCCHC5	chrX	-	77911566	77914825	2648
ENSG00000(	79.75598	73.46155	104.2337	26.21764	67.19154	65.75719	0.68492	0.057748	0.11012	FAM156B	chrX	+	52920336	52937587	2946
ENSG00000(	2.071584	2.408575	5.277655	68.16587	63.50981	59.18147	-4.1072	3.05E-12	2.02E-11	WSCD1	chr17	+	5675554	6027747	5884
ENSG00000(	1.035792	0	5.277655	61.42419	91.12277	56.71558	-4.7751	7.95E-13	5.48E-12	RAB39A	chr11	+	1.08E+08	1.08E+08	1830
ENSG00000(	984.0023	991.1288	928.8673	855.4443	790.6511	765.2493	0.26762	0.031651	0.065137	CLK3	chr15	+	74890841	74932057	3787
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	GS1-124K5	chr7	-	65970142	65971210	1069
ENSG00000(	0	0	0	9.737982	7.363456	8.219649	-3.9216	0.001025	0.002869	HLA-DQB1	chr6	-	32627244	32636160	4644
ENSG00000(	87.00652	55.39724	65.97069	1329.609	1709.242	1948.879	-4.5475	2.28E-119	2.38E-117	GATA2	chr3	-	1.28E+08	1.28E+08	3367
ENSG00000(	56.96855	75.87013	48.81831	2561.838	2488.848	2631.932	-5.3788	3.47E-223	1.32E-220	ARID3B	chr15	+	74833518	74890472	4271
ENSG00000(	6.214751	7.225726	2.638828	4.494453	3.681728	2.465895	0.51591	0.5866	0.70383	HMGN2P46	chr15	+	45803334	45878488	1923
ENSG00000(	0	2.408575	0	1.498151	1.840864	4.109825	-1.0557	0.41354	0.54398	TMEM31	chrX	+	1.03E+08	1.03E+08	728
ENSG00000(	1556.795	1549.918	1113.585	1307.886	1171.71	1400.628	0.1215	0.41133	0.54204	PACS2	chr14	+	1.06E+08	1.06E+08	6332
ENSG00000(	424.6747	479.3065	596.375	550.5705	576.1904	503.8645	-0.12184	0.44904	0.57882	ELMOD2	chr4	+	1.41E+08	1.41E+08	4409
ENSG00000(	31.07376	36.12863	35.62417	0	1.840864	4.109825	3.8255	4.92E-08	2.33E-07	EGR3	chr8	-	22545172	22550815	4336
ENSG00000(	4.143168	21.67718	9.235896	5.243529	4.60216	4.93179	1.1184	0.16187	0.25954	C1orf101	chr1	+	2.45E+08	2.45E+08	3333
ENSG00000(	5.17896	0	0	123.5975	88.36147	149.5976	-5.5916	1.14E-18	1.09E-17	GPC5	chr13	+	92050929	93519490	2889
ENSG00000(	544.8265	614.1867	397.1435	1268.185	1137.654	1216.508	-1.2133	1.64E-14	1.26E-13	VWA1	chr1	+	1370241	1378262	4511
ENSG00000(	140.8677	96.34302	91.03955	96.63075	103.0884	101.1017	0.13088	0.6192	0.73159	LINC00174	chr7	-	65841031	65866325	4702
ENSG00000(	430.8894	407.0492	432.7677	1089.156	903.8642	914.025	-1.1912	2.55E-17	2.27E-16	GEMIN4	chr17	-	647654	657239	4729
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AC073072.	chr7	-	22765014	22767239	1364
ENSG00000(	1177.695	982.6988	1051.573	1977.559	1764.468	1836.27	-0.79421	9.75E-11	5.78E-10	FJX1	chr11	+	35639735	35642419	2685
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP5-1027G	chr20	-	19222946	19265240	1789
ENSG00000(	75.61281	44.55865	104.2337	49.43899	59.82808	34.52253	0.62959	0.086157	0.15505	KLHL28	chr14	-	45397672	45511525	2395
ENSG00000(	0	0	0	26.96672	9.20432	10.68554	-4.7952	2.39E-05	8.45E-05	MKRN3	chr15	+	23810454	23873064	2711
ENSG00000(	266.1985	302.2762	319.2981	299.6302	330.4351	304.949	-0.07583	0.65214	0.758	ZBTB18	chr1	+	2.44E+08	2.44E+08	3851
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	EEF1A1P27	chr7	+	20621695	20622829	1135
ENSG00000(	0	2.408575	0	2.247227	0	1.64393	-0.37942	0.77921	0.85467	AL109806.	chr20	+	55097413	55097855	441
ENSG00000(	49.71801	42.15007	42.22124	41.94823	41.41944	30.4127	0.235	0.52951	0.65424	C14orf28	chr14	+	45366498	45376460	3498
ENSG00000(	93.22127	126.4502	88.40072	159.5531	127.94	154.5294	-0.51805	0.035304	0.071693	RP11-151N	chr15	-	44819455	44829121	2863
ENSG00000(	1037.863	873.1086	713.8029	1044.96	860.6039	1024.99	-0.15731	0.31024	0.43631	SHARPIN	chr8	-	1.45E+08	1.45E+08	1765
ENSG00000(	7.250543	3.612863	9.235896	14.98151	11.04518	12.32947	-0.86727	0.2277	0.34091	LBX2	chr2	-	74724644	74730443	1452
ENSG00000(	180.2278	197.5032	179.4403	113.1104	146.3487	136.4462	0.49209	0.021412	0.046109	DNHD1	chr11	+	6518490	6614988	14862

ENSG00000(	2.071584	1.204288	0	53.18436	65.35067	33.70056	-4.8946	3.09E-10	1.76E-09	SLITRK4	chrX	-	1.43E+08	1.43E+08	8555
ENSG00000(	1.035792	0	0	6.74168	7.363456	7.397684	-3.0281	0.009616	0.022454	HTR1D	chr1	-	23516993	23521222	2835
ENSG00000(	599.7235	519.048	624.0827	367.047	472.1816	436.4634	0.44985	0.004133	0.010416	GCC1	chr7	-	1.27E+08	1.27E+08	4149
ENSG00000(	6.214751	0	0	3.745378	6.443024	2.465895	-0.73648	0.52469	0.64968	LSMEM2	chr3	+	50316458	50325545	1494
ENSG00000(	2.071584	3.612863	0	2.247227	11.96562	1.64393	-1.1365	0.30635	0.43195	RNF151	chr16	+	2016824	2018976	853
ENSG00000(	11.39371	2.408575	6.597069	7.490755	10.12475	13.9734	-0.55957	0.46971	0.59888	CIITA	chr16	+	10971055	11026079	9438
ENSG00000(	472.3211	461.2422	320.6175	350.5674	379.218	284.3999	0.30757	0.10293	0.17959	ZFPM1	chr16	+	88519725	88601572	3528
ENSG00000(	9.322127	4.817151	3.958241	0	0	0	3.7411	0.002786	0.007239	PLD6	chr17	-	17104309	17109629	2560
ENSG00000(	0	2.408575	0	7.490755	0.920432	12.32947	-2.3178	0.045784	0.08993	GRM8	chr7	-	1.26E+08	1.27E+08	4057
ENSG00000(	1529.865	1410.221	1266.637	553.5668	578.0313	632.913	1.2514	1.63E-21	1.76E-20	CDC42EP4	chr17	-	71279763	71308314	3272
ENSG00000(	7.250543	1.204288	3.958241	12.73428	16.56778	12.32947	-1.5614	0.046163	0.090583	DGKZP1	chr13	+	44542560	44545335	2776
ENSG00000(	73.54123	92.73015	84.44248	113.1104	110.4518	122.4728	-0.46344	0.06916	0.12844	ZBTB42	chr14	+	1.05E+08	1.05E+08	3800
ENSG00000(	588.3298	581.671	769.2182	283.1506	277.9705	219.4646	1.3062	4.60E-14	3.44E-13	LACC1	chr13	+	44453420	44468068	4262
ENSG00000(	1038.899	859.8614	792.9677	1252.454	1071.383	1375.147	-0.45627	0.001813	0.00487	MAF1	chr8	+	1.45E+08	1.45E+08	1754
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	TPPP2	chr14	+	21492268	21504435	1696
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	ARL14	chr3	+	1.6E+08	1.6E+08	1286
ENSG00000(	16.57267	9.634302	1.319414	20.22504	10.12475	16.4393	-0.68816	0.33825	0.46684	KIAA1875	chr8	+	1.45E+08	1.45E+08	7119
ENSG00000(	4.143168	4.817151	6.597069	14.98151	23.93123	32.8786	-2.0738	0.001753	0.004719	PCED1B	chr12	+	47473386	47630443	2328
ENSG00000(	59.04014	33.72006	30.34652	68.16587	49.70333	56.71558	-0.48586	0.1934	0.29928	RP11-169K	chr1	-	16160560	16174642	2468
ENSG00000(	77.68439	69.84869	58.05421	18.72689	18.40864	16.4393	1.9038	5.75E-07	2.44E-06	APOBEC3B	chr22	+	39378352	39388809	1844
ENSG00000(	0	1.204288	1.319414	2.247227	2.761296	4.93179	-1.419	0.24746	0.36427	PIPOX	chr17	+	27277531	27384234	2410
ENSG00000(	1.035792	0	1.319414	0	0	0.821965	0.54471	0.68089	NA	ATP8B5P	chr9	+	35406752	35483026	3962
ENSG00000(	0	0	5.277655	0.749076	0	0.821965	0.90059	0.50557	0.63323	ATOH7	chr10	-	69990386	69991871	1486
ENSG00000(	2.071584	3.612863	1.319414	277.907	205.2563	218.6427	-6.3182	1.17E-29	1.75E-28	CDH5	chr16	+	66400533	66438686	4117
ENSG00000(	0	0	0	149.066	99.40666	123.2947	-7.6212	2.07E-14	1.57E-13	LRRC3B	chr3	+	26664297	26752267	1696
ENSG00000(	26.93059	45.76293	34.30476	0	0	0	6.3937	1.54E-09	8.30E-09	FAM216B	chr13	+	43355686	43365683	3300
ENSG00000(	311.7734	319.1362	249.3692	226.2208	218.1424	273.7143	0.29381	0.11635	0.19879	PCBP1-AS1	chr2	-	70189395	70315978	2451
ENSG00000(	2563.585	2695.196	2162.519	3657.736	3212.308	3421.84	-0.4706	9.53E-05	0.000312	MYADM	chr19	+	54369477	54379691	3186
ENSG00000(	191.6215	208.3418	186.0373	155.0586	201.5746	212.8889	0.042711	0.83576	0.8949	MROH1	chr8	+	1.45E+08	1.45E+08	5832
ENSG00000(	687.7658	652.7239	765.26	768.5515	801.6963	574.5535	-0.0267	0.86437	0.91431	SERTAD2	chr2	-	64858755	64977449	5549
ENSG00000(	2748.992	2533.821	2558.343	1752.837	1943.952	1731.058	0.53031	1.89E-06	7.61E-06	RBM15B	chr3	+	51428731	51435330	6600
ENSG00000(	3.107376	6.021439	15.83297	67.4168	95.72493	48.49593	-3.0091	4.44E-09	2.30E-08	AKAP5	chr14	+	64932217	64936425	2601
ENSG00000(	4.143168	37.33292	13.19414	1.498151	11.04518	5.753754	1.4399	0.070049	0.12984	NKPD1	chr19	-	45653008	45663408	4687
ENSG00000(	10.35792	10.83859	9.235896	2.996302	4.60216	1.64393	1.543	0.066586	0.12434	GIPC3	chr19	+	3585551	3593539	4335
ENSG00000(	75.61281	59.0101	31.66593	32.95932	29.45382	32.05663	0.80457	0.043577	0.086237	AC025335.	chr17	-	7816642	7819271	2529
ENSG00000(	49.71801	31.31148	58.05421	53.93344	31.29469	36.98842	0.17649	0.65456	0.75999	CITED4	chr1	-	41326729	41328018	1290
ENSG00000(	17.60846	26.49433	34.30476	1.498151	8.283888	1.64393	2.6084	0.00019	0.000595	ABCA13	chr7	+	48211055	48687092	17184
ENSG00000(	220.6237	155.3531	155.6908	220.9773	203.4155	171.7907	-0.16045	0.46366	0.59294	TIGD5	chr8	+	1.45E+08	1.45E+08	2412
ENSG00000(	1841.638	1769.099	2097.868	1477.177	1564.734	1319.254	0.38741	0.001805	0.00485	PDXDC1	chr16	+	15068448	15233196	4828
ENSG00000(	41.43168	26.49433	43.54065	20.22504	28.53339	27.12484	0.54382	0.20939	0.31902	PHC1P1	chr12	-	55804263	55808633	3553
ENSG00000(	1.035792	1.204288	3.958241	4.494453	2.761296	0.821965	-0.31108	0.78925	0.86218	C1orf194	chr1	-	1.1E+08	1.1E+08	956
ENSG00000(	532.397	479.3065	543.5985	191.0143	289.9361	203.0253	1.1828	1.43E-10	8.39E-10	ZNF154	chr19	-	58208735	58220579	5687
ENSG00000(	529.2897	550.3595	469.7113	266.6709	226.4263	266.3166	1.0244	1.73E-10	1.00E-09	R3HDM2	chr12	-	57643392	57824788	4372
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	B3GNT3	chr19	+	17905637	17923891	2226

ENSG00000(	0	0	2.638828	16.47966	18.40864	22.19305	-3.8331	4.79E-05	0.000163	NRXN1	chr2	-	50145643	51259674	7578
ENSG00000(	719.8754	622.6168	635.9574	731.0977	729.9026	812.9233	-0.19931	0.14108	0.23226	SEPHS2	chr16	-	30454952	30457502	2551
ENSG00000(	17.60846	2.408575	5.277655	4.494453	7.363456	9.863579	0.21779	0.79342	0.86496	GPBAR1	chr2	+	2.19E+08	2.19E+08	2003
ENSG00000(	213.3731	157.7617	141.1773	149.066	148.1896	165.2149	0.15114	0.50134	0.62948	ZNF784	chr19	-	56132108	56135967	2021
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	ZNF648	chr1	-	1.82E+08	1.82E+08	3649
ENSG00000(	674.3005	762.3141	610.8886	1125.111	682.9605	835.1164	-0.36759	0.036776	0.074348	C14orf119	chr14	+	23563974	23569665	3654
ENSG00000(	3.107376	6.021439	2.638828	3.745378	0.920432	2.465895	0.57204	0.59173	0.708	LINC00652	chr20	-	18768295	18774979	1713
ENSG00000(	321.0955	272.169	328.534	229.2171	211.6994	217.8207	0.48204	0.00623	0.015141	BBS10	chr12	-	76738254	76742222	3595
ENSG00000(	397.7441	355.2649	341.7282	482.4047	416.0353	443.8611	-0.29233	0.060448	0.11436	FIZ1	chr19	-	56102746	56113336	4686
ENSG00000(	2277.706	2062.945	1944.816	3938.639	3065.039	3507.324	-0.74001	4.27E-09	2.22E-08	PUF60	chr8	-	1.45E+08	1.45E+08	2412
ENSG00000(	312.8092	388.9849	237.4945	12.73428	32.21512	23.01502	3.7629	3.92E-37	7.47E-36	SSC5D	chr19	+	55999771	56030465	4845
ENSG00000(	406.0304	410.6621	299.5069	1017.994	744.6295	895.1198	-1.2453	1.78E-13	1.28E-12	DCTPP1	chr16	-	30434940	30441396	1222
ENSG00000(	355.2766	290.2333	266.5216	295.8848	201.5746	213.7109	0.35687	0.07915	0.14404	ZNF771	chr16	+	30418618	30440920	2371
ENSG00000(	22.78742	14.45145	22.43003	14.23244	12.88605	24.65895	0.19566	0.72142	0.81271	PPP1R14BI	chr4	-	1.4E+08	1.4E+08	445
ENSG00000(	24.85901	33.72006	25.06886	32.95932	41.41944	16.4393	-0.1129	0.81078	0.87724	RP11-1319	chr5	-	69390202	69424261	3544
ENSG00000(	100.4718	119.2245	109.5113	131.0882	119.6562	108.4994	-0.12709	0.59669	0.71245	CRIPAK	chr4	+	1385340	1389780	4441
ENSG00000(	1367.245	1347.598	1463.23	67.4168	86.52061	67.40112	4.2298	4.56E-155	7.34E-153	TSHZ1	chr18	+	72922710	73001905	7080
ENSG00000(	67.32647	62.62296	68.60952	74.15848	46.94203	41.09825	0.28291	0.40106	0.53228	PSTK	chr10	+	1.25E+08	1.25E+08	3538
ENSG00000(	398.7799	431.135	597.6944	638.2124	627.7346	485.7813	-0.29621	0.10054	0.17626	SOCS4	chr14	+	55493948	55516206	6779
ENSG00000(	1032.685	968.2473	1108.308	191.7633	158.3143	133.1583	2.6737	1.79E-61	6.49E-60	ZADH2	chr18	-	72907063	72921303	7732
ENSG00000(	7.250543	9.634302	14.51355	6.74168	9.20432	11.50751	0.17231	0.80695	0.87472	RP11-756P	chr4	+	1.9E+08	1.9E+08	1143
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC079741.	chr7	-	1.12E+08	1.12E+08	212
ENSG00000(	167.7983	173.4174	166.2461	567.7993	608.4055	602.5003	-1.8028	1.11E-29	1.68E-28	ZNF48	chr16	+	30389427	30411429	3234
ENSG00000(	1.035792	1.204288	2.638828	1.498151	0	0	0.92435	0.49172	0.62078	C3orf80	chr3	+	1.6E+08	1.6E+08	2577
ENSG00000(	2.071584	0	0	1.498151	0	0	0.18632	0.88758	NA	NKX2-6	chr8	-	23559964	23564111	906
ENSG00000(	1.035792	2.408575	0	0	2.761296	0	0.18734	0.89003	0.93174	TMEM150B	chr19	-	55824169	55845416	1197
ENSG00000(	0	1.204288	0	5.243529	0	2.465895	-1.5088	0.2587	0.37741	C10orf91	chr10	+	1.34E+08	1.34E+08	1846
ENSG00000(	0	0	0	12.73428	37.73771	32.8786	-5.6052	2.40E-07	1.06E-06	ANKRD18A	chr9	-	38540564	38620657	4041
ENSG00000(	6.214751	8.430014	6.597069	14.98151	12.88605	6.575719	-0.64496	0.37785	0.50856	TMEM86B	chr19	-	55738007	55741647	3061
ENSG00000(	4.143168	0	1.319414	14.98151	6.443024	9.041614	-2.067	0.031584	0.065016	1-Sep	chr16	-	30389454	30407312	2738
ENSG00000(	312.8092	376.9421	245.411	463.6778	487.829	477.5616	-0.60741	0.000533	0.00156	TRNAU1AP	chr1	+	28879597	28905051	2040
ENSG00000(	1494.648	1419.855	1203.305	809.0016	780.5263	854.8435	0.75135	7.30E-09	3.71E-08	EXOC3	chr5	+	443273	472052	5748
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	AC017081.	chr2	-	2.07E+08	2.07E+08	823
ENSG00000(	3.107376	0	3.958241	0.749076	0	0.821965	1.311	0.31886	0.44598	TDRD6	chr6	+	46655612	46672056	8887
ENSG00000(	0	2.408575	2.638828	0	0	0	1.6365	0.22501	NA	C12orf40	chr12	+	40019969	40302102	3061
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CSNK1A1L	chr13	-	37677398	37679803	2406
ENSG00000(	11.39371	10.83859	11.87472	11.23613	16.56778	6.575719	-0.00622	0.99256	0.99532	ACTA2-AS1	chr10	+	90692428	90700368	2422
ENSG00000(	0	0	1.319414	0	0.920432	3.28786	-0.84165	0.53503	NA	HMGN2P9	chr22	+	44198424	44198652	229
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC079753.	chr2	+	1.14E+08	1.14E+08	795
ENSG00000(	528.2539	508.2094	387.9077	226.9699	337.7985	331.2519	0.66864	0.000512	0.001504	LYNX1	chr8	-	1.44E+08	1.44E+08	4706
ENSG00000(	17.60846	14.45145	5.277655	0	0	0	4.8526	2.93E-05	0.000103	TH	chr11	-	2185159	2193107	1910
ENSG00000(	1.035792	8.430014	2.638828	2.247227	7.363456	1.64393	0.090118	0.93124	0.95867	AC018865.	chr2	-	1.31E+08	1.31E+08	3793
ENSG00000(	672.2289	664.7668	748.1076	1006.758	862.4448	674.8332	-0.28692	0.07088	0.13118	MED14	chrX	-	40507558	40595110	7984
ENSG00000(	658.7637	578.0581	484.2249	707.1273	641.5411	678.943	-0.234	0.11918	0.20263	FAHD1	chr16	+	1876968	1890208	1964

ENSG00000(	8.286335	7.225726	9.235896	4.494453	5.522592	4.109825	0.72906	0.37214	0.50273	HMGB1P14	chr14	+	58751491	58752116	591
ENSG00000(	83.89914	80.68728	65.97069	484.6519	555.9409	484.1373	-2.7051	2.82E-44	6.60E-43	C8orf42	chr8	-	439803	495781	3395
ENSG00000(	1034.756	894.7858	810.1201	1999.283	1868.477	2109.162	-1.1215	3.97E-18	3.69E-17	RCC1	chr1	+	28832455	28865812	2844
ENSG00000(	3.107376	0	0	3.745378	6.443024	4.93179	-1.6533	0.15381	0.24921	MYLPF	chr16	+	30382255	30389312	682
ENSG00000(	1.035792	0	2.638828	14.23244	5.522592	4.93179	-2.253	0.031485	0.064846	F2	chr11	+	46740730	46761056	2023
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	FAM71C	chr12	+	1E+08	1E+08	1796
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	RP11-179B	chr10	-	59972302	59972797	496
ENSG00000(	546.8981	499.7794	628.041	723.607	540.2936	594.2806	-0.15133	0.3419	0.47081	PRKRA	chr2	-	1.79E+08	1.79E+08	1851
ENSG00000(	667.05	696.0783	711.164	226.9699	261.4027	258.9189	1.4694	2.89E-23	3.33E-22	HERC2P3	chr15	-	20587869	20711433	4383
ENSG00000(	46.61064	40.94578	35.62417	199.2541	170.2799	152.0635	-2.0551	5.55E-14	4.12E-13	ZNRF2	chr7	+	30323923	30452118	3460
ENSG00000(	6.214751	0	3.958241	1.498151	2.761296	1.64393	0.61412	0.59418	0.71029	RRH	chr4	+	1.11E+08	1.11E+08	1455
ENSG00000(	2.071584	0	2.638828	1.498151	1.840864	1.64393	-0.05579	0.96464	0.97961	SLC9A4	chr2	+	1.03E+08	1.03E+08	4138
ENSG00000(	72.50543	61.41867	77.84541	115.3576	101.2475	64.11326	-0.40279	0.18621	0.29079	ZNF816	chr19	-	53430388	53466164	2697
ENSG00000(	886.6379	917.6672	1033.101	423.9768	520.9645	461.9443	1.0098	9.42E-13	6.46E-12	FGD6	chr12	-	95470525	95611258	9288
ENSG00000(	0	0	0	0.749076	0.920432	1.64393	-1.0185	0.44577	NA	GPR144	chr9	+	1.27E+08	1.27E+08	2892
ENSG00000(	3.107376	7.225726	3.958241	0	1.840864	3.28786	1.174	0.28802	0.41168	CTD-2568A	chr19	+	51320937	51322134	936
ENSG00000(	0	0	0	836.7174	754.7542	622.2274	-9.8858	1.59E-27	2.19E-26	PLD5	chr1	-	2.42E+08	2.43E+08	2830
ENSG00000(	1821.958	1863.033	1826.069	1313.879	1356.717	1619.271	0.36067	0.003195	0.008222	OAZ2	chr15	-	64979772	64995480	7102
ENSG00000(	0	0	5.277655	0.749076	0	0	1.2252	0.36584	0.49572	PNPLA1	chr6	+	36210980	36276372	2478
ENSG00000(	44.53905	61.41867	39.58241	32.95932	20.2495	22.19305	0.92105	0.025235	0.053418	ALX1	chr12	+	85673885	85695562	1445
ENSG00000(	249.6258	223.9975	279.7157	516.8621	393.9449	364.9524	-0.75848	4.57E-05	0.000156	CCDC43	chr17	-	42750437	42767147	2082
ENSG00000(	34.18113	28.90291	31.66593	29.96302	36.81728	17.26126	0.17222	0.70195	0.79743	C17orf104	chr17	+	42733762	42767676	4328
ENSG00000(	1754.631	1452.371	1519.965	1555.081	996.8279	891.8319	0.45456	0.010924	0.025182	FZD2	chr17	+	42634925	42636907	1983
ENSG00000(	1.035792	2.408575	1.319414	0	0	0	1.6865	0.21314	NA	AL035460.	chr20	+	2677351	2677781	414
ENSG00000(	56.96855	46.96722	71.24834	164.0475	157.3939	117.541	-1.315	2.14E-06	8.55E-06	TIGD2	chr4	+	90033968	90036050	2083
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	CCDC129	chr7	+	31553704	31698334	4544
ENSG00000(	197.8363	221.5889	229.578	31.46117	21.16994	22.19305	3.0743	1.46E-29	2.18E-28	HCLS1	chr3	-	1.21E+08	1.21E+08	2710
ENSG00000(	278.628	264.9433	266.5216	62.92235	89.2819	88.77221	1.7425	1.19E-15	9.71E-15	C7orf41	chr7	+	30174426	30202378	5937
ENSG00000(	1231.557	1110.353	1523.923	830.7248	1240.742	1088.282	0.29013	0.077179	0.14092	ZNF609	chr15	+	64752941	64978264	8743
ENSG00000(	1607.549	1548.714	1968.565	2091.419	2309.364	1840.379	-0.284	0.03548	0.072001	PAK2	chr3	+	1.96E+08	1.97E+08	6139
ENSG00000(	114.9729	107.1816	143.8161	176.7818	192.3703	188.23	-0.60552	0.005692	0.013944	CCDC66	chr3	+	56591189	56655846	3120
ENSG00000(	56.96855	83.09585	91.03955	137.0808	224.5854	183.2982	-1.2297	5.72E-06	2.18E-05	AC034193.	chr3	+	10028577	10048674	2882
ENSG00000(	2219.702	2280.921	2644.105	2711.653	2732.763	2474.936	-0.14869	0.20221	0.30999	MCFD2	chr2	-	47129009	47168994	4210
ENSG00000(	15.53688	14.45145	18.47179	1.498151	4.60216	4.93179	1.9728	0.007821	0.018637	LINC00304	chr16	+	89225554	89230653	2243
ENSG00000(	51.7896	38.53721	36.94359	62.92235	69.0324	85.48435	-0.75394	0.024457	0.051948	HARBI1	chr11	-	46624411	46639459	1967
ENSG00000(	12.4295	21.67718	21.11062	26.21764	22.09037	10.68554	-0.09956	0.85857	0.9101	C11orf71	chr11	-	1.14E+08	1.14E+08	1441
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CYP8B1	chr3	-	42897497	42917633	3950
ENSG00000(	0	0	0	2.996302	1.840864	6.575719	-2.6739	0.04084	0.081526	TPRXL	chr3	+	13978756	14124311	2350
ENSG00000(	4.143168	2.408575	5.277655	6.74168	5.522592	9.041614	-0.75083	0.39654	0.52756	SERTM1	chr13	+	37248049	37271976	3207
ENSG00000(	4842.327	4747.302	4631.142	679.4115	876.2513	744.7002	2.6241	1.63E-103	1.34E-101	GAS1	chr9	-	89559279	89562104	2826
ENSG00000(	98.40023	72.25726	47.4989	393.2647	391.1836	474.2738	-2.4961	4.63E-27	6.22E-26	HMHA1	chr19	+	1065922	1086627	4264
ENSG00000(	0	0	0	0.749076	1.840864	0.821965	-1.0455	0.43461	NA	CTD-3064H	chr19	-	38036372	38040073	3267
ENSG00000(	52.82539	26.49433	38.263	44.19546	29.45382	17.26126	0.36142	0.42806	0.55834	ZNF571	chr19	-	38045684	38085673	3844
ENSG00000(	12.4295	1.204288	14.51355	2.247227	0.920432	2.465895	1.9538	0.044107	0.087132	GLIPR1L2	chr12	+	75784850	75826468	2609

ENSG00000(	255.8406	273.3733	281.0351	189.5161	224.5854	160.2832	0.49453	0.01071	0.024724	FAM73A	chr1	+	78245309	78344106	5288
ENSG00000(	0	6.021439	1.319414	59.92604	38.65814	46.03004	-4.0332	3.03E-09	1.59E-08	KCNE1	chr21	-	35818988	35884573	3320
ENSG00000(	43.50326	33.72006	42.22124	3.745378	19.32907	18.90519	1.4609	0.006148	0.014963	PRR26	chr10	+	695888	709947	2249
ENSG00000(	307.6302	291.4376	523.8073	292.8885	545.8162	378.1039	-0.1157	0.63179	0.7417	NRIP1	chr21	-	16333556	16437321	7671
ENSG00000(	0	1.204288	0	1.498151	0.920432	4.93179	-1.5249	0.24953	0.36676	ZSCAN4	chr19	+	58180303	58190520	2246
ENSG00000(	3.107376	0	3.958241	1.498151	5.522592	3.28786	-0.4167	0.71227	0.8055	BHLHA15	chr7	+	97841566	97842271	706
ENSG00000(	134.6529	133.6759	158.3297	217.2319	133.4626	134.8022	-0.18926	0.44482	0.57434	RNF182	chr6	+	13924677	13980533	3706
ENSG00000(	0	1.204288	0	2.996302	0	4.109825	-1.4184	0.28996	0.4138	C9orf139	chr9	+	1.4E+08	1.4E+08	3815
ENSG00000(	196.8005	127.6545	133.2608	131.0882	140.8261	129.8705	0.19186	0.42064	0.55131	TSPYL5	chr8	-	98285717	98290176	4460
ENSG00000(	1080.331	1077.838	986.9215	319.1062	277.9705	289.3317	1.8215	3.08E-40	6.41E-39	HIST1H2AC	chr6	+	26124373	26139344	1668
ENSG00000(	16.57267	26.49433	25.06886	17.22874	17.48821	18.08323	0.34856	0.49624	0.62481	EIF2S3L	chr12	+	10658201	10675734	2142
ENSG00000(	20.71584	9.634302	21.11062	15.73059	25.7721	28.76877	-0.42647	0.43123	0.56102	SRP9P1	chr10	-	93565803	93567253	959
ENSG00000(	79.75598	89.11729	73.88717	238.9551	277.9705	273.7143	-1.6908	5.07E-15	4.00E-14	SKIDA1	chr10	-	21802407	21814611	6598
ENSG00000(	107.7224	108.3859	151.7326	28.46487	37.73771	32.05663	1.8815	7.43E-10	4.11E-09	HIST1H2BC	chr6	-	26115101	26124154	659
ENSG00000(	15.53688	10.83859	9.235896	2.996302	11.04518	8.219649	0.64216	0.3816	0.51225	ZBTB12P1	chr4	-	39771701	39773000	1260
ENSG00000(	82.86335	119.2245	120.0667	351.3164	327.6738	325.4981	-1.6382	1.63E-15	1.33E-14	MB21D2	chr3	-	1.93E+08	1.93E+08	3368
ENSG00000(	1.035792	6.021439	5.277655	13.48336	15.64734	4.109825	-1.2872	0.13329	0.22194	SSTR2	chr17	+	71161151	71167185	2096
ENSG00000(	94.25706	74.66584	101.5949	77.15478	104.0088	102.7456	-0.06736	0.80566	0.87405	ZNF594	chr17	-	5082831	5095178	4862
ENSG00000(	391.5293	342.0177	439.3648	1008.256	856.0018	898.4077	-1.2337	8.24E-17	7.15E-16	PCGF5	chr10	+	92979908	93044088	7018
ENSG00000(	2.071584	10.83859	0	2.247227	0.920432	0	1.4325	0.24118	0.35659	SLC47A2	chr17	-	19581601	19622292	3114
ENSG00000(	1.035792	1.204288	3.958241	0.749076	0	1.64393	0.86609	0.50339	0.63131	PRF1	chr10	-	72357104	72362531	2533
ENSG00000(	221.6595	291.4376	266.5216	0	0	0	8.9983	1.64E-21	1.77E-20	MAB21L1	chr13	-	36047926	36050832	2907
ENSG00000(	2.071584	1.204288	0	0	2.761296	1.64393	-0.23037	0.86206	0.91256	RPL21P8	chr14	-	65934525	65935059	535
ENSG00000(	104.615	111.9988	168.885	285.3978	268.7661	261.3848	-1.0808	7.99E-07	3.34E-06	YOD1	chr1	-	2.07E+08	2.07E+08	6291
ENSG00000(	191.6215	168.6003	146.4549	249.4422	256.8005	274.5363	-0.61685	0.001438	0.003922	AC007362.	chr2	+	2.07E+08	2.07E+08	1886
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	EXOC5P1	chr4	+	63682544	63684512	1969
ENSG00000(	2197.95	2288.147	2564.94	1339.347	1381.568	1245.277	0.82821	1.52E-12	1.03E-11	TMEM64	chr8	-	91634223	91803860	4997
ENSG00000(	2.071584	4.817151	0	0.749076	5.522592	0	0.1133	0.92806	0.95677	RP11-290F	chr4	-	1.85E+08	1.85E+08	2153
ENSG00000(	8.286335	7.225726	17.15238	5.243529	5.522592	5.753754	0.8894	0.2448	0.36107	CHRM4	chr11	-	46406640	46408107	1468
ENSG00000(	99.43602	134.8802	157.0102	19.47596	34.97642	23.83698	2.2938	2.65E-12	1.76E-11	SHISA2	chr13	-	26618735	26625169	2860
ENSG00000(	2.071584	12.04288	2.638828	2.247227	0.920432	0.821965	1.6259	0.13648	0.22603	S1PR5	chr19	-	10623623	10628607	2191
ENSG00000(	69.39806	72.25726	62.01245	50.18806	78.23672	50.96182	0.1862	0.56197	0.68192	CTD-2547E	chr16	-	21458004	21531765	4262
ENSG00000(	136.7245	111.9988	110.8308	531.8436	536.6119	521.1258	-2.1304	8.77E-34	1.52E-32	GPR157	chr1	-	9160364	9189229	5265
ENSG00000(	4.143168	8.430014	6.597069	2.247227	0	4.93179	1.1609	0.25282	0.37063	PIPSL	chr10	-	95717948	95721297	3350
ENSG00000(	80.79177	86.70872	72.56776	23.97042	28.53339	41.92021	1.3263	0.000125	0.000401	WDFY3-AS2	chr4	+	85887538	85932430	6434
ENSG00000(	764.4144	668.3797	654.4292	1557.328	1426.67	1398.162	-1.0666	4.85E-17	4.25E-16	SRSF8	chr11	+	94800056	94804388	4331
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AGTR2	chrX	+	1.15E+08	1.15E+08	2882
ENSG00000(	378.064	409.4578	488.1831	413.4897	346.0824	406.0507	0.12672	0.44181	0.57155	SLC36A4	chr11	-	92877341	92931130	6008
ENSG00000(	300.3797	222.7932	427.4901	141.5753	297.2995	161.9271	0.65693	0.015964	0.035437	ZDHHC20	chr13	-	21950263	22033509	1869
ENSG00000(	0	0	0	1.498151	0.920432	6.575719	-2.2833	0.087601	0.15723	ANKRD30B	chr18	+	14728271	14852737	4359
ENSG00000(	4.143168	0	5.277655	2.247227	4.60216	0	0.34498	0.77308	0.85088	ZFP3	chr17	+	4981543	4999669	5206
ENSG00000(	765.4502	734.6155	899.8402	806.7544	969.2149	826.0747	-0.11658	0.40769	0.53848	ARSJ	chr4	-	1.15E+08	1.15E+08	4657
ENSG00000(	96.32865	118.0202	126.6637	2.996302	0	1.64393	5.7835	2.15E-22	2.39E-21	HOXC9	chr12	+	54388679	54397121	1516
ENSG00000(	3.107376	7.225726	1.319414	27.7158	20.2495	30.4127	-2.5515	0.000202	0.000631	MAP3K15	chrX	-	19378174	19533379	4697

ENSG00000(	1755.667	1985.87	1750.862	3869.724	2727.24	2880.987	-0.78532	3.36E-08	1.62E-07	PPA1	chr10	-	71962587	71993667	1294
ENSG00000(	49.71801	83.09585	47.4989	0	0	0	7.0915	5.51E-12	3.58E-11	HOXC10	chr12	+	54378849	54384063	1936
ENSG00000(	327.3102	304.6848	271.7992	295.8848	312.9469	304.949	-0.01344	0.93585	0.96144	PSMG4	chr6	+	3231637	3303607	4603
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	BHLHE22	chr8	+	65492814	65496181	3368
ENSG00000(	47.64643	49.3758	42.22124	59.17697	47.86246	55.07165	-0.21621	0.52412	0.64923	MAP6D1	chr3	-	1.84E+08	1.84E+08	2111
ENSG00000(	6.214751	15.65574	10.55531	0.749076	8.283888	13.9734	0.44671	0.58675	0.70398	CSNK1G2-A	chr19	-	1952530	1954585	1288
ENSG00000(	26.93059	27.69862	31.66593	85.39461	87.44104	77.2647	-1.5143	7.35E-06	2.77E-05	ZNF443	chr19	-	12540521	12551926	2663
ENSG00000(	1.035792	0	3.958241	0	0	0	1.6134	0.2311	NA	C12orf36	chr12	-	13524023	13540101	2750
ENSG00000(	90.1139	62.62296	71.24834	73.4094	45.10117	76.44274	0.19694	0.53988	0.6633	PDIA3P	chr1	+	1.47E+08	1.47E+08	1510
ENSG00000(	0	0	0	0	0	4.93179	-1.2404	0.35057	NA	C1orf180	chr1	-	85093913	85100703	2884
ENSG00000(	0	0	0	5.243529	1.840864	12.32947	-3.4486	0.005771	0.014123	CXCR2	chr2	+	2.19E+08	2.19E+08	2879
ENSG00000(	303.487	360.082	348.3252	21.72319	48.7829	32.05663	3.288	1.73E-37	3.33E-36	GREM2	chr1	-	2.41E+08	2.41E+08	4170
ENSG00000(	5.17896	6.021439	1.319414	0	0	0.821965	2.5318	0.045099	0.088763	C11orf42	chr11	+	6226796	6232362	1142
ENSG00000(	4784.323	4414.919	3335.478	2131.12	1765.389	1930.796	1.1021	7.27E-15	5.69E-14	SSR4	chrX	+	1.53E+08	1.53E+08	2482
ENSG00000(	16.57267	25.29004	15.83297	5.992604	11.96562	6.575719	1.1735	0.061769	0.11646	CAPS2	chr12	-	75669759	75784708	3831
ENSG00000(	27.96638	19.2686	18.47179	22.47227	39.57858	22.19305	-0.33422	0.49412	0.62286	ZNF792	chr19	-	35447258	35454953	3888
ENSG00000(	2090.228	1920.839	1797.042	1340.845	1286.764	1347.201	0.54661	2.13E-06	8.54E-06	CUEDC1	chr17	-	55938604	56032684	3621
ENSG00000(	2161.698	2087.031	1794.403	4430.782	4820.302	5606.623	-1.2945	1.22E-24	1.48E-23	SCRIB	chr8	-	1.45E+08	1.45E+08	5218
ENSG00000(	798.5956	709.3255	715.1223	834.4702	687.5627	757.0297	-0.03579	0.79416	0.86541	KCTD2	chr17	+	73028670	73061984	3635
ENSG00000(	619.4036	631.0468	420.893	211.2393	254.9597	382.2137	0.97344	7.84E-06	2.95E-05	D2HGDH	chr2	+	2.43E+08	2.43E+08	4549
ENSG00000(	58.00435	37.33292	64.65128	91.38722	63.50981	70.68898	-0.49166	0.1373	0.22721	OXTR	chr3	-	8792094	8811314	4364
ENSG00000(	306.5944	254.1047	390.5465	334.0877	387.5019	316.4565	-0.1264	0.50326	0.63121	FTSJD1	chr16	-	71315292	71323618	4869
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	OR56B4	chr11	+	6128914	6130065	1152
ENSG00000(	20.71584	26.49433	18.47179	2206.777	2606.663	2756.048	-6.7958	1.48E-190	3.87E-188	FAM83H	chr8	-	1.45E+08	1.45E+08	5654
ENSG00000(	3.107376	7.225726	1.319414	0	0.920432	2.465895	1.324	0.26544	0.38536	GPR62	chr3	+	51989330	51991509	2180
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	OR56A1	chr11	-	6047901	6048971	1071
ENSG00000(	2.071584	1.204288	1.319414	2.996302	12.88605	5.753754	-1.8124	0.078559	0.1431	ZNF572	chr8	+	1.26E+08	1.26E+08	3275
ENSG00000(	16.57267	13.24716	19.79121	37.45378	29.45382	32.8786	-0.98085	0.039715	0.079517	ST20	chr15	-	80191182	80216044	1004
ENSG00000(	1349.637	1325.921	1467.188	1715.383	1469.009	1396.518	-0.14542	0.24673	0.36348	PITPNB	chr22	-	28247657	28316122	2926
ENSG00000(	1408.677	1581.23	1486.979	1016.496	814.5823	996.2215	0.66051	4.34E-07	1.87E-06	TCEAL8	chrX	-	1.03E+08	1.03E+08	1222
ENSG00000(	124.295	149.3317	158.3297	329.5932	281.6522	281.934	-1.0472	9.33E-08	4.29E-07	LRRC57	chr15	-	42834720	42841000	2649
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC123768.	chr15	-	32890499	32891012	504
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	OR52N2	chr11	+	5841544	5842578	1035
ENSG00000(	696.0522	564.8109	580.5421	884.6582	745.5499	896.7637	-0.45443	0.001792	0.004818	MRPL14	chr6	-	44081194	44095194	956
ENSG00000(	66.29068	63.82725	79.16483	60.67512	52.46462	39.45432	0.44573	0.16948	0.26947	GPR137C	chr14	+	53019866	53104431	5410
ENSG00000(	0	2.408575	1.319414	124.3465	101.2475	107.6774	-5.9988	2.47E-17	2.21E-16	C1orf105	chr1	+	1.72E+08	1.72E+08	985
ENSG00000(	78.72018	92.73015	88.40072	61.42419	67.19154	49.3179	0.53961	0.065437	0.12246	BBS12	chr4	+	1.24E+08	1.24E+08	3431
ENSG00000(	103.5792	145.7188	101.5949	125.8447	104.9292	84.66239	0.1505	0.572	0.69073	ZFP82	chr19	-	36874022	36909558	5718
ENSG00000(	12.4295	15.65574	22.43003	24.71949	20.2495	17.26126	-0.29969	0.57738	0.69565	LSMEM1	chr7	+	1.12E+08	1.12E+08	1870
ENSG00000(	1905.857	1865.442	1898.636	5137.909	4023.208	4658.075	-1.283	4.85E-27	6.51E-26	NQO1	chr16	-	69740899	69760854	2912
ENSG00000(	970.537	976.6773	1035.74	2453.222	3040.187	3349.507	-1.5641	1.78E-31	2.84E-30	AEN	chr15	+	89164527	89175513	5039
ENSG00000(	569.6855	551.5638	496.0996	768.5515	728.0617	844.9799	-0.53157	0.000123	0.000397	FKRP	chr19	+	47249303	47280245	3332
ENSG00000(	1.035792	0	1.319414	2.996302	0.920432	0.821965	-0.62286	0.63736	0.74586	TRAPPC5	chr19	+	7745729	7747744	790
ENSG00000(	0	1.204288	3.958241	3.745378	4.60216	0	-0.50532	0.68476	0.78423	RPH3AL	chr17	-	62293	236045	2809

ENSG00000(	219.5879	161.3746	240.1333	26.96672	55.22592	46.852	2.2501	3.89E-15	3.09E-14	SLC25A42	chr19	+	19174808	19223697	3120
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	FCRL6	chr1	+	1.6E+08	1.6E+08	1997
ENSG00000(	176.0846	155.3531	141.1773	157.3059	138.0648	129.8705	0.15303	0.48503	0.61422	METTL23	chr17	+	74722912	74730018	1184
ENSG00000(	157.4404	121.6331	139.8579	10.48706	8.283888	8.219649	3.876	3.43E-26	4.44E-25	ANKRD34A	chr1	+	1.45E+08	1.45E+08	3611
ENSG00000(	286.9144	307.0934	288.9516	257.682	249.4371	302.4831	0.12412	0.47288	0.60194	SLC26A11	chr17	+	78193498	78227299	2885
ENSG00000(	825.5261	790.0127	959.2138	2685.436	2255.058	2635.22	-1.5546	1.40E-33	2.40E-32	HIGD1A	chr3	-	42798669	42846023	1373
ENSG00000(	0	0	2.638828	88.39091	105.8497	98.63579	-6.1742	2.68E-15	2.16E-14	CHRM2	chr7	+	1.37E+08	1.37E+08	5918
ENSG00000(	20.71584	33.72006	18.47179	29.21395	24.85166	17.26126	0.029297	0.95266	0.97177	MAPK15	chr8	+	1.45E+08	1.45E+08	2240
ENSG00000(	1349.637	1123.6	1208.583	1637.479	2093.983	1857.641	-0.59976	6.37E-06	2.42E-05	EHMT1	chr9	+	1.41E+08	1.41E+08	7842
ENSG00000(	10.35792	14.45145	29.0271	5.992604	13.80648	16.4393	0.53232	0.40308	0.5341	RP11-429J1	chr8	+	1.45E+08	1.45E+08	1963
ENSG00000(	1281.275	1259.685	1455.313	856.1934	673.7562	644.4205	0.8743	1.05E-09	5.76E-09	F2R	chr5	+	76011868	76031606	3821
ENSG00000(	204.051	208.3418	139.8579	221.7264	275.2092	267.9606	-0.46254	0.027367	0.057402	ZNF707	chr8	+	1.45E+08	1.45E+08	3031
ENSG00000(	0	0	0	5.243529	8.283888	9.863579	-3.7897	0.001698	0.004578	MUC16	chr19	-	8959520	9092018	43816
ENSG00000(	25388.3	26201.69	21532.83	36032.03	29147.32	30106.11	-0.38116	0.001662	0.004489	NPM1	chr5	+	1.71E+08	1.71E+08	1758
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	FER1L6-AS1	chr8	-	1.25E+08	1.25E+08	2315
ENSG00000(	627.6899	578.0581	551.515	603.7549	685.7218	664.1477	-0.15076	0.27506	0.39644	PJA1	chrX	-	68380694	68385636	2755
ENSG00000(	426.7463	382.9635	476.3084	1173.052	1363.16	1131.846	-1.5084	4.62E-26	5.97E-25	DHTKD1	chr10	+	12110971	12165224	5159
ENSG00000(	6.214751	3.612863	11.87472	98.87797	90.20234	77.2647	-3.5313	2.64E-14	2.00E-13	PENK	chr8	-	57349233	57359293	1199
ENSG00000(	10.35792	1.204288	0	0	0	0	2.8173	0.035411	0.071874	HECW1-IT1	chr7	+	43157495	43202786	1839
ENSG00000(	138.7961	142.106	79.16483	162.5494	100.3271	127.4046	-0.11332	0.6848	0.78423	HIST3H2A	chr1	-	2.29E+08	2.29E+08	496
ENSG00000(	613.1888	684.0354	667.6234	634.467	656.268	692.9164	-0.01431	0.91443	0.9478	ZNF746	chr7	-	1.49E+08	1.49E+08	5051
ENSG00000(	5103.347	4746.098	5463.692	5439.038	6028.83	5166.05	-0.11914	0.28414	0.40714	POLR2A	chr17	+	7387685	7417933	6749
ENSG00000(	8.286335	19.2686	18.47179	1.498151	1.840864	4.93179	2.2288	0.005337	0.013147	RP4-682C2	chr1	-	76209103	76210461	1354
ENSG00000(	0	0	0	60.67512	101.2475	62.46933	-6.9586	8.92E-12	5.69E-11	TMEM132C	chr12	+	1.29E+08	1.29E+08	4947
ENSG00000(	5.17896	6.021439	3.958241	16.47966	6.443024	7.397684	-0.90544	0.26132	0.38057	SLC25A41	chr19	-	6426048	6433790	1630
ENSG00000(	280.6996	250.4918	317.9787	197.7559	208.9381	212.8889	0.45203	0.013202	0.029845	TMEM136	chr11	+	1.2E+08	1.2E+08	4143
ENSG00000(	79.75598	54.19295	77.84541	104.1215	134.3831	120.8288	-0.75183	0.006208	0.015092	FRAT2	chr10	-	99092255	99094458	2204
ENSG00000(	43.50326	51.78437	35.62417	125.8447	80.99802	124.9387	-1.3232	2.64E-05	9.31E-05	TMEM102	chr17	+	7338762	7340998	1973
ENSG00000(	0	0	0	52.43529	37.73771	42.74218	-6.2852	1.72E-09	9.23E-09	TMEM132E	chr17	+	32907768	32966337	4369
ENSG00000(	174.013	109.5902	224.3003	65.16957	99.40666	89.59418	0.9892	0.000512	0.001504	ZNF322	chr6	-	26636518	26659980	2910
ENSG00000(	7.250543	19.2686	36.94359	6.74168	3.681728	2.465895	2.0943	0.004287	0.010767	NME9	chr3	-	1.38E+08	1.38E+08	2133
ENSG00000(	1.035792	1.204288	3.958241	7.490755	6.443024	6.575719	-1.4766	0.13632	0.2258	HEPHL1	chr11	+	93754527	93846917	5345
ENSG00000(	31.07376	34.92434	27.70769	22.47227	33.13555	14.79537	0.40595	0.3863	0.51718	FAM211A	chr17	-	16344891	16395467	3157
ENSG00000(	1.035792	0	0	2.996302	4.60216	1.64393	-1.8702	0.14984	0.2438	OFCC1	chr6	-	9596343	10211841	2877
ENSG00000(	2.071584	0	0	2.996302	5.522592	0.821965	-1.3784	0.27945	0.40167	CCDC108	chr2	-	2.2E+08	2.2E+08	5953
ENSG00000(	224.7668	225.2018	312.7011	41.94823	33.13555	36.98842	2.7355	3.69E-27	4.98E-26	DDX60L	chr4	-	1.69E+08	1.69E+08	6781
ENSG00000(	4.143168	12.04288	3.958241	5.243529	3.681728	10.68554	0.029711	0.97226	0.98387	SYNE4	chr19	-	36494209	36499695	2339
ENSG00000(	1153.872	1174.181	898.5208	588.0243	703.21	794.0181	0.629	5.05E-05	0.000172	OGFOD3	chr17	-	80347099	80376513	4287
ENSG00000(	74.57702	87.913	81.80365	123.5975	97.56579	146.3098	-0.58655	0.027369	0.057402	XXyac-YRM	chr9	-	14511	29739	1837
ENSG00000(	0	0	0	2.996302	0.920432	0	-1.1048	0.40628	NA	UTS2R	chr17	+	80332153	80333462	1310
ENSG00000(	3.107376	0	5.277655	1.498151	0.920432	1.64393	0.74277	0.54175	0.66459	AATK	chr17	-	79091095	79139877	5257
ENSG00000(	14.50109	16.86003	9.235896	15.73059	9.20432	5.753754	0.37575	0.57472	0.69333	DDN	chr12	-	49388932	49393092	3749
ENSG00000(	0	0	0	4.494453	2.761296	0.821965	-2.1518	0.10874	0.18783	SAGE1	chrX	+	1.35E+08	1.35E+08	3045
ENSG00000(	107.7224	137.2888	94.99779	27.7158	35.89685	33.70056	1.7855	8.36E-09	4.22E-08	ZNF467	chr7	-	1.49E+08	1.49E+08	2553

ENSG00000(	194.7289	244.4704	199.2315	1.498151	10.12475	3.28786	5.3521	9.28E-38	1.80E-36	SOX2	chr3	+	1.81E+08	1.81E+08	2500
ENSG00000(	59.04014	63.82725	102.9143	80.15108	143.5874	56.71558	-0.30897	0.38293	0.51355	ZNF678	chr1	+	2.28E+08	2.28E+08	3052
ENSG00000(	2856.714	3138.374	2634.869	147.5679	159.2347	133.1583	4.2845	1.39E-213	4.66E-211	TMEM45A	chr3	+	1E+08	1E+08	4615
ENSG00000(	2684.773	2619.326	2533.274	1517.627	1757.105	1527.211	0.7061	5.42E-10	3.03E-09	RAP2B	chr3	+	1.53E+08	1.53E+08	6237
ENSG00000(	246.5185	232.4275	229.578	591.0206	545.8162	504.6865	-1.2073	2.25E-14	1.70E-13	ZBTB2	chr6	-	1.52E+08	1.52E+08	3090
ENSG00000(	224.7668	216.7718	232.2168	163.2985	132.5422	177.5444	0.50427	0.012412	0.028255	RNF135	chr17	+	29295803	29326929	2892
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	OR6T1	chr11	-	1.24E+08	1.24E+08	1089
ENSG00000(	39.36009	25.29004	48.81831	40.45008	36.81728	53.42772	-0.2029	0.60938	0.72335	ACBD4	chr17	+	43209967	43221548	2241
ENSG00000(	575.9003	692.4654	513.252	403.0026	421.5579	445.505	0.48732	0.001829	0.00491	SGSH	chr17	-	78180515	78194722	5562
ENSG00000(	4.143168	14.45145	7.916483	0	1.840864	6.575719	1.402	0.15076	0.24504	RPL24P4	chr6	-	42924083	42924503	421
ENSG00000(	36.25272	20.47289	18.47179	26.96672	40.49901	28.76877	-0.33048	0.47685	0.60611	MAB21L2	chr4	+	1.52E+08	1.52E+08	2767
ENSG00000(	31.07376	16.86003	27.70769	92.88537	113.2131	75.62077	-1.8568	2.44E-07	1.08E-06	FANCB	chrX	-	14861529	14891191	3008
ENSG00000(	0	0	0	5.243529	1.840864	1.64393	-2.2774	0.087849	0.15762	EDDM3B	chr14	+	21236586	21239107	896
ENSG00000(	891.8168	869.4957	1117.543	710.1236	951.7267	757.8517	0.24988	0.10658	0.18483	SETD2	chr3	-	47057919	47205457	8172
ENSG00000(	0	0	0	2.996302	0	0.821965	-1.0802	0.41594	NA	EDDM3A	chr14	+	21214051	21216539	927
ENSG00000(	15.53688	18.06432	10.55531	0	0	0	5.1336	5.86E-06	2.23E-05	C6orf223	chr6	+	43968317	43973695	3581
ENSG00000(	0	0	0	3.745378	0	2.465895	-1.6796	0.21567	0.32631	TMIE	chr3	+	46742823	46752376	1824
ENSG00000(	1681.09	1722.131	1328.65	3838.263	3412.962	3299.367	-1.1536	5.39E-19	5.21E-18	MEX3D	chr19	-	1554668	1568057	2850
ENSG00000(	582.1151	507.0051	575.2644	899.6397	701.3692	938.6839	-0.60829	6.09E-05	0.000204	MRPS23	chr17	-	55916842	55927417	921
ENSG00000(	76.6486	66.23582	109.5113	2.996302	2.761296	7.397684	4.1047	1.45E-16	1.24E-15	GPR135	chr14	-	59895740	59932060	4578
ENSG00000(	0	0	0	0	2.761296	4.109825	-1.797	0.1853	0.28968	P2RY13	chr3	-	1.51E+08	1.51E+08	2764
ENSG00000(	1.035792	0	0	171.5383	168.4391	145.4878	-7.3353	5.38E-18	4.97E-17	TNFSF15	chr9	-	1.18E+08	1.18E+08	2789
ENSG00000(	226.8384	260.1261	225.6198	229.9662	253.1188	250.6993	-0.04161	0.81709	0.88148	ZFP41	chr8	+	1.44E+08	1.44E+08	4797
ENSG00000(	375.9925	368.512	352.2835	1062.189	589.9969	624.6933	-1.0487	2.03E-07	9.04E-07	PHLDA2	chr11	-	2949503	2950685	955
ENSG00000(	19.68005	12.04288	6.597069	11.23613	10.12475	12.32947	0.18699	0.77681	0.85319	ATG9B	chr7	-	1.51E+08	1.51E+08	4571
ENSG00000(	7.250543	2.408575	11.87472	0	0	0	3.9743	0.001294	0.003567	GPR88	chr1	+	1.01E+08	1.01E+08	3491
ENSG00000(	506.5022	503.3923	484.2249	414.2388	451.0117	435.6414	0.20018	0.1606	0.25797	HKR1	chr19	+	37803739	37860267	3472
ENSG00000(	266.1985	255.309	366.797	105.6197	145.4283	90.41614	1.3706	3.07E-09	1.61E-08	PLAG1	chr8	-	57073463	57123883	7322
ENSG00000(	488.8938	578.0581	646.5128	812.747	859.6835	771.0031	-0.5124	0.000422	0.001256	YIPF6	chrX	+	67718165	67757127	6741
ENSG00000(	12.4295	30.10719	17.15238	0.749076	7.363456	8.219649	1.7351	0.017421	0.038359	ZBTB20	chr3	-	1.14E+08	1.15E+08	3740
ENSG00000(	2.071584	7.225726	9.235896	0	1.840864	5.753754	1.0449	0.32003	0.44719	FDX1P1	chr20	-	33063729	33064279	551
ENSG00000(	1534.008	1719.723	1671.697	760.3117	673.7562	581.9512	1.2848	1.36E-21	1.47E-20	C3orf58	chr3	+	1.44E+08	1.44E+08	4346
ENSG00000(	327.3102	339.6091	389.2271	861.4369	905.7051	828.5406	-1.2956	6.23E-20	6.29E-19	C5orf30	chr5	+	1.03E+08	1.03E+08	3049
ENSG00000(	10.35792	9.634302	32.98534	23.97042	36.81728	18.90519	-0.57481	0.3117	0.43794	AMIGO1	chr1	-	1.1E+08	1.1E+08	5088
ENSG00000(	30.03797	16.86003	25.06886	125.8447	99.40666	119.1849	-2.2173	4.86E-11	2.94E-10	GPR3	chr1	+	27719148	27722318	2115
ENSG00000(	1.035792	7.225726	1.319414	0	0	0.821965	2.1168	0.10531	0.18297	ODF3L2	chr19	-	463346	474983	1604
ENSG00000(	486.8222	516.6394	455.1978	1385.041	1116.484	1066.91	-1.287	7.92E-19	7.61E-18	SIAH2	chr3	-	1.5E+08	1.5E+08	2517
ENSG00000(	5802.506	5416.886	5529.663	2991.059	2939.86	2765.912	0.94425	2.09E-20	2.16E-19	COPG1	chr3	+	1.29E+08	1.29E+08	3231
ENSG00000(	58.00435	61.41867	19.79121	11.23613	6.443024	11.50751	2.1624	4.19E-05	0.000144	BAI1	chr8	+	1.44E+08	1.44E+08	6241
ENSG00000(	6.214751	6.021439	10.55531	2.996302	3.681728	13.9734	0.12016	0.88632	0.92915	LINC00471	chr2	-	2.32E+08	2.32E+08	1282
ENSG00000(	3.107376	4.817151	2.638828	1.498151	5.522592	4.109825	-0.05223	0.95919	0.97606	CELF2-AS1	chr10	-	11358797	11361847	2468
ENSG00000(	240.3037	264.9433	216.3839	14.98151	10.12475	4.109825	4.5391	2.60E-41	5.55E-40	SLC9A9	chr3	-	1.43E+08	1.44E+08	3627
ENSG00000(	439.1758	502.188	402.4212	572.2937	501.6354	435.6414	-0.16732	0.30344	0.42855	LSM10	chr1	-	36856839	36863493	1006
ENSG00000(	0	3.612863	0	0	1.840864	0	0.45719	0.73538	NA	KCTD9P2	chrX	+	1.05E+08	1.05E+08	1013

ENSG00000(	91.14969	72.25726	83.12307	69.66403	101.2475	83.01846	-0.03737	0.8952	0.93517	RELL1	chr4	-	37592422	37687998	1350
ENSG00000(	747.8418	788.8085	977.6856	560.3085	711.4939	545.7847	0.46637	0.003166	0.008149	RFX7	chr15	-	56379478	56535483	7194
ENSG00000(	1326.849	1119.988	1070.045	663.6809	691.2444	706.0679	0.77032	6.45E-09	3.29E-08	SLC35C1	chr11	+	45825623	45834566	4171
ENSG00000(	1.035792	0	2.638828	0	0	1.64393	0.56423	0.6775	NA	TIGIT	chr3	+	1.14E+08	1.14E+08	3710
ENSG00000(	947.7496	933.323	955.2556	773.795	709.6531	635.3789	0.41938	0.001403	0.003838	RNF41	chr12	-	56598285	56615717	3270
ENSG00000(	6.214751	10.83859	0	4.494453	0	0.821965	1.2708	0.26773	0.38797	SLC2A4	chr17	+	7184986	7191576	3426
ENSG00000(	481.6432	446.7907	426.1707	311.6154	415.1148	345.2253	0.33907	0.03919	0.078614	IBA57	chr1	+	2.28E+08	2.28E+08	9815
ENSG00000(	2.071584	2.408575	3.958241	1292.155	1407.341	1959.564	-8.7919	4.22E-70	1.83E-68	CLDN7	chr17	-	7163222	7167302	1923
ENSG00000(	252.7332	226.4061	294.2293	191.7633	200.6542	198.9155	0.38429	0.040752	0.081393	ZNF329	chr19	-	58637619	58666477	3410
ENSG00000(	92.18548	119.2245	96.31721	385.7739	344.2416	360.0206	-1.8171	2.50E-20	2.57E-19	ZNF101	chr19	+	19779605	19794318	4627
ENSG00000(	1450.109	1439.124	1965.927	847.9535	825.6275	759.4956	0.99299	7.98E-12	5.12E-11	C5orf24	chr5	+	1.34E+08	1.34E+08	5065
ENSG00000(	0	0	0	11.23613	4.60216	9.041614	-3.8788	0.001253	0.003459	AP003774.	chr11	+	64216546	64219126	2337
ENSG00000(	392.5651	339.6091	412.9765	512.3677	485.0677	417.5582	-0.30468	0.056888	0.10868	ADO	chr10	+	64564516	64568238	3723
ENSG00000(	1030.613	1035.687	802.2036	1250.956	989.4644	1112.941	-0.22421	0.12399	0.20927	COA4	chr11	-	73583712	73588033	1038
ENSG00000(	1162.159	1211.513	981.6439	770.0497	639.7002	696.2043	0.67009	1.26E-06	5.17E-06	PRKAG1	chr12	-	49396057	49412980	2071
ENSG00000(	83.89914	98.75159	60.69303	374.5378	363.5706	378.1039	-2.1793	3.66E-25	4.54E-24	GINS3	chr16	+	58328984	58440048	3202
ENSG00000(	385.3146	432.3393	457.8366	73.4094	109.5314	73.97684	2.3034	3.61E-29	5.32E-28	CCDC149	chr4	-	24807739	24981826	5604
ENSG00000(	617.332	605.7567	502.6967	940.0898	740.9478	747.1661	-0.49052	0.001294	0.003567	MRPS11	chr15	+	89010684	89022222	2002
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	LINC00301	chr11	+	60383209	60454622	852
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	AQP7P2	chr9	-	69633978	69650004	1041
ENSG00000(	0	0	2.638828	0	2.761296	0	-0.03456	0.97961	NA	RP11-651P	chr3	+	1.5E+08	1.5E+08	403
ENSG00000(	1056.508	1213.922	824.6336	1517.627	1502.145	1707.221	-0.6084	3.63E-05	0.000126	SNRPE	chr1	+	2.04E+08	2.04E+08	967
ENSG00000(	48.68222	38.53721	63.33186	515.364	445.4891	456.1905	-3.2209	3.69E-49	1.00E-47	RTKN2	chr10	-	63942794	64028466	6641
ENSG00000(	96.32865	60.21439	63.33186	82.39831	86.52061	82.19649	-0.18234	0.53718	0.66115	PNMAL1	chr19	-	46969748	46974820	3689
ENSG00000(	2.071584	0	0	0.749076	0	1.64393	-0.07972	0.95303	NA	RP11-381C	chr9	-	67017400	67032072	2566
ENSG00000(	944.6422	1117.579	1064.767	116.8558	123.3379	116.719	3.1215	2.86E-92	1.89E-90	CHST15	chr10	-	1.26E+08	1.26E+08	4810
ENSG00000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	ADIG	chr20	+	37209838	37217106	772
ENSG00000(	0	0	0	7.490755	8.283888	8.219649	-3.8398	0.001388	0.003803	USH1G	chr17	-	72912176	72919351	3561
ENSG00000(	1.035792	0	0	0	5.522592	3.28786	-1.695	0.20237	0.3102	TRPC2	chr11	+	3631131	3658789	3173
ENSG00000(	0	0	0	0.749076	5.522592	4.109825	-2.4974	0.058964	0.11206	MGAT4C	chr12	-	86372516	87232681	3193
ENSG00000(	0	0	3.958241	1.498151	0	0	0.61337	0.65027	NA	TRIM49B	chr11	+	49050504	49059579	1437
ENSG00000(	2322.245	2278.512	1721.835	2492.174	2498.052	2569.462	-0.25652	0.050019	0.097135	IDH2	chr15	-	90626277	90645736	2694
ENSG00000(	9.322127	10.83859	2.638828	11.23613	11.96562	4.109825	-0.22399	0.77731	0.85333	Z83851.3	chr22	+	42665759	42671202	1242
ENSG00000(	2445.505	2539.843	2066.202	2678.694	2309.364	2817.696	-0.14613	0.24841	0.36546	TMEM259	chr19	-	1006168	1021117	5098
ENSG00000(	461.9632	523.8652	525.1267	477.9102	422.4783	388.7894	0.22657	0.13914	0.22959	WRB	chr21	+	40752170	40800454	1616
ENSG00000(	8341.232	7399.144	7424.341	2094.415	3385.349	3157.989	1.419	3.51E-20	3.58E-19	TNRC18	chr7	-	5346421	5465045	10572
ENSG00000(	1.035792	7.225726	0	2.996302	1.840864	2.465895	0.13067	0.91113	0.94542	FAM181B	chr11	-	82443053	82444906	1854
ENSG00000(	9.322127	1.204288	2.638828	229.2171	231.0284	199.7375	-5.3969	1.71E-32	2.82E-31	TMEM30B	chr14	-	61744088	61748558	4471
ENSG00000(	2.071584	4.817151	1.319414	0	0.920432	7.397684	-0.01249	0.99159	0.99499	DEXI	chr16	-	11022748	11036317	1561
ENSG00000(	9.322127	14.45145	5.277655	5.992604	5.522592	20.54912	-0.12773	0.86534	0.91504	RP11-69E1	chr1	-	39987952	40011859	2241
ENSG00000(	1165.266	992.3331	949.9779	1955.087	1304.252	1735.99	-0.68231	1.16E-05	4.27E-05	NOP10	chr15	-	34633917	34635378	551
ENSG00000(	306.5944	327.5663	278.3963	552.0687	478.6246	506.3304	-0.74943	1.63E-06	6.60E-06	FAM89A	chr1	-	2.31E+08	2.31E+08	1576
ENSG00000(	66.29068	55.39724	30.34652	1.498151	2.761296	0	4.7925	9.85E-12	6.26E-11	KCNIP1	chr5	+	1.7E+08	1.7E+08	2014
ENSG00000(	34.18113	31.31148	23.74945	83.14739	110.4518	83.01846	-1.5967	2.45E-06	9.74E-06	TDRKH	chr1	-	1.52E+08	1.52E+08	3093

ENSG0000(	180.2278	213.1589	184.7179	308.6191	318.4695	250.6993	-0.59985	0.001582	0.004284	ZNF708	chr19	-	21473962	21512227	4004
ENSG0000(	1228.449	1398.178	1221.777	1815.759	1299.65	1409.67	-0.23367	0.10515	0.18274	IST1	chr16	+	71919136	71962913	2654
ENSG0000(	274.4849	275.7819	287.6322	182.7744	314.7877	174.2566	0.31924	0.15819	0.25477	ERCC6L2	chr9	+	98637983	98776842	4564
ENSG0000(	972.6086	933.323	840.4666	979.0417	738.1865	1059.513	-0.01594	0.91668	0.94924	MRPL41	chr9	+	1.4E+08	1.4E+08	1262
ENSG0000(	2342.961	2102.686	2798.477	810.4997	1128.45	817.8551	1.3899	2.73E-19	2.68E-18	CREB3L2	chr7	-	1.38E+08	1.38E+08	7412
ENSG0000(	193.6931	201.116	192.6344	213.4865	171.2004	267.1386	-0.15048	0.4754	0.60463	TP53TG1	chr7	-	86954541	86974831	855
ENSG0000(	3.107376	1.204288	10.55531	1081.665	1305.173	1097.323	-7.7482	4.61E-80	2.49E-78	UNC5C	chr4	-	96083655	96470357	9875
ENSG0000(	139.8319	196.2989	125.3443	397.7591	318.4695	381.3917	-1.2433	1.52E-09	8.17E-09	TSEN54	chr17	+	73512141	73520820	1944
ENSG0000(	570.7213	498.5751	440.6842	125.0956	154.6326	119.1849	1.9158	2.43E-25	3.04E-24	RGMA	chr15	-	93586636	93632433	3216
ENSG0000(	0	0	0	2.247227	0	2.465895	-1.3312	0.32317	NA	ASB18	chr2	-	2.37E+08	2.37E+08	3627
ENSG0000(	55.93276	61.41867	47.4989	2.996302	0	3.28786	4.3956	1.12E-12	7.62E-12	UBA7	chr3	-	49842640	49851379	3299
ENSG0000(	1443.894	1448.758	1161.084	2086.175	1961.441	2333.558	-0.65238	6.00E-07	2.55E-06	MRPS16	chr10	-	75006510	75012451	2634
ENSG0000(	0	0	0	2.996302	1.840864	4.109825	-2.3265	0.080173	0.14563	FAM159A	chr1	+	53099016	53135355	1992
ENSG0000(	56.96855	80.68728	76.526	68.16587	46.94203	49.3179	0.36867	0.25434	0.37244	RAD51B	chr14	+	68286496	69196935	2596
ENSG0000(	1815.743	1735.379	1510.729	626.2272	472.1816	471.8079	1.6829	1.79E-30	2.76E-29	LDOC1	chrX	-	1.4E+08	1.4E+08	1370
ENSG0000(	4.143168	6.021439	5.277655	2.247227	5.522592	11.50751	-0.28085	0.75318	0.83675	ARL6IP4	chr12	+	1.23E+08	1.23E+08	1782
ENSG0000(	1193.232	1193.449	1345.802	1623.996	1620.881	1533.787	-0.35642	0.00227	0.005993	EXT1	chr8	-	1.19E+08	1.19E+08	8270
ENSG0000(	5135.456	5369.919	4046.642	3891.447	3877.78	3878.852	0.32072	0.009292	0.021767	SHMT2	chr12	+	57623110	57628718	3416
ENSG0000(	322.1313	309.5019	296.8681	311.6154	311.106	423.3119	-0.17062	0.34138	0.47026	MOB2	chr11	-	1490687	1522477	3174
ENSG0000(	4.143168	0	3.958241	2.247227	0.920432	0.821965	0.72221	0.55607	0.67668	HIST2H4B	chr1	-	1.5E+08	1.5E+08	1696
ENSG0000(	52.82539	39.74149	50.13772	27.7158	29.45382	21.37109	0.845	0.032868	0.067287	HHIPL1	chr14	+	1E+08	1E+08	7390
ENSG0000(	2721.025	2724.099	2942.293	1730.365	1495.702	1397.34	0.85706	1.00E-12	6.85E-12	ATP6AP2	chrX	+	40440146	40465889	2093
ENSG0000(	6.214751	0	1.319414	0	0	0	2.1977	0.10512	0.18272	ZAR1	chr4	+	48492269	48496406	1460
ENSG0000(	341.8113	386.5764	360.2	405.2499	338.719	315.6345	0.037186	0.82382	0.88627	CYB5D1	chr17	+	7761064	7765600	3509
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	FAM153B	chr5	+	1.75E+08	1.76E+08	4330
ENSG0000(	362.5272	320.3405	361.5194	214.9847	215.3811	161.1051	0.81679	1.06E-05	3.93E-05	BACE2	chr21	+	42539728	42648524	2993
ENSG0000(	716.768	709.3255	595.0556	519.8584	508.0785	477.5616	0.42483	0.002871	0.007438	UBE2E2	chr3	+	23244511	23633284	2748
ENSG0000(	212.3373	209.5461	234.8557	429.9694	435.3643	458.6564	-1.0092	5.55E-10	3.10E-09	SYNM	chr15	+	99638420	99675798	7393
ENSG0000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	KCNA4	chr11	-	30031288	30038570	4172
ENSG0000(	23.82321	32.51577	17.15238	37.45378	41.41944	43.56414	-0.71343	0.095027	0.16808	GABRG3	chr15	+	27216429	27778373	2004
ENSG0000(	6.214751	8.430014	11.87472	0	0	0	4.3439	0.000281	0.000859	C22orf26	chr22	-	46445358	46450024	2817
ENSG0000(	0	0	1.319414	0.749076	0	1.64393	-0.40261	0.76414	NA	NLRP10	chr11	-	7980971	7986973	2350
ENSG0000(	95.29286	115.6116	130.622	500.3825	600.1217	441.3952	-2.1682	2.67E-28	3.80E-27	FIGN	chr2	-	1.64E+08	1.65E+08	9536
ENSG0000(	2.071584	0	0	0	1.840864	1.64393	-0.34884	0.79706	NA	IZUMO1	chr19	-	49244109	49250166	2218
ENSG0000(	2238.346	2224.319	1584.616	312.3645	289.9361	355.9108	2.649	4.31E-64	1.66E-62	B4GALNT4	chr11	+	369796	382116	3444
ENSG0000(	761.307	833.3671	899.8402	1976.81	1617.199	1500.908	-1.0289	1.64E-13	1.18E-12	AP1S2	chrX	-	15843929	15873054	3492
ENSG0000(	1036.828	958.613	938.1032	957.3186	913.989	886.9001	0.089218	0.46699	0.59626	C8orf33	chr8	+	1.46E+08	1.46E+08	2677
ENSG0000(	3.107376	3.612863	5.277655	20.97412	10.12475	23.01502	-2.0127	0.006418	0.015558	DCAF4L1	chr4	+	41983713	41988476	4764
ENSG0000(	147.0825	164.9874	145.1355	37.45378	48.7829	68.22309	1.5511	2.85E-08	1.38E-07	LINC00085	chr19	+	52196593	52215640	1960
ENSG0000(	277.5922	278.1905	228.2586	176.0328	152.7917	188.23	0.59794	0.002052	0.005461	ZSCAN22	chr19	+	58838385	58853698	4629
ENSG0000(	1178.731	1118.783	1155.806	4592.582	4284.611	4094.207	-1.9061	1.24E-68	5.27E-67	SGK223	chr8	-	8175258	8244008	4891
ENSG0000(	38.3243	31.31148	32.98534	52.43529	36.81728	45.20807	-0.38207	0.3196	0.44677	KCNJ14	chr19	+	48958766	48969367	3120
ENSG0000(	145.0109	110.7945	88.40072	307.121	183.166	292.6195	-1.1712	3.20E-06	1.26E-05	FBXL6	chr8	-	1.46E+08	1.46E+08	3108
ENSG0000(	610.0814	676.8097	556.7926	5.992604	4.60216	2.465895	6.9821	2.46E-76	1.23E-74	C1S	chr12	+	7096351	7178336	3076

ENSG00000(	16.57267	32.51577	27.70769	27.7158	20.2495	36.98842	-0.15054	0.7525	0.83619	GLTPD2	chr17	+	4692254	4693685	1023
ENSG00000(	0	2.408575	1.319414	0	1.840864	0	0.51994	0.70155	NA	AC079354.	chr2	+	2.03E+08	2.03E+08	5135
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	OR5P3	chr11	-	7846584	7847519	936
ENSG00000(	4.143168	0	3.958241	0	0	0	2.3234	0.08602	0.15487	RP11-39K2	chr9	-	5084999	5086112	1114
ENSG00000(	34.18113	45.76293	30.34652	28.46487	25.7721	32.8786	0.33167	0.42462	0.55514	KBTBD3	chr11	-	1.06E+08	1.06E+08	3751
ENSG00000(	451.6053	355.2649	281.0351	250.1912	253.1188	292.6195	0.45168	0.020493	0.044314	YBEY	chr21	+	47706251	47717665	1402
ENSG00000(	1.035792	1.204288	1.319414	0	5.522592	0	-0.37663	0.77526	0.85264	FAM87A	chr8	-	325931	333174	4013
ENSG00000(	6.214751	2.408575	2.638828	4.494453	8.283888	2.465895	-0.34914	0.71901	0.81066	FAM27A	chr9	+	45727107	45728274	616
ENSG00000(	924.9622	839.3885	960.5332	1077.171	1201.164	1227.194	-0.36249	0.004088	0.010312	CLN8	chr8	+	1703944	1734738	7113
ENSG00000(	6.214751	16.86003	13.19414	0.749076	5.522592	12.32947	0.86473	0.29316	0.41747	RP5-1142A	chr16	+	88809175	88812156	2137
ENSG00000(	857.6357	914.0544	630.6798	1689.914	1528.838	1750.785	-1.0444	1.61E-12	1.09E-11	PLCXD1	chrX	+	192989	220023	5507
ENSG00000(	448.4979	408.2535	325.8952	25.46857	24.85166	40.27628	3.6758	2.79E-50	7.74E-49	NXPH4	chr12	+	57610578	57620232	2007
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTD-2503C	chr5	-	74286014	74286462	449
ENSG00000(	18.64425	26.49433	27.70769	0	1.840864	2.465895	3.7086	2.71E-06	1.07E-05	CACNB4	chr2	-	1.53E+08	1.53E+08	8055
ENSG00000(	15.53688	19.2686	11.87472	0	2.761296	1.64393	3.0382	0.00048	0.001415	DNM1P46	chr15	-	1E+08	1E+08	3831
ENSG00000(	429.8536	522.6609	488.1831	399.2573	368.1728	343.5813	0.37207	0.017099	0.037713	TRAPPC6B	chr14	-	39617015	39639736	4533
ENSG00000(	4.143168	0	0	0	2.761296	1.64393	-0.01972	0.9882	0.99285	RP1-86D1.3	chr6	-	1.29E+08	1.29E+08	1904
ENSG00000(	34.18113	44.55865	46.17948	27.7158	25.7721	18.90519	0.76345	0.06804	0.12665	PGBD4	chr15	+	34394274	34396591	2318
ENSG00000(	1741.166	1505.36	1704.683	2865.963	2862.544	2863.726	-0.79374	9.15E-13	6.28E-12	NPLOC4	chr17	-	79523913	79615495	5538
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	OTOL1	chr3	+	1.61E+08	1.61E+08	1434
ENSG00000(	7.250543	0	1.319414	3.745378	10.12475	1.64393	-0.64935	0.54935	0.67086	TEX19	chr17	+	80317123	80321652	1936
ENSG00000(	126.3666	171.0089	200.5509	3.745378	14.72691	9.863579	4.0803	1.62E-26	2.13E-25	TSHZ2	chr20	+	51588946	52111869	12187
ENSG00000(	9.322127	19.2686	7.916483	11.98521	23.0108	16.4393	-0.46213	0.45721	0.58696	CAPN12	chr19	-	39220827	39260544	2762
ENSG00000(	1336.172	1233.191	1389.343	770.7987	1202.084	998.6874	0.41337	0.008141	0.019302	EXOC7	chr17	-	74077098	74117657	4751
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	OR2B8P	chr6	-	28021006	28021943	938
ENSG00000(	1849.924	1580.025	1835.305	10438.37	8421.032	8660.222	-2.381	8.10E-84	4.64E-82	KPNA2	chr17	+	66031635	66042958	2456
ENSG00000(	24.85901	19.2686	6.597069	14.98151	7.363456	16.4393	0.37083	0.56064	0.6811	WASH6P	chrX	+	1.55E+08	1.55E+08	4244
ENSG00000(	0	0	0	0.749076	3.681728	5.753754	-2.4707	0.062109	0.11705	NCF1B	chr7	+	72634611	72649979	1516
ENSG00000(	0	2.408575	1.319414	3.745378	1.840864	3.28786	-0.92481	0.44564	0.57519	XKRX	chrX	-	1E+08	1E+08	2851
ENSG00000(	6901.481	6556.142	5854.239	1009.754	1125.688	948.5475	2.6423	1.15E-111	1.04E-109	BGN	chrX	+	1.53E+08	1.53E+08	2402
ENSG00000(	330.4176	304.6848	238.8139	519.8584	424.3192	444.683	-0.66335	0.000151	0.00048	ORAI1	chr12	+	1.22E+08	1.22E+08	2139
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	ABHD17AP	chr22	-	22469236	22472374	900
ENSG00000(	262.0554	263.739	249.3692	354.3127	356.2072	315.6345	-0.40249	0.015457	0.034402	CEP97	chr3	+	1.01E+08	1.01E+08	8361
ENSG00000(	1.035792	0	2.638828	2.996302	3.681728	12.32947	-1.8768	0.089141	0.1595	LHFPL1	chrX	-	1.12E+08	1.12E+08	1675
ENSG00000(	33.14534	13.24716	13.19414	50.18806	56.14635	85.48435	-1.6197	0.000264	0.000809	FES	chr15	+	91426925	91439006	2829
ENSG00000(	940.499	946.5701	913.0343	1639.726	1584.984	1772.156	-0.83391	9.16E-13	6.28E-12	GLRX5	chr14	+	95999840	96011061	1863
ENSG00000(	181.2636	174.6217	141.1773	188.767	180.4047	178.3664	-0.13611	0.50791	0.63542	FAM104B	chrX	-	55169535	55187743	1229
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	TBPL2	chr14	-	55880259	55923444	2037
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-271M	chr10	-	15049812	15055672	1100
ENSG00000(	1.035792	0	0	0.749076	0.920432	0.821965	-0.44823	0.73997	NA	CAV3	chr3	+	8775486	8883492	1431
ENSG00000(	3952.582	3924.774	3959.561	1194.026	1012.475	943.6157	1.9055	5.67E-57	1.83E-55	MXRA7	chr17	-	74668633	74707098	5661
ENSG00000(	421.5673	397.4149	436.726	1010.503	1075.065	1066.088	-1.3246	4.35E-24	5.20E-23	LIMK2	chr22	+	31608225	31676066	3670
ENSG00000(	586.2582	570.8324	601.6527	644.954	670.9949	692.0945	-0.19081	0.14765	0.24077	MFSD5	chr12	+	53645035	53648189	2038
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RNASE10	chr14	+	20973696	20979328	1172

ENSG00000(	915.64	885.1515	823.3142	1408.262	1191.039	1223.084	-0.54125	2.20E-05	7.83E-05	ADI1	chr2	-	3501690	3523507	3870
ENSG00000(	277.5922	254.1047	257.2857	400.0063	280.7318	294.2634	-0.30491	0.1057	0.18355	RWDD4	chr4	-	1.85E+08	1.85E+08	2641
ENSG00000(	0	0	0	2.996302	8.283888	1.64393	-2.8372	0.028653	0.059711	SPNS3	chr17	+	4336983	4391503	2133
ENSG00000(	416.3883	357.6735	432.7677	542.3307	634.1776	511.2622	-0.48169	0.002122	0.005628	SATB1	chr3	-	18386864	18487080	7825
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	HIST1H3I	chr6	-	27839623	27840099	477
ENSG00000(	13.46529	22.88147	11.87472	31.46117	46.0216	41.09825	-1.2544	0.008302	0.019641	NXPH3	chr17	+	47653220	47661189	5194
ENSG00000(	14.50109	15.65574	35.62417	4.494453	1.840864	7.397684	2.0792	0.002884	0.007469	CSF1R	chr5	-	1.49E+08	1.49E+08	3989
ENSG00000(	196.8005	197.5032	151.7326	627.7253	713.3348	632.091	-1.8422	2.98E-28	4.22E-27	EPHB3	chr3	+	1.84E+08	1.84E+08	4236
ENSG00000(	0	4.817151	1.319414	0	0.920432	0	1.4368	0.28779	0.41144	VCX	chrX	+	7810303	7812184	967
ENSG00000(	24.85901	45.76293	21.11062	8.239831	15.64734	15.61733	1.1729	0.0286	0.05962	ACTL10	chr20	+	32254304	32256331	2028
ENSG00000(	11.39371	14.45145	19.79121	4.494453	7.363456	6.575719	1.2177	0.076551	0.14005	EPGN	chr4	+	75174190	75181024	1196
ENSG00000(	0	2.408575	1.319414	1.498151	0	0.821965	0.359	0.78993	0.86247	LINC00334	chr21	+	46654255	46678645	589
ENSG00000(	35.21692	19.2686	11.87472	19.47596	34.97642	31.23467	-0.33661	0.51185	0.63892	C2orf82	chr2	+	2.34E+08	2.34E+08	2782
ENSG00000(	0	0	0	58.42789	71.7937	76.44274	-6.8665	1.68E-11	1.05E-10	HS3ST4	chr16	+	25703347	26149009	3203
ENSG00000(	661.871	582.8753	766.5794	770.0497	845.877	666.6135	-0.18231	0.23063	0.34404	TRAK1	chr3	+	42055294	42267381	5536
ENSG00000(	1.035792	1.204288	6.597069	2.996302	14.72691	3.28786	-1.0593	0.29275	0.41701	HIST1H2AJ	chr6	-	27782112	27782607	496
ENSG00000(	58.00435	50.58008	65.97069	33.7084	31.29469	40.27628	0.71438	0.043833	0.086669	TSPAN10	chr17	+	79604197	79615779	1896
ENSG00000(	140.8677	132.4716	203.1897	101.8743	148.1896	111.7872	0.39331	0.11901	0.2024	PLCB1	chr20	+	8112824	8949003	7295
ENSG00000(	6.214751	0	2.638828	0	0	0	2.4522	0.069405	0.12882	RP11-123C	chr15	+	58978610	58978816	207
ENSG00000(	409.1378	432.3393	420.893	1053.2	922.2729	1001.153	-1.2354	2.94E-20	3.01E-19	SKA2	chr17	-	57187312	57232630	2798
ENSG00000(	0	1.204288	2.638828	0	0.920432	4.109825	-0.25871	0.84412	0.90059	RXFP3	chr5	+	33936491	33939023	2533
ENSG00000(	542.755	605.7567	510.6131	1162.565	893.7395	947.7256	-0.85435	7.33E-09	3.73E-08	NDN	chr15	-	23930565	23932450	1886
ENSG00000(	16.57267	19.2686	26.38828	14.23244	18.40864	23.83698	0.12975	0.80507	0.87364	FAM156A	chrX	-	52976462	53024651	2945
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	AC073871.	chr7	-	1.56E+08	1.56E+08	766
ENSG00000(	1199.447	1062.182	1256.082	290.6413	187.7681	255.6311	2.2488	3.45E-42	7.60E-41	NTM	chr11	+	1.31E+08	1.32E+08	3190
ENSG00000(	8685.115	8613.066	10622.6	1525.867	1596.95	1357.064	2.6344	1.04E-102	8.26E-101	TTC3	chr21	+	38445526	38575413	10363
ENSG00000(	0	1.204288	0	8.239831	14.72691	7.397684	-3.4719	0.001861	0.004989	KCNB2	chr8	+	73449626	73850584	3582
ENSG00000(	5.17896	0	3.958241	3.745378	1.840864	2.465895	0.14339	0.89877	0.93723	PPP1R27	chr17	-	79791368	79792926	1443
ENSG00000(	39.36009	28.90291	26.38828	103.3724	98.48622	122.4728	-1.742	5.74E-08	2.69E-07	BRICD5	chr16	-	2259254	2261951	1913
ENSG00000(	2.071584	0	0	11.23613	11.04518	7.397684	-2.9571	0.00524	0.012933	GALR2	chr17	+	74070875	74073622	1364
ENSG00000(	117.0445	115.6116	145.1355	38.95193	26.69253	27.94681	1.9794	6.84E-11	4.10E-10	IGIP	chr5	+	1.4E+08	1.4E+08	2871
ENSG00000(	1771.204	1759.464	1414.412	715.3671	694.9262	707.7118	1.221	8.90E-21	9.30E-20	TSKU	chr11	+	76493295	76509198	3554
ENSG00000(	43035.08	41169.78	37835.51	45593.23	35092.39	37817.78	0.042341	0.72347	0.81425	ANXA2	chr15	-	60639333	60695082	3528
ENSG00000(	0	0	0	2.996302	10.12475	0	-2.6944	0.042021	0.08358	SEPHS1P1	chr7	-	64312775	64313732	958
ENSG00000(	2.071584	6.021439	0	11.23613	11.96562	25.48091	-2.291	0.006504	0.015745	RGS6	chr14	+	72399156	73030654	3105
ENSG00000(	76.6486	57.80581	80.48424	36.7047	72.71413	69.04505	0.26852	0.43099	0.56086	HOXB4	chr17	-	46652875	46657473	3757
ENSG00000(	307.6302	309.5019	261.2439	471.1685	599.2012	683.8748	-0.99166	1.63E-08	8.03E-08	PAQR7	chr1	-	26187701	26197744	3297
ENSG00000(	1413.856	1390.952	1783.847	809.7507	902.9438	724.9731	0.90981	1.70E-10	9.93E-10	PAPPA	chr9	+	1.19E+08	1.19E+08	10959
ENSG00000(	5.17896	10.83859	5.277655	9.737982	2.761296	0.821965	0.56991	0.54047	0.66379	MAFA	chr8	-	1.45E+08	1.45E+08	2347
ENSG00000(	444.3547	443.1779	482.9054	599.2604	598.2808	604.9662	-0.39516	0.004245	0.010672	NGRN	chr15	+	90808891	90816463	2784
ENSG00000(	2.071584	9.634302	3.958241	37.45378	30.37426	35.34449	-2.5875	2.59E-05	9.12E-05	GRID1	chr10	-	87359312	88126250	5834
ENSG00000(	0	0	0	2.247227	2.761296	3.28786	-2.2198	0.096429	0.17025	HCAR2	chr12	-	1.23E+08	1.23E+08	2051
ENSG00000(	3.107376	16.86003	1.319414	9.737982	9.20432	4.109825	-0.10183	0.90763	0.94312	CCDC87	chr11	-	66357640	66360554	2915
ENSG00000(	0	1.204288	2.638828	15.73059	32.21512	21.37109	-3.7229	1.67E-05	6.04E-05	C1orf116	chr1	-	2.07E+08	2.07E+08	5493

ENSG0000(	160.5477	148.1274	121.3861	68.16587	87.44104	72.33291	0.9135	0.000305	0.000927	TMEM198B	chr12	+	56223529	56230030	2787
ENSG0000(	1.035792	0	2.638828	0	0.920432	1.64393	0.28893	0.83005	0.891	MAGEB17	chrX	+	16185604	16189587	1434
ENSG0000(	1224.306	1113.966	869.4937	152.8114	132.5422	170.9687	2.8017	1.21E-60	4.29E-59	CRIP2	chr14	+	1.06E+08	1.06E+08	1976
ENSG0000(	84.93494	75.87013	85.7619	182.7744	136.2239	179.1884	-1.0081	3.70E-05	0.000128	DDX28	chr16	-	68055179	68057770	2592
ENSG0000(	1123.834	1113.966	1413.092	653.943	694.9262	592.6367	0.90805	1.35E-10	7.95E-10	ACBD3	chr1	-	2.26E+08	2.26E+08	3573
ENSG0000(	1417.999	1346.394	1501.493	1048.706	929.6363	849.0898	0.59142	3.88E-06	1.51E-05	C16orf72	chr16	+	9185505	9215497	5953
ENSG0000(	4.143168	2.408575	3.958241	188.767	276.1296	184.1201	-5.7174	4.13E-30	6.29E-29	PLCXD3	chr5	-	41307056	41510730	7704
ENSG0000(	120.1519	156.5574	96.31721	232.2134	163.8369	303.3051	-0.8983	0.000505	0.001482	RRP7B	chr22	-	42951229	42978044	2375
ENSG0000(	2.071584	3.612863	1.319414	2.996302	1.840864	0.821965	0.22772	0.84668	0.90234	VMO1	chr17	-	4688580	4689728	766
ENSG0000(	709.5175	815.3028	573.945	770.7987	613.9281	618.1176	0.067328	0.6782	0.77943	ALG12	chr22	-	50296867	50312106	2360
ENSG0000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	LCK	chr1	+	32716840	32751766	2166
ENSG0000(	92.18548	55.39724	69.92893	2.247227	0.920432	3.28786	4.7885	4.99E-16	4.18E-15	GALNT9	chr12	-	1.33E+08	1.33E+08	2410
ENSG0000(	18612.14	17615.12	15815.81	5417.314	7088.247	7461.798	1.379	8.65E-26	1.11E-24	COL18A1	chr21	+	46825052	46933634	6607
ENSG0000(	1463.574	1501.747	1332.608	1776.807	1534.36	1656.259	-0.20844	0.080439	0.14604	RBM10	chrX	+	47004268	47046212	3747
ENSG0000(	40.39588	38.53721	31.66593	71.91125	65.35067	75.62077	-0.92645	0.005755	0.014088	RP11-181G	chr1	-	2113233	2115828	2260
ENSG0000(	3.107376	6.021439	6.597069	61.42419	80.07758	64.11326	-3.59	4.74E-12	3.10E-11	GLUD2	chrX	+	1.2E+08	1.2E+08	2333
ENSG0000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	TMEM95	chr17	+	7258442	7260538	1191
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	TCHHL1	chr1	-	1.52E+08	1.52E+08	3603
ENSG0000(	11468.29	12843.73	9840.188	6315.456	6534.147	8866.536	0.6514	6.39E-06	2.43E-05	RPL35A	chr3	+	1.98E+08	1.98E+08	1437
ENSG0000(	7.250543	3.612863	2.638828	17.97781	9.20432	10.68554	-1.3327	0.089192	0.15958	RGS7	chr1	-	2.41E+08	2.42E+08	2494
ENSG0000(	14.50109	19.2686	23.74945	34.45748	28.53339	28.76877	-0.66289	0.16241	0.2603	SLC25A18	chr22	+	18043139	18073647	2454
ENSG0000(	203.0152	240.8575	282.3545	232.2134	330.4351	262.2068	-0.1838	0.36357	0.49339	ZNF721	chr4	-	419604	492945	4492
ENSG0000(	135.6887	98.75159	94.99779	8.988907	21.16994	4.109825	3.2082	4.26E-14	3.19E-13	LENG9	chr19	-	54972981	54974894	1914
ENSG0000(	46.61064	27.69862	27.70769	20.97412	10.12475	6.575719	1.3727	0.011245	0.025855	C21orf90	chr21	+	45937099	45945835	2422
ENSG0000(	410.1736	457.6293	407.6989	198.505	212.6198	252.3432	0.93952	3.90E-08	1.86E-07	TCEAL7	chrX	+	1.03E+08	1.03E+08	1177
ENSG0000(	207.1584	232.4275	244.0915	238.206	215.3811	277.0022	-0.09787	0.60512	0.71987	C11orf54	chr11	+	93474757	93497915	4094
ENSG0000(	274.4849	285.4162	311.3817	385.0248	337.7985	286.8658	-0.2137	0.22605	0.33884	CEP63	chr3	+	1.34E+08	1.34E+08	5778
ENSG0000(	2155.483	2156.879	2282.586	1880.18	1529.758	1536.252	0.41358	0.000743	0.00213	SRPR	chr11	-	1.26E+08	1.26E+08	3069
ENSG0000(	4169.062	4130.707	4447.744	6606.846	6745.846	7418.233	-0.70342	1.48E-11	9.31E-11	EWSR1	chr22	+	29663998	29696515	7285
ENSG0000(	2.071584	0	1.319414	2.247227	0	0	0.2943	0.82824	NA	ODF3L1	chr15	+	76016318	76020029	1196
ENSG0000(	679.4795	611.7782	666.304	501.1315	437.2052	455.3686	0.48822	0.000522	0.001529	HMGN4	chr6	+	26538633	26546482	1225
ENSG0000(	108.7581	87.913	151.7326	231.4643	292.6974	215.3548	-1.0806	4.78E-06	1.84E-05	SPATA13	chr13	+	24553839	24895169	8603
ENSG0000(	1459.431	1530.65	1432.883	2737.871	2556.04	2607.273	-0.8358	1.06E-14	8.18E-14	GJC1	chr17	-	42875816	42908184	7640
ENSG0000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	SOX1	chr13	+	1.13E+08	1.13E+08	4108
ENSG0000(	333.525	329.9748	354.9223	623.9799	413.274	433.1755	-0.52942	0.003748	0.009524	CNOT10	chr3	+	32726637	32815367	2815
ENSG0000(	2024.973	1984.666	1493.576	2005.275	1779.195	2010.526	-0.0738	0.58996	0.70675	MTA1	chr14	+	1.06E+08	1.06E+08	2876
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	ZNF662	chr3	+	42947223	42960825	5629
ENSG0000(	138.7961	136.0845	131.9414	513.8658	497.9537	399.475	-1.7855	2.13E-22	2.37E-21	CADM1	chr11	-	1.15E+08	1.15E+08	4223
ENSG0000(	478.5359	553.9724	478.9472	910.8759	730.823	837.5823	-0.71285	9.62E-07	4.00E-06	ZNF320	chr19	-	53367043	53400946	6448
ENSG0000(	21.75163	15.65574	31.66593	42.69731	28.53339	31.23467	-0.56096	0.22452	0.33691	C12orf60	chr12	+	14956506	15059520	2870
ENSG0000(	2142.018	2024.408	1674.336	251.6894	272.4479	283.5779	2.848	2.92E-92	1.93E-90	PYCR1	chr17	-	79890260	79900288	1890
ENSG0000(	944.6422	829.7542	663.6651	466.6741	491.5107	655.106	0.59468	0.000577	0.001678	LSMD1	chr17	-	7760003	7788556	999
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	IQCA1P1	chr7	-	1.51E+08	1.51E+08	2456
ENSG0000(	6.214751	13.24716	6.597069	654.692	685.7218	814.5672	-6.2771	1.46E-77	7.51E-76	SPNS2	chr17	+	4402133	4442330	3447

ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	C19orf59	chr19	+	7741514	7744712	1730
ENSG0000(	2994.474	2880.656	2780.005	1910.143	1681.629	1652.149	0.72154	1.59E-10	9.29E-10	AP2A2	chr11	+	924894	1012239	4575
ENSG0000(	84.93494	93.93444	137.219	335.5858	410.5127	369.0622	-1.8148	2.21E-17	1.98E-16	SLC8A1	chr2	-	40339286	40838193	6111
ENSG0000(	11.39371	8.430014	19.79121	19.47596	37.73771	26.30288	-1.0352	0.060334	0.11418	SLC25A21	chr14	-	37147636	37642071	2785
ENSG0000(	10.35792	12.04288	15.83297	2.996302	1.840864	1.64393	2.2708	0.006457	0.015645	PCP4	chr21	+	41239243	41301322	706
ENSG0000(	141.9035	127.6545	179.4403	14.98151	33.13555	18.90519	2.717	1.70E-16	1.45E-15	ABAT	chr16	+	8768422	8878432	5586
ENSG0000(	12.4295	12.04288	22.43003	134.0845	100.3271	138.9121	-2.9562	8.90E-16	7.34E-15	SLC25A10	chr17	+	79670404	79688042	1946
ENSG0000(	817.2398	763.5184	1014.629	31.46117	19.32907	15.61733	5.2315	1.61E-109	1.41E-107	CAMK1D	chr10	+	12391481	12877545	8154
ENSG0000(	4.143168	1.204288	1.319414	0	2.761296	0	0.84086	0.51933	0.64554	RGPD6	chr2	-	1.11E+08	1.11E+08	7165
ENSG0000(	6.214751	0	0	0	0.920432	3.28786	0.37076	0.77851	0.85414	FAM133CP	chr10	+	60475314	60476017	704
ENSG0000(	146.0467	127.6545	170.2044	102.6234	104.0088	109.3213	0.48543	0.037015	0.0748	LYSMD4	chr15	-	1E+08	1E+08	3042
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	WBP2NL	chr22	+	42394729	42454460	3403
ENSG0000(	0	0	3.958241	2.996302	0	0	0.17782	0.89571	0.93537	IGSF5	chr21	+	41117334	41174023	2066
ENSG0000(	1.035792	0	0	8.239831	1.840864	4.93179	-2.5017	0.043216	0.085621	NKX2-5	chr5	-	1.73E+08	1.73E+08	1709
ENSG0000(	346.9903	313.1148	244.0915	406.748	325.8329	364.9524	-0.27635	0.12919	0.21612	AFMID	chr17	+	76183398	76203782	1730
ENSG0000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	GATSL1	chr7	+	74379083	74438803	990
ENSG0000(	1715.271	1653.487	1238.93	388.7702	285.3339	361.6646	2.1445	7.38E-40	1.52E-38	GAS6	chr13	-	1.15E+08	1.15E+08	2632
ENSG0000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	FREM3	chr4	-	1.44E+08	1.45E+08	6729
ENSG0000(	22.78742	12.04288	21.11062	22.47227	28.53339	26.30288	-0.44533	0.37516	0.50575	NEB	chr2	-	1.52E+08	1.53E+08	26202
ENSG0000(	418.4599	460.0379	282.3545	20.22504	40.49901	18.08323	3.856	3.38E-42	7.46E-41	BEGAIN	chr14	-	1.01E+08	1.01E+08	5811
ENSG0000(	902.1747	1083.859	1252.124	195.5087	185.0068	134.8022	2.6391	1.29E-50	3.63E-49	GPC6	chr13	+	93879095	95059655	6467
ENSG0000(	31.07376	27.69862	30.34652	64.4205	77.31629	43.56414	-1.0324	0.006638	0.01604	ARHGEF37	chr5	+	1.49E+08	1.49E+08	4968
ENSG0000(	55.93276	59.0101	40.90183	0.749076	0	0	6.237	8.32E-12	5.33E-11	FAM43B	chr1	+	20878932	20881512	2581
ENSG0000(	3.107376	0	1.319414	0	1.840864	0.821965	0.45541	0.73316	0.82147	CSMD1	chr8	-	2792875	4852494	12134
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	OR2A3P	chr7	+	1.44E+08	1.44E+08	953
ENSG0000(	0	0	0	0	2.761296	1.64393	-1.2339	0.35779	NA	CALHM3	chr10	-	1.05E+08	1.05E+08	1652
ENSG0000(	101.5076	71.05298	71.24834	0	1.840864	4.109825	5.0959	2.47E-17	2.21E-16	PTGDR2	chr11	-	60618413	60623444	2895
ENSG0000(	188.5141	195.0946	215.0644	283.1506	229.1876	229.3282	-0.31038	0.10515	0.18274	CEP57L1	chr6	+	1.09E+08	1.09E+08	3832
ENSG0000(	1.035792	1.204288	1.319414	1.498151	0	2.465895	-0.10882	0.93379	0.96025	DSCR6	chr21	+	38378450	38391959	2235
ENSG0000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	ANKRD20A	chr9	+	42368303	42411410	3511
ENSG0000(	2.071584	1.204288	5.277655	47.94084	39.57858	55.89361	-3.8529	2.12E-09	1.13E-08	GPR19	chr12	-	12813825	12849141	1751
ENSG0000(	1.035792	0	1.319414	4.494453	5.522592	3.28786	-1.8315	0.1207	0.20482	GJD3	chr17	-	38517235	38520067	891
ENSG0000(	0	6.021439	0	2.247227	0	4.93179	-0.17663	0.89038	0.93192	RP11-863K	chr8	-	37592279	37594944	2086
ENSG0000(	169.8699	183.0517	158.3297	388.7702	323.0716	283.5779	-0.95654	7.66E-07	3.21E-06	RABIF	chr1	-	2.03E+08	2.03E+08	2430
ENSG0000(	2768.672	2604.874	2232.448	23.97042	30.37426	23.83698	6.5784	5.74E-245	2.87E-242	TMEM119	chr12	-	1.09E+08	1.09E+08	2707
ENSG0000(	235.1248	280.599	230.8974	293.6376	211.6994	217.8207	0.043763	0.82578	0.8877	FANCF	chr11	-	22644079	22647387	3309
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CALN1	chr7	-	71244476	71912136	9459
ENSG0000(	3.107376	0	2.638828	0.749076	0	0	1.4577	0.28163	0.40421	RP11-49C9	chrX	+	1.49E+08	1.49E+08	2143
ENSG0000(	398.7799	366.1035	370.7553	286.8959	252.1984	367.4183	0.32345	0.071658	0.13243	SMDT1	chr22	+	42475695	42520105	1567
ENSG0000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	GABRR3	chr3	-	97705517	97754148	4826
ENSG0000(	22.78742	16.86003	6.597069	41.19916	70.87326	78.08667	-1.9546	2.40E-05	8.49E-05	C2CD4C	chr19	-	405445	409139	3091
ENSG0000(	61.11172	79.48299	98.95603	46.44268	70.87326	76.44274	0.29949	0.3506	0.48027	CHST6	chr16	-	75510949	75529282	2958
ENSG0000(	3.107376	3.612863	6.597069	11.23613	16.56778	13.9734	-1.5223	0.044231	0.087317	HSP90AB3I	chr4	+	88812995	88815167	2173
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	POTEC	chr18	-	14507338	14543584	6556

ENSG00000(	2414.431	2367.63	1911.831	4077.967	3377.065	4148.457	-0.79144	1.46E-09	7.86E-09	RUVBL2	chr19	+	49496705	49519252	2488
ENSG00000(	5.17896	7.225726	6.597069	23.22134	25.7721	19.72716	-1.7547	0.005065	0.012538	GDPGP1	chr15	+	90777040	90785315	1595
ENSG00000(	7.250543	2.408575	11.87472	1.498151	1.840864	0.821965	1.9567	0.055504	0.10639	CTNNA3	chr10	-	67679719	69455927	3232
ENSG00000(	3.107376	2.408575	0	1.498151	2.761296	0	0.26572	0.83671	0.89561	RP5-1120P	chr6	-	44056979	44057433	455
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	WT1-AS	chr11	+	32457064	32480315	3828
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RIMBP3C	chr22	-	21899646	21905750	5784
ENSG00000(	12.4295	2.408575	7.916483	61.42419	68.11197	60.8254	-2.9321	3.50E-09	1.83E-08	FLJ22184	chr19	-	7933605	7939326	4518
ENSG00000(	60.07593	44.55865	51.45714	26.21764	34.97642	44.38611	0.55762	0.13931	0.22982	C21orf67	chr21	-	46352729	46359828	2303
ENSG00000(	5255.608	4752.119	5169.463	5370.872	5188.475	4768.218	-0.01418	0.89352	0.93415	PTTG1IP	chr21	-	46269500	46293752	2760
ENSG00000(	2093.335	1984.666	1847.179	1325.115	1221.413	1333.227	0.60996	1.18E-07	5.38E-07	DDX41	chr5	-	1.77E+08	1.77E+08	2949
ENSG00000(	56.96855	51.78437	56.73479	109.365	105.8497	92.88204	-0.88665	0.001706	0.0046	ABHD16B	chr20	+	62492566	62494341	1776
ENSG00000(	0	0	0	25.46857	23.93123	16.4393	-5.3176	1.09E-06	4.53E-06	CCDC60	chr12	+	1.2E+08	1.2E+08	2450
ENSG00000(	14.50109	7.225726	7.916483	0.749076	3.681728	1.64393	2.0148	0.027687	0.057955	PLGLB1	chr2	-	87229682	87248975	2081
ENSG00000(	2032.224	1922.043	2000.231	1310.882	1220.493	1149.107	0.69271	1.31E-09	7.13E-09	DAZAP2	chr12	+	51632076	51665146	2450
ENSG00000(	58.00435	71.05298	88.40072	169.2911	173.0412	203.0253	-1.3227	1.12E-07	5.11E-07	CCBE1	chr18	-	57101149	57364612	3250
ENSG00000(	2263.205	2529.004	2262.795	2049.471	1522.395	1708.865	0.41634	0.001614	0.004369	15-Sep	chr1	-	87328132	87380107	1777
ENSG00000(	14.50109	26.49433	18.47179	9.737982	7.363456	17.26126	0.74418	0.21486	0.32549	RP11-556K	chr1	-	1.02E+08	1.02E+08	880
ENSG00000(	0	0	0	0.749076	5.522592	0.821965	-1.9257	0.15435	0.24989	OR5P2	chr11	-	7817452	7818520	1069
ENSG00000(	8.286335	14.45145	3.958241	17.22874	48.7829	26.30288	-1.6816	0.005827	0.014243	CECR6	chr22	-	17597189	17602257	4954
ENSG00000(	338.704	338.4048	481.586	209.7412	327.6738	251.5213	0.55159	0.00771	0.018404	ZNF623	chr8	+	1.45E+08	1.45E+08	3947
ENSG00000(	0	0	0	0	3.681728	3.28786	-1.8162	0.1806	0.28356	EPHA10	chr1	-	38179552	38230805	5425
ENSG00000(	43.50326	24.08575	35.62417	78.65293	108.611	101.1017	-1.4514	1.60E-05	5.79E-05	CCDC125	chr5	-	68576002	68628636	4198
ENSG00000(	0	7.225726	1.319414	0	1.840864	0.821965	1.11	0.38855	0.5193	C15orf60	chr15	+	73735499	73852355	927
ENSG00000(	340.7755	342.0177	365.4776	322.1025	454.6934	296.7293	-0.03286	0.86041	0.91126	BCOR	chrX	-	39909068	40036582	6390
ENSG00000(	388.422	466.0593	489.5025	214.9847	203.4155	169.3248	1.1862	2.50E-11	1.55E-10	JRKL	chr11	+	96123153	96240738	3570
ENSG00000(	13.46529	8.430014	2.638828	0	0.920432	0	3.4853	0.002587	0.006758	C10orf107	chr10	+	63422719	63526524	1685
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	GBP6	chr1	+	89829617	89852020	2987
ENSG00000(	378.064	285.4162	452.5589	194.7596	189.609	118.3629	1.1417	4.80E-07	2.06E-06	KIAA2026	chr9	-	5881596	6007901	6988
ENSG00000(	3.107376	3.612863	3.958241	26.96672	75.47542	51.78379	-3.6312	7.04E-09	3.58E-08	OVCH2	chr11	-	7710669	7727968	1764
ENSG00000(	0	0	0	4.494453	0	0.821965	-1.4611	0.2797	NA	SYNDIG1L	chr14	-	74872596	74892805	2607
ENSG00000(	1500.862	1455.984	1146.571	1137.097	945.2837	988.8238	0.41723	0.003056	0.007883	FHL3	chr1	-	38462442	38471278	1647
ENSG00000(	2.071584	1.204288	0	3.745378	0	0	-0.10524	0.93787	0.96232	PMCH	chr12	-	1.03E+08	1.03E+08	766
ENSG00000(	0	0	0	0	4.60216	3.28786	-1.9836	0.14291	0.23453	TMEM89	chr3	-	48658192	48659288	662
ENSG00000(	109.7939	78.2787	71.24834	53.18436	58.90765	55.07165	0.63187	0.037752	0.0761	C19orf71	chr19	+	3539152	3544028	674
ENSG00000(	68.36227	111.9988	43.54065	27.7158	36.81728	32.05663	1.1927	0.002022	0.005385	CCDC159	chr19	+	11455360	11465620	1408
ENSG00000(	39.36009	65.03154	38.263	51.68621	39.57858	64.11326	-0.12372	0.73905	0.82526	RPS7P1	chr17	+	26794814	26795460	647
ENSG00000(	4.143168	0	0	385.7739	419.717	350.979	-7.4601	2.73E-34	4.79E-33	RIPK4	chr21	-	43159529	43187266	4017
ENSG00000(	2.071584	7.225726	10.55531	5.243529	0	0.821965	1.3461	0.20576	0.31453	LRIT3	chr4	+	1.11E+08	1.11E+08	3781
ENSG00000(	154.333	189.0732	110.8308	107.1178	60.74851	69.04505	0.92548	0.001332	0.003664	NPIP	chr16	+	15016659	15045915	5343
ENSG00000(	1634.48	1676.369	1405.176	2760.343	2417.975	2416.577	-0.68575	1.68E-08	8.30E-08	SF3A3	chr1	-	38422647	38456593	3673
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	ZBTB8OSP1	chr4	+	1.52E+08	1.52E+08	498
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	TRIM61	chr4	-	1.66E+08	1.66E+08	1582
ENSG00000(	73.54123	52.98866	44.86007	85.39461	34.05598	60.8254	-0.07154	0.84982	0.90441	AC004967.	chr7	-	97595402	97596335	934
ENSG00000(	0	0	1.319414	20.22504	28.53339	18.08323	-4.599	4.61E-06	1.78E-05	GRIN2A	chr16	-	9852376	10276611	9335

ENSG00000(	238.2321	278.1905	224.3003	53.18436	115.054	117.541	1.3654	3.62E-07	1.57E-06	RP11-958N	chr16	+	15005408	15029565	6830
ENSG00000(	0	0	0	12.73428	11.04518	13.9734	-4.521	7.75E-05	0.000256	PRHOXNB	chr13	-	28552243	28562774	522
ENSG00000(	121.1877	157.7617	124.0249	287.645	221.8241	197.2716	-0.807	0.000312	0.000946	GTF2H2C	chr5	+	68856035	68890550	2952
ENSG00000(	210.2658	209.5461	257.2857	191.0143	170.2799	180.0103	0.31821	0.10226	0.17862	ASB7	chr15	+	1.01E+08	1.01E+08	4985
ENSG00000(	0	0	1.319414	1.498151	1.840864	0	-0.6531	0.62966	NA	SH2D7	chr15	+	78370150	78397251	2750
ENSG00000(	2.071584	3.612863	5.277655	13.48336	8.283888	18.08323	-1.7035	0.033403	0.068259	TREX2	chrX	-	1.53E+08	1.53E+08	2262
ENSG00000(	20.71584	12.04288	6.597069	1.498151	0.920432	0.821965	3.0881	0.000857	0.002429	GPR132	chr14	-	1.06E+08	1.06E+08	3658
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	MX2	chr21	+	42733870	42781317	4064
ENSG00000(	1489.469	1502.951	1489.618	1248.709	2011.144	1443.37	-0.06854	0.66486	0.76865	EP400	chr12	+	1.32E+08	1.33E+08	12376
ENSG00000(	273.4491	263.739	250.6886	259.1801	241.1532	242.4797	0.085072	0.62308	0.73484	MEX3B	chr15	-	82334119	82338482	4333
ENSG00000(	0	0	0	0	3.681728	4.109825	-1.9686	0.14605	0.23869	AL132868.	chr4	-	1961768	1962113	342
ENSG00000(	436.0684	441.9736	316.6593	569.2974	533.8506	666.6135	-0.56277	0.000921	0.002594	PI4KAP2	chr22	-	21827289	21871822	3872
ENSG00000(	8.286335	14.45145	11.87472	38.20285	34.05598	42.74218	-1.6815	0.000734	0.002105	FAM46C	chr1	+	1.18E+08	1.18E+08	5751
ENSG00000(	349.0619	332.3834	253.3274	286.8959	290.8565	300.8392	0.091811	0.60626	0.7209	COA5	chr2	-	99215773	99224978	1754
ENSG00000(	687.7658	592.5096	626.7215	1002.263	867.9674	974.8504	-0.57539	1.81E-05	6.50E-05	UTP11L	chr1	+	38474930	38490496	2019
ENSG00000(	438.14	450.4036	439.3648	1028.481	831.1501	926.3545	-1.0669	2.70E-14	2.04E-13	PSMG1	chr21	-	40546695	40555777	2154
ENSG00000(	1149.729	1154.912	1300.942	1071.178	1333.706	1035.676	0.067576	0.62118	0.73338	PRR14L	chr22	-	32072242	32146126	10826
ENSG00000(	42.46747	54.19295	62.01245	5.992604	35.89685	17.26126	1.3856	0.005726	0.014023	COL18A1-A	chr21	-	46839631	46844985	3425
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	ACSM5	chr16	+	20420856	20452658	2796
ENSG00000(	11.39371	6.021439	6.597069	0.749076	2.761296	2.465895	1.7383	0.06717	0.12526	HIST2H2AA	chr1	-	1.5E+08	1.5E+08	974
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	FOLR4	chr11	+	94038759	94040887	805
ENSG00000(	6.214751	3.612863	15.83297	3.745378	34.97642	10.68554	-0.86175	0.27023	0.39072	AC131971.	chr11	+	3011093	3012563	1471
ENSG00000(	69.39806	83.09585	50.13772	135.5827	124.2583	129.8705	-0.9307	0.000587	0.001706	SERHL2	chr22	+	42949623	42970388	2096
ENSG00000(	686.73	667.1754	554.1538	38.95193	16.56778	21.37109	4.574	6.77E-80	3.65E-78	PCBP3	chr21	+	47063608	47362368	2202
ENSG00000(	0	0	0	0	0.920432	4.109825	-1.3831	0.30514	NA	PGPEP1L	chr15	-	99511459	99551024	1483
ENSG00000(	680.5153	692.4654	723.0388	1241.218	1153.301	1079.24	-0.72797	7.35E-09	3.74E-08	SETD3	chr14	-	99864083	99947216	2878
ENSG00000(	3.107376	1.204288	7.916483	23.22134	15.64734	15.61733	-2.0014	0.007495	0.01794	TNFAIP8L3	chr15	-	51348795	51397473	2262
ENSG00000(	519.9675	546.7466	573.945	806.0053	1102.678	885.2562	-0.76546	3.68E-07	1.60E-06	ZNRF3	chr22	+	29279580	29453475	6851
ENSG00000(	1538.151	1507.768	1613.643	257.682	231.9489	196.4496	2.7551	9.11E-86	5.37E-84	FBXL7	chr5	+	15500305	15939900	4562
ENSG00000(	161.5835	144.5145	141.1773	143.0734	160.1552	123.2947	0.070981	0.7488	0.83302	TANGO2	chr22	+	20004537	20053449	3109
ENSG00000(	5.17896	2.408575	15.83297	0.749076	11.96562	4.93179	0.35613	0.70072	0.79658	HIST2H3D	chr1	-	1.5E+08	1.5E+08	411
ENSG00000(	41.43168	52.98866	56.73479	29.96302	24.85166	36.16646	0.71134	0.063199	0.1189	RP11-347C	chr16	-	30234230	30346695	5504
ENSG00000(	176.0846	173.4174	134.5802	315.3608	244.8349	241.6577	-0.72211	0.00048	0.001413	SFXN4	chr10	-	1.21E+08	1.21E+08	1363
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	GKN2	chr2	-	69172364	69180102	1498
ENSG00000(	12.4295	6.021439	7.916483	17.97781	9.20432	10.68554	-0.48152	0.48772	0.61689	FAM167B	chr1	+	32712834	32714457	936
ENSG00000(	457.82	437.1564	389.2271	376.785	354.3663	482.4934	0.081974	0.6279	0.73868	MRPL54	chr19	+	3762662	3768573	626
ENSG00000(	56.96855	48.17151	48.81831	41.94823	30.37426	32.05663	0.5488	0.13528	0.22452	ZNF438	chr10	-	31133563	31320866	3418
ENSG00000(	247.5543	226.4061	250.6886	1237.473	1121.086	1214.042	-2.2958	3.99E-61	1.44E-59	C3orf37	chr3	+	1.29E+08	1.29E+08	2515
ENSG00000(	0	0	0	34.45748	28.53339	36.16646	-5.892	2.75E-08	1.33E-07	CCR3	chr3	+	46205096	46308197	2000
ENSG00000(	35.21692	26.49433	29.0271	62.92235	81.91845	64.93523	-1.1811	0.000908	0.002562	DGCR6	chr22	+	18893541	18901751	3245
ENSG00000(	0	1.204288	3.958241	2.247227	0	0	0.63744	0.63604	0.74482	RP1L1	chr8	-	10463859	10569697	7973
ENSG00000(	5.17896	13.24716	3.958241	27.7158	6.443024	4.109825	-0.70577	0.3834	0.51403	C11orf88	chr11	+	1.11E+08	1.11E+08	3099
ENSG00000(	58.00435	68.6444	77.84541	130.3391	141.7465	156.1733	-1.0616	3.80E-05	0.000131	ZNF530	chr19	+	58111253	58124090	4367
ENSG00000(	352.1692	386.5764	395.8241	388.7702	398.5471	557.2922	-0.24497	0.16643	0.26531	NDUFB1	chr14	-	92582466	92588261	1333

ENSG00000(	2.071584	0	0	2.247227	1.840864	2.465895	-0.99858	0.4446	0.57419	11-Mar	chr5	-	16067248	16180871	1741
ENSG00000(	228.91	205.9332	248.0498	192.5124	209.8585	242.4797	0.082043	0.66962	0.77259	KLHL25	chr15	-	86302554	86338261	3758
ENSG00000(	2.071584	1.204288	1.319414	8.239831	8.283888	0	-1.4107	0.21367	0.32397	PP13439	chr3	-	1.72E+08	1.72E+08	2906
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-44N1	chr8	-	97080957	97081909	953
ENSG00000(	145.0109	133.6759	110.8308	223.2245	192.3703	216.9987	-0.69248	0.001073	0.002997	TRMT12	chr8	+	1.25E+08	1.25E+08	2215
ENSG00000(	118.0803	71.05298	114.789	110.8632	121.497	100.2797	-0.12703	0.63716	0.7458	GUSBP1	chr5	+	21341942	21544886	1305
ENSG00000(	0	0	0	25.46857	25.7721	19.72716	-5.4275	5.47E-07	2.34E-06	PSG9	chr19	-	43715943	43773682	2830
ENSG00000(	118.0803	124.0416	91.03955	32.21025	12.88605	10.68554	2.5098	1.03E-10	6.08E-10	GPR1	chr2	-	2.07E+08	2.07E+08	2295
ENSG00000(	0	0	0	3.745378	13.80648	10.68554	-4.0397	0.000703	0.002022	LINC00518	chr6	-	10429488	10435107	1548
ENSG00000(	3.107376	2.408575	3.958241	2.247227	5.522592	0	0.22988	0.83978	0.89743	BMP8A	chr1	+	39957318	39991607	1692
ENSG00000(	906.3179	759.9056	791.6483	2673.451	2494.371	2764.268	-1.6859	4.19E-44	9.78E-43	ALYREF	chr17	-	79845713	79849462	1095
ENSG00000(	521.0033	479.3065	609.5692	313.8627	202.495	206.3132	1.1462	3.52E-09	1.84E-08	FAM101B	chr17	-	289769	295730	3621
ENSG00000(	11.39371	15.65574	6.597069	0.749076	0	0.821965	3.5271	0.000615	0.001784	EFHC2	chrX	-	44007128	44202923	3251
ENSG00000(	12.4295	10.83859	9.235896	467.4231	590.9173	563.8679	-5.5474	7.37E-69	3.15E-67	NOG	chr17	+	54671060	54672951	1892
ENSG00000(	32.10955	33.72006	17.15238	1309.384	964.6127	1004.441	-5.2451	2.65E-109	2.30E-107	UPP1	chr7	+	48128225	48148330	2782
ENSG00000(	6.214751	1.204288	6.597069	11.98521	2.761296	3.28786	-0.32131	0.73467	0.82247	OPCML	chr11	-	1.32E+08	1.33E+08	6833
ENSG00000(	125.3308	133.6759	180.7597	69.66403	93.88406	80.55256	0.84101	0.00112	0.003116	TRIM52	chr5	-	1.81E+08	1.81E+08	3467
ENSG00000(	1635.515	1553.531	1567.464	688.4004	829.3092	1010.195	0.90989	4.23E-10	2.39E-09	LHFP	chr13	-	39917029	40177665	2110
ENSG00000(	273.4491	315.5234	361.5194	732.5959	1051.133	901.6955	-1.4943	1.95E-18	1.83E-17	CMTM4	chr16	-	66648653	66730610	7026
ENSG00000(	1199.447	1191.041	1198.028	1065.185	1010.634	1126.914	0.16356	0.16409	0.26236	TMEM50A	chr1	+	25664408	25688852	2683
ENSG00000(	0	0	1.319414	91.38722	112.2927	78.08667	-6.5927	6.41E-14	4.74E-13	NPBWR1	chr8	+	53850991	53853677	2687
ENSG00000(	6.214751	3.612863	0	1.498151	0	0	1.6842	0.19509	0.30148	ASCL2	chr11	-	2289725	2292182	1852
ENSG00000(	410.1736	454.0165	423.5318	415.7369	401.3084	327.964	0.1684	0.29336	0.41765	TBK1	chr12	+	64845660	64895888	3256
ENSG00000(	2489.008	2202.642	2699.521	484.6519	739.1069	621.4055	1.9971	9.30E-39	1.86E-37	CBX6	chr22	-	39257455	39268319	6122
ENSG00000(	1.035792	1.204288	2.638828	447.1981	577.1109	493.179	-7.8277	1.85E-38	3.68E-37	MACC1	chr7	-	20174278	20257027	9159
ENSG00000(	2.071584	0	0	0	3.681728	0	-0.35836	0.79134	NA	MRC1L1	chr10	+	17851362	17953178	5171
ENSG00000(	706.4101	592.5096	562.0703	1447.214	1196.562	1338.981	-1.0934	5.66E-15	4.46E-14	TBL3	chr16	+	2022038	2032934	6803
ENSG00000(	0	2.408575	0	2.247227	0	0.821965	-0.18813	0.88971	NA	PAPL	chr19	+	39574553	39602133	2966
ENSG00000(	609.0456	557.5852	513.252	245.6968	370.0137	290.9756	0.88933	4.46E-07	1.92E-06	KREMEN1	chr22	+	29469066	29564321	6182
ENSG00000(	118.0803	85.50443	64.65128	410.4934	267.8457	321.3883	-1.8746	1.67E-14	1.28E-13	TRAIP	chr3	-	49866034	49894007	2026
ENSG00000(	194.7289	250.4918	229.578	392.5156	333.1964	343.5813	-0.66427	0.000205	0.00064	CHEK2	chr22	-	29083731	29138410	2560
ENSG00000(	137.7603	98.75159	117.4278	200.0032	197.8929	175.0785	-0.68721	0.002003	0.005338	FOXL2	chr3	-	1.39E+08	1.39E+08	2917
ENSG00000(	2.071584	6.021439	1.319414	2.996302	4.60216	5.753754	-0.41607	0.68221	0.78258	AIFM3	chr22	+	21319396	21335649	2850
ENSG00000(	133.6172	164.9874	242.7721	12.73428	19.32907	12.32947	3.5578	1.50E-25	1.90E-24	KCTD16	chr5	+	1.44E+08	1.44E+08	5646
ENSG00000(	5.17896	9.634302	9.235896	5.243529	2.761296	3.28786	0.95093	0.27044	0.39094	B3GALT5	chr21	+	40928369	41034816	2922
ENSG00000(	1222.234	965.8388	938.1032	2749.107	2952.746	2723.17	-1.4254	4.54E-28	6.37E-27	ZNF703	chr8	+	37553269	37557537	3347
ENSG00000(	2.071584	0	1.319414	5.243529	6.443024	9.863579	-2.1178	0.046099	0.090466	SLC35F3	chr1	+	2.34E+08	2.34E+08	2891
ENSG00000(	4.143168	1.204288	6.597069	4.494453	3.681728	1.64393	0.22553	0.82687	0.8884	KCTD8	chr4	-	44175926	44450824	2587
ENSG00000(	0	0	0	17.97781	17.48821	13.9734	-4.9139	1.05E-05	3.89E-05	C9orf66	chr9	-	213108	215893	2786
ENSG00000(	6.214751	6.021439	3.958241	0	4.60216	0.821965	1.2892	0.23709	0.35169	TUBA8	chr22	+	18593097	18614498	2018
ENSG00000(	0	1.204288	0	0	4.60216	0	-0.85017	0.52991	NA	TCEB3C	chr18	-	44554573	44556449	1877
ENSG00000(	53.86118	34.92434	25.06886	53.93344	25.7721	24.65895	0.12457	0.78409	0.85786	PKD1P1	chr16	-	15457516	15474904	1053
ENSG00000(	9.322127	2.408575	13.19414	23.22134	22.09037	30.4127	-1.5212	0.013993	0.031505	EMILIN3	chr20	-	39988606	39995467	3796
ENSG00000(	51.7896	59.0101	42.22124	56.18067	64.43024	46.03004	-0.11729	0.73001	0.81913	OLFML1	chr11	+	7506619	7532608	2792

ENSG00000(	0	3.612863	0	7.490755	3.681728	7.397684	-1.8406	0.10008	0.17561	FAM162B	chr6	-	1.17E+08	1.17E+08	1033
ENSG00000(	275.5206	276.9862	348.3252	311.6154	451.0117	315.6345	-0.25812	0.1836	0.28757	RBM12B	chr8	-	94741584	94753245	7269
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	CCR4	chr3	+	32993066	32997841	3095
ENSG00000(	74.57702	68.6444	76.526	268.169	223.665	216.1768	-1.6773	1.49E-13	1.08E-12	LIN9	chr1	-	2.26E+08	2.26E+08	3567
ENSG00000(	418.4599	454.0165	477.6278	140.8262	205.2563	198.0935	1.3069	2.08E-12	1.40E-11	BTBD9	chr6	-	38136227	38607924	8525
ENSG00000(	61.11172	50.58008	58.05421	133.3354	105.8497	158.6392	-1.2155	1.42E-05	5.17E-05	NUDT14	chr14	-	1.06E+08	1.06E+08	1042
ENSG00000(	18.64425	22.88147	26.38828	41.19916	37.73771	36.16646	-0.74872	0.081709	0.14803	ANKRD45	chr1	-	1.74E+08	1.74E+08	1824
ENSG00000(	3.107376	3.612863	3.958241	15.73059	10.12475	9.041614	-1.5449	0.057344	0.10944	MAATS1	chr3	+	1.19E+08	1.19E+08	4433
ENSG00000(	2.071584	4.817151	0	0	0.920432	1.64393	0.92304	0.47796	0.60703	PNMA3	chrX	+	1.52E+08	1.52E+08	3751
ENSG00000(	14.50109	2.408575	9.235896	16.47966	18.40864	15.61733	-0.87273	0.19698	0.3039	GPR39	chr2	+	1.33E+08	1.33E+08	2784
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	FAM3B	chr21	+	42676139	42729358	2742
ENSG00000(	14.50109	14.45145	47.4989	87.64184	124.2583	112.6092	-2.0601	2.85E-07	1.25E-06	ZNF730	chr19	+	23258012	23330021	2374
ENSG00000(	3303.14	3098.632	3466.1	2662.964	3614.536	3093.876	0.074582	0.56187	0.68183	KIRREL	chr1	+	1.58E+08	1.58E+08	6870
ENSG00000(	323.1671	305.8891	331.1729	1095.898	1388.011	1278.977	-1.9645	1.45E-42	3.24E-41	IQGAP3	chr1	-	1.56E+08	1.57E+08	5988
ENSG00000(	1621.014	1745.013	1731.071	1269.683	1712.924	1525.567	0.17712	0.18145	0.28461	TOB2	chr22	-	41829496	41843027	4561
ENSG00000(	7.250543	7.225726	3.958241	48.68991	77.31629	65.75719	-3.2334	2.24E-10	1.29E-09	SCN5A	chr3	-	38589548	38691164	8504
ENSG00000(	82.86335	81.89156	96.31721	183.5235	231.9489	240.0138	-1.32	7.77E-09	3.94E-08	ARSI	chr5	-	1.5E+08	1.5E+08	3161
ENSG00000(	248.5901	216.7718	213.745	157.3059	187.7681	138.9121	0.48922	0.016626	0.036771	UTY	chrY	-	15360259	15592553	6529
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	C1orf64	chr1	+	16330731	16335302	3039
ENSG00000(	3.107376	2.408575	2.638828	5.992604	1.840864	10.68554	-0.99695	0.31337	0.43979	PKD1P1	chr16	+	16411301	16444447	4514
ENSG00000(	60.07593	49.3758	60.69303	45.69361	57.98722	57.53754	0.078983	0.8099	0.87669	TTC32	chr2	-	20096404	20101747	822
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	LRRC55	chr11	+	56949221	56959191	5410
ENSG00000(	9.322127	1.204288	2.638828	0	1.840864	1.64393	1.4664	0.21047	0.32029	RPL21P132	chrX	+	1.01E+08	1.01E+08	462
ENSG00000(	9.322127	1.204288	0	0	0	1.64393	1.687	0.19499	0.30134	DNAH2	chr17	+	7620672	7737062	14955
ENSG00000(	5.17896	0	1.319414	0	2.761296	2.465895	0.23976	0.84993	0.90441	SDR42E2	chr16	+	22177618	22203075	2528
ENSG00000(	43.50326	36.12863	42.22124	11.23613	11.96562	10.68554	1.7907	0.000142	0.000454	DUSP5P1	chr1	+	2.29E+08	2.29E+08	2463
ENSG00000(	87.00652	121.6331	149.0938	191.0143	179.4842	173.4346	-0.60697	0.010863	0.025054	HTR7P1	chr12	+	13152812	13157764	4411
ENSG00000(	1.035792	2.408575	0	0.749076	0	3.28786	-0.13465	0.91943	0.95101	HIST2H4A	chr1	+	1.5E+08	1.5E+08	1696
ENSG00000(	471.2853	484.1237	490.8219	742.3339	784.2081	682.2309	-0.60951	8.32E-06	3.12E-05	PRKX	chrX	-	3522411	3631649	6031
ENSG00000(	672.2289	785.1956	709.8446	1125.111	1118.325	1070.198	-0.61176	1.32E-06	5.39E-06	SETD8	chr12	+	1.24E+08	1.24E+08	3140
ENSG00000(	0	0	0	24.71949	23.0108	25.48091	-5.4746	4.02E-07	1.74E-06	KCNH8	chr3	+	19189946	19577138	5137
ENSG00000(	1520.543	1401.791	1318.094	693.644	882.6943	962.5209	0.73907	2.79E-07	1.23E-06	SMTN	chr22	+	31460091	31500610	5080
ENSG00000(	149.154	175.826	108.1919	29.21395	12.88605	25.48091	2.6267	6.33E-15	4.97E-14	NPW	chr16	+	2059927	2070756	1015
ENSG00000(	6.214751	0	5.277655	6.74168	3.681728	2.465895	-0.13526	0.89626	0.93574	PP2D1	chr3	-	20021453	20053822	2151
ENSG00000(	455.7484	557.5852	411.6571	663.6809	520.0441	517.0159	-0.25471	0.12927	0.21625	COA3	chr17	-	40947165	40950722	1374
ENSG00000(	531.3612	503.3923	558.112	600.7586	594.5991	490.7131	-0.08208	0.57774	0.69604	ST6GALNAC	chr1	+	76540404	77100286	6861
ENSG00000(	4042.696	3962.107	4208.93	3385.072	3118.424	2928.661	0.37207	0.000531	0.001554	PTP4A2	chr1	-	32372022	32410457	3929
ENSG00000(	98181.68	91293.44	87471.86	119983.9	99529.99	93319.32	-0.17545	0.13544	0.22471	ACTG1	chr17	-	79476997	79490873	2256
ENSG00000(	0	2.408575	0	9.737982	11.96562	10.68554	-3.0311	0.003468	0.008865	TMPRSS2	chr21	-	42836478	42903043	3240
ENSG00000(	1960.754	1881.097	1870.929	1926.622	1961.441	1794.349	0.007947	0.94194	0.96498	DENND5A	chr11	-	9160372	9286937	5031
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	OR2T10	chr1	-	2.49E+08	2.49E+08	1049
ENSG00000(	1.035792	0	0	0.749076	0	2.465895	-0.63474	0.6383	NA	TMEM236	chr10	+	18041218	18089855	5465
ENSG00000(	64.2191	95.13873	93.67838	39.701	45.10117	60.8254	0.78242	0.015578	0.034635	DIABLO	chr12	-	1.23E+08	1.23E+08	2569
ENSG00000(	268.2701	286.6205	250.6886	315.3608	267.8457	318.9224	-0.16314	0.34702	0.47658	VPS33B	chr15	-	91541646	91565833	2767

ENSG00000(	572.7929	500.9837	443.323	304.8737	161.0756	224.3964	1.1268	8.90E-08	4.10E-07	TBX1	chr22	+	19744226	19771116	2082
ENSG00000(	1.035792	1.204288	9.235896	11.98521	6.443024	5.753754	-0.96251	0.3029	0.42804	ADAP2	chr17	+	29233362	29286340	2934
ENSG00000(	101.5076	54.19295	71.24834	134.8336	88.36147	94.52597	-0.47605	0.11968	0.20327	RP5-821D1	chr22	-	42227219	42230669	2989
ENSG00000(	1048.221	968.2473	874.7713	1108.632	1081.508	1293.773	-0.26752	0.044444	0.087671	UQCR10	chr22	+	30163358	30166402	916
ENSG00000(	151.2256	174.6217	219.0227	133.3354	106.7701	116.719	0.60077	0.009009	0.021169	FAM120C	chrX	-	54094757	54209714	8057
ENSG00000(	1.035792	1.204288	2.638828	3.745378	0	1.64393	-0.12258	0.92255	0.95302	RP11-67F2	chr3	+	1.6E+08	1.6E+08	1969
ENSG00000(	0	0	1.319414	0	0	1.64393	-0.1317	0.91874	NA	TREML3P	chr6	-	41176292	41190382	1224
ENSG00000(	1.035792	0	0	1.498151	1.840864	2.465895	-1.3098	0.32827	0.45602	TRIML1	chr4	+	1.89E+08	1.89E+08	1797
ENSG00000(	507.538	468.4679	478.9472	308.6191	386.5814	435.6414	0.36367	0.028835	0.060057	EIF3C	chr16	+	28699879	28747051	3957
ENSG00000(	2.071584	2.408575	0	0	3.681728	1.64393	-0.13837	0.91471	0.948	RP11-366I:	chr10	-	94356609	94357044	436
ENSG00000(	3.107376	2.408575	7.916483	12.73428	8.283888	9.863579	-1.1005	0.179	0.28166	CLDN5	chr22	-	19510547	19515068	2548
ENSG00000(	1184.946	1178.998	989.5603	846.4554	820.1049	734.0147	0.48182	0.000295	0.000898	NIPSNAP1	chr22	-	29950797	29977326	2237
ENSG00000(	0	0	0	2.996302	1.840864	0	-1.3549	0.31496	NA	CNTN2	chr1	+	2.05E+08	2.05E+08	8141
ENSG00000(	98.40023	132.4716	158.3297	78.65293	88.36147	120.8288	0.42686	0.11884	0.20218	LRTOMT	chr11	+	71791382	71821828	3822
ENSG00000(	18.64425	25.29004	26.38828	15.73059	5.522592	3.28786	1.411	0.027307	0.057281	KCNQ3	chr8	-	1.33E+08	1.33E+08	11441
ENSG00000(	45.57484	49.3758	42.22124	98.87797	92.0432	86.30632	-1.0019	0.000848	0.002406	ADRA2C	chr4	+	3768075	3770251	2127
ENSG00000(	70.43385	95.13873	75.20659	247.1949	181.3251	219.4646	-1.4205	2.62E-09	1.38E-08	NR2C2AP	chr19	-	19312218	19314220	1565
ENSG00000(	14.50109	36.12863	13.19414	16.47966	11.04518	42.74218	-0.13472	0.82078	0.88422	FAM132A	chr1	-	1177826	1182102	1036
ENSG00000(	885.6021	796.0342	789.0094	837.4665	719.7778	891.01	0.013253	0.92284	0.95327	CRELD2	chr22	+	50311815	50321188	2622
ENSG00000(	422.6031	362.4906	419.5736	257.682	306.5039	272.8924	0.5248	0.001496	0.004068	SCFD2	chr4	-	53739149	54232242	3176
ENSG00000(	114.9729	114.4073	109.5113	232.9625	144.5078	151.2415	-0.63835	0.009946	0.023148	UBE2F	chr2	+	2.39E+08	2.39E+08	2009
ENSG00000(	118.0803	81.89156	97.63662	60.67512	84.67974	86.30632	0.36277	0.20217	0.30995	KCNJ12	chr17	+	21279509	21323179	5420
ENSG00000(	417.4241	427.5221	327.2146	115.3576	133.4626	152.8855	1.5396	2.65E-15	2.14E-14	GPR173	chrX	+	53078273	53109797	4485
ENSG00000(	587.294	581.671	668.9428	1216.499	1150.54	1042.252	-0.89042	2.13E-11	1.32E-10	PPP1R2	chr3	-	1.95E+08	1.95E+08	3452
ENSG00000(	953.9643	1194.653	927.5479	374.5378	462.0569	466.0541	1.2367	8.28E-16	6.84E-15	TSPYL2	chrX	+	53111549	53117722	4178
ENSG00000(	27.96638	30.10719	30.34652	3.745378	7.363456	11.50751	1.8803	0.001071	0.002991	GOLGA6L4	chr15	+	84904525	84914120	4563
ENSG00000(	403.9588	286.6205	286.3128	1367.812	1034.566	1171.3	-1.8608	2.31E-28	3.30E-27	PGP	chr16	-	2261998	2264808	2727
ENSG00000(	157.4404	233.6318	154.3714	185.0217	230.108	231.7941	-0.24385	0.26952	0.38988	C22orf46	chr22	+	42084943	42094140	4975
ENSG00000(	264.1269	339.6091	267.841	205.2467	218.1424	282.7559	0.30184	0.12526	0.21096	SNRNP35	chr12	+	1.24E+08	1.24E+08	2161
ENSG00000(	785.1303	749.067	643.8739	2701.916	2682.139	2950.032	-1.9305	1.09E-55	3.44E-54	IRAK1	chrX	-	1.53E+08	1.53E+08	3666
ENSG00000(	200.9436	195.0946	208.4674	681.6587	376.4567	532.6333	-1.3896	1.85E-11	1.16E-10	CMSS1	chr3	+	99536678	99897447	2145
ENSG00000(	0	0	0	1.498151	1.840864	0	-0.93652	0.47589	NA	OLIG1	chr21	+	34442450	34444726	2277
ENSG00000(	134.6529	91.52587	139.8579	146.8188	240.2328	205.4912	-0.68658	0.00629	0.015276	PCDH9	chr13	-	66876967	67804468	6226
ENSG00000(	48.68222	39.74149	54.09597	17.22874	22.09037	23.01502	1.1671	0.004622	0.011533	ACOT1	chr14	+	74003818	74010498	1713
ENSG00000(	1893.428	1852.195	1760.098	1177.547	1085.189	1055.403	0.72922	2.23E-10	1.29E-09	OAF	chr11	+	1.2E+08	1.2E+08	2525
ENSG00000(	1.035792	3.612863	15.83297	6.74168	12.88605	8.219649	-0.41598	0.62563	0.737	ALDH1A3	chr15	+	1.01E+08	1.01E+08	3924
ENSG00000(	103.5792	63.82725	76.526	2.247227	8.283888	9.863579	3.4916	1.29E-13	9.40E-13	CDR1	chrX	-	1.4E+08	1.4E+08	1299
ENSG00000(	10.35792	4.817151	13.19414	9.737982	28.53339	13.15144	-0.79675	0.23699	0.35156	HIST2H2AC	chr1	+	1.5E+08	1.5E+08	437
ENSG00000(	39.36009	21.67718	23.74945	135.5827	111.3723	129.0485	-2.1038	9.37E-11	5.56E-10	KCNK12	chr2	-	47747910	47798078	2037
ENSG00000(	6.214751	0	0	0	1.840864	1.64393	0.53811	0.68423	0.78409	HIST2H2AB	chr1	-	1.5E+08	1.5E+08	448
ENSG00000(	180.2278	168.6003	147.7743	44.19546	50.62376	39.45432	1.8737	6.30E-13	4.37E-12	POU6F1	chr12	-	51580719	51611477	5157
ENSG00000(	1.035792	2.408575	3.958241	0	0.920432	4.93179	0.23402	0.84792	0.90301	LINC00315	chr21	-	46720160	46725172	2323
ENSG00000(	0	1.204288	0	0	1.840864	0	-0.18234	0.88799	NA	DEFB108B	chr11	+	71544246	71548756	608
ENSG00000(	407.0662	413.0707	372.0747	402.2536	330.4351	369.8842	0.11189	0.48045	0.60957	TM2D3	chr15	-	1.02E+08	1.02E+08	3102

ENSG00000(	599.7235	596.1224	567.3479	987.2816	914.9094	1113.762	-0.77236	9.17E-09	4.61E-08	TSSC4	chr11	+	2421718	2425106	1686
ENSG00000(	5.17896	0	2.638828	223.9736	224.5854	169.3248	-5.9625	2.64E-28	3.75E-27	TACSTD2	chr1	-	59041099	59043166	2068
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	SIX6	chr14	+	60975669	60979568	2787
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	DRD5P1	chr2	-	91872473	91874507	1438
ENSG00000(	25.8948	48.17151	34.30476	76.40571	106.7701	71.51095	-1.215	0.000545	0.001591	PRKD1	chr14	-	30045687	30661104	3726
ENSG00000(	0	0	0	13.48336	49.70333	36.98842	-5.8409	6.01E-08	2.82E-07	CCSER1	chr4	+	91048686	92523064	5847
ENSG00000(	27.96638	24.08575	35.62417	71.16218	55.22592	63.2913	-1.0987	0.002831	0.007344	ZDHHC23	chr3	+	1.14E+08	1.14E+08	5280
ENSG00000(	0	1.204288	1.319414	3.745378	0	4.109825	-1.0821	0.40245	0.53363	MROH7	chr1	+	55107459	55207981	5951
ENSG00000(	602.8309	628.6382	492.1413	654.692	551.3388	676.4771	-0.12632	0.4097	0.54047	AC002055.	chr22	+	51195376	51239737	2987
ENSG00000(	9.322127	7.225726	2.638828	12.73428	16.56778	4.109825	-0.70621	0.37269	0.50321	SRPK3	chrX	+	1.53E+08	1.53E+08	4479
ENSG00000(	126.3666	127.6545	126.6637	370.7924	463.8977	360.8426	-1.6417	7.09E-18	6.49E-17	SLIT3	chr5	-	1.68E+08	1.69E+08	9706
ENSG00000(	14.50109	14.45145	7.916483	5.243529	12.88605	2.465895	0.78641	0.2997	0.4246	HIST1H2AK	chr6	-	27805658	27806117	460
ENSG00000(	650.4773	721.3683	686.0952	809.0016	849.5587	766.0713	-0.23627	0.068762	0.12777	EFNA5	chr5	-	1.07E+08	1.07E+08	5335
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	KRTAP19-1	chr21	-	31852018	31852663	646
ENSG00000(	0	0	0	0	6.443024	0	-1.5465	0.25144	0.36902	HIST1H1B	chr6	-	27834570	27835359	790
ENSG00000(	4.143168	3.612863	7.916483	0	0	1.64393	2.3505	0.047647	0.093075	SPATA32	chr17	-	43331760	43339479	1907
ENSG00000(	0	0	0	393.2647	338.719	423.3119	-9.0645	5.16E-22	5.67E-21	PKP3	chr11	+	392614	404908	2809
ENSG00000(	11.39371	19.2686	22.43003	55.43159	49.70333	60.00344	-1.6113	0.000154	0.00049	MAP7D2	chrX	-	20024831	20135035	3930
ENSG00000(	1442.858	1480.07	1394.62	388.0211	381.9793	295.0854	2.0139	2.77E-46	6.85E-45	CSF1	chr1	+	1.1E+08	1.1E+08	4210
ENSG00000(	0	0	2.638828	3.745378	2.761296	10.68554	-2.057	0.078356	0.14281	COLEC10	chr8	+	1.2E+08	1.2E+08	1266
ENSG00000(	121.1877	107.1816	135.8996	60.67512	44.18074	48.49593	1.2296	1.12E-05	4.14E-05	ACTRT3	chr3	-	1.69E+08	1.69E+08	2005
ENSG00000(	181.2636	196.2989	150.4132	78.65293	80.99802	101.1017	1.0115	2.04E-05	7.28E-05	PLA2G6	chr22	-	38507502	38601697	3271
ENSG00000(	646.3341	623.821	870.8131	269.6672	404.9901	309.8808	1.1164	1.63E-09	8.78E-09	MAML2	chr11	-	95709762	96076382	7106
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	PABPC1L2E	chrX	+	72223352	72225551	2200
ENSG00000(	0	0	1.319414	3.745378	4.60216	0	-1.5638	0.23894	0.35393	A3GALT2	chr1	-	33772367	33778491	1000
ENSG00000(	481.6432	500.9837	468.3919	462.1796	497.9537	532.6333	-0.04027	0.77969	0.85491	SS18L1	chr20	+	60718822	60757540	4493
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	KCND2	chr7	+	1.2E+08	1.2E+08	5331
ENSG00000(	0	0	3.958241	0.749076	3.681728	17.26126	-1.8951	0.10031	0.1759	RP11-44M(	chr7	+	1E+08	1E+08	1006
ENSG00000(	670.1574	747.8627	597.6944	464.4268	488.7494	500.5766	0.471	0.001082	0.003018	TOP1MT	chr8	-	1.44E+08	1.44E+08	2029
ENSG00000(	4486.015	4387.22	5107.451	2874.203	2998.767	2795.503	0.68833	3.11E-10	1.78E-09	COPB2	chr3	-	1.39E+08	1.39E+08	3524
ENSG00000(	1.035792	0	1.319414	0	2.761296	1.64393	-0.50913	0.70413	0.79928	LRRC19	chr9	-	26993134	27005691	3609
ENSG00000(	240.3037	184.256	175.482	368.5452	281.6522	304.949	-0.66453	0.000777	0.002218	THAP7	chr22	-	21353393	21356485	1957
ENSG00000(	5.17896	7.225726	26.38828	10.48706	11.04518	18.90519	-0.07432	0.91475	0.948	AP001062.	chr21	+	45751117	45755734	4354
ENSG00000(	193.6931	215.5675	270.4798	764.8061	724.38	584.4171	-1.6064	7.94E-20	7.97E-19	KNTC1	chr12	+	1.23E+08	1.23E+08	6975
ENSG00000(	17.60846	6.021439	17.15238	0.749076	11.04518	3.28786	1.3098	0.11348	0.19464	CCR10	chr17	-	40830907	40835935	1942
ENSG00000(	0	0	0	3.745378	0	2.465895	-1.6796	0.21567	0.32631	NCMAP	chr1	+	24882602	24935819	4063
ENSG00000(	562.435	649.1111	609.5692	442.7036	571.5883	498.1107	0.26781	0.076489	0.13995	WDR27	chr6	-	1.7E+08	1.7E+08	3511
ENSG00000(	4.143168	16.86003	6.597069	299.6302	208.0176	230.9721	-4.6667	1.90E-34	3.35E-33	TXNRD2	chr22	-	19863040	19929341	3130
ENSG00000(	112.9013	132.4716	85.7619	316.859	500.715	621.4055	-2.0991	5.85E-18	5.39E-17	FOXO4	chrX	+	70316047	70323385	3301
ENSG00000(	4.143168	2.408575	13.19414	60.67512	113.2131	79.7306	-3.5848	2.10E-12	1.41E-11	POU3F2	chr6	+	99282580	99286660	4081
ENSG00000(	61.11172	54.19295	46.17948	157.3059	117.8153	156.1733	-1.3989	3.48E-07	1.52E-06	PTP4A3	chr8	+	1.42E+08	1.42E+08	1866
ENSG00000(	3.107376	2.408575	3.958241	0	0	5.753754	0.51451	0.67268	0.77494	FOXD4L1	chr2	+	1.14E+08	1.14E+08	2068
ENSG00000(	55.93276	55.39724	43.54065	15.73059	16.56778	13.9734	1.7034	5.12E-05	0.000174	TMEM255B	chr13	+	1.14E+08	1.15E+08	1031
ENSG00000(	593.5088	745.4541	766.5794	798.5145	740.0273	701.958	-0.09125	0.52919	0.65392	PROS1	chr3	-	93591881	93692910	3556

ENSG00000(	0	0	0	5.243529	0	1.64393	-1.8073	0.18279	0.2864	GAST	chr17	+	39868578	39872221	470
ENSG00000(	3.107376	0	1.319414	5.992604	1.840864	3.28786	-0.98414	0.39876	0.52978	NUTM1	chr15	+	34635516	34649938	4102
ENSG00000(	18.64425	25.29004	31.66593	56.92974	56.14635	59.18147	-1.1741	0.002473	0.006481	HDDC3	chr15	-	91474148	91475799	1220
ENSG00000(	0	0	0	2.247227	2.761296	4.93179	-2.4799	0.060179	0.114	BEX5	chrX	-	1.01E+08	1.01E+08	860
ENSG00000(	198.872	196.2989	220.3421	187.2689	137.1444	120.8288	0.46078	0.038242	0.076976	ZFP1	chr16	+	75182390	75206134	3250
ENSG00000(	60.07593	80.68728	50.13772	3.745378	15.64734	13.9734	2.4553	2.41E-07	1.07E-06	CEND1	chr11	-	787104	790123	1649
ENSG00000(	4.143168	0	1.319414	5.243529	12.88605	4.109825	-1.6222	0.11596	0.19826	C6orf58	chr6	+	1.28E+08	1.28E+08	1200
ENSG00000(	95.29286	75.87013	65.97069	451.6926	401.3084	452.0807	-2.4382	1.88E-33	3.21E-32	DUSP8	chr11	-	1575274	1593150	4480
ENSG00000(	7.250543	12.04288	10.55531	0.749076	11.04518	8.219649	0.52666	0.52398	0.64913	AC132872.	chr17	+	80206943	80209703	2759
ENSG00000(	3651.166	3788.689	3104.581	463.6778	651.6659	695.3823	2.5352	1.31E-62	4.86E-61	SOCS3	chr17	-	76352864	76356158	2729
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	C17orf74	chr17	+	7328934	7330887	1651
ENSG00000(	10.35792	16.86003	7.916483	137.8299	95.72493	115.0751	-3.237	2.34E-16	1.99E-15	SLITRK6	chr13	-	86366925	86373623	4318
ENSG00000(	6.214751	10.83859	9.235896	2.996302	0	0	2.4863	0.017561	0.038638	LPAR5	chr12	-	6728001	6745613	3171
ENSG00000(	2279.778	2330.297	2465.984	2391.798	2297.398	1931.618	0.095494	0.42612	0.55648	XPOT	chr12	+	64798130	64844907	6414
ENSG00000(	1263.666	1069.407	957.8944	8.239831	1.840864	4.109825	7.6573	4.64E-102	3.66E-100	TMEM173	chr5	-	1.39E+08	1.39E+08	3200
ENSG00000(	29.00217	6.021439	25.06886	69.66403	89.2819	61.64737	-1.8173	3.62E-05	0.000125	PDE4B	chr1	+	66258197	66840259	4546
ENSG00000(	3.107376	21.67718	3.958241	8.988907	6.443024	13.15144	0.000937	0.99906	0.99932	AF207550.	chrX	+	48797263	48798079	813
ENSG00000(	1.035792	0	1.319414	1.498151	1.840864	5.753754	-1.3339	0.28591	0.4092	FAM19A3	chr1	+	1.13E+08	1.13E+08	1282
ENSG00000(	864.8862	865.8829	981.6439	734.094	888.2169	873.7487	0.11962	0.37815	0.50885	SNN	chr16	+	11762270	11773015	3312
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	C8orf12	chr8	+	11225911	11296167	1222
ENSG00000(	0	0	0	26.96672	42.33987	17.26126	-5.6736	1.41E-07	6.39E-07	KCNH7	chr2	-	1.63E+08	1.64E+08	4113
ENSG00000(	2.071584	2.408575	1.319414	3.745378	5.522592	3.28786	-0.88586	0.40975	0.5405	RPL7P26	chr6	-	17531130	17531883	754
ENSG00000(	15.53688	13.24716	29.0271	469.6704	479.5451	507.1524	-4.6337	1.22E-65	4.85E-64	NELL2	chr12	-	44902058	45315631	3612
ENSG00000(	17.60846	14.45145	9.235896	9.737982	3.681728	18.08323	0.36392	0.59935	0.71468	AC004166.	chr7	-	74320406	74331163	2819
ENSG00000(	4.143168	0	2.638828	2.247227	2.761296	1.64393	0.032964	0.97785	0.98705	ZNF840	chr20	+	45113100	45121279	1996
ENSG00000(	5.17896	14.45145	14.51355	2.996302	8.283888	4.93179	0.9782	0.21158	0.32152	KRBA2	chr17	-	8271955	8280029	2562
ENSG00000(	1553.688	1629.401	1517.326	843.4591	1122.927	1030.744	0.64855	1.25E-06	5.15E-06	MED12	chrX	+	70338406	70362303	6977
ENSG00000(	83.89914	102.3645	96.31721	608.9984	451.0117	452.9027	-2.4113	5.39E-33	9.05E-32	ZNF93	chr19	+	20011722	20046384	2648
ENSG00000(	23576.7	22215.5	20198.91	8639.088	9345.146	9749.326	1.2488	1.52E-31	2.42E-30	9-Sep	chr17	+	75276651	75496678	4453
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	PRSS55	chr8	+	10383056	10411676	2374
ENSG00000(	146.0467	179.4389	184.7179	659.9356	688.4831	588.5269	-1.9212	2.40E-30	3.68E-29	CDCA2	chr8	+	25316513	25365436	3731
ENSG00000(	2.071584	0	2.638828	59.92604	31.29469	21.37109	-4.135	1.16E-07	5.27E-07	OR7E14P	chr11	+	17035545	17074583	1012
ENSG00000(	0	0	0	6.74168	15.64734	8.219649	-4.182	0.000376	0.001127	RALYL	chr8	+	85095022	85834079	2701
ENSG00000(	2.071584	0	0	0.749076	0	0	0.47431	0.71145	NA	GSTT1	chr22	-	24376133	24384680	2066
ENSG00000(	179.192	163.7831	189.9956	205.9958	358.9685	276.1802	-0.65198	0.003232	0.008312	AMER1	chrX	-	63404997	63425624	8443
ENSG00000(	747.8418	652.7239	800.8842	546.0761	740.0273	655.928	0.18115	0.23862	0.35356	ZBTB40	chr1	+	22778344	22857650	8992
ENSG00000(	496.1443	432.3393	439.3648	129.5901	115.054	124.1167	1.8826	6.60E-27	8.82E-26	HIST2H2BE	chr1	-	1.5E+08	1.5E+08	2223
ENSG00000(	25.8948	12.04288	10.55531	0	0	0	5.2529	3.36E-06	1.31E-05	C11orf89	chr11	-	1910375	1912084	1710
ENSG00000(	1.035792	9.634302	15.83297	14842.18	13186.11	15799.81	-10.071	3.93E-57	1.29E-55	CLDN6	chr16	-	3064713	3070072	1739
ENSG00000(	854.5283	863.4743	697.9699	36.7047	25.7721	55.07165	4.3264	1.03E-88	6.32E-87	5-Sep	chr22	+	19701987	19712295	4113
ENSG00000(	259.9838	260.1261	281.0351	335.5858	380.1384	299.1952	-0.3398	0.049047	0.095469	EIF4ENIF1	chr22	-	31835349	31892094	3695
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	LRRC26	chr9	-	1.4E+08	1.4E+08	1209
ENSG00000(	76.6486	83.09585	77.84541	118.3539	78.23672	97.81383	-0.30959	0.26454	0.38438	RNLS	chr10	-	90033621	90344287	3385
ENSG00000(	0	0	0	5.243529	4.60216	1.64393	-2.6872	0.039591	0.079296	APOBR	chr16	+	28505970	28510291	3792

ENSG00000(	0	1.204288	0	59.92604	49.70333	40.27628	-5.7384	5.47E-10	3.06E-09	FAM110C	chr2	-	38814	46870	3760
ENSG00000(	1719.415	1846.173	1645.309	814.9942	776.8446	703.602	1.1803	5.41E-22	5.94E-21	ATL3	chr11	-	63391559	63439393	7135
ENSG00000(	554.1487	594.9181	514.5714	708.6255	671.9154	874.5707	-0.43735	0.003541	0.009035	NDUFA12	chr12	-	95290831	95397546	813
ENSG00000(	0	2.408575	0	1.498151	4.60216	0.821965	-0.95486	0.46449	0.59365	RP11-480I1	chr1	+	2.03E+08	2.03E+08	2810
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RPS17	chr15	-	82821158	82824972	1922
ENSG00000(	20.71584	55.39724	54.09597	29.96302	51.54419	43.56414	0.051262	0.90468	0.94101	SMIM10	chrX	+	1.34E+08	1.34E+08	1534
ENSG00000(	5.17896	8.430014	10.55531	2.247227	9.20432	5.753754	0.44248	0.59521	0.711	TCTE3	chr6	-	1.7E+08	1.7E+08	769
ENSG00000(	1461.502	1492.112	1357.677	2134.865	2153.811	2037.651	-0.55196	6.21E-07	2.63E-06	UBE2G2	chr21	-	46188955	46221934	4340
ENSG00000(	64.2191	68.6444	96.31721	92.13629	90.20234	73.97684	-0.16505	0.5696	0.68872	SATL1	chrX	-	84347293	84364054	2224
ENSG00000(	99.43602	115.6116	105.5531	24.71949	58.90765	52.60575	1.2229	0.000234	0.000723	OSBP2	chr22	+	31089769	31303811	4340
ENSG00000(	5.17896	10.83859	9.235896	1.498151	0	0.821965	2.7391	0.008746	0.020608	C21orf88	chr21	-	40969074	40984748	1357
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	TUSC5	chr17	+	1182957	1204281	3596
ENSG00000(	1.035792	1.204288	2.638828	0	7.363456	3.28786	-0.82791	0.48826	0.61734	HIST1H2AH	chr6	+	27114861	27115317	457
ENSG00000(	0	1.204288	0	17.22874	12.88605	9.863579	-3.8776	0.000301	0.000916	ZBTB7C	chr18	-	45553044	45937123	4949
ENSG00000(	196.8005	169.8046	153.052	244.9477	161.996	229.3282	-0.2897	0.18899	0.29408	APOO	chrX	-	23851470	23926057	1118
ENSG00000(	118.0803	146.9231	141.1773	18.72689	14.72691	13.15144	3.0688	1.47E-20	1.52E-19	PRR16	chr5	+	1.2E+08	1.2E+08	1826
ENSG00000(	6198.179	5872.107	5553.413	3854.743	3513.289	4696.708	0.54556	1.36E-05	4.96E-05	TMED9	chr5	+	1.77E+08	1.77E+08	1473
ENSG00000(	54.89697	48.17151	65.97069	0	0	0	7.0196	8.87E-12	5.66E-11	DRD1	chr5	-	1.75E+08	1.75E+08	4054
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	LINC00308	chr21	+	23470936	23488847	727
ENSG00000(	80.79177	72.25726	108.1919	132.5864	139.9057	158.6392	-0.7204	0.004453	0.011138	TMEM186	chr16	-	8874241	8891505	1448
ENSG00000(	1043.042	1029.666	1310.178	767.8024	914.9094	782.5106	0.455	0.001416	0.003869	RBM33	chr7	+	1.55E+08	1.56E+08	10149
ENSG00000(	1634.48	1543.897	1636.073	880.9128	938.8406	786.6204	0.8839	4.96E-13	3.47E-12	ARMCX2	chrX	-	1.01E+08	1.01E+08	2762
ENSG00000(	163.6551	124.0416	215.0644	665.9282	462.9773	569.6217	-1.7499	3.71E-17	3.28E-16	PIGW	chr17	+	34890847	34895159	2333
ENSG00000(	731.2691	653.9282	584.5003	543.0798	485.9881	481.6714	0.38252	0.009012	0.021173	BTBD6	chr14	+	1.06E+08	1.06E+08	2195
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	SRY	chrY	-	2654896	2655740	845
ENSG00000(	1146.622	1010.397	811.4395	2495.171	2251.377	2524.254	-1.2876	1.45E-20	1.51E-19	H1FX	chr3	-	1.29E+08	1.29E+08	1506
ENSG00000(	193.6931	251.6961	258.6051	39.701	42.33987	45.20807	2.4462	2.46E-23	2.84E-22	RBM43	chr2	-	1.52E+08	1.52E+08	4192
ENSG00000(	1962.826	1940.108	1884.123	2070.445	1877.681	2026.144	-0.04594	0.67337	0.77555	SUMO3	chr21	-	46225532	46238694	1807
ENSG00000(	131.5456	99.95588	91.03955	158.0549	98.48622	121.6508	-0.2259	0.39791	0.52889	IMMP2L	chr7	-	1.1E+08	1.11E+08	1519
ENSG00000(	0	0	0	0	0.920432	4.109825	-1.3831	0.30514	NA	TCEAL2	chrX	+	1.01E+08	1.01E+08	1100
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC129778.	chr9	-	42845768	42859085	960
ENSG00000(	0	1.204288	6.597069	6.74168	0.920432	2.465895	-0.32275	0.78091	0.85569	CLCNKB	chr1	+	16370272	16383803	2567
ENSG00000(	14.50109	18.06432	5.277655	68.91495	69.95283	86.30632	-2.4878	9.36E-09	4.70E-08	JAG2	chr14	-	1.06E+08	1.06E+08	5835
ENSG00000(	14.50109	10.83859	10.55531	17.22874	27.61296	18.90519	-0.7794	0.17227	0.27333	FMNL1	chr17	+	43298811	43324687	4919
ENSG00000(	37.28851	33.72006	50.13772	17.97781	34.97642	45.20807	0.29632	0.49607	0.62469	NUTM2A	chr10	+	88985205	88996665	3974
ENSG00000(	128.4382	167.396	106.8725	113.1104	101.2475	80.55256	0.44553	0.088596	0.15867	PTRHD1	chr2	-	25012855	25016251	1014
ENSG00000(	0	0	0	1.498151	2.761296	2.465895	-1.9136	0.15629	0.25228	LCN12	chr9	+	1.4E+08	1.4E+08	1804
ENSG00000(	0	0	0	5.992604	0.920432	6.575719	-2.8972	0.025255	0.053454	WT1	chr11	-	32409321	32457176	3122
ENSG00000(	72.50543	61.41867	79.16483	32.21025	38.65814	27.12484	1.1045	0.001336	0.003674	ZFP90	chr16	+	68563993	68609975	4664
ENSG00000(	129.474	130.0631	163.6073	57.67882	54.30549	35.34449	1.5029	1.14E-07	5.21E-07	FAM227A	chr22	-	38974125	39052634	10322
ENSG00000(	16.57267	28.90291	27.70769	1.498151	10.12475	10.68554	1.6179	0.013407	0.03029	MUC6	chr11	-	1012821	1036706	8006
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	AL772307.	chr9	-	42128839	42129419	581
ENSG00000(	373.9209	355.2649	331.1729	843.4591	654.4271	714.2875	-1.0571	6.25E-12	4.04E-11	NOC4L	chr12	+	1.33E+08	1.33E+08	1632
ENSG00000(	7.250543	1.204288	1.319414	49.43899	29.45382	31.23467	-3.1977	1.89E-06	7.63E-06	USP18	chr22	+	18632666	18660164	2129

ENSG00000(	1066.866	942.9573	796.9259	981.289	977.4988	1149.107	-0.1453	0.31111	0.43735	NDUFA6	chr22	-	42481529	42486959	1256
ENSG00000(	0	0	1.319414	4.494453	3.681728	4.93179	-2.2779	0.066224	0.12373	CHRM5	chr15	+	34260921	34357291	3043
ENSG00000(	242.3753	261.3304	221.6615	5.243529	9.20432	9.041614	4.8845	1.58E-45	3.84E-44	SORCS2	chr4	+	7194265	7744554	6152
ENSG00000(	87.00652	83.09585	29.0271	49.43899	32.21512	46.03004	0.63032	0.11743	0.20036	TMEM121	chr14	+	1.06E+08	1.06E+08	1532
ENSG00000(	160.5477	164.9874	130.622	41.94823	50.62376	43.56414	1.7323	7.52E-11	4.49E-10	TMEM106A	chr17	+	41363854	41372061	3267
ENSG00000(	655.6563	696.0783	596.375	1671.188	1282.162	1863.394	-1.3018	1.04E-17	9.44E-17	SIVA1	chr14	+	1.05E+08	1.05E+08	4142
ENSG00000(	227.8742	255.309	230.8974	929.6028	1084.269	928.8204	-2.0368	5.68E-43	1.28E-41	BRI3BP	chr12	+	1.25E+08	1.26E+08	6648
ENSG00000(	33.14534	12.04288	3.958241	7.490755	6.443024	2.465895	1.4515	0.063117	0.11875	IFNE	chr9	-	21480841	21482312	1472
ENSG00000(	519.9675	528.6823	397.1435	387.2721	353.4459	360.8426	0.39207	0.016307	0.036116	DGAT1	chr8	-	1.46E+08	1.46E+08	2004
ENSG00000(	0	0	0	3.745378	4.60216	2.465895	-2.6105	0.046181	0.090601	RFX6	chr6	+	1.17E+08	1.17E+08	3460
ENSG00000(	112.9013	78.2787	175.482	43.44638	56.14635	43.56414	1.3367	3.89E-05	0.000134	ROBO2	chr3	+	75955846	77699115	9570
ENSG00000(	759.2355	793.6256	914.3538	1613.509	1464.407	1321.72	-0.83379	4.51E-10	2.54E-09	AP3M1	chr10	-	75881524	75910821	3613
ENSG00000(	31.07376	28.90291	32.98534	32.21025	15.64734	10.68554	0.63457	0.21132	0.32124	F8	chrX	-	1.54E+08	1.54E+08	9059
ENSG00000(	1.035792	1.204288	1.319414	0	0.920432	0	0.95183	0.48289	NA	NT5C1B	chr2	-	18737050	18770838	2678
ENSG00000(	80.79177	87.913	80.48424	109.365	69.95283	75.62077	-0.03628	0.89975	0.9378	CA13	chr8	+	86132816	86196302	3815
ENSG00000(	171.9415	134.8802	108.1919	155.8077	128.8605	124.9387	0.022536	0.92629	0.95558	UBOX5	chr20	-	3088219	3140842	4631
ENSG00000(	6.214751	6.021439	3.958241	19.47596	9.20432	7.397684	-1.051	0.17319	0.27452	RP11-111G	chr9	+	40293025	40339528	3601
ENSG00000(	271.3775	242.0618	193.9538	327.346	247.5962	327.964	-0.34843	0.077409	0.1413	MAFF	chr22	+	38597889	38612518	2490
ENSG00000(	755.0923	694.874	606.9303	653.943	611.1668	799.7719	-0.00464	0.97573	0.98601	BRF1	chr14	-	1.06E+08	1.06E+08	18259
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	LRRC14B	chr5	+	191626	195468	1573
ENSG00000(	399.8157	457.6293	390.5465	258.4311	205.2563	254.8091	0.79155	4.24E-06	1.64E-05	SEMA4B	chr15	+	90703836	90772911	3807
ENSG00000(	1.035792	0	0	5.992604	0.920432	0.821965	-1.6172	0.22313	0.33531	MROH2A	chr2	+	2.35E+08	2.35E+08	5361
ENSG00000(	4.143168	0	5.277655	0.749076	3.681728	1.64393	0.48709	0.67751	0.77883	AC004980.	chr7	-	76163011	76170884	882
ENSG00000(	524.1107	503.3923	424.8512	415.7369	270.607	313.9906	0.53443	0.003621	0.009228	CIB1	chr15	-	90773207	90777279	1247
ENSG00000(	3.107376	7.225726	1.319414	3.745378	0.920432	0.821965	0.83468	0.45742	0.58711	RP11-435B	chr1	-	1.43E+08	1.43E+08	1789
ENSG00000(	121.1877	193.8903	186.0373	2.996302	11.96562	2.465895	4.7665	2.79E-28	3.96E-27	ANKS1B	chr12	-	99120235	1E+08	3885
ENSG00000(	626.6541	600.9396	456.5172	780.5367	700.4487	797.306	-0.43295	0.004758	0.011836	NELFA	chr4	-	1984441	2043630	3343
ENSG00000(	9.322127	4.817151	27.70769	28.46487	33.13555	9.041614	-0.72154	0.27	0.39045	SLC24A3	chr20	+	19193290	19703581	3929
ENSG00000(	0	10.83859	0	0	0	0	2.5435	0.060316	0.11416	SGCZ	chr8	-	13947373	15095848	2234
ENSG00000(	12.4295	14.45145	13.19414	29.96302	11.04518	4.93179	-0.19275	0.77558	0.85283	EFCAB10	chr7	-	1.05E+08	1.05E+08	1550
ENSG00000(	0	0	2.638828	0	1.840864	1.64393	-0.22543	0.86786	0.91696	C5orf47	chr5	+	1.73E+08	1.73E+08	2522
ENSG00000(	3.107376	3.612863	1.319414	11.98521	11.96562	10.68554	-1.8561	0.028879	0.060133	AC000068.	chr22	+	19435416	19437628	2097
ENSG00000(	484.7506	480.5108	395.8241	710.1236	625.8938	780.0447	-0.63352	3.28E-05	0.000114	GTF2H5	chr6	+	1.59E+08	1.59E+08	2125
ENSG00000(	845.2062	888.7643	899.8402	258.4311	276.1296	207.9571	1.8215	3.96E-33	6.68E-32	FLRT2	chr14	+	85996488	86095034	7943
ENSG00000(	658.7637	650.3154	534.3626	647.9503	745.5499	714.2875	-0.19086	0.18406	0.28817	INTS5	chr11	-	62414320	62420774	3285
ENSG00000(	1916.215	1922.043	1738.987	1533.358	1368.682	1881.478	0.22092	0.104	0.18112	RPS27L	chr15	-	63418071	63450220	2944
ENSG00000(	4.143168	14.45145	11.87472	23.22134	31.29469	16.4393	-1.168	0.055288	0.10606	MANEAL	chr1	+	38259474	38266809	2685
ENSG00000(	24.85901	15.65574	17.15238	2.996302	16.56778	8.219649	1.0072	0.12806	0.21476	ADSSL1	chr14	+	1.05E+08	1.05E+08	2600
ENSG00000(	3.107376	0	1.319414	22.47227	20.2495	33.70056	-3.6168	8.99E-06	3.36E-05	ANO9	chr11	-	417933	442011	5487
ENSG00000(	393.6009	408.2535	348.3252	1039.717	936.0793	757.8517	-1.244	2.46E-15	1.99E-14	FAF1	chr1	-	50905150	51425935	4367
ENSG00000(	5.17896	4.817151	2.638828	0	2.761296	0	1.6264	0.17735	0.2795	MYADML2	chr17	-	79897521	79905109	2452
ENSG00000(	2550.12	2347.157	2741.742	173.0365	140.8261	179.1884	3.9399	3.85E-176	8.45E-174	FAM43A	chr3	+	1.94E+08	1.94E+08	3141
ENSG00000(	498.2159	547.9509	444.6424	408.2462	350.6846	378.1039	0.38927	0.012287	0.027994	NDNL2	chr15	-	29560353	29562033	1681
ENSG00000(	2019.794	1899.162	1479.063	2656.222	2291.876	2478.224	-0.45844	0.000693	0.001995	HSF1	chr8	+	1.46E+08	1.46E+08	3451

ENSG00000(	672.2289	647.9068	754.7047	620.2346	600.1217	419.2021	0.33787	0.043085	0.085392	C6orf120	chr6	+	1.7E+08	1.7E+08	4145
ENSG00000(	79.75598	109.5902	65.97069	43.44638	45.10117	90.41614	0.50449	0.15031	0.24439	TBC1D3F	chr17	+	36283971	36294915	3389
ENSG00000(	214.4089	233.6318	245.411	328.0951	311.106	280.29	-0.40731	0.020335	0.04402	PURA	chr5	+	1.39E+08	1.39E+08	2614
ENSG00000(	6.214751	6.021439	10.55531	11.23613	19.32907	10.68554	-0.79992	0.25039	0.36782	HIST1H2BL	chr6	-	27775257	27775709	453
ENSG00000(	6.214751	8.430014	9.235896	35.95563	69.95283	43.56414	-2.5509	9.97E-07	4.14E-06	INPP5J	chr22	+	31518717	31530682	3347
ENSG00000(	0	0	0	2.996302	1.840864	10.68554	-3.107	0.01503	0.033547	NPY2R	chr4	+	1.56E+08	1.56E+08	3626
ENSG00000(	1.035792	0	5.277655	5.243529	5.522592	5.753754	-1.1505	0.28012	0.40233	MIXL1	chr1	+	2.26E+08	2.26E+08	2005
ENSG00000(	0	0	0	5.243529	4.60216	5.753754	-3.1787	0.011718	0.026806	MFSD6L	chr17	-	8700436	8702667	2232
ENSG00000(	109.7939	107.1816	79.16483	104.1215	110.4518	86.30632	-0.01826	0.94489	0.96694	LRRC37B	chr17	+	30334891	30380523	3162
ENSG00000(	292.0933	337.2006	240.1333	469.6704	498.8741	646.0644	-0.88756	1.22E-06	5.03E-06	DDX51	chr12	-	1.33E+08	1.33E+08	4718
ENSG00000(	1094.832	1122.396	1410.453	526.6001	756.5951	605.7881	0.93868	4.62E-09	2.39E-08	NOMO2	chr16	-	18511182	18573533	4352
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	LINC00482	chr17	-	79277571	79283048	2023
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	GOLGA8DP	chr15	-	22704721	22715604	2786
ENSG00000(	3.107376	1.204288	0	0	0.920432	3.28786	0.043413	0.9737	0.98475	LINC00313	chr21	-	44881974	44899414	967
ENSG00000(	107.7224	59.0101	71.24834	196.2578	138.9852	156.9953	-1.0321	0.000171	0.00054	SIGIRR	chr11	-	405716	417455	1867
ENSG00000(	657.7279	657.5411	543.5985	194.0106	245.7553	231.7941	1.4664	6.43E-19	6.20E-18	NRBP2	chr8	-	1.45E+08	1.45E+08	3877
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	PRSS57	chr19	-	685521	695460	1077
ENSG00000(	883.5305	930.9144	694.0116	59.92604	31.29469	60.8254	4.0082	1.48E-78	7.76E-77	IFITM2	chr11	+	307631	315272	659
ENSG00000(	216.4805	151.7403	174.1626	72.66033	54.30549	81.37453	1.3669	9.32E-08	4.29E-07	TNFAIP2	chr14	+	1.04E+08	1.04E+08	4683
ENSG00000(	986.0739	951.3873	1099.072	617.2383	969.2149	837.5823	0.32464	0.045778	0.089925	ZNF445	chr3	-	44481262	44519162	10243
ENSG00000(	107.7224	120.4288	85.7619	190.2652	156.4734	158.6392	-0.68042	0.003836	0.009726	PGBD2	chr1	+	2.49E+08	2.49E+08	2879
ENSG00000(	2158.59	2005.139	2149.325	1641.225	1712.004	2059.022	0.22173	0.07297	0.13437	WBP5	chrX	+	1.03E+08	1.03E+08	1096
ENSG00000(	2290.136	2189.395	1775.931	2428.503	1766.309	2030.253	0.007101	0.9607	0.97722	RAB11B	chr19	+	8454865	8469318	1751
ENSG00000(	160.5477	198.7075	175.482	371.5415	351.605	304.127	-0.93926	4.05E-07	1.75E-06	PRMT3	chr11	+	20409076	20530840	4159
ENSG00000(	17.60846	56.60152	50.13772	38.20285	46.0216	47.67397	-0.09147	0.83068	0.8914	GP1BA	chr17	+	4835592	4838325	2501
ENSG00000(	536.5402	553.9724	597.6944	465.925	532.0097	501.3986	0.17059	0.22928	0.34272	PRPF39	chr14	+	45553302	45585485	3507
ENSG00000(	0	0	0	0.749076	2.761296	1.64393	-1.5386	0.25678	NA	MAGEA11	chrX	+	1.49E+08	1.49E+08	3370
ENSG00000(	17.60846	24.08575	19.79121	14.23244	11.04518	13.9734	0.61442	0.26607	0.38612	PPIL6	chr6	-	1.1E+08	1.1E+08	4031
ENSG00000(	485.7864	474.4894	393.1853	537.8362	540.2936	577.8413	-0.28839	0.052893	0.10201	ZNF74	chr22	+	20748405	20762745	3879
ENSG00000(	21.75163	27.69862	56.73479	33.7084	13.80648	14.79537	0.72302	0.16433	0.26263	KIAA0825	chr5	-	93488671	93954309	5751
ENSG00000(	105.6508	86.70872	69.92893	375.2868	432.603	403.5848	-2.1856	1.15E-26	1.52E-25	UBALD2	chr17	+	74261283	74267375	1588
ENSG00000(	6.214751	28.90291	18.47179	18.72689	9.20432	15.61733	0.2675	0.67104	0.7737	CDNF	chr10	-	14861249	14880574	1492
ENSG00000(	3.107376	6.021439	5.277655	106.3687	95.72493	106.8554	-4.2915	2.28E-18	2.14E-17	NOTUM	chr17	-	79910388	79919716	2324
ENSG00000(	1.035792	0	1.319414	0	1.840864	0	0.17192	0.89859	NA	KLHL33	chr14	-	20896970	20903801	1863
ENSG00000(	0	0	0	7.490755	13.80648	8.219649	-4.1386	0.00044	0.001303	RBM11	chr21	+	15588451	15600693	1992
ENSG00000(	1.035792	0	0	337.8331	377.3771	300.8392	-8.3143	2.21E-24	2.68E-23	WBSCR17	chr7	+	70597155	71178585	3884
ENSG00000(	249.6258	172.2131	267.841	1824.748	2379.317	1904.493	-3.1347	1.10E-77	5.72E-76	CD24P4	chrY	-	21154353	21154595	243
ENSG00000(	27.96638	26.49433	50.13772	17.22874	36.81728	16.4393	0.5524	0.25657	0.37493	ZBTB37	chr1	+	1.74E+08	1.74E+08	2940
ENSG00000(	82.86335	75.87013	87.08131	62.92235	70.87326	98.63579	0.079933	0.78482	0.85854	IL3RA	chrX	+	1455509	1501578	1706
ENSG00000(	871.101	743.0455	694.0116	1508.638	1374.205	1757.361	-1.0035	1.27E-12	8.66E-12	CCDC137	chr17	+	79633394	79640934	2468
ENSG00000(	0	3.612863	0	0	0	0.821965	0.85103	0.52479	NA	SFTPA2	chr10	-	81315608	81320153	2189
ENSG00000(	10.35792	3.612863	1.319414	0	0	0	3.4183	0.007869	0.018748	RGPD2	chr2	-	88055474	88285309	6931
ENSG00000(	198.872	221.5889	266.5216	323.6006	381.0588	379.7478	-0.65823	0.000286	0.000872	ARL15	chr5	-	53179775	53606412	3248
ENSG00000(	1.035792	0	0	0.749076	0.920432	2.465895	-0.92447	0.49522	NA	C12orf56	chr12	-	64660217	64784972	3242

ENSG00000(	793.4166	881.5386	675.5399	928.8537	751.9929	901.6955	-0.1354	0.35797	0.4875	CDK10	chr16	+	89747145	89762772	3344
ENSG00000(	0	0	0	1.498151	5.522592	9.041614	-3.165	0.012765	0.028954	TMEM105	chr17	-	79285074	79304474	3317
ENSG00000(	65.25489	48.17151	51.45714	297.383	254.9597	214.5328	-2.1934	4.88E-19	4.73E-18	SOCS1	chr16	-	11348262	11350036	1225
ENSG00000(	1046.15	1156.116	1055.531	501.8806	415.1148	387.1455	1.3159	3.54E-20	3.61E-19	TCN2	chr22	+	31002825	31023265	2535
ENSG00000(	703.3027	640.6811	548.8761	668.9245	554.1001	534.2772	0.10759	0.48632	0.61542	GAS2L1	chr22	+	29702572	29708774	3381
ENSG00000(	247.5543	298.6634	288.9516	557.3122	520.9645	495.6448	-0.91345	7.96E-09	4.02E-08	ATP6V0A2	chr12	+	1.24E+08	1.24E+08	5789
ENSG00000(	38.3243	27.69862	43.54065	5.243529	0.920432	4.109825	3.1896	2.70E-07	1.19E-06	PARK2	chr6	-	1.62E+08	1.63E+08	4180
ENSG00000(	76.6486	67.44011	63.33186	389.5193	402.2288	540.8529	-2.6618	7.18E-35	1.28E-33	C14orf80	chr14	+	1.06E+08	1.06E+08	4437
ENSG00000(	0	0	0	2.996302	2.761296	5.753754	-2.7018	0.038142	0.076801	HS6ST3	chr13	+	96743093	97485671	1659
ENSG00000(	2606.052	2619.326	2046.411	1853.962	1863.875	2266.979	0.28073	0.038796	0.077916	HGS	chr17	+	79650356	79670168	2970
ENSG00000(	208.1942	156.5574	147.7743	188.767	175.8025	203.0253	-0.14258	0.50372	0.63148	TNFAIP8L1	chr19	+	4639530	4655580	3845
ENSG00000(	96.32865	85.50443	117.4278	81.64923	103.0884	110.1433	0.02044	0.93872	0.9628	RAD51D	chr17	-	33426811	33448541	2404
ENSG00000(	591.4372	638.2725	423.5318	74.90755	63.50981	108.4994	2.7236	1.06E-34	1.88E-33	MAPK11	chr22	-	50702142	50709196	2431
ENSG00000(	160.5477	151.7403	151.7326	64.4205	43.2603	35.34449	1.6745	2.44E-09	1.29E-08	SP140L	chr2	+	2.31E+08	2.31E+08	3591
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	MRPL30	chr2	+	99771461	99814089	2605
ENSG00000(	329.3818	396.2107	290.271	241.9514	208.9381	195.6277	0.64842	0.000543	0.001586	TARSL2	chr15	-	1.02E+08	1.02E+08	3610
ENSG00000(	830.7051	893.5815	707.2058	158.0549	97.56579	143.0219	2.5917	2.10E-44	4.92E-43	SMYD3	chr1	-	2.46E+08	2.47E+08	1863
ENSG00000(	1575.439	1736.583	1580.658	686.1532	821.9458	814.5672	1.0732	2.90E-17	2.57E-16	METTL7A	chr12	+	51317255	51326300	4076
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	LINC00158	chr21	-	26758133	26804013	1476
ENSG00000(	0	0	0	119.8521	155.553	145.4878	-7.7821	3.73E-15	2.98E-14	IFNLR1	chr1	-	24480647	24514449	4549
ENSG00000(	54.89697	26.49433	31.66593	32.21025	30.37426	44.38611	0.085659	0.83971	0.89743	SH3BGR	chr21	+	40817781	40887433	1251
ENSG00000(	30.03797	32.51577	26.38828	38.20285	30.37426	45.20807	-0.34739	0.39866	0.52972	FAM174B	chr15	-	93160673	93353114	2792
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	FAM47A	chrX	-	34147869	34150447	2579
ENSG00000(	118.0803	114.4073	124.0249	86.14369	109.5314	161.1051	-0.00053	0.99843	0.99905	C19orf68	chr19	+	48673949	48700877	2277
ENSG00000(	193.6931	202.3203	157.0102	181.2763	123.3379	105.2115	0.4276	0.080832	0.14669	TMEM179B	chr11	+	62554887	62557877	1023
ENSG00000(	0	0	0	22.47227	85.60018	45.20807	-6.4024	1.21E-09	6.61E-09	GPRIN3	chr4	-	90165429	90229161	6352
ENSG00000(	68.36227	72.25726	93.67838	141.5753	202.495	179.1884	-1.1521	5.68E-06	2.17E-05	PARPBP	chr12	+	1.03E+08	1.03E+08	3189
ENSG00000(	26.93059	30.10719	7.916483	9.737982	13.80648	12.32947	0.82372	0.17252	0.27364	STAC3	chr12	-	57637236	57644976	1656
ENSG00000(	764.4144	780.3784	993.5186	1206.761	1423.908	991.2897	-0.51184	0.0013	0.003581	ROR1	chr1	+	64239693	64647181	5832
ENSG00000(	270.3417	344.4263	287.6322	299.6302	289.0156	301.6611	0.018234	0.91559	0.94853	SDHAP1	chr3	-	1.96E+08	1.96E+08	2491
ENSG00000(	0	2.408575	0	0	0	3.28786	-0.21349	0.87474	NA	RP11-504P	chr1	+	2.24E+08	2.24E+08	1881
ENSG00000(	151.2256	142.106	113.4696	11.98521	8.283888	20.54912	3.2527	7.39E-20	7.43E-19	MUC1	chr1	-	1.55E+08	1.55E+08	1811
ENSG00000(	966.3938	1140.46	802.2036	988.7797	868.8878	978.9602	0.036492	0.80492	0.87353	C17orf70	chr17	-	79506911	79520987	3822
ENSG00000(	99.43602	93.93444	88.40072	152.0623	118.7357	140.556	-0.54147	0.025693	0.05426	IRF7	chr11	-	612553	615999	2051
ENSG00000(	136.7245	136.0845	88.40072	86.89276	107.6905	97.81383	0.30788	0.24131	0.35675	L3MBTL1	chr20	+	42136320	42179590	4322
ENSG00000(	361.4914	361.2863	459.156	663.6809	697.6875	647.7084	-0.76505	4.51E-07	1.94E-06	BRCC3	chrX	+	1.54E+08	1.54E+08	2846
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	SV2B	chr15	+	91643180	91844539	11279
ENSG00000(	3.107376	4.817151	10.55531	0.749076	0	0	3.1146	0.00965	0.022522	FAM131C	chr1	-	16384264	16400127	1695
ENSG00000(	14.50109	6.021439	3.958241	17.97781	9.20432	15.61733	-0.72947	0.3022	0.42732	C11orf35	chr11	-	554855	560779	2084
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	C1orf227	chr1	-	2.13E+08	2.13E+08	506
ENSG00000(	2.071584	0	2.638828	3.745378	7.363456	0	-0.88874	0.46357	0.59285	PDE6G	chr17	-	79617489	79630142	1505
ENSG00000(	66.29068	80.68728	110.8308	37.45378	36.81728	43.56414	1.1071	0.00075	0.002147	PRKG1	chr10	+	52750945	54058110	6928
ENSG00000(	9078.716	8411.95	9184.439	3379.08	3828.077	3017.433	1.3811	1.59E-32	2.62E-31	NR2F2	chr15	+	96869167	96883492	5275
ENSG00000(	389.4578	375.7378	233.5362	1.498151	5.522592	4.93179	6.257	2.34E-48	6.18E-47	DLK1	chr14	+	1.01E+08	1.01E+08	1700

ENSG00000(	27.96638	19.2686	31.66593	12.73428	4.60216	4.93179	1.7115	0.004786	0.011898	TLCD2	chr17	-	1611064	1613732	991
ENSG00000(	586.2582	566.0152	617.4856	92.13629	110.4518	69.04505	2.6939	3.99E-46	9.79E-45	LSAMP	chr3	-	1.16E+08	1.18E+08	1740
ENSG00000(	4777.072	4749.711	6116.802	18.72689	29.45382	28.76877	7.6389	0	0	AHNAK2	chr14	-	1.05E+08	1.05E+08	18335
ENSG00000(	1033.72	1003.172	1029.143	419.4823	531.0893	423.3119	1.1566	2.29E-16	1.95E-15	OLFML2A	chr9	+	1.28E+08	1.28E+08	6425
ENSG00000(	1383.818	1393.361	1691.488	1305.639	1420.227	1283.909	0.15547	0.22045	0.33216	SP1	chr12	+	53773960	53810230	7603
ENSG00000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	SPATA8	chr15	+	97326619	97328845	1386
ENSG00000(	358.384	367.3078	207.148	290.6413	285.3339	388.7894	-0.04567	0.83539	0.89473	WASH3P	chr15	+	1.03E+08	1.03E+08	1721
ENSG00000(	0	0	3.958241	2.247227	1.840864	5.753754	-0.96451	0.43376	0.56351	ACTBP7	chr15	-	44281259	44282382	1124
ENSG00000(	480.6074	439.565	377.3523	738.5885	585.3947	623.0494	-0.5824	0.000224	0.000693	MRPL40	chr22	+	19419425	19423598	1387
ENSG00000(	0	0	0	2.247227	0	1.64393	-1.1086	0.40518	NA	DBX2	chr12	-	45408455	45444882	2806
ENSG00000(	21.75163	33.72006	22.43003	19.47596	29.45382	23.01502	0.11401	0.8103	0.87689	FAM212A	chr3	+	49840687	49842463	1040
ENSG00000(	2.071584	0	2.638828	0.749076	0	0	1.2345	0.36288	NA	PDIA2	chr16	+	333152	337215	1956
ENSG00000(	1507.077	1374.092	1570.102	1170.805	1156.983	1101.433	0.37548	0.001419	0.003876	PCGF3	chr4	+	699537	764428	5685
ENSG00000(	219.5879	233.6318	287.6322	98.1289	87.44104	95.34793	1.3865	9.75E-11	5.78E-10	LMLN	chr3	+	1.98E+08	1.98E+08	7043
ENSG00000(	25419.37	24679.47	21663.45	11080.33	10843.61	9603.016	1.1847	7.98E-27	1.06E-25	P4HB	chr17	-	79801035	79818570	2603
ENSG00000(	1708.021	1574.004	1464.549	2737.871	2261.501	2486.444	-0.65563	7.81E-08	3.62E-07	PSMD13	chr11	+	236546	252983	2200
ENSG00000(	453.6769	458.8336	490.8219	1039.717	1274.798	1002.797	-1.2378	4.61E-18	4.26E-17	PBX1	chr1	+	1.65E+08	1.65E+08	11321
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	AC017079.	chr2	+	1.29E+08	1.29E+08	415
ENSG00000(	666.0142	765.927	419.5736	5.243529	15.64734	9.863579	5.8623	1.19E-74	5.64E-73	NDUFA4L2	chr12	-	57628686	57634498	1200
ENSG00000(	38.3243	36.12863	51.45714	38.95193	30.37426	19.72716	0.48154	0.25072	0.36814	SHC4	chr15	-	49115932	49255641	4558
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	FTH1P14	chrX	+	34165153	34165703	551
ENSG00000(	95.29286	150.536	72.56776	104.1215	73.63456	110.9653	0.1384	0.64761	0.75409	CTD-2287C	chr5	-	1.15E+08	1.15E+08	375
ENSG00000(	8563.927	8508.293	8405.985	4166.358	5073.421	3878.852	0.95601	1.17E-15	9.62E-15	ZFP36L1	chr14	-	69254377	69263190	3190
ENSG00000(	2492.115	2471.198	2225.851	3496.685	2958.268	3004.282	-0.39509	0.000713	0.002048	UBE2L3	chr22	+	21903736	21978323	3451
ENSG00000(	14.50109	6.021439	11.87472	208.9921	188.6886	197.2716	-4.11	6.70E-31	1.05E-29	NTF3	chr12	+	5541278	5630702	1167
ENSG00000(	484.7506	403.4364	675.5399	423.9768	446.4095	397.0091	0.30027	0.10378	0.18085	BRWD1	chr21	-	40556102	40693485	12929
ENSG00000(	15.53688	7.225726	13.19414	104.8706	76.39586	136.4462	-3.0605	1.18E-13	8.60E-13	PMEL	chr12	-	56347889	56367101	2757
ENSG00000(	0	1.204288	0	1.498151	0	0	-0.08768	0.94524	NA	SYN3	chr22	-	32908539	33454358	3126
ENSG00000(	10.35792	7.225726	5.277655	24.71949	8.283888	10.68554	-0.86064	0.22732	0.34042	POU3F1	chr1	-	38509523	38512450	2928
ENSG00000(	61.11172	87.913	73.88717	23.22134	13.80648	18.90519	1.9436	3.62E-07	1.57E-06	SNAI3	chr16	-	88744090	88752901	1732
ENSG00000(	119.1161	125.2459	108.1919	146.8188	111.3723	155.3514	-0.22939	0.33706	0.46556	ZBTB3	chr11	-	62515791	62521660	2978
ENSG00000(	8.286335	6.021439	11.87472	8.988907	9.20432	7.397684	0.025567	0.97224	0.98387	LYG2	chr2	-	99858709	99871745	878
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	MORN5	chr9	+	1.25E+08	1.25E+08	1543
ENSG00000(	291.0575	311.9105	273.1187	190.2652	242.994	239.1918	0.38204	0.037393	0.075487	EP400NL	chr12	+	1.33E+08	1.33E+08	3935
ENSG00000(	9.322127	9.634302	3.958241	2.247227	8.283888	1.64393	0.8197	0.36512	0.49491	C6orf201	chr6	+	4079440	4131185	2496
ENSG00000(	87.00652	87.913	126.6637	286.1469	333.1964	281.112	-1.5736	3.66E-13	2.59E-12	MYBL1	chr8	-	67474410	67526482	5192
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-645C	chr16	-	21890659	21930477	4131
ENSG00000(	247.5543	215.5675	294.2293	120.6012	119.6562	119.1849	1.0675	2.28E-07	1.01E-06	C16orf52	chr16	+	22018959	22098855	4360
ENSG00000(	1149.729	1004.376	971.0885	1881.678	1383.409	1460.632	-0.59468	3.84E-05	0.000132	DRG1	chr22	+	31795509	31924726	1746
ENSG00000(	1088.617	1003.172	1595.171	844.9572	1112.802	678.1211	0.48152	0.012187	0.02778	ANKFY1	chr17	-	4067201	4167274	7418
ENSG00000(	1410.749	1474.048	2014.745	1439.723	1671.505	1307.746	0.14789	0.33514	0.46326	YTHDF3	chr8	+	64081112	64125346	5162
ENSG00000(	206.1226	195.0946	178.1209	321.3534	296.3791	263.8507	-0.60141	0.001109	0.003089	ZNF696	chr8	+	1.44E+08	1.44E+08	2795
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	ADARB2	chr10	-	1228073	1779670	3606
ENSG00000(	1.035792	7.225726	5.277655	0	0.920432	0	2.5793	0.039713	0.079517	NRG3	chr10	+	83635070	84746935	3530

ENSG00000(	0	2.408575	2.638828	0	0	0	1.6365	0.22501	NA	SRL	chr16	-	4239375	4292081	5587
ENSG00000(	1289.561	1076.633	1679.614	31.46117	29.45382	27.94681	5.4709	5.06E-141	6.95E-139	C11orf87	chr11	+	1.09E+08	1.09E+08	5884
ENSG00000(	220.6237	227.6104	203.1897	15.73059	15.64734	12.32947	3.8509	1.83E-38	3.64E-37	IFIT1	chr10	+	91152303	91163745	2769
ENSG00000(	95.29286	99.95588	67.2901	95.88167	102.168	72.33291	-0.03764	0.89476	0.93492	CXorf38	chrX	-	40488285	40506819	2783
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	CLDN24	chr4	-	1.84E+08	1.84E+08	663
ENSG00000(	69.39806	42.15007	67.2901	36.7047	20.2495	13.9734	1.2936	0.002552	0.006671	KCNQ5	chr6	+	73331520	73908574	6688
ENSG00000(	62.14751	49.3758	34.30476	74.15848	46.94203	51.78379	-0.23696	0.51281	0.6398	ADAMTSL5	chr19	-	1505017	1513603	2851
ENSG00000(	31.07376	28.90291	34.30476	34.45748	48.7829	54.24968	-0.5316	0.17725	0.27944	KCNIP4	chr4	-	20730239	21950422	2481
ENSG00000(	6891.124	6759.667	6793.662	5363.381	5379.925	5652.653	0.31798	0.00104	0.002909	MORF4L1	chr15	+	79102829	79190475	2359
ENSG00000(	1.035792	0	0	0	2.761296	0	-0.44657	0.73574	NA	NLRP9	chr19	-	56219798	56249768	3484
ENSG00000(	75.61281	75.87013	88.40072	162.5494	173.0412	193.9837	-1.1363	1.44E-06	5.86E-06	WDR53	chr3	-	1.96E+08	1.96E+08	1671
ENSG00000(	1250.201	1074.225	1041.017	676.4152	825.6275	1017.593	0.41721	0.008294	0.019628	DMWD	chr19	-	46286205	46296060	3305
ENSG00000(	649.4415	646.7025	584.5003	1260.694	918.5911	1208.288	-0.84656	1.32E-08	6.54E-08	SLC52A2	chr8	+	1.46E+08	1.46E+08	2147
ENSG00000(	177.1204	145.7188	122.7055	129.5901	128.8605	143.0219	0.15335	0.50412	0.63178	PIGP	chr21	-	38435146	38445470	3437
ENSG00000(	0	0	0	6.74168	18.40864	9.041614	-4.3375	0.000197	0.000616	IKZF1	chr7	+	50343720	50472799	6189
ENSG00000(	970.537	1050.139	956.575	1144.587	1110.961	1269.114	-0.24312	0.048718	0.094876	PCYT2	chr17	-	79858841	79869340	5147
ENSG00000(	4.143168	12.04288	17.15238	52.43529	45.10117	46.852	-2.0696	3.77E-05	0.00013	NAT8L	chr4	+	2061239	2070816	5870
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	NPAP1	chr15	+	24920541	24928593	8053
ENSG00000(	3787.891	3452.693	3248.397	3523.651	2863.464	3269.776	0.11905	0.31978	0.44694	BCAP31	chrX	-	1.53E+08	1.53E+08	1810
ENSG00000(	40.39588	48.17151	42.22124	35.95563	47.86246	46.852	0.002891	0.99366	0.996	ARL17A	chr17	-	44594068	44657088	3945
ENSG00000(	69.39806	71.05298	43.54065	47.94084	38.65814	83.84042	0.11073	0.76445	0.84443	RPL12P4	chr20	+	53691155	53691685	529
ENSG00000(	3.107376	10.83859	1.319414	2.247227	0.920432	0	1.7039	0.13997	0.23073	CECR5-AS1	chr22	+	17640274	17646335	616
ENSG00000(	114.9729	108.3859	104.2337	374.5378	267.8457	350.1571	-1.5895	2.05E-14	1.56E-13	GNB1L	chr22	-	19770747	19842462	6706
ENSG00000(	1.035792	0	1.319414	3.745378	3.681728	4.109825	-1.651	0.16956	0.26957	RP4-592A1	chr1	-	59096513	59097202	690
ENSG00000(	101.5076	114.4073	116.1084	152.0623	150.9508	178.3664	-0.53444	0.018063	0.039587	DNAH14	chr1	+	2.25E+08	2.26E+08	13788
ENSG00000(	0	0	0	83.14739	107.6905	126.5826	-7.4159	1.47E-13	1.07E-12	RP1-46F2.2	chr12	+	1.11E+08	1.11E+08	705
ENSG00000(	1.035792	6.021439	3.958241	2.247227	4.60216	1.64393	0.30021	0.7785	0.85414	C1orf110	chr1	-	1.63E+08	1.63E+08	2607
ENSG00000(	6.214751	0	2.638828	0	2.761296	7.397684	-0.13204	0.91074	0.94514	EVI2B	chr17	-	29630784	29641130	1999
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	TMEM210	chr9	-	1.4E+08	1.4E+08	873
ENSG00000(	81.82756	85.50443	85.7619	131.0882	130.7013	115.0751	-0.57033	0.020948	0.045221	61E3.4	chr16	-	21845890	21892148	3807
ENSG00000(	45.57484	33.72006	29.0271	84.64554	95.72493	89.59418	-1.2877	7.57E-05	0.000251	ZNF829	chr19	-	37379026	37407193	4977
ENSG00000(	170.9057	215.5675	170.2044	126.5938	132.5422	98.63579	0.63367	0.005218	0.012889	THNSL1	chr10	+	25305587	25315593	3788
ENSG00000(	754.0565	811.6899	740.1911	269.6672	208.0176	194.8057	1.7691	1.40E-27	1.93E-26	TRIM69	chr15	+	45021186	45060027	5691
ENSG00000(	9.322127	18.06432	3.958241	8.988907	8.283888	10.68554	0.1558	0.83069	0.8914	ATP6V0C	chr16	+	2563871	2570219	1175
ENSG00000(	411.2094	466.0593	427.4901	8.239831	22.09037	20.54912	4.6583	7.74E-67	3.15E-65	IFITM1	chr11	+	313506	315272	855
ENSG00000(	9700.191	9749.913	9454.919	7855.555	8637.334	9448.487	0.15589	0.14388	0.2358	LAMP1	chr13	+	1.14E+08	1.14E+08	5242
ENSG00000(	127.4024	139.6974	244.0915	92.13629	186.8477	116.719	0.36452	0.21998	0.33166	SGK196	chr8	+	42948658	42978577	1865
ENSG00000(	0	1.204288	1.319414	2.247227	0.920432	0	-0.19834	0.88336	NA	OR11N1P	chrX	-	1.3E+08	1.3E+08	853
ENSG00000(	364.5988	350.4477	267.841	377.5341	411.4331	430.7096	-0.30715	0.072475	0.13363	KLHDC8B	chr3	+	49209044	49213917	1957
ENSG00000(	0	0	1.319414	5.243529	10.12475	8.219649	-3.0958	0.00714	0.017169	KLHL34	chrX	-	21673609	21676448	2840
ENSG00000(	273.4491	209.5461	215.0644	382.7776	337.7985	420.846	-0.70373	0.000111	0.00036	SETD4	chr21	-	37406839	37451687	4272
ENSG00000(	485.7864	503.3923	482.9054	289.1432	533.8506	436.4634	0.22589	0.25054	0.36794	PTCH1	chr9	-	98205262	98279339	10631
ENSG00000(	29.00217	31.31148	14.51355	20.97412	34.05598	21.37109	-0.01724	0.97206	0.98379	RTN4RL1	chr17	-	1839299	1928178	1836
ENSG00000(	232.0174	287.8248	219.0227	228.468	287.1748	369.8842	-0.25877	0.21757	0.32888	PAGR1	chr16	+	29827285	29831759	2011

ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CALHM1	chr10	-	1.05E+08	1.05E+08	3053
ENSG00000(	3.107376	0	0	3.745378	3.681728	5.753754	-1.4804	0.21121	0.32113	NKAIN3	chr8	+	63161150	63912211	1988
ENSG00000(	117.0445	136.0845	135.8996	118.3539	116.8949	98.63579	0.21689	0.35728	0.48676	RNPC3	chr1	+	1.04E+08	1.04E+08	3658
ENSG00000(	22.78742	32.51577	54.09597	42.69731	40.49901	27.12484	-0.02245	0.95863	0.97566	ZNF267	chr16	+	31885079	31928668	3307
ENSG00000(	371.8493	398.6192	501.3772	920.6138	1043.77	752.0979	-1.0925	5.33E-11	3.22E-10	IRS2	chr13	-	1.1E+08	1.1E+08	6999
ENSG00000(	6.214751	7.225726	1.319414	4.494453	5.522592	5.753754	-0.06884	0.94026	0.96401	C7orf61	chr7	-	1E+08	1E+08	1004
ENSG00000(	1.035792	13.24716	1.319414	3.745378	1.840864	1.64393	0.88188	0.41216	0.54272	FAM186A	chr12	-	50720013	50790405	8200
ENSG00000(	43.50326	22.88147	52.77655	2.996302	2.761296	8.219649	2.9268	1.03E-06	4.28E-06	SHOX	chrX	+	585079	620146	3757
ENSG00000(	1108.297	1092.289	1332.608	1102.639	1336.467	1154.039	-0.02445	0.85642	0.90907	BICD2	chr9	-	95473645	95527094	6427
ENSG00000(	13.46529	15.65574	5.277655	0	0	0	4.733	5.15E-05	0.000175	CCIN	chr9	+	36169389	36171329	1941
ENSG00000(	119.1161	104.773	118.7472	101.1252	103.0884	61.64737	0.36295	0.18684	0.29148	TMLHE	chrX	-	1.55E+08	1.55E+08	2832
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	GRK1	chr13	+	1.14E+08	1.14E+08	2101
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	H2AFB3	chrX	-	1.55E+08	1.55E+08	517
ENSG00000(	0	0	0	1.498151	1.840864	0.821965	-1.2806	0.34348	NA	SLITRK2	chrX	+	1.45E+08	1.45E+08	7672
ENSG00000(	4.143168	4.817151	7.916483	110.1141	85.60018	95.34793	-4.0004	6.44E-17	5.61E-16	SDHAP3	chr5	-	1568637	1594735	1026
ENSG00000(	10.35792	8.430014	9.235896	2.247227	1.840864	3.28786	1.6941	0.053089	0.10234	PLK5	chr19	+	1524073	1535455	2106
ENSG00000(	2420.646	2368.834	2297.099	429.9694	619.4507	590.1708	2.1076	6.84E-49	1.84E-47	RASA3	chr13	-	1.15E+08	1.15E+08	4191
ENSG00000(	5.17896	3.612863	5.277655	5.243529	2.761296	4.93179	0.098948	0.91576	0.94858	F8A3	chrX	-	1.55E+08	1.55E+08	1701
ENSG00000(	1173.552	1263.298	1260.04	1004.51	854.1609	816.2112	0.46483	0.000337	0.001018	LRCH3	chr3	+	1.98E+08	1.98E+08	7394
ENSG00000(	1.035792	0	0	3.745378	1.840864	14.79537	-2.875	0.017153	0.03783	LEMD1	chr1	-	2.05E+08	2.05E+08	929
ENSG00000(	2.071584	0	1.319414	0.749076	0	3.28786	-0.14577	0.91283	0.94661	ATP4B	chr13	-	1.14E+08	1.14E+08	1488
ENSG00000(	2.071584	30.10719	13.19414	6.74168	15.64734	28.76877	-0.16598	0.81928	0.88331	NDUFA13	chr19	+	19626545	19639863	1166
ENSG00000(	166.7625	261.3304	192.6344	230.7153	158.3143	174.2566	0.13544	0.55623	0.6768	ZNF566	chr19	-	36936021	36980804	5253
ENSG00000(	9.322127	6.021439	10.55531	2.247227	1.840864	0	2.2259	0.024605	0.052225	AC084219.	chr19	-	44609616	44617298	3199
ENSG00000(	226.8384	237.2447	261.2439	219.4791	189.609	188.23	0.27612	0.14068	0.2318	ZNF529	chr19	-	37025676	37096178	5238
ENSG00000(	96.32865	131.2674	104.2337	45.69361	46.0216	50.13986	1.2109	2.52E-05	8.92E-05	ZNF284	chr19	+	44576297	44593766	4351
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	HTR3E	chr3	+	1.84E+08	1.84E+08	2139
ENSG00000(	4.143168	0	5.277655	4.494453	0.920432	0.821965	0.43081	0.71465	0.80745	DLEU7	chr13	-	51285144	51418075	2291
ENSG00000(	5.17896	0	0	0	0	0.821965	1.2091	0.37233	0.50277	TAL2	chr9	+	1.08E+08	1.08E+08	630
ENSG00000(	6.214751	8.430014	7.916483	9.737982	2.761296	2.465895	0.50745	0.55797	0.6785	MATN1-AS1	chr1	+	31191351	31199674	3925
ENSG00000(	847.2778	902.0115	1025.185	1212.004	1110.041	1020.88	-0.26954	0.042735	0.084827	AIDA	chr1	-	2.23E+08	2.23E+08	4050
ENSG00000(	136.7245	127.6545	125.3443	611.9947	535.6914	618.9396	-2.1704	4.49E-37	8.53E-36	C15orf41	chr15	+	36871812	37102449	5843
ENSG00000(	38.3243	43.35436	47.4989	42.69731	33.13555	54.24968	-0.01527	0.96746	0.98087	RP11-887P	chr12	-	94034598	94035362	765
ENSG00000(	2.071584	1.204288	1.319414	9.737982	8.283888	16.4393	-2.4797	0.007651	0.018269	GSAP	chr7	-	76940068	77045717	3458
ENSG00000(	0	2.408575	0	3.745378	1.840864	4.93179	-1.4737	0.23588	0.35027	AGBL4	chr1	-	48998527	50489585	3938
ENSG00000(	122.2234	166.1917	204.5091	154.3096	150.9508	119.1849	0.20927	0.38863	0.5193	CYP2R1	chr11	-	14899553	14913798	2325
ENSG00000(	1.035792	0	0	0	1.840864	0	-0.17777	0.89006	NA	LRRC70	chr5	+	61874562	61877275	2249
ENSG00000(	135.6887	130.0631	154.3714	319.8553	258.6414	267.1386	-1.0068	3.99E-07	1.73E-06	ANKRD46	chr8	-	1.02E+08	1.02E+08	3270
ENSG00000(	2741.741	2594.036	2388.139	910.1268	1174.471	1146.641	1.2553	8.61E-22	9.40E-21	PIP5K1C	chr19	-	3630181	3700477	5080
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CYP4F2	chr19	-	15988834	16008930	2406
ENSG00000(	1.035792	2.408575	2.638828	0.749076	0.920432	0.821965	0.85949	0.49881	0.6271	TEX38	chr1	+	47134527	47139266	1003
ENSG00000(	199.9078	171.0089	226.9392	182.0254	243.9145	251.5213	-0.17884	0.39147	0.52217	ZBTB6	chr9	-	1.26E+08	1.26E+08	4106
ENSG00000(	72.50543	89.11729	100.2754	65.16957	66.2711	92.88204	0.21675	0.45837	0.58781	C2orf76	chr2	-	1.2E+08	1.2E+08	1150
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	TAS2R42	chr12	-	11338599	11339543	945

ENSG00000(	584.1866	584.0795	490.8219	585.028	463.8977	410.1605	0.18461	0.26912	0.38946	POLR3C	chr1	-	1.46E+08	1.46E+08	1851
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	C2orf53	chr2	-	27359723	27362278	2001
ENSG00000(	96.32865	127.6545	102.9143	101.1252	90.20234	129.0485	0.026599	0.91864	0.9507	WWOX	chr16	+	78133310	79246564	2482
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	CYP4Z1	chr1	+	47533160	47583991	1906
ENSG00000(	124.295	115.6116	121.3861	183.5235	134.3831	138.9121	-0.33772	0.14719	0.24025	CIDECP	chr3	-	10055932	10068049	1784
ENSG00000(	180.2278	258.9219	179.4403	648.6994	492.4311	600.8564	-1.4879	2.76E-15	2.22E-14	CCDC84	chr11	+	1.19E+08	1.19E+08	1781
ENSG00000(	3074.23	3109.471	2816.948	1916.884	2734.603	2553.845	0.32067	0.020049	0.04347	BCL9L	chr11	-	1.19E+08	1.19E+08	10005
ENSG00000(	2297.386	2306.211	2030.578	1804.523	1364.08	1657.903	0.45757	0.000498	0.001464	POLR1D	chr13	+	28194903	28241548	1945
ENSG00000(	368.7419	407.0492	327.2146	1232.978	1413.784	1521.457	-1.9113	2.77E-40	5.78E-39	KIF18B	chr17	-	43002077	43025082	4217
ENSG00000(	624.5825	620.2082	562.0703	349.0692	445.4891	389.6114	0.60986	6.19E-05	0.000207	ZNRF1	chr16	+	75032928	75144892	5331
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	FFAR4	chr10	+	95326422	95364237	3653
ENSG00000(	90.1139	72.25726	64.65128	411.2425	434.4439	512.0841	-2.5571	2.07E-35	3.74E-34	SAPCD2	chr9	-	1.4E+08	1.4E+08	3843
ENSG00000(	0	0	0	24.71949	35.89685	22.19305	-5.6335	1.58E-07	7.12E-07	EDARADD	chr1	+	2.37E+08	2.37E+08	3097
ENSG00000(	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	SLC51B	chr15	+	65337708	65345734	940
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	CYP4F12	chr19	+	15783567	15807984	3256
ENSG00000(	2.071584	1.204288	5.277655	384.2758	265.0844	296.7293	-6.5542	8.77E-36	1.61E-34	1-Mar	chr1	+	2.21E+08	2.21E+08	2707
ENSG00000(	1.035792	0	0	97.37982	104.0088	78.90863	-6.5973	6.64E-14	4.91E-13	SOWAHB	chr4	-	77816082	77819002	2921
ENSG00000(	313.8449	350.4477	294.2293	278.6561	229.1876	341.1154	0.17345	0.35869	0.48835	BLOC1S4	chr4	+	6717842	6719387	1546
ENSG00000(	74.57702	126.4502	93.67838	77.15478	132.5422	102.7456	-0.08259	0.77849	0.85414	ZNF749	chr19	+	57946697	57956853	2587
ENSG00000(	0	1.204288	3.958241	4.494453	4.60216	2.465895	-0.92375	0.42059	0.55131	KLHL32	chr6	+	97372605	97588630	3698
ENSG00000(	9.322127	16.86003	26.38828	6.74168	9.20432	15.61733	0.68295	0.28805	0.41168	AC016757.	chr2	-	2.39E+08	2.39E+08	1888
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-1079	chr17	-	47477791	47478162	372
ENSG00000(	226.8384	199.9118	414.2959	190.2652	429.8417	214.5328	0.010591	0.98229	0.98984	MKL2	chr16	+	14165178	14360630	8799
ENSG00000(	0	4.817151	1.319414	0	1.840864	0	0.99425	0.45909	0.58866	BTLA	chr3	-	1.12E+08	1.12E+08	3213
ENSG00000(	60.07593	65.03154	91.03955	47.94084	52.46462	45.20807	0.55775	0.084791	0.15299	ZNF17	chr19	+	57922531	57933307	2750
ENSG00000(	78.72018	110.7945	94.99779	63.67142	93.88406	64.93523	0.35203	0.22653	0.33945	NBPF12	chr1	+	1.46E+08	1.46E+08	12455
ENSG00000(	13.46529	13.24716	19.79121	50.18806	45.10117	50.96182	-1.6179	0.00024	0.000739	KDM4D	chr11	+	94706845	94732682	2978
ENSG00000(	0	0	1.319414	0	0	1.64393	-0.1317	0.91874	NA	GPAT2	chr2	-	96687694	96705199	4407
ENSG00000(	472.3211	395.0064	394.5047	623.2309	524.6462	655.928	-0.51279	0.001035	0.002898	TOR3A	chr1	+	1.79E+08	1.79E+08	2724
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	PABPC1L2A	chrX	-	72297115	72299351	2237
ENSG00000(	20.71584	27.69862	17.15238	30.7121	23.0108	29.59074	-0.33558	0.47847	0.60751	GABRA5	chr15	+	27111510	27194354	3251
ENSG00000(	3054.55	2957.731	3087.428	4104.185	3667.922	3402.935	-0.29603	0.00817	0.019364	PPP1CC	chr12	-	1.11E+08	1.11E+08	2797
ENSG00000(	90.1139	101.1602	125.3443	51.68621	62.58938	60.00344	0.85033	0.002694	0.007022	ZNF555	chr19	+	2841433	2860482	8557
ENSG00000(	24.85901	13.24716	7.916483	19.47596	21.16994	31.23467	-0.59673	0.28814	0.41172	MST1P2	chr1	+	16972069	16976914	2368
ENSG00000(	83.89914	116.8159	84.44248	154.3096	94.8045	106.8554	-0.3203	0.25012	0.36747	NAP1L3	chrX	-	92925929	92928567	2639
ENSG00000(	206.1226	211.9546	217.7033	373.0396	241.1532	244.9455	-0.43435	0.037878	0.076327	CA5BP1	chrX	+	15693055	15721847	1264
ENSG00000(	259.9838	256.5133	221.6615	113.1104	115.054	110.1433	1.1211	2.49E-08	1.21E-07	PRELID2	chr5	-	1.45E+08	1.45E+08	2140
ENSG00000(	1227.413	1082.655	1246.846	301.1284	295.4587	240.0138	2.082	1.21E-46	3.02E-45	BACE1	chr11	-	1.17E+08	1.17E+08	9924
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	RP13-608F	chr15	+	82804003	82810874	1776
ENSG00000(	2.071584	12.04288	7.916483	1.498151	0	4.93179	1.4463	0.1602	0.25748	RGS9BP	chr19	+	33166313	33169206	2894
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	SLC36A3	chr5	-	1.51E+08	1.51E+08	3558
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	SLC36A2	chr5	-	1.51E+08	1.51E+08	3421
ENSG00000(	3030.727	2784.313	3534.71	17.22874	10.12475	10.68554	7.8527	1.10E-225	4.29E-223	THBS2	chr6	-	1.7E+08	1.7E+08	5811
ENSG00000(	1499.827	1567.983	1486.979	453.9398	693.0853	724.1511	1.28	3.79E-15	3.02E-14	RXRA	chr9	+	1.37E+08	1.37E+08	5770

ENSG00000(	74.57702	34.92434	31.66593	17.22874	40.49901	35.34449	0.59798	0.18972	0.29491	ANKRD37	chr4	+	1.86E+08	1.86E+08	1444
ENSG00000(	33.14534	28.90291	29.0271	6.74168	42.33987	26.30288	0.27232	0.61716	0.7297	C9orf47	chr9	+	91605778	91611055	4837
ENSG00000(	38.3243	27.69862	22.43003	31.46117	15.64734	31.23467	0.17092	0.71784	0.80997	NUDT17	chr1	-	1.46E+08	1.46E+08	2342
ENSG00000(	2.071584	0	2.638828	4.494453	0	3.28786	-0.51371	0.68079	0.78136	KIAA1024L	chr5	+	1.29E+08	1.29E+08	2354
ENSG00000(	0	0	0	2.247227	2.761296	10.68554	-3.128	0.014157	0.031829	LINC00643	chr14	+	62584197	62596352	1962
ENSG00000(	233.0532	227.6104	304.7846	106.3687	151.8713	96.1699	1.1045	1.67E-06	6.77E-06	ZNF75D	chrX	-	1.34E+08	1.34E+08	5592
ENSG00000(	0	0	0	4.494453	5.522592	0.821965	-2.5683	0.051285	0.099274	CYP4X1	chr1	+	47427036	47516423	2357
ENSG00000(	676.3721	698.4869	617.4856	301.1284	360.8093	528.5234	0.74003	9.32E-05	0.000305	KRT10	chr17	-	38974369	38978847	2124
ENSG00000(	12.4295	10.83859	10.55531	0	0	9.041614	1.6083	0.099634	0.17493	GOLGA8R	chr15	-	30695943	30706463	3062
ENSG00000(	21.75163	21.67718	27.70769	31.46117	34.97642	44.38611	-0.62635	0.14911	0.2428	CCDC30	chr1	+	42929001	43120335	6827
ENSG00000(	207.1584	175.826	219.0227	354.3127	343.3211	321.3883	-0.75665	2.07E-05	7.37E-05	NKRF	chrX	-	1.19E+08	1.19E+08	3741
ENSG00000(	0	0	0	0.749076	0.920432	1.64393	-1.0185	0.44577	NA	GLDN	chr15	+	51633826	51700210	4971
ENSG00000(	1174.588	1115.17	1333.927	2516.894	2259.661	2034.363	-0.90904	1.42E-12	9.62E-12	KPNA4	chr3	-	1.6E+08	1.6E+08	8981
ENSG00000(	0	0	0	6.74168	0.920432	0.821965	-2.1851	0.10382	0.18087	TRDN	chr6	-	1.24E+08	1.24E+08	4746
ENSG00000(	0	0	0	5.243529	0.920432	2.465895	-2.2485	0.09265	0.16463	KRT3	chr12	-	53183469	53189901	2319
ENSG00000(	95.29286	81.89156	89.72014	68.91495	77.31629	53.42772	0.41652	0.14821	0.24145	ZNF501	chr3	+	44771088	44778575	3099
ENSG00000(	515.8244	499.7794	621.4439	347.5711	388.4223	381.3917	0.54858	0.000388	0.00116	ZNF197	chr3	+	44626380	44689963	4299
ENSG00000(	7.250543	12.04288	0	8.988907	4.60216	3.28786	0.17027	0.85656	0.90907	SPATA12	chr3	+	57094469	57109460	2413
ENSG00000(	0	0	0	1.498151	1.840864	0	-0.93652	0.47589	NA	TMPRSS12	chr12	+	51236703	51281667	3336
ENSG00000(	1.035792	0	3.958241	0	0	0	1.6134	0.2311	NA	FAM228A	chr2	+	24397938	24423718	1774
ENSG00000(	0	0	0	20.97412	13.80648	21.37109	-5.093	4.04E-06	1.57E-05	NAP1L2	chrX	-	72432135	72434684	2550
ENSG00000(	15.53688	16.86003	7.916483	5.992604	8.283888	24.65895	0.053202	0.93813	0.96242	AQP7P1	chr9	-	67272038	67289492	1375
ENSG00000(	4404.187	4694.314	4257.748	2318.389	1858.352	1851.887	1.1449	7.58E-21	7.94E-20	RPS23	chr5	-	81569177	81574396	3437
ENSG00000(	462.999	479.3065	507.9743	92.88537	102.168	70.68898	2.4376	1.01E-37	1.95E-36	GNG2	chr14	+	52292913	52446060	3729
ENSG00000(	525.1465	517.8437	447.2813	71.16218	64.43024	43.56414	3.0375	2.27E-48	5.99E-47	BTN3A2	chr6	+	26365387	26378546	3017
ENSG00000(	0	0	1.319414	6.74168	3.681728	0.821965	-2.0218	0.11337	0.19447	AKAP14	chrX	+	1.19E+08	1.19E+08	977
ENSG00000(	93.22127	81.89156	112.1502	92.13629	121.497	69.04505	0.023602	0.93461	0.96066	PCLO	chr7	-	82387442	82792246	17144
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RGS7BP	chr5	+	63802084	63908139	4160
ENSG00000(	1373.46	1318.695	1657.184	370.7924	351.605	308.2368	2.0705	3.88E-47	9.79E-46	INSIG1	chr7	+	1.55E+08	1.55E+08	3010
ENSG00000(	0	0	0	26.96672	39.57858	30.4127	-5.8546	3.64E-08	1.74E-07	ANKRD20A	chr18	+	14179096	14249455	3410
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	MYT1L	chr2	-	1792885	2335032	7063
ENSG00000(	93.22127	95.13873	46.17948	53.18436	59.82808	45.20807	0.56556	0.09747	0.1717	C5orf38	chr5	+	2752245	2755508	1441
ENSG00000(	15.53688	18.06432	6.597069	13.48336	17.48821	14.79537	-0.16585	0.78666	0.85998	ZNF396	chr18	-	32946661	32957301	2788
ENSG00000(	1100.011	995.9459	851.0219	1090.654	746.4703	905.8053	0.10318	0.51649	0.64297	TMEM222	chr1	+	27648651	27662891	2861
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	CLCNKA	chr1	+	16345370	16360545	3060
ENSG00000(	2.071584	14.45145	17.15238	8.239831	7.363456	23.83698	-0.22598	0.76271	0.84327	ARHGAP30	chr1	-	1.61E+08	1.61E+08	4857
ENSG00000(	1219.127	1199.471	1461.91	1247.96	1179.073	989.6458	0.18241	0.18594	0.29049	10-Sep	chr2	-	1.1E+08	1.1E+08	3091
ENSG00000(	14.50109	16.86003	9.235896	50.18806	30.37426	18.08323	-1.2244	0.024211	0.051504	FAM86B1	chr8	-	12039605	12051642	2394
ENSG00000(	0	6.021439	0	0.749076	0	0	1.3768	0.31019	0.43627	CYP4F3	chr19	+	15751707	15773634	5050
ENSG00000(	20.71584	9.634302	11.87472	22.47227	36.81728	22.19305	-0.89247	0.099933	0.17539	XKR5	chr8	-	6666038	6693166	4894
ENSG00000(	282.7712	305.8891	237.4945	494.3899	438.1256	598.3905	-0.88517	5.32E-07	2.28E-06	SMYD4	chr17	-	1682779	1733928	4384
ENSG00000(	7.250543	3.612863	1.319414	2.996302	3.681728	9.863579	-0.35501	0.71274	0.80579	FOXD2	chr1	+	47901689	47906363	4675
ENSG00000(	928.0695	1117.579	1192.75	782.7839	1046.531	734.8366	0.33564	0.034938	0.071043	GPATCH8	chr17	-	42472652	42580798	8109
ENSG00000(	133.6172	208.3418	150.4132	162.5494	90.20234	115.0751	0.41169	0.12299	0.2081	CEACAM19	chr19	+	45165545	45187631	3278

ENSG0000(	1172.516	1169.363	1059.489	1210.506	1144.097	1217.33	-0.07012	0.55425	0.67505	NF2	chr22	+	29999545	30094587	6025
ENSG0000(	290.0217	343.222	236.1751	169.2911	168.4391	210.423	0.66273	0.00107	0.002988	C6orf1	chr6	-	34214157	34217247	1487
ENSG0000(	0	4.817151	2.638828	0	0	0	2.1804	0.10782	0.18657	SPATC1	chr8	+	1.45E+08	1.45E+08	1954
ENSG0000(	4390.722	4106.621	4661.489	1574.557	1836.262	1612.695	1.3871	6.71E-34	1.17E-32	UBE2H	chr7	-	1.29E+08	1.3E+08	5151
ENSG0000(	411.2094	470.8765	444.6424	400.0063	242.0736	267.9606	0.53811	0.00587	0.014335	MIR22HG	chr17	-	1614805	1620468	2626
ENSG0000(	32.10955	37.33292	21.11062	136.3317	115.054	159.4612	-2.1453	9.73E-12	6.19E-11	HPDL	chr1	+	45792545	45794347	1803
ENSG0000(	71.46964	75.87013	43.54065	71.16218	79.15715	46.03004	-0.03423	0.92014	0.95145	KTN1-AS1	chr14	-	55965996	56046828	2185
ENSG0000(	295.2007	267.3519	288.9516	259.9292	231.9489	230.1502	0.23648	0.17378	0.27529	KATNA1	chr6	-	1.5E+08	1.5E+08	1894
ENSG0000(	38.3243	28.90291	29.0271	28.46487	25.7721	46.852	-0.06566	0.8792	0.92454	FSD2	chr15	-	83424114	83474822	6418
ENSG0000(	1176.66	1295.814	1143.932	264.4237	352.5255	391.2553	1.8381	1.70E-31	2.71E-30	ARAP1	chr11	-	72396114	72504644	5767
ENSG0000(	58.00435	42.15007	68.60952	140.0771	204.3359	189.8739	-1.6462	1.91E-09	1.02E-08	KIF24	chr9	-	34252379	34329198	6226
ENSG0000(	0	2.408575	2.638828	2.996302	0.920432	4.109825	-0.51419	0.67	0.7728	PDE2A	chr11	-	72287185	72385635	4315
ENSG0000(	5.17896	2.408575	5.277655	5.992604	4.60216	3.28786	-0.09565	0.91934	0.951	SPDYE9P	chr7	-	76651635	76661674	2884
ENSG0000(	2.071584	1.204288	3.958241	0	6.443024	0	0.12802	0.91865	0.9507	LRRC16B	chr14	+	24521206	24538937	4597
ENSG0000(	194.7289	173.4174	137.219	160.3022	140.8261	193.1618	0.034305	0.8791	0.92447	PRR5	chr22	+	45064593	45133561	2279
ENSG0000(	1132.121	1095.902	1287.748	1319.122	1129.37	1029.922	0.014463	0.91533	0.94835	ZFP91	chr11	+	58346584	58388515	5220
ENSG0000(	179.192	111.9988	137.219	268.9181	175.8025	189.8739	-0.56072	0.021247	0.045813	C17orf58	chr17	-	65987217	65989765	1654
ENSG0000(	30.03797	24.08575	35.62417	20.97412	25.7721	16.4393	0.49171	0.29331	0.4176	BCDIN3D	chr12	-	50231573	50236912	1502
ENSG0000(	0	0	0	4.494453	1.840864	0.821965	-1.9797	0.14229	0.23373	MAGEE2	chrX	-	75002823	75005079	2257
ENSG0000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	EEF1GP1	chr7	+	1.25E+08	1.25E+08	1299
ENSG0000(	90.1139	74.66584	60.69303	104.1215	142.667	131.5144	-0.7311	0.0071	0.017078	CYP27C1	chr2	-	1.28E+08	1.28E+08	4401
ENSG0000(	400.8515	422.705	463.1142	426.224	405.9105	393.7212	0.06801	0.6512	0.7573	LYRM7	chr5	+	1.31E+08	1.31E+08	6351
ENSG0000(	7.250543	8.430014	10.55531	2.996302	12.88605	4.109825	0.36382	0.65291	0.75864	DTX2P1	chr7	+	76607934	76673092	1652
ENSG0000(	4.143168	1.204288	0	0	0	0.821965	1.3467	0.32051	0.44773	CCDC42B	chr12	+	1.14E+08	1.14E+08	1514
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CCDC73	chr11	-	32623792	32816204	4381
ENSG0000(	3.107376	10.83859	1.319414	7.490755	2.761296	7.397684	-0.18561	0.84241	0.89946	MST1L	chr1	-	17081405	17096732	4377
ENSG0000(	1052.365	963.4302	1006.713	1524.369	1855.591	1551.87	-0.70406	2.91E-08	1.41E-07	BCR	chr22	+	23521891	23660224	7082
ENSG0000(	39.36009	33.72006	38.263	13.48336	29.45382	25.48091	0.69077	0.1258	0.21171	FSCN2	chr17	+	79495422	79504156	1665
ENSG0000(	132.5814	162.5788	153.052	410.4934	488.7494	381.3917	-1.5091	5.80E-16	4.85E-15	SPIN4	chrX	-	62567107	62571223	4117
ENSG0000(	41.43168	45.76293	25.06886	145.3207	211.6994	193.1618	-2.2555	1.30E-14	1.00E-13	ZNF732	chr4	-	264464	299110	2193
ENSG0000(	106.6866	107.1816	108.1919	63.67142	54.30549	65.75719	0.79949	0.003079	0.007936	SPIN2B	chrX	-	57144984	57147980	1258
ENSG0000(	1.035792	0	0	68.16587	23.0108	23.83698	-5.3339	3.83E-08	1.83E-07	FOXE3	chr1	+	47881744	47883723	1980
ENSG0000(	139.8319	179.4389	143.8161	88.39091	66.2711	60.00344	1.0952	2.39E-05	8.45E-05	HYAL3	chr3	-	50330262	50336899	1942
ENSG0000(	15.53688	28.90291	21.11062	36.7047	48.7829	53.42772	-1.0599	0.014082	0.031687	VSIG10L	chr19	-	51834790	51845378	3397
ENSG0000(	2.071584	4.817151	1.319414	0	1.840864	0	1.4149	0.27394	0.39503	CXCR3	chrX	-	70835766	70838367	1861
ENSG0000(	301.4154	361.2863	350.9641	133.3354	169.3595	123.2947	1.2456	1.98E-10	1.15E-09	ZNF397	chr18	+	32820994	32847097	2637
ENSG0000(	346.9903	435.9522	325.8952	202.2504	221.8241	203.0253	0.81958	5.63E-06	2.15E-05	ZSCAN30	chr18	-	32831032	32870196	4323
ENSG0000(	1202.554	1304.244	1182.195	643.4559	721.6187	704.4239	0.83278	2.46E-11	1.52E-10	TPCN1	chr12	+	1.14E+08	1.14E+08	5345
ENSG0000(	3.107376	1.204288	0	0	0.920432	0.821965	0.74712	0.57953	0.6978	TNFRSF4	chr1	-	1146706	1149518	1707
ENSG0000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	KRT17P2	chr17	+	18330175	18335162	1314
ENSG0000(	5.17896	0	1.319414	4.494453	5.522592	4.109825	-0.86233	0.4272	0.55742	KRT16	chr17	-	39766030	39772151	1644
ENSG0000(	892.8526	817.7114	903.7984	800.0127	1245.344	1186.917	-0.30418	0.06249	0.11769	HEXIM1	chr17	+	43224684	43229468	4785
ENSG0000(	0	0	0	3.745378	14.72691	9.041614	-3.9977	0.000832	0.002363	SELV	chr19	+	40005753	40011326	1704
ENSG0000(	1.035792	0	7.916483	4.494453	3.681728	0.821965	-0.02842	0.98041	0.98857	LINC00846	chr21	-	33944548	33948191	1778

ENSG00000(	6.214751	1.204288	6.597069	2.247227	2.761296	0	1.1631	0.29954	0.42451	KRT14	chr17	-	39738531	39743173	1662
ENSG00000(	71.46964	61.41867	80.48424	55.43159	33.13555	24.65895	0.89049	0.015732	0.034959	TRABD2A	chr2	-	85048774	85134132	3895
ENSG00000(	13.46529	30.10719	30.34652	17.97781	12.88605	18.08323	0.55832	0.29555	0.41993	PDZD7	chr10	-	1.03E+08	1.03E+08	4306
ENSG00000(	2182.414	2103.891	1923.705	670.4226	744.6295	784.1545	1.4954	2.80E-34	4.91E-33	POFUT2	chr21	-	46683843	46707813	4825
ENSG00000(	31.07376	19.2686	21.11062	127.3428	130.7013	101.1017	-2.2808	9.28E-12	5.91E-11	QRFPR	chr4	-	1.22E+08	1.22E+08	1708
ENSG00000(	41.43168	54.19295	44.86007	21.72319	38.65814	32.8786	0.5827	0.14194	0.23345	MAPT	chr17	+	43971748	44105700	6816
ENSG00000(	64.2191	56.60152	60.69303	400.7554	359.8889	309.8808	-2.5419	2.92E-31	4.62E-30	ERCC6L	chrX	-	71424510	71458897	4341
ENSG00000(	55.93276	59.0101	64.65128	63.67142	22.09037	39.45432	0.49968	0.20364	0.31176	TMEM17	chr2	-	62727356	62739029	2460
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	TNFRSF18	chr1	-	1138888	1142071	1179
ENSG00000(	0	1.204288	0	0	0	3.28786	-0.57455	0.66797	NA	FGF3	chr11	-	69624992	69633792	892
ENSG00000(	18.64425	16.86003	13.19414	0	0.920432	3.28786	3.1168	0.000348	0.001048	C1QL4	chr12	-	49726200	49730971	2065
ENSG00000(	35.21692	48.17151	18.47179	9.737982	3.681728	5.753754	2.2752	0.000118	0.00038	RTN4RL2	chr11	+	57228022	57245007	2203
ENSG00000(	541.7192	609.3696	785.0512	381.2795	419.717	369.8842	0.72147	1.38E-05	5.05E-05	ZDHHC17	chr12	+	77157368	77247476	5259
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	P2RY4	chrX	-	69478016	69479654	1639
ENSG00000(	1536.079	1789.572	1308.858	841.9609	1014.316	857.3094	0.77097	8.68E-08	4.00E-07	ZNF395	chr8	-	28203102	28260218	4808
ENSG00000(	8.286335	14.45145	11.87472	4.494453	8.283888	13.15144	0.38475	0.58935	0.7063	ZACN	chr17	+	74068042	74079747	2651
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CHCHD2P9	chr9	+	82006219	82006674	456
ENSG00000(	243.4111	264.9433	283.674	54.68252	77.31629	86.30632	1.8486	6.78E-16	5.64E-15	PPARA	chr22	+	46546424	46639653	10048
ENSG00000(	3.107376	4.817151	6.597069	5.992604	2.761296	1.64393	0.38958	0.69129	0.7894	TMEM232	chr5	-	1.1E+08	1.1E+08	4217
ENSG00000(	6.214751	1.204288	9.235896	2.247227	6.443024	9.041614	-0.07811	0.93232	0.95944	FAM183A	chr1	+	43610824	43622067	530
ENSG00000(	11.39371	15.65574	7.916483	5.992604	11.96562	9.041614	0.35683	0.6073	0.72163	EFCAB6	chr22	-	43924624	44208217	5120
ENSG00000(	7.250543	14.45145	3.958241	42.69731	32.21512	46.852	-2.148	7.51E-05	0.000249	KANK3	chr19	-	8387468	8408146	2787
ENSG00000(	111.8655	130.0631	89.72014	20.22504	20.2495	24.65895	2.3139	2.67E-12	1.77E-11	EMID1	chr22	+	29601840	29655586	2173
ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	ACTL7A	chr9	+	1.12E+08	1.12E+08	1433
ENSG00000(	11.39371	13.24716	15.83297	5.992604	1.840864	3.28786	1.6754	0.030163	0.062475	PKD1L3	chr16	-	71963441	72033877	5195
ENSG00000(	20.71584	20.47289	11.87472	4.494453	9.20432	5.753754	1.3707	0.039221	0.07867	RHD	chr1	+	25598884	25656936	2930
ENSG00000(	23.82321	24.08575	26.38828	6.74168	8.283888	8.219649	1.5999	0.005238	0.01293	C17orf82	chr17	+	59489112	59490641	1530
ENSG00000(	3.107376	4.817151	6.597069	2.996302	6.443024	9.041614	-0.31156	0.72734	0.81731	ESPN	chr1	+	6484848	6521430	3531
ENSG00000(	3.107376	0	6.597069	0.749076	2.761296	3.28786	0.38902	0.73654	0.82369	GPR141	chr7	+	37723399	37873390	1270
ENSG00000(	10.35792	27.69862	3.958241	0	1.840864	0.821965	3.3612	0.000643	0.001859	TMPRSS6	chr22	-	37461476	37505603	3260
ENSG00000(	102.5434	137.2888	98.95603	229.2171	145.4283	147.9537	-0.62221	0.015313	0.034115	TMEM216	chr11	+	61159159	61166335	1955
ENSG00000(	1135.228	964.6345	872.1325	1914.637	1597.87	1892.985	-0.85977	3.53E-10	2.00E-09	RPS19BP1	chr22	-	39925098	39928860	2801
ENSG00000(	0	2.408575	3.958241	0.749076	0	0	1.5556	0.2495	0.36676	TMPRSS11A	chr4	-	68775103	68829858	3247
ENSG00000(	2.071584	2.408575	3.958241	0	3.681728	0	0.84038	0.50426	0.63192	RP11-187C	chr9	+	45562979	45563576	598
ENSG00000(	6.214751	13.24716	6.597069	0.749076	5.522592	4.109825	1.1771	0.18903	0.29411	AP003068.	chr11	-	64852451	64856847	4129
ENSG00000(	50.7538	54.19295	64.65128	51.68621	81.91845	69.86702	-0.25873	0.4259	0.55622	C3orf70	chr3	-	1.85E+08	1.85E+08	5901
ENSG00000(	2948.9	2700.013	4141.64	2459.964	3024.54	2386.164	0.31366	0.046189	0.090603	TEAD1	chr11	+	12695969	12966298	9430
ENSG00000(	489.9296	564.8109	448.6007	277.907	254.0392	272.0704	0.89938	2.30E-08	1.12E-07	PLCD1	chr3	-	38048987	38071253	3271
ENSG00000(	0	0	0	9.737982	2.761296	4.109825	-3.2451	0.0101	0.023463	CCK	chr3	-	42299317	42307699	1527
ENSG00000(	296.2365	292.6419	397.1435	185.0217	198.8133	162.7491	0.84533	1.34E-05	4.91E-05	ENTPD5	chr14	-	74424713	74486102	5842
ENSG00000(	31.07376	24.08575	46.17948	32.21025	32.21512	35.34449	0.016391	0.96893	0.98173	MITF	chr3	+	69788586	70017488	4814
ENSG00000(	16.57267	0	1.319414	11.98521	5.522592	7.397684	-0.38486	0.68617	0.78531	HEATR4	chr14	-	73945189	74025651	3523
ENSG00000(	15016.91	15523.27	15190.41	12336.53	10588.65	10053.45	0.47079	1.70E-05	6.14E-05	NAP1L1	chr12	-	76438670	76478813	5202
ENSG00000(	204.051	254.1047	163.6073	205.9958	188.6886	236.7259	-0.02124	0.92042	0.95162	CMC1	chr3	+	28283075	28366633	6033

ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	SLIT1	chr10	-	98757795	98945677	7925
ENSG00000(	89.0781	65.03154	80.48424	1100.392	1219.572	1024.99	-3.8129	1.85E-104	1.53E-102	LYPD6	chr2	+	1.5E+08	1.5E+08	4071
ENSG00000(	855.5641	800.8513	800.8842	108.616	91.12277	91.23811	3.0642	1.38E-79	7.37E-78	AKR1C1	chr10	+	4934796	5025475	6705
ENSG00000(	0	0	0	11.23613	13.80648	7.397684	-4.2838	0.000236	0.000729	VSTM2B	chr19	+	30017406	30055386	1488
ENSG00000(	0	0	1.319414	11.98521	11.04518	13.9734	-3.7588	0.000495	0.001455	FOXD3	chr1	+	63788730	63790797	2068
ENSG00000(	0	6.021439	1.319414	0	0	4.93179	0.36083	0.78164	0.85625	SPATA21	chr1	-	16713612	16763919	3619
ENSG00000(	1395.212	1305.448	1124.141	1513.882	1195.641	1769.69	-0.22688	0.13738	0.22726	MRPS21	chr1	+	1.5E+08	1.5E+08	1463
ENSG00000(	448.4979	421.5007	350.9641	564.803	444.5687	757.8517	-0.53003	0.005779	0.014138	RNF220	chr1	+	44870866	45117396	3835
ENSG00000(	7.250543	2.408575	1.319414	6.74168	0	0	0.50804	0.67314	0.77541	ANGPTL5	chr11	-	1.02E+08	1.02E+08	2368
ENSG00000(	88.04231	126.4502	127.9831	1132.602	1199.323	918.1348	-3.2396	1.02E-71	4.59E-70	KIAA1598	chr10	-	1.19E+08	1.19E+08	3941
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	BAGE2	chr21	-	10996026	11098980	2598
ENSG00000(	1.035792	0	0	1.498151	2.761296	4.93179	-1.8602	0.15259	0.24764	CTD-2600C	chr16	+	57832098	57850850	1309
ENSG00000(	1.035792	0	1.319414	0	4.60216	0	-0.50488	0.70898	0.80325	RP11-195F	chr9	-	34664160	34666109	1525
ENSG00000(	82.86335	72.25726	81.80365	28.46487	50.62376	26.30288	1.1569	0.000998	0.002798	ZNF546	chr19	+	40490041	40523514	4553
ENSG00000(	644.2626	651.5197	761.3018	560.3085	719.7778	684.6968	0.065989	0.65825	0.76292	TSPYL4	chr6	-	1.17E+08	1.17E+08	4111
ENSG00000(	6.214751	9.634302	10.55531	2.996302	3.681728	0	1.6978	0.073854	0.13584	MT1X	chr16	+	56716336	56718108	1727
ENSG00000(	297.2723	317.932	274.4381	192.5124	186.8477	183.2982	0.65848	0.000217	0.000674	GCNT1	chr9	+	79034752	79122332	5972
ENSG00000(	18.64425	10.83859	6.597069	0	7.363456	0.821965	1.8834	0.044298	0.087427	RP11-161I2	chr8	+	18578415	18591915	2054
ENSG00000(	1773.276	1732.97	2034.536	433.7147	451.0117	409.3385	2.0935	1.17E-60	4.15E-59	SESTD1	chr2	-	1.8E+08	1.8E+08	10615
ENSG00000(	1245.022	1132.03	1026.504	745.3302	872.5695	700.3141	0.55409	6.36E-05	0.000213	FNBP1	chr9	-	1.33E+08	1.33E+08	5398
ENSG00000(	980.8949	909.2372	1225.735	516.8621	522.8054	413.4484	1.0962	2.72E-12	1.81E-11	DYNC2H1	chr11	+	1.03E+08	1.03E+08	13678
ENSG00000(	1.035792	2.408575	1.319414	0	0	1.64393	0.85879	0.52286	0.64815	KRT12	chr17	-	39017555	39023462	1867
ENSG00000(	39.36009	71.05298	42.22124	13.48336	13.80648	18.90519	1.675	0.00017	0.000536	MAGED4B	chrX	-	51804923	51812368	3230
ENSG00000(	167.7983	138.4931	114.789	705.6292	776.8446	926.3545	-2.4981	5.22E-43	1.18E-41	BCAM	chr19	+	45312328	45324673	2686
ENSG00000(	208.1942	162.5788	186.0373	300.3793	222.7445	258.097	-0.48582	0.015501	0.034481	RSBN1L	chr7	+	77325760	77409008	3091
ENSG00000(	0	0	0	0.749076	2.761296	0	-0.97685	0.45852	NA	NPSR1	chr7	+	34697851	34917944	1567
ENSG00000(	222.6953	237.2447	230.8974	325.8479	427.0804	402.7628	-0.73841	2.84E-05	9.96E-05	WDR86	chr7	-	1.51E+08	1.51E+08	2023
ENSG00000(	33.14534	22.88147	27.70769	81.64923	75.47542	80.55256	-1.4752	2.16E-05	7.68E-05	EPOR	chr19	-	11488236	11495018	2133
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	FAM9C	chrX	-	13053737	13062801	5858
ENSG00000(	8.286335	12.04288	15.83297	1.498151	1.840864	3.28786	2.1697	0.010625	0.024543	CIDEC	chr3	-	9908398	9921938	1277
ENSG00000(	188.5141	244.4704	365.4776	22.47227	51.54419	28.76877	2.9282	4.06E-21	4.30E-20	DCC	chr18	+	49866542	51057784	5721
ENSG00000(	471.2853	447.995	496.0996	491.3936	412.3535	332.8958	0.19292	0.25858	0.37728	TAF9B	chrX	-	77385245	77395203	2713
ENSG00000(	65.25489	50.58008	102.9143	32.21025	27.61296	27.94681	1.286	0.000551	0.001606	PCDHB13	chr5	+	1.41E+08	1.41E+08	3485
ENSG00000(	111.8655	111.9988	110.8308	21.72319	29.45382	23.01502	2.15	8.86E-12	5.66E-11	MAGI2	chr7	-	77646393	79082890	6861
ENSG00000(	19.68005	20.47289	18.47179	110.8632	91.12277	87.95025	-2.2654	1.91E-10	1.11E-09	LUZP2	chr11	+	24518516	25104150	5016
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	LHFPL3	chr7	+	1.04E+08	1.05E+08	3174
ENSG00000(	1655.195	1530.65	1304.9	1557.328	1561.973	1384.189	-0.00318	0.98026	0.98847	CHP1	chr15	+	41523037	41574043	3284
ENSG00000(	0	0	3.958241	38.20285	20.2495	28.76877	-4.0433	1.53E-06	6.22E-06	RDM1	chr17	-	34245070	34257777	1535
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	FPR3	chr19	+	52298416	52329442	2620
ENSG00000(	5.17896	1.204288	5.277655	0.749076	0	0	2.4533	0.054565	0.10488	HIST1H1T	chr6	-	26107640	26108364	725
ENSG00000(	87.00652	51.78437	100.2754	22.47227	11.04518	13.15144	2.2878	3.25E-08	1.57E-07	C11orf96	chr11	+	43946892	43965888	1834
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	HSD3BP1	chr1	+	1.2E+08	1.2E+08	1111
ENSG00000(	0	0	0	11.98521	17.48821	17.26126	-4.8273	1.69E-05	6.10E-05	KCNJ11	chr11	-	17407406	17410878	2801
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CDHR4	chr3	-	49828165	49837268	2476

ENSG00000(	6208.537	6182.813	7334.621	8093.761	10026.27	8942.156	-0.45535	0.000153	0.000487	COL4A1	chr13	-	1.11E+08	1.11E+08	6524
ENSG00000(	0	1.204288	2.638828	0	0	0	1.2853	0.33195	NA	PLEKHG7	chr12	+	93115281	93166231	3584
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	GJA4	chr1	+	35258599	35261348	1622
ENSG00000(	18517.89	18309.99	16069.14	21114.94	19695.4	21688.37	-0.24023	0.022145	0.047514	PTMA	chr2	+	2.33E+08	2.33E+08	1635
ENSG00000(	0	0	3.958241	0	0	4.109825	-0.04632	0.9727	0.98414	CXorf27	chrX	+	37850070	37850569	500
ENSG00000(	252.7332	219.1804	307.4234	680.9097	598.2808	555.6483	-1.2329	5.20E-13	3.63E-12	HSPA14	chr10	+	14880163	14913740	1904
ENSG00000(	2.071584	0	0	0	0	4.109825	-0.45547	0.73699	0.82369	ATP13A5	chr3	-	1.93E+08	1.93E+08	4027
ENSG00000(	285.8786	357.6735	321.937	644.205	570.6678	654.2841	-0.95198	8.34E-10	4.60E-09	SIRT7	chr17	-	79869815	79879199	3445
ENSG00000(	46.61064	39.74149	51.45714	29.21395	31.29469	47.67397	0.34116	0.37696	0.5076	CTC-471F3.	chr19	-	40448563	40449634	976
ENSG00000(	780.9871	862.27	794.2871	244.1986	296.3791	287.6877	1.5542	4.67E-26	6.03E-25	IFT140	chr16	-	1560428	1662111	5270
ENSG00000(	2.071584	0	1.319414	0	0	1.64393	0.51016	0.70682	NA	TPM3P7	chr2	-	26032794	26033525	732
ENSG00000(	101.5076	137.2888	84.44248	0.749076	0.920432	0.821965	6.4223	1.66E-19	1.64E-18	AGMO	chr7	-	15239943	15601640	2475
ENSG00000(	0	0	0	2.996302	0.920432	0	-1.1048	0.40628	NA	SBK2	chr19	-	56041100	56048456	1085
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CYP26C1	chr10	+	94821021	94828454	1569
ENSG00000(	9.322127	9.634302	15.83297	3.745378	6.443024	3.28786	1.2482	0.10731	0.1859	TLR5	chr1	-	2.23E+08	2.23E+08	4088
ENSG00000(	1684.198	1549.918	1861.693	2337.865	2129.88	1787.774	-0.2955	0.026281	0.055383	USP7	chr16	-	8985951	9058371	5412
ENSG00000(	6.214751	1.204288	1.319414	1.498151	4.60216	0.821965	0.2893	0.8012	0.87065	NANOS3	chr19	+	13972877	13991571	776
ENSG00000(	2.071584	1.204288	1.319414	2.247227	0	0	0.58387	0.66258	0.7668	FOXD4L3	chr9	+	70917276	70920000	2725
ENSG00000(	13.46529	16.86003	5.277655	0.749076	0	1.64393	3.218	0.001127	0.003134	NHLRC1	chr6	-	18120718	18122851	2134
ENSG00000(	3.107376	16.86003	14.51355	79.40201	64.43024	113.4312	-2.8425	8.67E-10	4.78E-09	PLEKHN1	chr1	+	901877	911245	2455
ENSG00000(	8.286335	2.408575	3.958241	14.98151	20.2495	8.219649	-1.408	0.065434	0.12246	ZNF385C	chr17	-	40177594	40217383	2085
ENSG00000(	2.071584	0	0	2.247227	0	0	-0.04193	0.97501	NA	TMEM247	chr2	+	46656329	46711564	741
ENSG00000(	341.8113	308.2977	270.4798	175.2837	145.4283	212.0669	0.78498	8.71E-05	0.000286	MAGEH1	chrX	+	55478538	55479998	1461
ENSG00000(	374.9567	447.995	453.8783	647.9503	1052.054	764.4274	-0.94464	1.72E-07	7.69E-07	TET3	chr2	+	74229840	74335303	10983
ENSG00000(	566.5782	546.7466	464.4337	544.5779	531.0893	517.8379	-0.01285	0.92932	0.95737	ZNF286A	chr17	+	15602891	15640874	5616
ENSG00000(	301.4154	281.8033	254.6469	110.8632	63.50981	79.7306	1.7035	1.94E-13	1.39E-12	ISG15	chr1	+	948803	949920	711
ENSG00000(	213.3731	232.4275	162.2879	89.13999	131.6218	101.1017	0.91616	0.000119	0.000384	EXD3	chr9	-	1.4E+08	1.4E+08	2932
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	TCL6	chr14	+	96116835	96146170	4232
ENSG00000(	34.18113	31.31148	35.62417	33.7084	23.0108	22.19305	0.34382	0.42681	0.55703	C17orf97	chr17	+	260118	273510	1839
ENSG00000(	114.9729	124.0416	135.8996	86.89276	106.7701	107.6774	0.31235	0.1993	0.30691	ZKSCAN4	chr6	-	28212401	28227011	2375
ENSG00000(	6.214751	0	1.319414	0	0	0	2.1977	0.10512	0.18272	RGPD1	chr2	+	87135076	87241104	6697
ENSG00000(	155.3688	162.5788	127.9831	219.4791	121.497	103.5676	0.002692	0.99227	0.99518	DHRS4L2	chr14	+	24439148	24475617	1370
ENSG00000(	76.6486	66.23582	43.54065	80.90016	73.63456	80.55256	-0.32351	0.29704	0.42158	SAMD11	chr1	+	860260	879955	2551
ENSG00000(	4.143168	2.408575	0	23.22134	16.56778	19.72716	-2.8127	0.000427	0.001269	C1orf170	chr1	-	910579	917497	3064
ENSG00000(	63.18331	103.5687	102.9143	65.91865	70.87326	113.4312	0.10178	0.74573	0.83076	VMAC	chr19	+	5904869	5910864	2254
ENSG00000(	180.2278	161.3746	164.9267	149.8151	127.0196	175.9005	0.16068	0.46053	0.59	TMSB4XP8	chr4	-	91759652	91760263	565
ENSG00000(	59.04014	92.73015	68.60952	9.737982	12.88605	5.753754	2.8843	4.73E-11	2.87E-10	WHAMMP3	chr15	-	23187728	23208737	3649
ENSG00000(	1.035792	6.021439	7.916483	34.45748	40.49901	28.76877	-2.6738	1.97E-05	7.05E-05	ERC2	chr3	-	55542336	56502391	6138
ENSG00000(	119.1161	79.48299	135.8996	348.3201	281.6522	318.1004	-1.4952	1.32E-11	8.33E-11	B3GALTL	chr13	+	31774073	31906413	4254
ENSG00000(	893.8884	880.3343	1038.379	1637.479	1858.352	1662.013	-0.87357	3.53E-12	2.33E-11	SPRY4	chr5	-	1.42E+08	1.42E+08	4938
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	ERAS	chrX	+	48687283	48688548	1266
ENSG00000(	6.214751	1.204288	6.597069	0	0.920432	1.64393	1.836	0.11738	0.20029	RP11-687M	chr11	+	1.25E+08	1.25E+08	3338
ENSG00000(	43.50326	45.76293	48.81831	29.96302	12.88605	18.08323	1.137	0.009558	0.022332	TRPV2	chr17	+	16318856	16340317	2808
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	CXorf67	chrX	+	51149767	51151687	1921

ENSG00000(	0	0	2.638828	2.996302	4.60216	1.64393	-1.2613	0.31668	0.44356	RP11-723C	chr3	-	1.29E+08	1.29E+08	2291
ENSG00000(	26.93059	24.08575	32.98534	15.73059	47.86246	21.37109	-0.0092	0.98529	0.99132	C2orf88	chr2	+	1.91E+08	1.91E+08	4035
ENSG00000(	544.8265	514.2309	391.8659	757.3154	567.9065	647.7084	-0.44054	0.008858	0.020833	TMEM203	chr9	-	1.4E+08	1.4E+08	1557
ENSG00000(	1.035792	0	0	238.206	122.4175	146.3098	-7.3707	6.30E-18	5.79E-17	SLC18A3	chr10	+	50818347	50820765	2419
ENSG00000(	509.6096	413.0707	529.0849	271.1653	407.7514	327.142	0.52868	0.003827	0.009706	THSD4	chr15	+	71389291	72075722	9200
ENSG00000(	0	1.204288	0	8.988907	3.681728	1.64393	-2.3831	0.055305	0.10609	DNAJB13	chr11	+	73661364	73681411	1875
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	GABRD	chr1	+	1950780	1962192	1913
ENSG00000(	1248.129	1292.201	1289.067	2155.09	1765.389	1654.615	-0.54114	3.06E-05	0.000107	TCEA1	chr8	-	54879112	54935089	2966
ENSG00000(	5.17896	6.021439	9.235896	2.247227	0.920432	0	2.1365	0.044902	0.088441	NHEJ1	chr2	-	2.2E+08	2.2E+08	2113
ENSG00000(	223.7311	219.1804	208.4674	518.3603	659.0293	591.8147	-1.4343	2.31E-18	2.16E-17	FANCA	chr16	-	89803957	89883065	5451
ENSG00000(	605.9383	614.1867	577.9032	715.3671	823.7866	685.5187	-0.3054	0.026527	0.055845	SECISBP2	chr9	+	91933421	91974557	5405
ENSG00000(	3.107376	4.817151	2.638828	0	0	0	2.885	0.028519	0.059468	OR52B6	chr11	+	5602107	5603114	1008
ENSG00000(	5.17896	6.021439	0	4.494453	2.761296	0	0.47961	0.68082	0.78136	C9orf153	chr9	-	88835180	88874572	1845
ENSG00000(	1.035792	1.204288	0	0	2.761296	0.821965	-0.34444	0.79878	NA	ADH1A	chr4	-	1E+08	1E+08	1499
ENSG00000(	2.071584	2.408575	2.638828	0	3.681728	4.93179	-0.20263	0.86181	0.91233	RP11-527B	chr6	+	34991299	34991608	310
ENSG00000(	0	0	2.638828	1.498151	0	0	0.308	0.81734	NA	OR2B7P	chr6	+	28014212	28015145	934
ENSG00000(	54.89697	43.35436	40.90183	329.5932	412.3535	337.0056	-2.9231	2.02E-36	3.76E-35	SEMA4D	chr9	-	91975702	92113045	5684
ENSG00000(	13.46529	8.430014	21.11062	1541.597	1669.664	1246.921	-6.6432	7.42E-126	8.33E-124	LIN28B	chr6	+	1.05E+08	1.06E+08	5505
ENSG00000(	49.71801	55.39724	39.58241	67.4168	36.81728	61.64737	-0.19557	0.58908	0.70609	DNAH17	chr17	-	76419778	76573476	13792
ENSG00000(	858.6715	832.1628	796.9259	1250.956	1088.871	1131.846	-0.47969	0.000118	0.000382	MCRS1	chr12	-	49950327	49961936	2450
ENSG00000(	2.071584	2.408575	0	8.239831	19.32907	6.575719	-2.4444	0.010832	0.024991	TMEM72	chr10	+	45406648	45432450	3009
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	SCXB	chr8	+	1.45E+08	1.45E+08	606
ENSG00000(	55.93276	75.87013	118.7472	189.5161	169.3595	135.6242	-0.97984	0.000547	0.001597	FANCM	chr14	+	45605143	45670093	7111
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	FAM205CP	chr9	-	34889061	34895775	4148
ENSG00000(	350.0977	387.7806	308.7428	120.6012	148.1896	143.8439	1.339	1.91E-12	1.28E-11	ZNF70	chr22	-	24083769	24093279	4020
ENSG00000(	223.7311	240.8575	213.745	194.0106	217.222	291.7975	-0.05062	0.80444	0.87316	CARD9	chr9	-	1.39E+08	1.39E+08	4574
ENSG00000(	83.89914	61.41867	75.20659	143.0734	170.2799	106.8554	-0.91693	0.000813	0.002313	PEAR1	chr1	+	1.57E+08	1.57E+08	4970
ENSG00000(	50.7538	24.08575	43.54065	24.71949	38.65814	22.19305	0.46336	0.29455	0.41896	ZFP69B	chr1	+	40915774	40929390	2382
ENSG00000(	10.35792	16.86003	9.235896	12.73428	8.283888	10.68554	0.18439	0.78035	0.85524	SOWAHD	chrX	+	1.19E+08	1.19E+08	1589
ENSG00000(	63.18331	66.23582	60.69303	56.92974	58.90765	51.78379	0.18012	0.56231	0.68222	ZFP69	chr1	+	40942887	40962015	2871
ENSG00000(	61.11172	49.3758	63.33186	49.43899	52.46462	37.81039	0.31092	0.36025	0.48982	TMEM220	chr17	-	10602332	10633633	3106
ENSG00000(	722.9827	727.3898	684.7758	569.2974	655.3476	643.5985	0.19322	0.15005	0.2441	HIST1H1C	chr6	-	26055968	26056699	732
ENSG00000(	1.035792	1.204288	1.319414	0.749076	0	0.821965	0.63435	0.63824	NA	PLSCR3	chr17	-	7293046	7307416	2557
ENSG00000(	2417.538	2388.103	1683.572	1435.229	1263.753	1431.041	0.65038	9.34E-06	3.48E-05	EIF4EBP1	chr8	+	37887859	37917883	1020
ENSG00000(	0	0	1.319414	8.239831	1.840864	8.219649	-2.7055	0.024427	0.051899	P2RX2	chr12	+	1.33E+08	1.33E+08	1867
ENSG00000(	171.9415	172.2131	158.3297	117.6049	105.8497	114.2531	0.56938	0.008802	0.020724	CCDC157	chr22	+	30752624	30774647	4789
ENSG00000(	0	0	2.638828	0	0.920432	0.821965	0.26148	0.84655	NA	TTC24	chr1	+	1.57E+08	1.57E+08	2005
ENSG00000(	266.1985	237.2447	333.8117	345.3238	275.2092	250.6993	-0.06001	0.76035	0.84156	FAM122A	chr9	+	71394964	71398609	3646
ENSG00000(	142.9393	131.2674	112.1502	22.47227	45.10117	74.79881	1.4206	5.27E-05	0.000178	PALM3	chr19	-	14164177	14169971	2262
ENSG00000(	0	0	0	5.243529	3.681728	6.575719	-3.164	0.012273	0.027968	C1orf168	chr1	-	57184477	57285369	3135
ENSG00000(	3.107376	9.634302	1.319414	0.749076	0.920432	0	2.2055	0.066752	0.12457	SHISA7	chr19	-	55940107	55954230	6033
ENSG00000(	0	2.408575	0	0	3.681728	0.821965	-0.4807	0.72209	0.81311	AC097382.	chr4	+	6997068	7000685	591
ENSG00000(	1.035792	6.021439	0	0.749076	3.681728	0.821965	0.3134	0.80037	0.86991	AC002472.	chr22	+	21400249	21418457	4803
ENSG00000(	4.143168	2.408575	3.958241	0	0	0.821965	2.3084	0.071626	0.13238	DMBT1	chr10	+	1.24E+08	1.24E+08	7686

ENSG00000(	0	1.204288	0	0	0	1.64393	-0.12916	0.91993	NA	CLEC17A	chr19	+	14693896	14721969	2065
ENSG00000(	1.035792	2.408575	2.638828	2.247227	6.443024	0.821965	-0.49651	0.66453	0.76842	LDLRAD2	chr1	+	22138758	22151714	4012
ENSG00000(	32.10955	13.24716	15.83297	0	5.522592	9.041614	1.9042	0.013776	0.031066	C2orf66	chr2	-	1.98E+08	1.98E+08	1669
ENSG00000(	22.78742	6.021439	17.15238	0	3.681728	9.863579	1.5766	0.064252	0.12051	OVCH1	chr12	-	29565407	29650619	3405
ENSG00000(	91.14969	74.66584	92.35896	134.0845	280.7318	232.6161	-1.3099	2.03E-06	8.15E-06	ARHGAP11	chr15	+	30916697	31060329	2043
ENSG00000(	1.035792	0	1.319414	0.749076	0	2.465895	-0.24695	0.85513	NA	HS6ST1P1	chr1	+	21754796	21756030	1234
ENSG00000(	150.1898	250.4918	187.3568	134.0845	134.3831	129.0485	0.5586	0.015877	0.035267	PMS2CL	chr7	+	6749759	6793493	3327
ENSG00000(	712.6248	668.3797	584.5003	764.0571	695.8466	766.8933	-0.17859	0.19535	0.3018	CYHR1	chr8	-	1.46E+08	1.46E+08	6158
ENSG00000(	551.0413	475.6936	548.8761	32.95932	41.41944	33.70056	3.849	3.90E-75	1.89E-73	COL14A1	chr8	+	1.21E+08	1.21E+08	6466
ENSG00000(	170.9057	140.9017	158.3297	12.73428	19.32907	20.54912	3.126	2.92E-23	3.37E-22	DNER	chr2	-	2.3E+08	2.31E+08	3260
ENSG00000(	0	0	1.319414	0.749076	2.761296	0.821965	-0.93317	0.49046	NA	CPSF4L	chr17	-	71244588	71258491	1275
ENSG00000(	309.7018	405.845	327.2146	291.3904	222.7445	272.8924	0.40168	0.029437	0.061139	KLHL17	chr1	+	895967	901095	2560
ENSG00000(	20.71584	44.55865	15.83297	47.19176	29.45382	62.46933	-0.75668	0.10359	0.18058	ANKRD19P	chr9	+	95571670	95650975	2370
ENSG00000(	33.14534	42.15007	51.45714	0.749076	12.88605	10.68554	2.2814	0.000112	0.000363	ZSCAN23	chr6	-	28399707	28411279	3126
ENSG00000(	41.43168	18.06432	22.43003	22.47227	15.64734	22.19305	0.43171	0.39318	0.52397	HIST1H2BG	chr6	-	26216428	26216872	445
ENSG00000(	11.39371	9.634302	7.916483	39.701	19.32907	46.03004	-1.7746	0.001299	0.003578	RINL	chr19	-	39358470	39368919	3021
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC093393.	chr2	+	33861569	33862492	924
ENSG00000(	1.035792	3.612863	3.958241	0	0	0.821965	2.0059	0.12612	0.21212	OR7D2	chr19	+	9296279	9299493	3215
ENSG00000(	18.64425	22.88147	10.55531	2.247227	8.283888	6.575719	1.508	0.032274	0.066256	TPRG1	chr3	+	1.89E+08	1.89E+08	5479
ENSG00000(	0	0	0	46.44268	40.49901	62.46933	-6.4357	5.66E-10	3.16E-09	RP11-43F1	chr5	-	1599035	1634120	2338
ENSG00000(	4.143168	4.817151	3.958241	3.745378	2.761296	7.397684	-0.09349	0.92127	0.95228	C1orf204	chr1	-	1.6E+08	1.6E+08	2501
ENSG00000(	259.9838	314.3191	258.6051	144.5716	142.667	148.7757	0.92873	1.23E-06	5.06E-06	MORN2	chr2	+	39103103	39156213	919
ENSG00000(	5.17896	2.408575	0	0	0	0	2.2334	0.099381	0.17452	CXXC11	chr2	+	2.43E+08	2.43E+08	2602
ENSG00000(	0	0	0	2.996302	0.920432	7.397684	-2.6284	0.045605	0.089631	MEIS3P2	chr17	+	20492371	20494013	1643
ENSG00000(	113.9371	113.203	84.44248	224.7227	149.11	199.7375	-0.87171	0.000337	0.001017	S100A3	chr1	-	1.54E+08	1.54E+08	856
ENSG00000(	1373.46	1236.803	1471.146	865.9313	976.5783	805.5256	0.62297	2.11E-06	8.44E-06	UBQLN2	chrX	+	56590026	56593443	3418
ENSG00000(	339.7397	351.652	292.9099	165.5457	178.5638	209.6011	0.82764	7.66E-06	2.88E-05	RILPL1	chr12	-	1.24E+08	1.24E+08	2608
ENSG00000(	5.17896	1.204288	0	0	0	0.821965	1.5441	0.25291	0.37073	C19orf67	chr19	-	14192431	14196687	1427
ENSG00000(	32.10955	7.225726	46.17948	12.73428	22.09037	17.26126	0.6823	0.2404	0.35566	ZNF490	chr19	-	12688775	12750912	4237
ENSG00000(	0	3.612863	0	4.494453	1.840864	0.821965	-0.6614	0.60594	0.72063	CLCN1	chr7	+	1.43E+08	1.43E+08	3172
ENSG00000(	0	0	0	0.749076	0.920432	7.397684	-2.2635	0.091196	0.16256	NWD1	chr19	+	16830787	16928774	8393
ENSG00000(	2953.043	2780.7	3192.981	2701.166	2841.374	2811.12	0.095473	0.3768	0.50741	ARL4C	chr2	-	2.35E+08	2.35E+08	4013
ENSG00000(	1.035792	3.612863	1.319414	8.239831	0	3.28786	-0.73286	0.52904	0.65382	TMEM221	chr19	-	17546318	17559376	1930
ENSG00000(	72.50543	95.13873	35.62417	5.992604	9.20432	8.219649	3.0257	4.70E-10	2.64E-09	RAB42	chr1	+	28918712	28921955	1950
ENSG00000(	134.6529	127.6545	113.4696	29.96302	30.37426	41.92021	1.8565	3.31E-10	1.88E-09	WNT7B	chr22	-	46316242	46373009	3919
ENSG00000(	1521.578	1584.843	1840.582	734.8431	901.1029	923.0666	0.94862	4.02E-12	2.64E-11	C11orf95	chr11	-	63527364	63536113	5582
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	PRSS45	chr3	-	46783582	46854048	3128
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	PLA2G4E	chr15	-	42273780	42343388	5266
ENSG00000(	21.75163	33.72006	44.86007	14.98151	23.0108	20.54912	0.74889	0.11672	0.19934	GPR89B	chr1	+	1.47E+08	1.47E+08	2701
ENSG00000(	0	2.408575	1.319414	0.749076	2.761296	0	0.050856	0.96962	0.98212	MESP2	chr15	+	90303822	90321982	1552
ENSG00000(	17.60846	7.225726	23.74945	11.98521	13.80648	12.32947	0.32873	0.5954	0.71116	EYS	chr6	-	64429876	66417118	10589
ENSG00000(	242.3753	220.3847	215.0644	927.3555	929.6363	1063.623	-2.0989	9.42E-46	2.30E-44	C6orf132	chr6	-	42068856	42110357	6210
ENSG00000(	689.8374	668.3797	605.6109	150.5642	110.4518	129.0485	2.3192	6.26E-42	1.37E-40	MAPK12	chr22	-	50683879	50700254	6248
ENSG00000(	0	0	0	8.239831	17.48821	21.37109	-4.8135	2.01E-05	7.19E-05	TMEM215	chr9	+	32783497	32787397	3581

ENSG00000(	21.75163	34.92434	23.74945	41.19916	64.43024	43.56414	-0.86955	0.034358	0.070015	NUTMG	chr9	+	99690592	99702535	2851
ENSG00000(	997.4676	936.9358	1293.026	1206.012	1458.885	1158.149	-0.2441	0.1063	0.18442	COL4A5	chrX	+	1.08E+08	1.08E+08	6483
ENSG00000(	9772.697	8869.579	9036.665	5808.332	8425.634	8259.925	0.29865	0.031208	0.064349	AGRN	chr1	+	955503	991496	7323
ENSG00000(	88.04231	72.25726	134.5802	29.21395	46.94203	45.20807	1.2616	0.000201	0.000627	NHS	chrX	+	17393543	17754114	8761
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	OTOG	chr11	+	17568920	17668697	9953
ENSG00000(	2.071584	4.817151	0	0.749076	0.920432	0	1.2553	0.34062	0.46936	FAM166A	chr9	-	1.4E+08	1.4E+08	1720
ENSG00000(	32.10955	33.72006	58.05421	23.97042	126.0992	76.44274	-0.84519	0.068298	0.12704	TMPPE	chr3	-	33131913	33138293	3962
ENSG00000(	67.32647	72.25726	93.67838	268.169	237.4715	247.4114	-1.6864	5.60E-14	4.16E-13	ZNF626	chr19	-	20802867	20844402	5963
ENSG00000(	59.04014	43.35436	40.90183	406.748	360.8093	360.8426	-2.9452	7.08E-39	1.42E-37	SMTNL2	chr17	+	4487294	4511614	2280
ENSG00000(	159.512	156.5574	213.745	41.19916	79.15715	56.71558	1.5695	1.94E-08	9.52E-08	ZC3H6	chr2	+	1.13E+08	1.13E+08	11540
ENSG00000(	113.9371	124.0416	113.4696	110.8632	123.3379	117.541	-0.00035	0.99879	0.99913	LINC00265	chr7	+	39773231	39832691	3049
ENSG00000(	1123.834	1065.795	911.7149	752.8209	742.7886	1211.576	0.19567	0.27683	0.3984	LAMTOR4	chr7	+	99746530	99753567	730
ENSG00000(	349.0619	322.7491	294.2293	872.673	890.0577	973.2065	-1.4955	1.05E-25	1.33E-24	PRKAR1B	chr7	-	588834	767287	2553
ENSG00000(	25.8948	13.24716	19.79121	9.737982	14.72691	17.26126	0.48339	0.39772	0.5287	NUTM2B	chr10	+	81462983	81474437	3970
ENSG00000(	87.00652	67.44011	127.9831	80.90016	75.47542	59.18147	0.38048	0.21523	0.32593	HNRNPU-A	chr1	-	2.45E+08	2.45E+08	5007
ENSG00000(	279.6638	261.3304	407.6989	108.616	115.9744	101.9236	1.5271	2.81E-12	1.87E-11	NCR3LG1	chr11	+	17373273	17398888	6438
ENSG00000(	493.0369	522.6609	568.6673	142.3244	199.7337	166.0369	1.6364	1.70E-20	1.76E-19	DCUN1D3	chr16	-	20869396	20911706	3013
ENSG00000(	146.0467	137.2888	146.4549	266.6709	277.9705	264.6727	-0.90821	1.58E-06	6.40E-06	ZNF793	chr19	+	37997841	38039664	6712
ENSG00000(	3663.596	3474.37	3167.912	17197.28	12937.59	14218.35	-2.1009	5.95E-63	2.22E-61	TUBB4B	chr9	+	1.4E+08	1.4E+08	2035
ENSG00000(	72.50543	34.92434	39.58241	71.16218	50.62376	40.27628	-0.1316	0.7341	0.8222	AGAP4	chr10	-	46321042	46349323	2439
ENSG00000(	151.2256	158.966	170.2044	104.1215	91.12277	92.06007	0.73361	0.001258	0.003473	CTD-2228K	chr5	-	466239	473213	1876
ENSG00000(	1062.722	1069.407	980.3244	910.1268	636.0185	824.4308	0.39078	0.008694	0.020497	COMMD6	chr13	-	76099350	76123575	1793
ENSG00000(	0	1.204288	0	19.47596	21.16994	14.79537	-4.348	2.30E-05	8.16E-05	PLA2G2A	chr1	-	20301925	20306932	1306
ENSG00000(	15.53688	2.408575	14.51355	7.490755	2.761296	7.397684	0.78529	0.33451	0.46248	AGPHD1	chr15	+	78799906	78829714	2180
ENSG00000(	1.035792	0	0	1.498151	0	1.64393	-0.62149	0.64536	NA	OR7A5	chr19	-	14903302	14946188	1048
ENSG00000(	26.93059	30.10719	19.79121	16.47966	23.93123	23.83698	0.25642	0.59602	0.7118	C15orf62	chr15	+	41062159	41064643	2485
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	FAM230A	chr22	+	20692438	20716938	8854
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RUFY4	chr2	+	2.19E+08	2.19E+08	3568
ENSG00000(	134.6529	108.3859	84.44248	83.89646	53.38506	69.86702	0.65341	0.025938	0.054722	ZNF383	chr19	+	37708828	37734828	2268
ENSG00000(	24.85901	15.65574	22.43003	229.2171	170.2799	241.6577	-3.2999	8.24E-27	1.10E-25	HES4	chr1	-	934342	935552	1040
ENSG00000(	118.0803	103.5687	114.789	217.2319	204.3359	176.7225	-0.82474	0.000144	0.00046	ZNF669	chr1	-	2.47E+08	2.47E+08	1951
ENSG00000(	16.57267	13.24716	5.277655	0.749076	0	5.753754	2.0855	0.026678	0.056122	C19orf35	chr19	-	2274631	2282181	2564
ENSG00000(	1.035792	0	3.958241	0	3.681728	0	0.26263	0.84428	0.90064	LRRIQ4	chr3	+	1.7E+08	1.7E+08	1827
ENSG00000(	59.04014	85.50443	75.20659	109.365	88.36147	86.30632	-0.37145	0.19144	0.29708	CENPP	chr9	+	95087766	95382815	8766
ENSG00000(	212.3373	232.4275	215.0644	1513.882	1619.04	1573.241	-2.8278	3.05E-98	2.26E-96	PLSCR1	chr3	-	1.46E+08	1.46E+08	2233
ENSG00000(	168.8341	183.0517	160.9685	154.3096	161.996	175.9005	0.059656	0.77027	0.84906	C3orf62	chr3	-	49306035	49315342	4235
ENSG00000(	2.071584	13.24716	2.638828	29.96302	14.72691	29.59074	-1.9134	0.005924	0.014461	ENO4	chr10	+	1.19E+08	1.19E+08	2779
ENSG00000(	126.3666	160.1703	130.622	98.1289	82.83888	114.2531	0.49233	0.045817	0.089988	ZNF559	chr19	+	9434448	9461838	3042
ENSG00000(	30.03797	44.55865	62.01245	361.0544	553.1796	465.2321	-3.3233	2.22E-39	4.52E-38	SBK1	chr16	+	28303840	28335170	4992
ENSG00000(	3.107376	0	0	7.490755	1.840864	3.28786	-1.4167	0.23937	0.3544	SLC38A3	chr3	+	50242679	50258411	2470
ENSG00000(	568.6498	633.4553	649.1516	634.467	582.6335	618.9396	0.01035	0.93957	0.96348	GTF2F2	chr13	+	45694650	45858237	1432
ENSG00000(	492.0012	559.9938	534.3626	519.8584	433.5235	424.9559	0.20049	0.18653	0.29112	FAM92A1	chr8	+	94710789	94743755	4241
ENSG00000(	872.1368	839.3885	1055.531	742.3339	889.1373	590.9928	0.315	0.054276	0.10439	FOCAD	chr9	+	20658308	20995954	6096
ENSG00000(	16.57267	14.45145	7.916483	5.243529	7.363456	10.68554	0.69902	0.31703	0.44399	AC092171.	chr7	+	5459477	5462753	753

ENSG00000(	73.54123	45.76293	40.90183	47.94084	36.81728	25.48091	0.53194	0.17898	0.28164	PRR19	chr19	+	42806250	42814973	1956
ENSG00000(	12.4295	10.83859	7.916483	18.72689	7.363456	16.4393	-0.41948	0.52461	0.64964	ZP3	chr7	+	76026835	76071388	1846
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	H3F3C	chr12	-	31944123	31945175	1053
ENSG00000(	0	0	0	0	5.522592	7.397684	-2.6884	0.04234	0.084093	IFNA2	chr9	-	21384254	21385396	1143
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	AC018892.	chr2	+	97746835	97748986	1056
ENSG00000(	4.143168	8.430014	5.277655	2.247227	10.12475	10.68554	-0.32469	0.70305	0.79834	RP11-152F	chr15	+	82751614	82769399	4809
ENSG00000(	5.17896	3.612863	6.597069	0	0.920432	4.93179	1.1082	0.31165	0.43791	JAKMIP3	chr10	+	1.34E+08	1.34E+08	6626
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	PPP3R2	chr9	-	1.04E+08	1.04E+08	3387
ENSG00000(	2.071584	4.817151	1.319414	0	0	0	2.4706	0.065789	0.12303	GOLGA6L3	chr15	+	85783703	85790410	1679
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	PDCD1	chr2	-	2.43E+08	2.43E+08	2114
ENSG00000(	2.071584	0	2.638828	0	1.840864	0	0.7447	0.58184	0.69955	CLEC2A	chr12	-	10051272	10084980	916
ENSG00000(	5.17896	6.021439	5.277655	1.498151	0	0	2.483	0.034432	0.070142	GPR21	chr9	+	1.26E+08	1.26E+08	1170
ENSG00000(	13.46529	24.08575	5.277655	2.996302	3.681728	1.64393	2.1269	0.009762	0.022753	TCTEX1D4	chr1	-	45271585	45272957	1262
ENSG00000(	0	0	0	5.992604	13.80648	9.041614	-4.0968	0.00053	0.001551	ANKRD36P	chrY	+	28555962	28566682	659
ENSG00000(	0	0	0	15.73059	17.48821	13.15144	-4.8201	1.73E-05	6.24E-05	SELL	chr1	-	1.7E+08	1.7E+08	2436
ENSG00000(	345.9545	425.1136	484.2249	352.0655	291.7769	270.4265	0.45199	0.012687	0.028799	CHM	chrX	-	85116185	85302566	5442
ENSG00000(	140.8677	144.5145	110.8308	287.645	181.3251	193.9837	-0.73671	0.001897	0.005075	BLOC1S5	chr6	-	8013800	8064647	2684
ENSG00000(	3.107376	2.408575	9.235896	1.498151	7.363456	18.08323	-0.76804	0.40045	0.53167	SRP72P2	chr6	-	1.59E+08	1.59E+08	1979
ENSG00000(	147.0825	155.3531	175.482	65.16957	53.38506	51.78379	1.4708	6.32E-09	3.23E-08	CERKL	chr2	-	1.82E+08	1.83E+08	3208
ENSG00000(	0	1.204288	1.319414	0.749076	0	0	0.61214	0.64459	NA	WASF4P	chrX	+	47657325	47664188	1878
ENSG00000(	0	2.408575	0	11.23613	15.64734	10.68554	-3.2425	0.00137	0.003759	SLC24A5	chr15	+	48413169	48434869	2984
ENSG00000(	1317.527	1209.105	955.2556	1408.262	973.8171	817.8551	0.1214	0.50867	0.63616	IER5L	chr9	-	1.32E+08	1.32E+08	2706
ENSG00000(	1179.767	876.7215	901.1596	7998.629	6260.778	6098.158	-2.7738	1.03E-80	5.59E-79	H2AFX	chr11	-	1.19E+08	1.19E+08	1614
ENSG00000(	0	0	0	3.745378	1.840864	3.28786	-2.3167	0.081577	0.1478	INSC	chr11	+	15133970	15268754	2954
ENSG00000(	4.143168	1.204288	0	0.749076	0	1.64393	0.7087	0.59322	0.70931	SERPINA5	chr14	+	95027779	95059457	2312
ENSG00000(	298.3081	243.2661	278.3963	322.1025	312.9469	313.1686	-0.2079	0.21987	0.33159	C19orf54	chr19	-	41246761	41257458	2753
ENSG00000(	20.71584	31.31148	21.11062	66.66772	37.73771	53.42772	-1.0882	0.008822	0.02076	LCTL	chr15	-	66839517	66858317	3147
ENSG00000(	0	0	0	0	7.363456	0.821965	-1.9869	0.14257	0.2341	NCCRP1	chr19	+	39687601	39692524	1978
ENSG00000(	0	0	0	8.988907	0.920432	4.93179	-3.0309	0.018449	0.040355	KRTDAP	chr19	-	35978226	35986460	491
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	RP1-273G1	chr8	-	33827079	33827397	318
ENSG00000(	45.57484	59.0101	84.44248	75.65663	78.23672	64.93523	-0.21595	0.5009	0.62899	COL25A1	chr4	-	1.1E+08	1.1E+08	4630
ENSG00000(	129.474	155.3531	151.7326	566.3011	599.2012	621.4055	-2.0286	8.57E-34	1.49E-32	FAM83G	chr17	-	18872102	18908117	5266
ENSG00000(	2.071584	4.817151	3.958241	2.247227	0.920432	0.821965	1.0894	0.3405	0.46923	C9orf171	chr9	+	1.35E+08	1.35E+08	1818
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC010969.	chr2	-	10143286	10146158	2412
ENSG00000(	1507.077	1510.177	1803.639	2417.267	2103.187	2035.185	-0.44332	0.000455	0.001345	SRSF10	chr1	-	24291294	24307417	3957
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	HBA2	chr16	+	222846	223709	640
ENSG00000(	41.43168	43.35436	44.86007	47.94084	27.61296	57.53754	-0.04227	0.91303	0.94677	DUSP28	chr2	+	2.41E+08	2.42E+08	3461
ENSG00000(	97.36444	33.72006	68.60952	11.23613	13.80648	23.83698	1.9752	1.78E-05	6.40E-05	C15orf52	chr15	-	40623653	40633168	5021
ENSG00000(	941.5348	986.3116	1138.654	523.6038	587.2356	499.7547	0.92635	2.51E-11	1.55E-10	NBR1	chr17	+	41322498	41363708	4973
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	OR2G6	chr1	+	2.49E+08	2.49E+08	1049
ENSG00000(	277.5922	310.7062	274.4381	194.0106	340.5598	283.5779	0.078588	0.70814	0.80273	RALGAPA2	chr20	-	20370196	20693266	8769
ENSG00000(	265.1627	275.7819	254.6469	526.6001	613.9281	672.3673	-1.1831	1.52E-13	1.10E-12	NDOR1	chr9	+	1.4E+08	1.4E+08	2497
ENSG00000(	56.96855	51.78437	34.30476	27.7158	14.72691	14.79537	1.281	0.004029	0.010173	FBLL1	chr5	+	1.68E+08	1.68E+08	1519
ENSG00000(	1.035792	1.204288	3.958241	0	4.60216	0	0.28911	0.82288	0.88569	NKAIN2	chr6	+	1.24E+08	1.25E+08	3115

ENSG00000(	6.214751	13.24716	2.638828	6.74168	7.363456	8.219649	-0.00821	0.99191	0.99508	PAQR9	chr3	-	1.43E+08	1.43E+08	2103
ENSG00000(	36.25272	25.29004	26.38828	0.749076	2.761296	0.821965	4.0012	1.15E-07	5.23E-07	C12orf55	chr12	+	96883349	97040905	2756
ENSG00000(	16.57267	10.83859	18.47179	23.97042	11.04518	9.863579	0.022103	0.97121	0.98327	NPIPP1	chr16	-	15198178	15225458	2902
ENSG00000(	5.17896	1.204288	7.916483	4.494453	11.04518	9.863579	-0.73435	0.39677	0.52782	CLN3	chr16	-	28477983	28506896	3081
ENSG00000(	29.00217	26.49433	34.30476	137.0808	154.6326	151.2415	-2.2783	1.01E-14	7.80E-14	FAM72B	chr1	+	1.21E+08	1.21E+08	2374
ENSG00000(	14.50109	1.204288	10.55531	23.22134	8.283888	9.863579	-0.59713	0.43247	0.56233	ASAH2	chr10	-	51944621	52008370	4797
ENSG00000(	2549.084	2631.369	2361.751	2898.922	2932.496	3380.742	-0.28786	0.011856	0.027101	SUMO2	chr17	-	73163408	73179078	1463
ENSG00000(	108.7581	163.7831	126.6637	283.1506	263.2436	257.275	-1.0065	1.61E-06	6.54E-06	NANOS1	chr10	+	1.21E+08	1.21E+08	4627
ENSG00000(	0	0	0	2.996302	3.681728	0.821965	-2.0473	0.12821	0.21482	IGFL3	chr19	-	46623328	46627931	662
ENSG00000(	1.035792	1.204288	1.319414	0	3.681728	0.821965	-0.20106	0.87786	0.92371	GOLGA8M	chr15	-	28947100	28983530	1899
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	ZNF177	chr19	+	9435021	9493293	2429
ENSG00000(	1139.371	1068.203	1244.207	537.8362	786.0489	625.5153	0.82281	8.67E-08	4.00E-07	LDOC1L	chr22	-	44888452	44894178	5495
ENSG00000(	80.79177	63.82725	89.72014	58.42789	27.61296	51.78379	0.74568	0.03218	0.066086	DPYD	chr1	-	97543299	98386605	4412
ENSG00000(	646.3341	670.7883	518.5296	774.5441	610.2464	696.2043	-0.18003	0.24294	0.35881	S100A16	chr1	-	1.54E+08	1.54E+08	1146
ENSG00000(	921.8548	938.1401	1390.662	563.3048	621.2916	489.8911	0.95237	2.93E-08	1.41E-07	PTAR1	chr9	-	72324438	72374875	9876
ENSG00000(	39.36009	25.29004	50.13772	63.67142	64.43024	62.46933	-0.72171	0.044083	0.087091	FAM154B	chr15	+	82555151	82577271	3134
ENSG00000(	1.035792	3.612863	5.277655	7.490755	8.283888	7.397684	-1.0888	0.23083	0.3442	LINC00319	chr21	+	44866481	44873773	3507
ENSG00000(	4.143168	4.817151	2.638828	0	0	0	3.0363	0.020144	0.043652	HILS1	chr17	-	48248789	48258539	1219
ENSG00000(	10.35792	4.817151	2.638828	0	0	2.465895	2.1554	0.061632	0.11622	RHCE	chr1	-	25688740	25756683	1810
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	IDO2	chr8	+	39792133	39873910	4264
ENSG00000(	170.9057	162.5788	130.622	103.3724	96.64536	97.81383	0.63733	0.006162	0.014992	PARVB	chr22	+	44395091	44565106	1706
ENSG00000(	74.57702	87.913	50.13772	50.18806	41.41944	53.42772	0.54482	0.1034	0.1803	TEKT4P2	chr21	-	9907190	9968585	2180
ENSG00000(	2.071584	7.225726	1.319414	20.22504	16.56778	5.753754	-1.7895	0.031967	0.065714	SLC4A5	chr2	-	74443369	74570541	6576
ENSG00000(	1259.523	1171.772	985.6021	921.3629	652.5863	701.1361	0.58454	0.000203	0.000633	UROS	chr10	-	1.27E+08	1.28E+08	1556
ENSG00000(	4.143168	8.430014	3.958241	2.996302	0	2.465895	1.2724	0.2309	0.34427	CTB-161K2	chr7	+	91763918	91810039	2957
ENSG00000(	1957.647	2040.063	2010.787	1071.178	949.8858	813.7453	1.0808	6.00E-17	5.23E-16	ZDHHC9	chrX	-	1.29E+08	1.29E+08	4569
ENSG00000(	0	0	0	5.992604	8.283888	4.93179	-3.4914	0.00465	0.011594	C7orf29	chr7	+	1.5E+08	1.5E+08	2871
ENSG00000(	8.286335	2.408575	1.319414	3.745378	2.761296	3.28786	0.26241	0.79927	0.86912	QRFP	chr9	-	1.34E+08	1.34E+08	411
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	DUPD1	chr10	-	76797594	76818272	663
ENSG00000(	645.2984	516.6394	634.638	809.7507	675.5971	590.1708	-0.20779	0.19354	0.29943	SMIM15	chr5	-	60453536	60458301	2889
ENSG00000(	1.035792	2.408575	1.319414	3.745378	0	0	0.1951	0.88235	0.92656	OSTN	chr3	+	1.91E+08	1.91E+08	3134
ENSG00000(	1.035792	0	0	5.243529	0.920432	3.28786	-1.8883	0.14668	0.23956	VWC2	chr7	+	49813257	49952138	1891
ENSG00000(	32.10955	40.94578	11.87472	83.14739	134.3831	97.81383	-1.841	1.36E-06	5.55E-06	FAM221A	chr7	+	23719749	23742868	4154
ENSG00000(	855.5641	843.0014	712.4834	665.9282	600.1217	674.0112	0.31328	0.022995	0.049109	TMEM120B	chr12	+	1.22E+08	1.22E+08	7461
ENSG00000(	29.00217	61.41867	55.41538	19.47596	22.09037	24.65895	1.1046	0.010201	0.023674	FSIP2	chr2	+	1.87E+08	1.87E+08	21054
ENSG00000(	21.75163	12.04288	5.277655	5.992604	11.04518	12.32947	0.40177	0.56691	0.68613	RBM34	chr1	-	2.35E+08	2.35E+08	2054
ENSG00000(	0	9.634302	2.638828	53.18436	41.41944	110.1433	-3.8597	5.92E-10	3.30E-09	NOXA1	chr9	+	1.4E+08	1.4E+08	1678
ENSG00000(	140.8677	137.2888	109.5113	179.0291	128.8605	178.3664	-0.32372	0.16788	0.26733	TMEM198	chr2	+	2.2E+08	2.2E+08	2393
ENSG00000(	6.214751	1.204288	2.638828	3.745378	1.840864	3.28786	0.15533	0.8844	0.9278	BCL2L15	chr1	-	1.14E+08	1.14E+08	4041
ENSG00000(	64.2191	60.21439	92.35896	30.7121	23.0108	11.50751	1.6858	3.47E-05	0.00012	FZD9	chr7	+	72848109	72850450	2342
ENSG00000(	63.18331	50.58008	85.7619	8.239831	9.20432	13.15144	2.6307	2.18E-09	1.16E-08	SPRED3	chr19	+	38879061	38886881	1539
ENSG00000(	2.071584	0	1.319414	0	1.840864	0	0.45539	0.73712	NA	OPTC	chr1	+	2.03E+08	2.03E+08	1359
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	C11orf34	chr11	-	1.12E+08	1.12E+08	1541
ENSG00000(	8.286335	8.430014	3.958241	2.996302	0	0.821965	1.9443	0.065258	0.12216	SKOR1	chr15	+	68112042	68126899	3675

ENSG00000(	9.322127	12.04288	3.958241	60.67512	63.50981	41.92021	-2.6012	1.96E-07	8.74E-07	PRELP	chr1	+	2.03E+08	2.03E+08	5747
ENSG00000(	181.2636	167.396	135.8996	143.8225	125.1788	144.6658	0.22863	0.30137	0.42651	ZNF548	chr19	+	57901218	57912786	3381
ENSG00000(	411.2094	444.3822	504.0161	248.6931	380.1384	378.1039	0.43174	0.021739	0.046732	MTF1	chr1	-	38275239	38325292	7972
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	TMCO2	chr1	+	40711619	40717363	739
ENSG00000(	7.250543	1.204288	5.277655	2.247227	2.761296	23.01502	-0.87595	0.35448	0.48423	ZNF322P1	chr9	-	99959537	99961910	2374
ENSG00000(	0	0	0	9.737982	11.04518	19.72716	-4.6065	5.45E-05	0.000184	SHISA6	chr17	+	11144580	11467380	7575
ENSG00000(	343.8829	332.3834	277.0769	554.3159	591.8378	620.5835	-0.88456	1.09E-08	5.46E-08	TMEM201	chr1	+	9648932	9674935	3851
ENSG00000(	158.4762	173.4174	179.4403	184.2726	222.7445	188.23	-0.21818	0.27805	0.4	NHLRC3	chr13	+	39612443	39624246	3549
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	HMX2	chr10	+	1.25E+08	1.25E+08	1628
ENSG00000(	27.96638	20.47289	17.15238	130.3391	144.5078	204.6693	-2.8116	2.18E-17	1.95E-16	ZDHHC11	chr5	-	710471	851101	3923
ENSG00000(	9.322127	14.45145	13.19414	22.47227	7.363456	11.50751	-0.16544	0.80003	0.86975	FAM26F	chr6	+	1.17E+08	1.17E+08	1109
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	CNR2	chr1	-	24197016	24285549	5350
ENSG00000(	17.60846	22.88147	22.43003	9.737982	8.283888	2.465895	1.5159	0.019155	0.041746	CTD-3014M	chr17	-	41447213	41466567	2890
ENSG00000(	418.4599	380.5549	391.8659	298.1321	498.8741	368.2403	0.033845	0.85912	0.91045	SLX4	chr16	-	3631182	3661599	7307
ENSG00000(	1.035792	3.612863	1.319414	0	0	0.821965	1.5446	0.25043	0.36783	GLRA4	chrX	-	1.03E+08	1.03E+08	1837
ENSG00000(	2.071584	0	0	0.749076	4.60216	9.863579	-1.9693	0.10486	0.18237	ENTPD8	chr9	-	1.4E+08	1.4E+08	2836
ENSG00000(	24080.09	24504.85	18647.27	15599.5	14483.92	16430.26	0.53043	1.80E-05	6.48E-05	RPL14	chr3	+	40498783	40503861	966
ENSG00000(	0	0	1.319414	5.992604	11.96562	9.863579	-3.332	0.003074	0.007925	BEND4	chr4	-	42112955	42154895	8765
ENSG00000(	0	0	0	1.498151	0	2.465895	-1.1271	0.39798	NA	RP11-159F	chr5	+	43336266	43348818	432
ENSG00000(	225.8026	236.0404	255.9663	191.7633	197.8929	138.0901	0.44054	0.032067	0.065901	RPSAP47	chr8	+	81471105	81471992	888
ENSG00000(	11.39371	2.408575	1.319414	6.74168	10.12475	4.93179	-0.42821	0.63588	0.74475	FAM78B	chr1	-	1.66E+08	1.66E+08	4399
ENSG00000(	12.4295	26.49433	3.958241	21.72319	16.56778	36.98842	-0.76396	0.21304	0.32328	ZNF563	chr19	-	12428291	12444534	2754
ENSG00000(	4.143168	0	10.55531	0	0	1.64393	2.1264	0.088958	0.15922	TMC3	chr15	-	81623558	81666554	4644
ENSG00000(	14.50109	39.74149	36.94359	35.95563	28.53339	50.13986	-0.33236	0.46928	0.59853	FBF1	chr17	-	73905655	73937221	4825
ENSG00000(	1.035792	0	0	86.14369	83.75931	97.81383	-6.5388	1.24E-13	9.05E-13	KLRG2	chr7	-	1.39E+08	1.39E+08	2197
ENSG00000(	2.071584	2.408575	0	0	0.920432	7.397684	-0.59258	0.6394	0.74749	GPR179	chr17	-	36481413	36499730	7980
ENSG00000(	1530.9	1593.273	1787.806	1301.144	1502.145	1330.761	0.24808	0.043312	0.085783	MSL1	chr17	+	38278551	38293040	3424
ENSG00000(	1.035792	3.612863	1.319414	2.247227	6.443024	0	-0.39121	0.74439	0.82968	CTD-3088G	chr16	-	11453702	11617444	7627
ENSG00000(	0	1.204288	1.319414	0	0	0.821965	0.59385	0.65509	NA	LRRK2	chr12	+	40590546	40763087	9158
ENSG00000(	0	0	0	27.7158	13.80648	21.37109	-5.2461	1.77E-06	7.14E-06	GJB3	chr1	+	35246790	35251970	2217
ENSG00000(	44.53905	45.76293	26.38828	9.737982	19.32907	5.753754	1.6922	0.001338	0.00368	FAM196A	chr10	-	1.29E+08	1.29E+08	4403
ENSG00000(	174.013	145.7188	160.9685	356.56	286.2544	318.9224	-0.99527	1.52E-07	6.85E-07	TRMT2B	chrX	-	1E+08	1E+08	3421
ENSG00000(	180.2278	149.3317	187.3568	134.8336	149.11	157.8173	0.22585	0.28943	0.41316	PTPLAD2	chr9	-	20995306	21031635	4161
ENSG00000(	153.2972	149.3317	196.5927	62.92235	108.611	101.9236	0.86244	0.001002	0.002808	C1orf192	chr1	-	1.61E+08	1.61E+08	774
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	USP32P1	chr17	+	16689803	16719854	3846
ENSG00000(	0	7.225726	1.319414	0.749076	11.04518	2.465895	-0.57108	0.61291	0.72627	NYX	chrX	+	41306687	41334963	2713
ENSG00000(	328.346	334.792	303.4652	598.5114	486.9085	563.046	-0.76773	8.32E-07	3.48E-06	FAM120AO	chr9	-	96208776	96215874	2771
ENSG00000(	5.17896	8.430014	6.597069	2.996302	2.761296	0.821965	1.371	0.15683	0.25288	UTS2B	chr3	-	1.91E+08	1.91E+08	2395
ENSG00000(	1.035792	2.408575	0	1.498151	0.920432	0	0.28377	0.83341	NA	C9orf152	chr9	-	1.13E+08	1.13E+08	2717
ENSG00000(	438.14	381.7592	533.0432	241.9514	345.162	244.9455	0.6989	0.000279	0.000854	AAK1	chr2	-	69686414	69693664	3657
ENSG00000(	2195.879	2061.741	1971.204	3655.489	3795.862	3984.064	-0.87464	3.82E-16	3.22E-15	NOC2L	chr1	-	879584	894689	4201
ENSG00000(	12.4295	14.45145	14.51355	5.992604	15.64734	16.4393	0.11804	0.85324	0.90645	MSANTD1	chr4	+	3246096	3273465	3164
ENSG00000(	0	0	0	2.996302	3.681728	2.465895	-2.3627	0.074875	0.13743	AADACL3	chr1	+	12776118	12788726	3832
ENSG00000(	3.107376	8.430014	1.319414	16.47966	23.93123	18.90519	-2.0256	0.005259	0.012975	DHFRP1	chr18	-	23749724	23751313	1474

ENSG00000(	1696.627	1458.392	1261.36	2695.174	2069.131	2684.537	-0.7514	2.22E-07	9.84E-07	NELFB	chr9	+	1.4E+08	1.4E+08	2698
ENSG00000(	12.4295	14.45145	17.15238	2.247227	13.80648	9.041614	0.76248	0.28195	0.40461	HIST1H4D	chr6	-	26188938	26189304	367
ENSG00000(	15.53688	4.817151	15.83297	8.239831	11.96562	4.109825	0.53409	0.46825	0.59747	LIPI	chr21	-	15481134	15583166	1652
ENSG00000(	35.21692	46.96722	43.54065	14.98151	3.681728	4.109825	2.3292	2.91E-05	0.000102	LRRC66	chr4	-	52859868	52883786	3327
ENSG00000(	576.9361	676.8097	924.9091	338.5821	384.7406	263.8507	1.1354	3.88E-09	2.02E-08	ZNF292	chr6	+	87862551	87973914	10610
ENSG00000(	3.107376	0	0	10.48706	4.60216	0.821965	-1.6786	0.1573	0.25351	HUS1B	chr6	-	655939	656963	1025
ENSG00000(	302.4512	301.0719	287.6322	249.4422	192.3703	209.6011	0.44849	0.013487	0.030459	KCTD21	chr11	-	77882295	77899868	3585
ENSG00000(	2.071584	1.204288	5.277655	0.749076	0	3.28786	0.75765	0.53614	0.66028	SBSN	chr19	-	36014269	36019253	1945
ENSG00000(	163.6551	171.0089	162.2879	138.579	101.2475	147.1317	0.3558	0.1177	0.20067	ADAT2	chr6	-	1.44E+08	1.44E+08	2065
ENSG00000(	0	0	1.319414	0.749076	4.60216	3.28786	-1.6864	0.19647	0.30318	AC138783.	chr7	-	74702428	74714647	905
ENSG00000(	0	2.408575	3.958241	6.74168	5.522592	5.753754	-1.2674	0.22127	0.33302	FAM35DP	chr10	+	47379727	47420712	2712
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	VHLL	chr1	-	1.56E+08	1.56E+08	1014
ENSG00000(	80.79177	85.50443	85.7619	148.317	121.497	107.6774	-0.57984	0.02365	0.050411	ZNF567	chr19	+	37178514	37218603	3734
ENSG00000(	1615.835	1610.133	1361.635	1791.789	1423.908	1814.077	-0.13234	0.32704	0.45474	NDUFA4	chr7	-	10971578	10979883	2130
ENSG00000(	13.46529	6.021439	5.277655	7.490755	7.363456	16.4393	-0.29505	0.69328	0.79084	ANKDD1B	chr5	+	74907284	74967671	2569
ENSG00000(	164.6909	197.5032	118.7472	129.5901	92.96363	175.9005	0.26873	0.32151	0.44875	ALKBH2	chr12	-	1.1E+08	1.1E+08	1159
ENSG00000(	102.5434	151.7403	130.622	134.8336	96.64536	109.3213	0.16865	0.50685	0.6345	RNFT1	chr17	-	58029601	58042122	2101
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RNF222	chr17	-	8294022	8301144	3062
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	CGB5	chr19	+	49547141	49548568	841
ENSG00000(	1.035792	6.021439	0	518.3603	588.156	431.5316	-7.4182	1.72E-43	3.94E-42	RELN	chr7	-	1.03E+08	1.04E+08	11571
ENSG00000(	36.25272	34.92434	43.54065	763.308	634.1776	628.8032	-4.1227	8.04E-81	4.39E-79	FAM111B	chr11	+	58874658	58894883	3488
ENSG00000(	131.5456	157.7617	135.8996	0	1.840864	0.821965	6.81	6.08E-23	6.93E-22	APOD	chr3	-	1.95E+08	1.95E+08	1210
ENSG00000(	3938.081	3812.775	3702.275	2951.358	3872.257	4026.806	0.078126	0.54666	0.66859	H1F0	chr22	+	38201114	38203442	2329
ENSG00000(	254.8048	240.8575	207.148	1276.425	1158.824	1156.505	-2.3437	2.19E-59	7.53E-58	LITAF	chr16	-	11641853	11730237	2357
ENSG00000(	0	0	0	4.494453	0	0	-1.1446	0.38559	NA	VSTM1	chr19	-	54544079	54567207	1041
ENSG00000(	815.1682	887.56	633.3186	352.8146	251.2779	319.7444	1.3317	2.67E-14	2.02E-13	TMEM120A	chr7	-	75616155	75623977	1456
ENSG00000(	293.1291	283.0076	399.7824	423.2277	471.2612	337.0056	-0.3357	0.076982	0.14064	ARID2	chr12	+	46123448	46301823	8642
ENSG00000(	7.250543	6.021439	1.319414	0.749076	0	0.821965	2.3075	0.052732	0.10172	RIMKLBP1	chr21	+	37422512	37423675	1164
ENSG00000(	3015.19	2922.806	3072.915	3951.374	3867.655	3246.761	-0.29587	0.009977	0.023207	SF3B3	chr16	+	70557691	70608820	6969
ENSG00000(	0	0	1.319414	0.749076	2.761296	2.465895	-1.2635	0.34445	0.47364	PRSS48	chr4	+	1.52E+08	1.52E+08	989
ENSG00000(	1.035792	0	1.319414	1.498151	4.60216	6.575719	-1.7465	0.14544	0.238	IL1RAPL2	chrX	+	1.04E+08	1.05E+08	2985
ENSG00000(	301.4154	311.9105	233.5362	192.5124	155.553	189.0519	0.65357	0.000924	0.002602	BLOC1S3	chr19	+	45682003	45685059	2601
ENSG00000(	4.143168	2.408575	2.638828	746.0792	1145.017	1366.928	-8.1324	2.04E-62	7.53E-61	SP6	chr17	-	45922279	45933240	3848
ENSG00000(	0	0	0	35.95563	46.0216	51.78379	-6.2902	1.67E-09	8.95E-09	ANKRD34B	chr5	-	79852574	79866307	3938
ENSG00000(	397.7441	382.9635	249.3692	29.21395	49.70333	49.3179	2.9877	1.07E-30	1.66E-29	PLAC9	chr10	+	81891477	81905115	785
ENSG00000(	3.107376	0	0	5.992604	0	0.821965	-0.66714	0.61431	0.72765	NKAPL	chr6	+	28227098	28228736	1639
ENSG00000(	54.89697	98.75159	94.99779	5.992604	9.20432	8.219649	3.3203	6.97E-14	5.14E-13	UBE2Q2P1	chr15	-	85070012	85114447	2150
ENSG00000(	15.53688	8.430014	17.15238	3700.433	3352.213	3948.719	-7.9843	2.60E-198	7.19E-196	CLDN4	chr7	+	73213872	73247014	4163
ENSG00000(	97.36444	96.34302	89.72014	31.46117	60.74851	52.60575	0.96249	0.002486	0.006513	ZNF573	chr19	-	38226734	38307940	2516
ENSG00000(	7.250543	12.04288	19.79121	6.74168	12.88605	15.61733	0.13143	0.84386	0.90048	CRYM-AS1	chr16	+	21312170	21329912	2028
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	GRAPL	chr17	+	19030782	19062489	1308
ENSG00000(	0	2.408575	0	2.996302	3.681728	1.64393	-1.1871	0.35186	0.48164	FAM47E	chr4	+	77135193	77232282	6249
ENSG00000(	2841.177	2892.699	2549.107	4808.316	4025.97	4940.009	-0.73227	7.95E-10	4.40E-09	HN1	chr17	-	73131343	73164376	2289
ENSG00000(	143.9751	126.4502	130.622	70.4131	57.06678	74.79881	0.97719	0.00014	0.000446	ZNF527	chr19	+	37861963	37883968	5333

ENSG00000(	0	0	0	2.996302	4.60216	2.465895	-2.5009	0.057636	0.10993	ZAR1L	chr13	-	32877837	32889481	1564
ENSG00000(	816.204	865.8829	564.7091	919.8648	788.8102	842.514	-0.18161	0.26632	0.3863	S100A13	chr1	-	1.54E+08	1.54E+08	2184
ENSG00000(	300.3797	358.8777	336.4505	352.8146	344.2416	352.623	-0.07739	0.62968	0.73985	ZNF33A	chr10	+	38299578	38354016	6117
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	OR14I1	chr1	-	2.49E+08	2.49E+08	1002
ENSG00000(	906.3179	824.9371	1042.337	1071.927	1002.35	868.8169	-0.08614	0.54073	0.66379	PCDH18	chr4	-	1.38E+08	1.38E+08	5906
ENSG00000(	46.61064	25.29004	36.94359	120.6012	85.60018	103.5676	-1.4816	7.09E-06	2.68E-05	ZNF600	chr19	-	53267448	53290044	3829
ENSG00000(	5.17896	3.612863	10.55531	0.749076	2.761296	4.109825	1.1363	0.24704	0.36383	BTBD8	chr1	+	92545862	92613393	1616
ENSG00000(	2.071584	0	2.638828	0.749076	2.761296	2.465895	-0.23431	0.85083	0.90495	RP11-129B	chr3	-	64064037	64073039	2129
ENSG00000(	0	0	5.277655	12.73428	17.48821	6.575719	-2.4241	0.012703	0.028832	DPY19L2P1	chr7	-	35119601	35225934	3914
ENSG00000(	201.9794	146.9231	213.745	47.94084	57.06678	30.4127	2.0355	5.86E-13	4.07E-12	MAOA	chrX	+	43515467	43606068	4015
ENSG00000(	1700.77	1820.883	1778.57	502.6297	417.8761	447.1489	1.9486	1.35E-53	4.04E-52	AC016683.	chr2	+	1.14E+08	1.14E+08	2687
ENSG00000(	42.46747	27.69862	42.22124	46.44268	31.29469	30.4127	0.051372	0.89986	0.9378	C15orf61	chr15	+	67813406	67819628	1400
ENSG00000(	41.43168	31.31148	32.98534	56.92974	64.43024	66.57916	-0.81	0.020814	0.044953	AC069277.	chr3	+	6532166	6777816	1083
ENSG00000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	NUGGC	chr8	-	27879481	27941388	3887
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	RP11-173C	chr12	+	1.27E+08	1.27E+08	2815
ENSG00000(	2099.55	2176.148	1830.027	1040.466	1462.566	1346.379	0.66464	3.32E-06	1.30E-05	TSPYL1	chr6	-	1.17E+08	1.17E+08	3326
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	TRIM64B	chr11	-	89602450	89609185	2689
ENSG00000(	1191.161	1305.448	1324.691	1951.342	1956.838	1675.165	-0.54647	6.57E-06	2.49E-05	PNRC2	chr1	+	24285599	24289952	2416
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	C22orf43	chr22	-	23950639	23974508	1300
ENSG00000(	0	0	0	2.996302	1.840864	0	-1.3549	0.31496	NA	AL450307.	chr10	-	1.34E+08	1.34E+08	3384
ENSG00000(	2.071584	0	0	3.745378	0	6.575719	-1.4449	0.26276	0.3824	GJB5	chr1	+	35220648	35224113	1355
ENSG00000(	18.64425	31.31148	23.74945	62.17327	69.95283	79.7306	-1.4989	6.42E-05	0.000215	FHIT	chr3	-	59735036	61237133	3063
ENSG00000(	7.250543	10.83859	2.638828	3.745378	3.681728	5.753754	0.57996	0.51266	0.63966	FAM150B	chr2	-	279558	288851	1389
ENSG00000(	109.7939	98.75159	117.4278	83.89646	104.9292	87.95025	0.23551	0.35464	0.48435	ZKSCAN3	chr6	+	28317691	28334531	2340
ENSG00000(	749.9133	741.8412	605.6109	1569.313	1429.431	1789.418	-1.1866	1.92E-17	1.72E-16	RRP7A	chr22	-	42905974	42915808	3801
ENSG00000(	208.1942	245.6747	248.0498	533.3418	453.773	364.9524	-0.94388	3.83E-07	1.66E-06	LIN54	chr4	-	83831126	83934079	6127
ENSG00000(	1480.147	1347.598	1352.399	496.6371	482.3064	517.0159	1.4796	7.79E-33	1.30E-31	FAM53B	chr10	-	1.26E+08	1.26E+08	5431
ENSG00000(	23.82321	12.04288	14.51355	0	0	0	5.3229	2.08E-06	8.34E-06	FAM180A	chr7	-	1.35E+08	1.35E+08	1800
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	C6orf222	chr6	-	36283534	36304662	3736
ENSG00000(	0	1.204288	1.319414	11.98521	12.88605	30.4127	-3.7812	7.83E-05	0.000259	S100A14	chr1	-	1.54E+08	1.54E+08	1218
ENSG00000(	198.872	219.1804	284.9934	257.682	248.5166	258.9189	-0.12539	0.51444	0.64123	KAZN	chr1	+	14925200	15444539	6030
ENSG00000(	2023.937	1947.333	2117.659	834.4702	1098.075	866.351	1.1195	4.57E-17	4.02E-16	SLC35E2B	chr1	-	1592939	1624167	6261
ENSG00000(	16569.56	16231.39	12620.19	9295.278	8826.022	10498.96	0.66493	1.75E-07	7.85E-07	RPS2P46	chr17	-	19349246	19350169	923
ENSG00000(	0	0	0	2.247227	0	1.64393	-1.1086	0.40518	NA	FAM90A27	chr19	+	53784808	53788200	1383
ENSG00000(	2.071584	2.408575	2.638828	1.498151	4.60216	2.465895	-0.20373	0.85477	0.90762	FAM179A	chr2	+	29179477	29284239	12691
ENSG00000(	39.36009	46.96722	46.17948	80.15108	137.1444	81.37453	-1.1545	0.00044	0.001303	TMEM194B	chr2	-	1.91E+08	1.91E+08	6168
ENSG00000(	1.035792	0	0	3.745378	0.920432	0.821965	-1.2325	0.36015	0.48975	ALG1L	chr3	-	1.26E+08	1.26E+08	805
ENSG00000(	6.214751	2.408575	5.277655	0	5.522592	0	1.0332	0.37571	0.50624	KIAA0408	chr6	-	1.28E+08	1.28E+08	6580
ENSG00000(	280.6996	278.1905	311.3817	350.5674	439.9665	376.4599	-0.42143	0.012133	0.027674	GSPT2	chrX	+	51486481	51489324	2844
ENSG00000(	22.78742	8.430014	5.277655	30.7121	16.56778	26.30288	-0.93819	0.12175	0.20633	C8orf76	chr8	-	1.24E+08	1.24E+08	1342
ENSG00000(	0	0	6.597069	0	0	0	1.83	0.17508	0.27674	CXCL17	chr19	-	42932440	42947200	1172
ENSG00000(	2.071584	1.204288	0	17.22874	46.94203	28.76877	-4.177	6.80E-07	2.87E-06	OR7E12P	chr11	-	3412010	3412982	973
ENSG00000(	4628.954	4681.066	4578.366	11376.96	11465.82	12191.38	-1.3331	8.50E-43	1.92E-41	HMGB1	chr13	-	31032884	31191734	4199
ENSG00000(	24.85901	33.72006	31.66593	2.996302	12.88605	9.041614	1.7821	0.002221	0.00587	MMP23B	chr1	+	1567474	1570639	1531

ENSG00000(	33.14534	27.69862	43.54065	100.3761	86.52061	89.59418	-1.3911	1.96E-05	7.02E-05	SH2D5	chr1	-	21046225	21059330	3705
ENSG00000(	0	1.204288	1.319414	2.247227	1.840864	4.109825	-1.1864	0.34433	0.47357	RP11-168G	chr15	-	1.01E+08	1.01E+08	2072
ENSG00000(	11.39371	2.408575	6.597069	43.44638	41.41944	39.45432	-2.4668	9.64E-06	3.59E-05	USP32P3	chr17	+	20318860	20334321	1174
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	NCR1	chr19	+	55417508	55427508	1612
ENSG00000(	0	0	0	4.494453	6.443024	22.19305	-4.2456	0.000335	0.001013	RASSF10	chr11	+	13030696	13032647	1848
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	OR2L13	chr1	+	2.48E+08	2.48E+08	1883
ENSG00000(	681.5511	670.7883	666.304	1077.92	879.0126	1133.49	-0.61326	9.65E-06	3.59E-05	BLOC1S2	chr10	-	1.02E+08	1.02E+08	2024
ENSG00000(	55.93276	50.58008	46.17948	9.737982	20.2495	9.863579	1.8976	2.93E-05	0.000103	SYCP2	chr20	-	58438618	58508710	5567
ENSG00000(	42.46747	45.76293	36.94359	241.9514	281.6522	259.7409	-2.6202	6.07E-27	8.12E-26	ZNF724P	chr19	-	23404401	23433192	2764
ENSG00000(	97.36444	101.1602	167.5656	28.46487	23.0108	14.79537	2.4157	8.59E-12	5.49E-11	IL1RAP	chr3	+	1.9E+08	1.9E+08	4778
ENSG00000(	0	0	0	7.490755	1.840864	6.575719	-3.1747	0.012296	0.028007	PTPRT	chr20	-	40701392	41818610	12755
ENSG00000(	0	0	0	3.745378	0.920432	0.821965	-1.6164	0.23349	NA	PAX5	chr9	-	36833272	37034103	8536
ENSG00000(	0	2.408575	3.958241	1.498151	2.761296	0	0.3766	0.76856	0.8477	AC079610.	chr2	-	2.14E+08	2.14E+08	1727
ENSG00000(	22.78742	34.92434	23.74945	11.23613	4.60216	5.753754	1.8034	0.00234	0.006164	SPOCK3	chr4	-	1.68E+08	1.68E+08	2986
ENSG00000(	34.18113	34.92434	63.33186	14.23244	24.85166	14.79537	1.2603	0.006462	0.015654	ZNF699	chr19	-	9404951	9420514	3358
ENSG00000(	2.071584	1.204288	0	6.74168	0	0	-0.62242	0.63869	0.74685	RP3-391O2	chr6	-	34544035	34544433	399
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	ADAM5	chr8	+	39172110	39274897	1998
ENSG00000(	38.3243	13.24716	15.83297	67.4168	77.31629	50.13986	-1.4711	0.000703	0.002021	TDRD7	chr9	+	1E+08	1E+08	3834
ENSG00000(	3.107376	1.204288	2.638828	5.992604	0.920432	9.041614	-0.9772	0.35312	0.4828	C16orf93	chr16	-	30768744	30774031	2114
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	OR8A1	chr11	+	1.24E+08	1.24E+08	1145
ENSG00000(	1032.685	1085.063	823.3142	182.0254	293.6178	350.979	1.8232	1.32E-19	1.32E-18	KIAA0895L	chr16	-	67209505	67217943	3550
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	HLA-DRB1	chr6	-	32546546	32557625	1229
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	MYT1	chr20	+	62783144	62873604	5614
ENSG00000(	7.250543	18.06432	7.916483	3.745378	2.761296	3.28786	1.5718	0.057421	0.10957	SERPINA3	chr14	+	95058395	95090983	3067
ENSG00000(	219.5879	152.9445	175.482	6.74168	9.20432	5.753754	4.5805	2.32E-34	4.09E-33	AKR1C3	chr10	+	5077546	5149878	1807
ENSG00000(	1759.81	1460.801	1541.075	2853.978	2367.351	2190.537	-0.63655	1.90E-06	7.65E-06	SPATS2L	chr2	+	2.01E+08	2.01E+08	2698
ENSG00000(	292.0933	245.6747	248.0498	174.5346	165.6778	146.3098	0.68954	0.000352	0.001059	ZNF250	chr8	-	1.46E+08	1.46E+08	6364
ENSG00000(	87.00652	79.48299	88.40072	196.2578	140.8261	176.7225	-1.0053	3.30E-05	0.000115	WDSUB1	chr2	-	1.6E+08	1.6E+08	1920
ENSG00000(	133.6172	163.7831	153.052	116.8558	127.94	152.0635	0.18024	0.427	0.55722	ZNF79	chr9	+	1.3E+08	1.3E+08	2078
ENSG00000(	1042.007	1012.806	876.0908	226.2208	209.8585	280.29	2.0256	2.63E-38	5.20E-37	S100A4	chr1	-	1.54E+08	1.54E+08	755
ENSG00000(	196.8005	240.8575	145.1355	8.988907	4.60216	5.753754	4.7867	8.51E-35	1.52E-33	PLEKHG4	chr16	+	67311413	67323402	6949
ENSG00000(	1552.652	1547.51	2128.214	70.4131	64.43024	58.35951	4.7349	2.07E-154	3.31E-152	FAT4	chr4	+	1.26E+08	1.26E+08	16123
ENSG00000(	2.071584	0	0	0	0	1.64393	0.14412	0.91322	NA	C11orf92	chr11	-	1.11E+08	1.11E+08	5496
ENSG00000(	20.71584	25.29004	34.30476	168.542	129.7809	143.0219	-2.44	6.15E-15	4.84E-14	ZNF681	chr19	-	23921997	23941693	6497
ENSG00000(	2.071584	6.021439	5.277655	2.247227	28.53339	20.54912	-1.7443	0.035233	0.071574	HIST1H4A	chr6	+	26021907	26022278	372
ENSG00000(	163.6551	183.0517	201.8703	176.0328	120.5766	133.1583	0.34469	0.12597	0.21195	ACADSB	chr10	+	1.25E+08	1.25E+08	5859
ENSG00000(	1351.708	1306.652	1209.902	1645.719	2197.071	2148.616	-0.62879	3.87E-06	1.51E-05	STK40	chr1	-	36805225	36851497	4837
ENSG00000(	2.071584	2.408575	0	0	0	4.93179	-0.07559	0.95457	0.97296	RPS2P4	chr14	-	1.05E+08	1.05E+08	891
ENSG00000(	426.7463	451.6079	336.4505	561.0576	776.8446	762.7834	-0.7846	5.76E-06	2.20E-05	TMEM63A	chr1	-	2.26E+08	2.26E+08	5407
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	CTSE	chr1	+	2.06E+08	2.06E+08	2243
ENSG00000(	20.71584	2.408575	11.87472	0.749076	6.443024	3.28786	1.5501	0.082668	0.14959	SEMA4A	chr1	+	1.56E+08	1.56E+08	3300
ENSG00000(	1.035792	1.204288	0	0.749076	0	0	0.55357	0.6746	NA	AC034229.	chr5	+	10201621	10201960	337
ENSG00000(	29.00217	46.96722	59.37362	0	0	1.64393	5.5273	6.21E-11	3.73E-10	HRCT1	chr9	+	35906189	35907138	950
ENSG00000(	861.7789	847.8186	828.5919	943.0861	882.6943	755.3858	-0.02413	0.8569	0.90909	MPHOSPH8	chr13	+	20207788	20247599	4235

ENSG00000(	293.1291	299.8676	323.2564	483.9028	392.104	376.4599	-0.45124	0.007251	0.017409	RNF216P1	chr7	+	5013619	5080306	3632
ENSG00000(	2948.9	3308.178	3028.055	1692.162	1601.552	2121.491	0.7759	2.46E-09	1.31E-08	EEF1A1P5	chr9	+	1.36E+08	1.36E+08	1676
ENSG00000(	27.96638	26.49433	17.15238	170.0401	255.8801	179.1884	-3.0236	1.76E-22	1.97E-21	GREB1	chr2	+	11674242	11782914	8484
ENSG00000(	0	0	0	2.247227	0.920432	0.821965	-1.2297	0.36205	NA	SIRPB2	chr20	-	1451386	1472233	2642
ENSG00000(	337.6682	325.1577	374.7135	293.6376	254.9597	295.9074	0.2939	0.078653	0.14323	ZNF766	chr19	+	52772824	52795977	2975
ENSG00000(	1.035792	0	0	16.47966	19.32907	24.65895	-4.4881	1.08E-05	3.99E-05	RYR1	chr19	+	38924339	39078204	15377
ENSG00000(	503.3949	498.5751	560.7509	62.92235	112.2927	76.44274	2.6268	1.21E-36	2.28E-35	SRGAP3	chr3	-	9022275	9404737	8656
ENSG00000(	0	1.204288	0	0	0	4.109825	-0.75943	0.57378	NA	HIST1H2BB	chr6	-	26043455	26043885	431
ENSG00000(	460.9274	402.2321	501.3772	539.3344	595.5195	503.0425	-0.26263	0.085512	0.15412	FAM217B	chr20	+	58508819	58523735	5152
ENSG00000(	0	1.204288	2.638828	0	0.920432	0	0.94343	0.48603	NA	SULT1C3	chr2	+	1.09E+08	1.09E+08	915
ENSG00000(	35562.88	34531.75	32427.23	66332.89	52083.56	55449.75	-0.76067	4.19E-11	2.55E-10	TUBB	chr6	+	30687978	30693203	2903
ENSG00000(	370.8135	319.1362	500.0578	343.0766	514.5215	331.2519	0.001375	0.99475	0.9967	LCOR	chr10	+	98592017	98740800	7777
ENSG00000(	3992.978	3999.44	3546.584	3119.151	3287.783	3570.616	0.20968	0.059229	0.11241	SUPT5H	chr19	+	39926796	39967310	3902
ENSG00000(	902.1747	945.3659	766.5794	954.3222	838.5135	900.8736	-0.04281	0.75061	0.8346	XPNPEP3	chr22	+	41253081	41368585	7988
ENSG00000(	125.3308	151.7403	166.2461	317.608	372.775	320.5663	-1.1868	7.70E-10	4.26E-09	ZNF107	chr7	+	64126511	64171404	6094
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	OR10S1	chr11	-	1.24E+08	1.24E+08	1121
ENSG00000(	28507.06	29063.08	24837.96	27323.28	25744.48	27963.25	0.024301	0.81734	0.88166	PPIA	chr7	+	44836279	44864163	2238
ENSG00000(	11.39371	16.86003	19.79121	0.749076	5.522592	0.821965	2.5027	0.002522	0.006601	ZNF471	chr19	+	57019212	57041590	6287
ENSG00000(	83.89914	67.44011	72.56776	65.16957	63.50981	68.22309	0.18536	0.52546	0.65045	ZNF836	chr19	-	52657117	52674896	3333
ENSG00000(	85.97073	115.6116	122.7055	154.3096	191.4499	120.8288	-0.52297	0.041227	0.082173	ZNF493	chr19	+	21579921	21610375	5023
ENSG00000(	4.143168	1.204288	1.319414	0	0	0	2.1615	0.11037	0.19002	LINC00523	chr14	+	1.01E+08	1.01E+08	2071
ENSG00000(	3.107376	1.204288	0	0	0	0	1.4526	0.27741	NA	AC090519.	chr15	-	44595115	44595293	177
ENSG00000(	99.43602	89.11729	84.44248	41.94823	44.18074	33.70056	1.1753	0.000136	0.000436	GTF2IRD2	chr7	-	74210483	74267847	3558
ENSG00000(	11.39371	6.021439	2.638828	0	0	0	3.881	0.001798	0.004833	GRM7	chr3	+	6811688	7783215	4236
ENSG00000(	147.0825	177.0303	121.3861	286.1469	157.3939	159.4612	-0.43402	0.097844	0.1722	SUPT3H	chr6	-	44777054	45345690	2389
ENSG00000(	259.9838	208.3418	192.6344	659.1865	509.9193	507.1524	-1.3337	2.05E-13	1.47E-12	NIF3L1	chr2	+	2.02E+08	2.02E+08	1680
ENSG00000(	279.6638	250.4918	291.5904	119.8521	133.4626	138.9121	1.0623	4.31E-08	2.05E-07	AC005154.	chr7	-	30555925	30634425	4034
ENSG00000(	44.53905	71.05298	39.58241	38.95193	15.64734	35.34449	0.75936	0.076664	0.14018	ATP2A1	chr16	+	28889726	28915830	3536
ENSG00000(	3023.477	2983.021	3153.399	3839.761	3656.876	3104.561	-0.21057	0.069435	0.12886	IARS	chr9	-	94972489	95056038	4656
ENSG00000(	74.57702	66.23582	117.4278	75.65663	118.7357	133.9803	-0.34496	0.26081	0.37994	HIATL2	chr9	-	99708327	99775862	786
ENSG00000(	1726.665	1613.746	1545.034	996.2705	2034.155	1435.151	0.12993	0.49292	0.62189	POM121	chr7	+	72349936	72421979	7011
ENSG00000(	251.6974	213.1589	273.1187	263.6746	306.5039	246.5895	-0.14524	0.43522	0.56493	ZBTB44	chr11	-	1.3E+08	1.3E+08	9315
ENSG00000(	20.71584	20.47289	3.958241	8.239831	70.87326	32.8786	-1.2135	0.061477	0.11596	HIST1H2BC	chr6	+	27861203	27861669	467
ENSG00000(	0	0	0	12.73428	9.20432	6.575719	-4.0917	0.000535	0.001564	STK31	chr7	+	23749786	23872132	3732
ENSG00000(	3.107376	0	5.277655	2.996302	1.840864	0.821965	0.40968	0.7306	0.81963	CGB7	chr19	-	49557531	49562117	3386
ENSG00000(	14.50109	42.15007	26.38828	23.22134	5.522592	18.08323	0.77108	0.18744	0.29212	NLGN3	chrX	+	70364681	70391051	3913
ENSG00000(	2.071584	3.612863	3.958241	0	0	0	2.7354	0.039239	0.078686	ADH7	chr4	-	1E+08	1E+08	2516
ENSG00000(	162.6193	125.2459	200.5509	57.67882	79.15715	63.2913	1.2768	1.64E-06	6.64E-06	ZKSCAN7	chr3	+	44596685	44635665	3477
ENSG00000(	282.7712	302.2762	242.7721	410.4934	272.4479	295.0854	-0.2401	0.22297	0.33512	CD55	chr1	+	2.07E+08	2.08E+08	2760
ENSG00000(	6.214751	1.204288	2.638828	5.992604	0	4.93179	-0.09255	0.93312	0.95995	CPNE4	chr3	-	1.31E+08	1.32E+08	5431
ENSG00000(	9.322127	10.83859	5.277655	2.996302	0	0	2.4418	0.020838	0.044997	AC021860.	chr4	-	38628029	38666430	1896
ENSG00000(	94.25706	98.75159	67.2901	51.68621	37.73771	37.81039	1.0171	0.001593	0.004315	ZNF565	chr19	-	36673188	36737159	2519
ENSG00000(	4.143168	3.612863	3.958241	0.749076	5.522592	4.109825	0.15728	0.87828	0.92394	NTNG2	chr9	+	1.35E+08	1.35E+08	4792
ENSG00000(	6.214751	0	1.319414	0	0.920432	3.28786	0.58185	0.64834	0.75486	ELAVL3	chr19	-	11562141	11591861	4729

ENSG00000(	1130.049	1099.515	982.9633	1806.77	1757.105	1934.905	-0.7732	7.71E-11	4.60E-10	WDR5	chr9	+	1.37E+08	1.37E+08	3151
ENSG00000(	2859.821	3023.966	2327.446	3480.205	3169.968	3435.813	-0.29578	0.016894	0.037303	LONP1	chr19	-	5691845	5720583	3236
ENSG00000(	3.107376	3.612863	14.51355	16.47966	11.04518	13.9734	-0.91597	0.21685	0.32794	C9orf163	chr9	+	1.39E+08	1.39E+08	2572
ENSG00000(	1339.279	1327.125	1756.14	1339.347	1525.156	1251.853	0.1027	0.47145	0.60042	TRRAP	chr7	+	98475556	98610866	12677
ENSG00000(	514.7886	572.0367	496.0996	446.449	365.4115	330.4299	0.468	0.004072	0.010273	NUDT11	chrX	-	51232863	51239448	2385
ENSG00000(	112.9013	90.32158	212.4256	86.14369	223.665	109.3213	-0.01196	0.97244	0.98396	SRGAP2B	chr1	+	1.44E+08	1.44E+08	1334
ENSG00000(	91.14969	85.50443	106.8725	289.1432	300.0608	327.964	-1.6869	1.50E-16	1.29E-15	FUT4	chr11	+	94277017	94283063	6047
ENSG00000(	135.6887	131.2674	147.7743	221.7264	248.5166	241.6577	-0.77581	8.82E-05	0.00029	ASB13	chr10	-	5680830	5708558	2780
ENSG00000(	2.071584	3.612863	3.958241	4.494453	11.96562	11.50751	-1.3576	0.12346	0.20859	HIST1H2BM	chr6	+	27782822	27783267	446
ENSG00000(	0	0	1.319414	98.87797	90.20234	92.88204	-6.6019	5.12E-14	3.82E-13	SLC35F1	chr6	+	1.18E+08	1.19E+08	4852
ENSG00000(	55.93276	40.94578	55.41538	40.45008	55.22592	41.92021	0.14783	0.67642	0.77809	ZNF34	chr8	-	1.46E+08	1.46E+08	2056
ENSG00000(	15.53688	20.47289	14.51355	23.22134	26.69253	15.61733	-0.3583	0.50002	0.62826	ZNF781	chr19	-	38158652	38183223	3147
ENSG00000(	332.4892	256.5133	310.0622	280.9033	241.1532	235.082	0.24671	0.17597	0.27785	ZNF140	chr12	+	1.34E+08	1.34E+08	3550
ENSG00000(	30.03797	43.35436	35.62417	20.22504	18.40864	46.852	0.33676	0.46959	0.59883	INCA1	chr17	-	4891425	4900905	1552
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	CTD-2503C	chr5	+	74225705	74226391	687
ENSG00000(	6.214751	3.612863	15.83297	25.46857	32.21512	41.09825	-1.8704	0.001411	0.003856	ZNF774	chr15	+	90895477	90909324	3202
ENSG00000(	1490.505	1464.414	1496.215	1695.907	1895.169	2029.431	-0.33569	0.004263	0.010712	PTPN1	chr20	+	49126891	49201299	3529
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	BX255923.	chr9	+	69252845	69254032	1188
ENSG00000(	1679.019	1737.787	1314.136	447.9472	480.4655	475.0957	1.7494	1.63E-35	2.97E-34	EVL	chr14	+	1E+08	1.01E+08	3704
ENSG00000(	3.107376	0	1.319414	2.247227	3.681728	0	-0.25909	0.84023	0.89774	SPANXD	chrX	-	1.41E+08	1.41E+08	682
ENSG00000(	1.035792	9.634302	11.87472	17.22874	18.40864	19.72716	-1.23	0.07861	0.14317	THEM5	chr1	-	1.52E+08	1.52E+08	2503
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	NOXO1	chr16	-	2028918	2034193	1618
ENSG00000(	49.71801	31.31148	59.37362	35.95563	33.13555	35.34449	0.41547	0.2848	0.40783	ZNF658	chr9	-	40760700	40836415	4155
ENSG00000(	3307.284	2956.526	2923.821	3152.859	3688.171	3331.424	-0.14612	0.19944	0.30704	EPHB4	chr7	-	1E+08	1E+08	5058
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	PRTN3	chr19	+	840974	848180	1041
ENSG00000(	198.872	201.116	166.2461	245.6968	277.9705	252.3432	-0.44955	0.016907	0.03733	ZNF765	chr19	+	53893046	53930574	4569
ENSG00000(	139.8319	127.6545	157.0102	380.5304	344.2416	332.0738	-1.3119	2.06E-12	1.38E-11	ZNF124	chr1	-	2.47E+08	2.47E+08	2243
ENSG00000(	5871.904	5422.908	5337.029	10775.45	9882.678	9415.608	-0.85315	5.84E-16	4.88E-15	XRCC6	chr22	+	42017123	42060044	2709
ENSG00000(	1.035792	4.817151	2.638828	2.247227	0	0.821965	1.0013	0.41892	0.54961	S100A5	chr1	-	1.54E+08	1.54E+08	710
ENSG00000(	4.143168	15.65574	5.277655	9.737982	6.443024	8.219649	0.02781	0.97165	0.98351	LINC00176	chr20	+	62665697	62671315	4303
ENSG00000(	222.6953	166.1917	236.1751	484.6519	781.4468	789.9083	-1.7072	1.23E-16	1.06E-15	PPP1R26	chr9	+	1.38E+08	1.38E+08	4932
ENSG00000(	891.8168	934.5273	1092.475	1112.377	1251.788	967.4527	-0.19089	0.17734	0.2795	TSC22D2	chr3	+	1.5E+08	1.5E+08	4839
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	CRYBA4	chr22	+	27017928	27026636	811
ENSG00000(	4.143168	3.612863	0	0	0	0.821965	1.7977	0.17864	0.28126	ASMT	chrX	+	1733894	1761974	1388
ENSG00000(	27.96638	27.69862	17.15238	38.20285	25.7721	19.72716	-0.1919	0.68999	0.78842	NPIPL2	chr16	+	74411776	74425978	1428
ENSG00000(	133.6172	132.4716	108.1919	105.6197	102.168	110.9653	0.23196	0.33025	0.45802	ZNF569	chr19	-	37902057	37960177	4061
ENSG00000(	174.013	204.7289	257.2857	78.65293	254.0392	174.2566	0.32478	0.2924	0.41664	ARMCX4	chrX	+	1.01E+08	1.01E+08	7420
ENSG00000(	131.5456	198.7075	180.7597	425.4749	312.0264	433.1755	-1.1938	9.25E-09	4.64E-08	YRDC	chr1	-	38268616	38273857	1826
ENSG00000(	485.7864	496.1665	343.0476	755.0682	605.6443	550.7165	-0.52505	0.003285	0.008436	ZNF777	chr7	-	1.49E+08	1.49E+08	3233
ENSG00000(	242.3753	191.4817	365.4776	551.3196	537.5323	443.0391	-0.93592	7.96E-06	2.99E-05	PIK3R4	chr3	-	1.3E+08	1.3E+08	5015
ENSG00000(	450.5695	351.652	349.6447	407.4971	386.5814	364.9524	-0.00674	0.96756	0.98093	ZNF775	chr7	+	1.5E+08	1.5E+08	2582
ENSG00000(	534.4686	611.7782	551.515	217.2319	316.6286	223.5745	1.162	6.67E-11	4.00E-10	ZNF605	chr12	-	1.33E+08	1.34E+08	6215
ENSG00000(	292.0933	334.792	292.9099	307.121	373.6954	309.0588	-0.10446	0.54122	0.66411	TRAPPC2	chrX	-	13730363	13752754	3108
ENSG00000(	248.5901	313.1148	188.6762	0	0	0	8.9408	4.22E-21	4.46E-20	RFX8	chr2	-	1.02E+08	1.02E+08	1948

ENSG00000(	1719.415	1743.809	1486.979	674.168	745.5499	955.1232	1.0571	8.00E-13	5.51E-12	MYL6B	chr12	+	56546040	56551771	1305
ENSG00000(	46.61064	9.634302	29.0271	73.4094	46.0216	54.24968	-0.98833	0.030898	0.063778	ZNF799	chr19	-	12500830	12512085	4076
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	FGF16	chrX	+	76709648	76712769	1106
ENSG00000(	84.93494	97.54731	89.72014	141.5753	125.1788	143.8439	-0.59045	0.014113	0.031741	SIAH1	chr16	-	48390275	48482313	3352
ENSG00000(	178.1562	201.116	219.0227	152.0623	110.4518	125.7606	0.61482	0.004933	0.012235	C20orf96	chr20	-	251504	271390	1575
ENSG00000(	0	0	0	4.494453	9.20432	9.863579	-3.7928	0.001699	0.00458	ESRRG	chr1	-	2.17E+08	2.17E+08	5532
ENSG00000(	0	0	2.638828	2.996302	0	4.109825	-0.90349	0.4937	0.62258	IPO4	chr14	-	24649425	24658170	3646
ENSG00000(	11049.83	10147.33	9123.746	3155.855	5360.596	5064.126	1.1548	1.81E-12	1.22E-11	NCOR2	chr12	-	1.25E+08	1.25E+08	8708
ENSG00000(	2.071584	6.021439	0	0	6.443024	7.397684	-0.58206	0.61136	0.72514	SULT1A1	chr16	-	28616903	28634946	7948
ENSG00000(	52.82539	45.76293	71.24834	8.988907	4.60216	17.26126	2.3683	9.84E-07	4.09E-06	ARL9	chr4	+	57371509	57390614	1258
ENSG00000(	1531.936	1406.608	1708.641	2757.347	2428.1	2149.438	-0.65737	5.36E-07	2.29E-06	PRPF40A	chr2	-	1.54E+08	1.54E+08	8048
ENSG00000(	138.7961	87.913	155.6908	199.2541	227.3467	168.5028	-0.63279	0.009679	0.022585	GDAP2	chr1	-	1.18E+08	1.18E+08	2898
ENSG00000(	1027.506	921.2801	948.6585	59.17697	105.8497	110.9653	3.3815	2.16E-67	8.92E-66	TCEAL3	chrX	+	1.03E+08	1.03E+08	1221
ENSG00000(	473.3569	505.8008	530.4043	1185.787	916.7503	1076.774	-1.0733	6.53E-14	4.83E-13	ANAPC7	chr12	-	1.11E+08	1.11E+08	3045
ENSG00000(	48.68222	25.29004	59.37362	40.45008	30.37426	36.16646	0.30598	0.45498	0.58467	TPK1	chr7	-	1.44E+08	1.45E+08	4429
ENSG00000(	242.3753	276.9862	200.5509	334.8368	320.3103	433.1755	-0.59207	0.00209	0.00555	SLC6A9	chr1	-	44457172	44497139	3130
ENSG00000(	1171.481	1221.148	1431.564	1008.256	1334.626	1168.834	0.12261	0.38521	0.51605	AFAP1	chr4	-	7760441	7941653	7768
ENSG00000(	15230.28	16079.65	12890.67	11060.85	9105.834	10128.25	0.5439	6.39E-06	2.43E-05	NACA	chr12	-	57106212	57125412	6629
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	C1orf186	chr1	-	2.06E+08	2.06E+08	1665
ENSG00000(	398.7799	393.8021	444.6424	219.4791	655.3476	417.5582	-0.06074	0.88796	0.93033	MYO18A	chr17	-	27400528	27507430	7597
ENSG00000(	1.035792	2.408575	3.958241	2.247227	6.443024	6.575719	-0.87501	0.39577	0.52689	SPTSSB	chr3	-	1.61E+08	1.61E+08	3103
ENSG00000(	180.2278	166.1917	172.8432	131.0882	145.4283	130.6924	0.35028	0.093834	0.16642	C17orf59	chr17	-	8091652	8093564	1913
ENSG00000(	183.3352	197.5032	211.1062	332.5895	352.5255	314.8126	-0.7548	1.71E-05	6.17E-05	MAN2A2	chr15	+	91445448	91465814	6268
ENSG00000(	9404.99	10388.19	11796.88	6985.129	7856.808	6366.118	0.57362	2.91E-06	1.15E-05	MME	chr3	+	1.55E+08	1.55E+08	5622
ENSG00000(	15.53688	42.15007	25.06886	117.6049	135.3035	148.7757	-2.2526	4.35E-11	2.64E-10	FAM72A	chr1	+	2.06E+08	2.06E+08	2398
ENSG00000(	3.107376	1.204288	0	0	2.761296	1.64393	0.011369	0.99308	0.9956	LINC00238	chr14	+	66953072	66965271	1142
ENSG00000(	242.3753	239.6533	263.8828	5.243529	24.85166	29.59074	3.4693	3.34E-09	1.75E-08	CACNA1H	chr16	+	1203241	1271771	8084
ENSG00000(	29.00217	31.31148	23.74945	19.47596	30.37426	23.01502	0.2072	0.65241	0.75824	LINC00610	chr11	-	36290834	36294971	2738
ENSG00000(	2551.155	2692.787	2409.25	1837.482	1874.92	1754.073	0.48487	8.86E-06	3.31E-05	SULF2	chr20	-	46285092	46415360	4915
ENSG00000(	0	0	1.319414	4.494453	0	0	-0.82548	0.54208	NA	HBG2	chr11	-	5274420	5667019	1772
ENSG00000(	3751.638	3585.165	5044.119	137.0808	185.9273	130.6924	4.7562	3.78E-181	8.98E-179	LAMA2	chr6	+	1.29E+08	1.3E+08	9640
ENSG00000(	12269.99	12227.13	11621.4	3119.9	3579.56	3762.955	1.7848	2.18E-60	7.69E-59	PLXNB2	chr22	-	50713408	50746056	6383
ENSG00000(	0	0	0	53.18436	107.6905	72.33291	-7.0007	6.76E-12	4.36E-11	AJAP1	chr1	+	4714792	4843850	2922
ENSG00000(	98.40023	101.1602	139.8579	913.8722	870.7287	892.6539	-2.9759	4.51E-68	1.90E-66	XRCC2	chr7	-	1.52E+08	1.52E+08	4728
ENSG00000(	331.4534	344.4263	490.8219	835.9683	983.0214	850.7337	-1.1924	1.20E-12	8.19E-12	MYO6	chr6	+	76458909	76629254	8665
ENSG00000(	904.2463	779.1742	823.3142	911.6249	1001.43	999.5093	-0.21493	0.09326	0.16555	MKL1	chr22	-	40806285	41032706	4505
ENSG00000(	2772.815	2749.389	2727.228	5638.292	5048.57	5007.41	-0.92654	1.11E-18	1.06E-17	HDAC2	chr6	-	1.14E+08	1.14E+08	9874
ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	ANKRD20A	chr13	-	24513696	24520921	2796
ENSG00000(	27.96638	40.94578	59.37362	41.94823	46.0216	56.71558	-0.17934	0.64136	0.749	ZNF782	chr9	-	99578754	99637905	4213
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	POTEF	chr2	-	1.31E+08	1.31E+08	4031
ENSG00000(	159.512	205.9332	166.2461	61.42419	75.47542	85.48435	1.2485	3.81E-07	1.65E-06	ZNF846	chr19	-	9862669	9903856	2016
ENSG00000(	12.4295	0	6.597069	48.68991	36.81728	50.96182	-2.6685	6.77E-06	2.56E-05	MMP1	chr11	-	1.03E+08	1.03E+08	1970
ENSG00000(	22.78742	8.430014	17.15238	0.749076	0	0.821965	4.0523	3.21E-05	0.000112	ADH1B	chr4	-	1E+08	1E+08	4072
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	UGT2B15	chr4	-	69512348	69536346	2077

ENSG00000(	9.322127	1.204288	2.638828	4.494453	11.96562	6.575719	-0.67093	0.46105	0.59047	RIMBP3	chr22	-	20456003	20461786	5784
ENSG00000(	3048.336	2952.913	3978.033	768.5515	1059.417	869.6389	1.882	1.09E-35	1.98E-34	TCF4	chr18	-	52889562	53332018	8332
ENSG00000(	149.154	143.3102	229.578	152.8114	162.9165	125.7606	0.23658	0.32457	0.45206	WNK3	chrX	-	54219256	54385075	11341
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP3-337D2	chr6	+	1.47E+08	1.48E+08	453
ENSG00000(	105.6508	104.773	100.2754	289.1432	226.4263	259.7409	-1.3118	4.20E-10	2.37E-09	ACN9	chr7	+	96745902	96811075	2060
ENSG00000(	870.0652	887.56	810.1201	1.498151	1.840864	3.28786	8.3111	1.97E-69	8.53E-68	HRH1	chr3	+	11178779	11305243	4711
ENSG00000(	2741.741	2610.896	2336.682	4178.343	4072.912	4919.46	-0.77453	1.11E-10	6.53E-10	RABL6	chr9	+	1.4E+08	1.4E+08	3949
ENSG00000(	135.6887	132.4716	122.7055	80.90016	98.48622	107.6774	0.44445	0.068699	0.12771	ZNF136	chr19	+	12273879	12300064	3579
ENSG00000(	16.57267	24.08575	13.19414	41.94823	18.40864	25.48091	-0.65089	0.21092	0.32081	GOLGA6L9	chr15	+	83098710	83108085	6545
ENSG00000(	426.7463	446.7907	409.0183	423.2277	489.6698	437.2853	-0.07272	0.62672	0.73786	ZKSCAN5	chr7	+	99102274	99132323	5626
ENSG00000(	0	0	0	8.239831	5.522592	6.575719	-3.5854	0.003422	0.00876	ZNF502	chr3	+	44754135	44765323	3270
ENSG00000(	550.0055	519.048	423.5318	946.0824	705.9713	714.2875	-0.66155	5.56E-05	0.000188	TRAPPC4	chr11	+	1.19E+08	1.19E+08	1924
ENSG00000(	52.82539	55.39724	43.54065	147.5679	95.72493	152.0635	-1.3642	3.67E-06	1.43E-05	AC004057.	chr4	-	1.14E+08	1.14E+08	442
ENSG00000(	37.28851	44.55865	58.05421	71.91125	95.72493	59.18147	-0.69049	0.041742	0.083088	TTC30B	chr2	-	1.78E+08	1.78E+08	2770
ENSG00000(	213.3731	266.1476	236.1751	0	1.840864	0.821965	7.5365	1.83E-29	2.72E-28	SLC30A10	chr1	-	2.2E+08	2.2E+08	3650
ENSG00000(	663.9426	614.1867	711.164	424.7258	530.1688	464.4102	0.4865	0.000988	0.002772	TECPR2	chr14	+	1.03E+08	1.03E+08	8686
ENSG00000(	0	0	0	8.239831	0.920432	0.821965	-2.4036	0.071523	0.13225	TLR7	chrX	+	12885202	12908499	5011
ENSG00000(	0	1.204288	5.277655	0	0	1.64393	1.1002	0.41222	0.54272	FAM180B	chr11	+	47608198	47610746	1435
ENSG00000(	10.35792	4.817151	3.958241	8.988907	7.363456	0	0.20236	0.83334	0.89318	LINC00173	chr12	+	1.17E+08	1.17E+08	1597
ENSG00000(	303.487	240.8575	299.5069	297.383	358.9685	338.6495	-0.23521	0.18219	0.28561	ZFP62	chr5	-	1.8E+08	1.8E+08	4020
ENSG00000(	6.214751	6.021439	9.235896	0	0.920432	4.93179	1.5452	0.13327	0.22193	Z98881.1	chr16	+	653555	653904	348
ENSG00000(	80.79177	96.34302	130.622	170.0401	213.5402	150.4196	-0.79297	0.001661	0.004485	ERI2	chr16	-	20791515	20911671	3846
ENSG00000(	1640.694	1806.432	1337.886	710.1236	680.1992	1297.061	0.82771	4.61E-05	0.000157	TOMM7	chr7	-	22852251	22862470	778
ENSG00000(	0	0	0	0	0	4.93179	-1.2404	0.35057	NA	HSH2D	chr19	+	16244838	16269386	2474
ENSG00000(	12.4295	8.430014	6.597069	1.498151	17.48821	15.61733	-0.28666	0.71498	0.80766	TRPV1	chr17	-	3468738	3500392	4170
ENSG00000(	212.3373	255.309	281.0351	354.3127	405.9105	421.668	-0.6585	0.000186	0.000582	ZNF33B	chr10	-	43069633	43134016	5945
ENSG00000(	21.75163	45.76293	17.15238	26.96672	21.16994	27.94681	0.14729	0.76389	0.84398	PDXDC2P	chr16	-	70010200	70099851	4184
ENSG00000(	1327.885	1463.21	1205.944	846.4554	1108.2	1336.515	0.27996	0.081283	0.1474	ZNF512B	chr20	-	62588055	62680113	5926
ENSG00000(	702.2669	684.0354	608.2498	1057.695	732.6639	864.7071	-0.41153	0.0083	0.019637	AMZ2	chr17	+	66243715	66253297	2402
ENSG00000(	178.1562	272.169	208.4674	535.589	502.5559	460.3004	-1.1825	1.21E-10	7.12E-10	ZNF431	chr19	+	21324827	21373034	3843
ENSG00000(	0	0	0	2.996302	10.12475	4.93179	-3.3662	0.007049	0.016961	FAM150A	chr8	-	53446597	53478067	1217
ENSG00000(	1084.474	1052.547	1382.746	956.5695	1243.504	937.04	0.16538	0.28328	0.4061	NF1	chr17	+	29421945	29709134	12425
ENSG00000(	726.0901	724.9812	835.1889	1244.214	1223.254	1194.315	-0.67918	5.10E-08	2.40E-07	VKORC1L1	chr7	+	65338254	65424550	5899
ENSG00000(	134.6529	122.8373	133.2608	88.39091	125.1788	109.3213	0.27628	0.25552	0.37375	ZNF418	chr19	-	58433252	58446761	3694
ENSG00000(	657.7279	646.7025	721.7193	1025.484	1114.643	954.3013	-0.60986	3.15E-06	1.24E-05	DAPK1	chr9	+	90112143	90323548	6012
ENSG00000(	3367.359	3644.175	3476.655	522.1057	709.6531	810.4574	2.3544	4.83E-57	1.57E-55	COL27A1	chr9	+	1.17E+08	1.17E+08	7790
ENSG00000(	47.64643	42.15007	42.22124	39.701	28.53339	18.90519	0.58302	0.15924	0.25619	CXorf24	chrX	+	47342970	47344207	1238
ENSG00000(	1476.003	1434.307	1303.581	3274.958	2957.348	2929.483	-1.118	1.16E-22	1.31E-21	GM2A	chr5	+	1.51E+08	1.51E+08	3896
ENSG00000(	33.14534	32.51577	38.263	4.494453	25.7721	21.37109	0.97708	0.072381	0.13351	HIST1H2AI	chr6	+	27775899	27776429	531
ENSG00000(	0	0	0	1.498151	0	3.28786	-1.3443	0.31856	NA	CLPSL2	chr6	+	35744371	35747329	532
ENSG00000(	78.72018	51.78437	79.16483	16.47966	5.522592	23.83698	2.1204	2.31E-06	9.19E-06	S100A2	chr1	-	1.54E+08	1.54E+08	998
ENSG00000(	327.3102	354.0606	294.2293	684.6551	541.214	579.4853	-0.88485	3.22E-08	1.55E-07	RP4-564F2	chr20	-	37049235	37063996	2138
ENSG00000(	129.474	173.4174	166.2461	145.3207	156.4734	144.6658	0.068522	0.75442	0.83765	ZNF700	chr19	+	12035883	12061588	3113
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	POU3F4	chrX	+	82763269	82764775	1507

ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	ANKRD20A	chr9	+	67926761	67969840	3511
ENSG0000(	1632.408	1736.583	1688.85	820.2377	885.4556	797.306	1.0132	4.23E-18	3.92E-17	CD47	chr3	-	1.08E+08	1.08E+08	6796
ENSG0000(	1407.641	1416.242	1366.913	1388.037	1471.771	1235.413	0.033561	0.77939	0.85472	TLE1	chr9	-	84198598	84304220	3893
ENSG0000(	191.6215	142.106	172.8432	53.93344	100.3271	69.86702	1.1718	1.54E-05	5.61E-05	MAML3	chr4	-	1.41E+08	1.41E+08	6844
ENSG0000(	130.5098	96.34302	101.5949	98.87797	104.0088	101.1017	0.11488	0.64815	0.75468	HIST1H2AG	chr6	+	27100832	27103070	2239
ENSG0000(	377.0283	372.1249	463.1142	523.6038	502.5559	383.8576	-0.21869	0.20487	0.31338	STRN3	chr14	-	31363005	31495607	3970
ENSG0000(	90.1139	78.2787	63.33186	102.6234	109.5314	78.08667	-0.31574	0.2655	0.38541	ZNF239	chr10	-	44051792	44070066	2389
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CTB-134H2	chr16	+	29049923	29064047	1350
ENSG0000(	313.8449	263.739	299.5069	265.9218	242.994	296.7293	0.12208	0.48892	0.61804	CTBP1-AS1	chr4	+	1243088	1282079	5652
ENSG0000(	13.46529	16.86003	13.19414	2.247227	4.60216	9.041614	1.3424	0.067427	0.12571	CHRNG	chr2	+	2.33E+08	2.33E+08	2262
ENSG0000(	31.07376	28.90291	14.51355	79.40201	34.97642	53.42772	-1.1343	0.0098	0.022834	ZSCAN16	chr6	+	28092338	28097860	1328
ENSG0000(	309.7018	387.7806	354.9223	63.67142	73.63456	65.75719	2.3614	1.69E-30	2.60E-29	MVB12B	chr9	+	1.29E+08	1.29E+08	4819
ENSG0000(	1597.191	1666.734	1678.294	1640.475	2429.02	2273.555	-0.35865	0.013596	0.030684	C6orf106	chr6	-	34555065	34664636	4418
ENSG0000(	155.3688	137.2888	91.03955	84.64554	80.07758	78.08667	0.65793	0.014684	0.032857	ADA	chr20	-	43248163	43280874	1770
ENSG0000(	734.3765	753.8841	550.1955	171.5383	119.6562	128.2265	2.2671	6.18E-33	1.03E-31	ARID5A	chr2	+	97202480	97218375	3079
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	PATE2	chr11	-	1.26E+08	1.26E+08	1657
ENSG0000(	359.4198	322.7491	428.8095	376.0359	473.102	335.3617	-0.09206	0.61233	0.72574	PPTC7	chr12	-	1.11E+08	1.11E+08	6926
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	KRT39	chr17	-	39114669	39123144	1696
ENSG0000(	3.107376	7.225726	0	16.47966	9.20432	7.397684	-1.4645	0.098056	0.17251	TOMM20L	chr14	+	58862634	58875419	620
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RGPD4	chr2	+	1.08E+08	1.09E+08	5464
ENSG0000(	273.4491	298.6634	407.6989	380.5304	424.3192	351.801	-0.24093	0.19161	0.29723	NHLRC2	chr10	+	1.16E+08	1.16E+08	11051
ENSG0000(	129.474	157.7617	159.6491	51.68621	52.46462	62.46933	1.4081	5.36E-08	2.52E-07	ZFP28	chr19	+	57050317	57068169	4086
ENSG0000(	21.75163	19.2686	19.79121	13.48336	10.12475	4.109825	1.0687	0.08357	0.15098	KIAA1211L	chr2	-	99410309	99552722	3907
ENSG0000(	18.64425	19.2686	26.38828	45.69361	38.65814	46.03004	-1.0023	0.018232	0.039921	CBWD3	chr9	+	70856397	70914929	2195
ENSG0000(	253.769	227.6104	407.6989	22.47227	34.97642	20.54912	3.4773	1.39E-32	2.30E-31	SCN8A	chr12	+	51984050	52203558	8466
ENSG0000(	77.68439	39.74149	51.45714	55.43159	69.0324	83.84042	-0.28979	0.39999	0.53115	LAMB3	chr1	-	2.1E+08	2.1E+08	4305
ENSG0000(	0	0	1.319414	0.749076	1.840864	1.64393	-0.92219	0.49549	NA	HIST3H2BB	chr1	+	2.29E+08	2.29E+08	452
ENSG0000(	158.4762	169.8046	189.9956	206.7449	191.4499	105.2115	0.039965	0.87499	0.92156	KPNA5	chr6	+	1.17E+08	1.17E+08	5089
ENSG0000(	42.46747	21.67718	39.58241	39.701	34.05598	30.4127	-0.00503	0.99046	0.99461	ANKRD36B	chr2	-	98108978	98206428	5986
ENSG0000(	1873.748	1861.829	2683.688	1334.853	1654.937	1159.793	0.62691	0.000148	0.000473	ARHGEF12	chr11	+	1.2E+08	1.2E+08	9660
ENSG0000(	0	0	0	0	9.20432	3.28786	-2.6221	0.0485	0.094498	HCAR1	chr12	-	1.23E+08	1.23E+08	3612
ENSG0000(	320.0597	351.652	364.1582	313.1136	304.663	285.2218	0.19585	0.22706	0.34007	ZNF252P	chr8	-	1.46E+08	1.46E+08	5210
ENSG0000(	4957.3	5025.493	3757.69	6128.187	5275.916	6194.328	-0.35597	0.006994	0.016849	PDLIM7	chr5	-	1.77E+08	1.77E+08	1904
ENSG0000(	58200.11	57053.13	55807.24	49837.49	61507.87	68778.74	-0.07432	0.546	0.66809	FLNA	chrX	-	1.54E+08	1.54E+08	8486
ENSG0000(	59.04014	61.41867	65.97069	2.247227	1.840864	2.465895	4.5686	1.19E-14	9.17E-14	TMEM26	chr10	-	63166401	63213208	5151
ENSG0000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	RPS26P11	chrX	+	71264395	71264742	348
ENSG0000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	RIMBP3B	chr22	+	21737663	21743446	5784
ENSG0000(	402.9231	342.0177	444.6424	115.3576	195.1316	147.9537	1.3711	6.94E-11	4.15E-10	SRGAP1	chr12	+	64238073	64541613	8943
ENSG0000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	OR2L8	chr1	+	2.48E+08	2.48E+08	939
ENSG0000(	1627.229	1724.54	1911.831	2055.463	2087.54	2197.112	-0.2686	0.019267	0.041964	FAM3C	chr7	-	1.21E+08	1.21E+08	2508
ENSG0000(	279.6638	257.7176	354.9223	373.7887	550.4183	401.9408	-0.56907	0.003279	0.008422	NOP9	chr14	+	24769068	24778330	6033
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	ZNF705A	chr12	+	8290733	8332642	3455
ENSG0000(	391.5293	402.2321	546.2373	862.935	879.0126	831.0065	-0.94075	1.36E-09	7.38E-09	SLC39A10	chr2	+	1.96E+08	1.97E+08	5432
ENSG0000(	6.214751	8.430014	2.638828	13.48336	9.20432	9.041614	-0.79136	0.30746	0.43321	RP11-425I:	chr4	-	1.41E+08	1.41E+08	1985

ENSG00000(	350.0977	411.8664	250.6886	22.47227	11.04518	28.76877	3.9629	8.67E-42	1.88E-40	CASP4	chr11	-	1.05E+08	1.05E+08	4745
ENSG00000(	113.9371	102.3645	159.6491	3.745378	7.363456	0	4.9357	1.54E-23	1.80E-22	AL117340.	chr10	-	31650356	31652937	2582
ENSG00000(	6292.436	5782.99	5040.161	3974.595	3258.329	3346.219	0.69264	2.87E-08	1.39E-07	AP2A1	chr19	+	50270225	50310370	3388
ENSG00000(	238.2321	205.9332	290.271	80.15108	44.18074	38.63235	2.1407	1.08E-14	8.39E-14	PCDHB16	chr5	+	1.41E+08	1.41E+08	4814
ENSG00000(	52.82539	39.74149	38.263	8.988907	18.40864	5.753754	1.9268	0.000137	0.000438	HIST1H3E	chr6	+	26225383	26225844	462
ENSG00000(	94.25706	121.6331	178.1209	44.19546	56.14635	39.45432	1.4736	1.81E-06	7.30E-06	ZNF585A	chr19	-	37597636	37663643	6547
ENSG00000(	518.9317	510.618	515.8908	340.8294	361.7298	349.3351	0.55398	0.000128	0.000411	FUT11	chr10	+	75532049	75538821	2408
ENSG00000(	58.00435	59.0101	55.41538	20.97412	21.16994	19.72716	1.4492	0.000158	0.000501	LINC00087	chrX	-	1.34E+08	1.34E+08	2696
ENSG00000(	686.73	787.6042	650.471	976.0454	746.4703	757.0297	-0.22269	0.14155	0.23293	ANXA4	chr2	+	69947923	70053596	4418
ENSG00000(	236.1606	207.1375	168.885	243.4496	222.7445	281.112	-0.28319	0.15728	0.25348	LAGE3	chrX	-	1.54E+08	1.54E+08	949
ENSG00000(	3.107376	1.204288	1.319414	0	0	0	1.9243	0.1561	NA	AL360004.	chr9	-	1.33E+08	1.33E+08	3258
ENSG00000(	120.1519	120.4288	151.7326	101.8743	93.88406	124.9387	0.28494	0.24591	0.36242	WDR5B	chr3	-	1.22E+08	1.22E+08	4168
ENSG00000(	0	0	0	0.749076	1.840864	8.219649	-2.5313	0.055869	0.10698	LCA10	chrX	+	1.53E+08	1.53E+08	1391
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	FAM163B	chr9	-	1.36E+08	1.36E+08	811
ENSG00000(	4.143168	3.612863	10.55531	4.494453	0.920432	4.109825	0.77878	0.42052	0.55127	A-575C2.4	chr16	+	28763108	28784128	2123
ENSG00000(	130.5098	127.6545	133.2608	101.1252	96.64536	97.81383	0.40146	0.085828	0.15463	WDR45	chrX	-	48929385	48958108	3079
ENSG00000(	2506.616	2504.918	2465.984	1773.811	1535.281	1430.219	0.65631	3.46E-08	1.66E-07	METTL9	chr16	+	21608539	21668794	5603
ENSG00000(	73.54123	57.80581	81.80365	173.0365	183.166	125.7606	-1.1665	1.02E-05	3.79E-05	ZNF138	chr7	+	64254766	64294054	2582
ENSG00000(	69.39806	51.78437	69.92893	140.0771	138.9852	129.0485	-1.0836	3.60E-05	0.000124	ZNF429	chr19	+	21679484	21739072	2233
ENSG00000(	284.8428	293.8462	281.0351	101.1252	138.9852	133.9803	1.1971	2.60E-09	1.38E-08	ZNF470	chr19	+	57078880	57100279	7151
ENSG00000(	261.0196	220.3847	219.0227	425.4749	325.8329	396.1871	-0.70809	8.30E-05	0.000273	SERTAD1	chr19	-	40927499	40931932	2114
ENSG00000(	101.5076	114.4073	137.219	391.7665	345.162	321.3883	-1.5807	2.26E-15	1.82E-14	ZNF100	chr19	-	21905568	21950430	5745
ENSG00000(	556.2203	526.2737	504.0161	382.0285	422.4783	410.9825	0.38472	0.007871	0.018748	CXorf40B	chrX	-	1.49E+08	1.49E+08	1653
ENSG00000(	314.8807	287.8248	382.63	331.0914	275.2092	253.1652	0.19372	0.29354	0.4178	ZNF398	chr7	+	1.49E+08	1.49E+08	5427
ENSG00000(	251.6974	281.8033	314.0205	514.6149	654.4271	586.061	-1.048	2.01E-10	1.17E-09	ZSCAN25	chr7	+	99214569	99230030	5722
ENSG00000(	10895.5	10595.32	10484.06	2298.164	2338.818	2161.768	2.2307	4.57E-112	4.17E-110	ANXA6	chr5	-	1.5E+08	1.51E+08	2593
ENSG00000(	76.6486	81.89156	67.2901	14.23244	42.33987	24.65895	1.4564	0.00023	0.000712	ZNF441	chr19	+	11877815	11894893	4356
ENSG00000(	941.5348	979.0859	1353.719	1221.742	1222.334	1088.282	-0.11039	0.46605	0.59525	GMFB	chr14	-	54941202	54955914	6721
ENSG00000(	20.71584	30.10719	18.47179	4.494453	0	3.28786	2.8569	0.000111	0.000359	SIGLEC15	chr18	+	43405477	43424045	2580
ENSG00000(	9.322127	7.225726	5.277655	61.42419	23.93123	46.852	-2.4715	9.75E-06	3.63E-05	Z73979.1	chr22	-	33210035	33210372	333
ENSG00000(	56.96855	54.19295	64.65128	77.90386	71.7937	73.97684	-0.34569	0.24717	0.36391	ZNF420	chr19	+	37498759	37621216	3535
ENSG00000(	4.143168	4.817151	2.638828	2.996302	11.04518	8.219649	-0.80764	0.36997	0.50043	ZNF763	chr19	+	12035890	12091196	2621
ENSG00000(	293.1291	323.9534	327.2146	543.8288	506.2376	410.9825	-0.62874	0.000154	0.000491	ZMYM1	chr1	+	35525387	35581460	4203
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	DTHD1	chr4	+	36283244	36347378	4335
ENSG00000(	7.250543	15.65574	5.277655	2.996302	41.41944	22.19305	-1.1324	0.12545	0.21123	HIST1H4C	chr6	+	26104104	26104518	415
ENSG00000(	338.704	289.0291	304.7846	134.0845	155.553	104.3895	1.2386	1.26E-09	6.84E-09	RP5-874C2	chr6	+	28234788	28245974	2808
ENSG00000(	740.5912	720.1641	708.5252	901.887	948.045	1115.406	-0.44946	0.000812	0.002312	MAFG	chr17	-	79876146	79885590	5040
ENSG00000(	242.3753	196.2989	205.8285	701.1347	715.1757	919.7787	-1.848	1.45E-27	1.99E-26	ARRDC1	chr9	+	1.41E+08	1.41E+08	3185
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	AC010243.	chr5	+	87514708	87515080	369
ENSG00000(	42.46747	40.94578	62.01245	248.6931	359.8889	247.4114	-2.5406	1.35E-22	1.51E-21	KIAA1671	chr22	+	25348697	25593415	10490
ENSG00000(	7165.608	6660.915	8684.382	2998.549	4834.109	3701.308	0.96163	1.29E-09	6.99E-09	IGF2R	chr6	+	1.6E+08	1.61E+08	9091
ENSG00000(	0	0	0	2.247227	0.920432	4.93179	-2.1553	0.10814	0.18694	NPSR1-AS1	chr7	-	34386124	34911194	4740
ENSG00000(	278.628	303.4805	211.1062	84.64554	104.9292	149.5976	1.2184	4.78E-07	2.05E-06	GAL3ST4	chr7	-	99756867	99766373	3162
ENSG00000(	7534.35	6904.181	9535.403	4276.472	6166.894	4319.426	0.69725	8.37E-06	3.13E-05	DYNC1H1	chr14	+	1.02E+08	1.03E+08	14333

ENSG0000(	13.46529	31.31148	7.916483	20.22504	8.283888	4.93179	0.60348	0.38164	0.51228	SLC6A17	chr1	+	1.11E+08	1.11E+08	6427
ENSG0000(	4523.303	4882.182	4041.364	4471.232	3558.39	4313.672	0.1232	0.32285	0.45019	PCBP2	chr12	+	53835525	53874946	3167
ENSG0000(	420.5315	372.1249	341.7282	471.1685	549.4979	769.3592	-0.65322	0.000508	0.001492	ZGPAT	chr20	+	62338794	62370456	4232
ENSG0000(	1056.508	979.0859	848.3831	1099.643	1120.166	1398.984	-0.32555	0.022751	0.04864	SLC25A29	chr14	-	1.01E+08	1.01E+08	5169
ENSG0000(	644.2626	731.0026	890.6043	188.018	283.4931	179.1884	1.7928	1.79E-20	1.85E-19	PGAP1	chr2	-	1.98E+08	1.98E+08	8942
ENSG0000(	658.7637	678.014	563.3897	693.644	959.0901	917.3128	-0.43258	0.005686	0.013932	SRC	chr20	+	35973088	36034453	4631
ENSG0000(	44.53905	52.98866	27.70769	233.7116	186.8477	191.5178	-2.2582	2.32E-16	1.97E-15	ZNF682	chr19	-	20107867	20150315	3769
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	OR8B8	chr11	-	1.24E+08	1.24E+08	1033
ENSG0000(	146.0467	133.6759	201.8703	145.3207	135.3035	154.5294	0.14128	0.53807	0.6619	ZNF772	chr19	-	57978031	57988938	5419
ENSG0000(	1309.241	1260.889	1312.817	1767.818	1888.726	1638.998	-0.4466	0.000113	0.000365	PCNXL3	chr11	+	65383244	65404910	7105
ENSG0000(	21.75163	22.88147	32.98534	11.23613	11.96562	9.041614	1.2106	0.026058	0.054964	ADAM32	chr8	+	38964509	39142430	6871
ENSG0000(	10.35792	9.634302	13.19414	10.48706	16.56778	13.15144	-0.26005	0.68316	0.78321	ACSL5	chr10	+	1.14E+08	1.14E+08	3380
ENSG0000(	2.071584	14.45145	15.83297	4.494453	11.04518	9.041614	0.35212	0.65284	0.7586	AL133458.	chr6	-	1.67E+08	1.67E+08	2298
ENSG0000(	125.3308	119.2245	162.2879	223.2245	208.0176	183.2982	-0.59495	0.006111	0.014883	LRRC8B	chr1	+	89990395	90063423	7593
ENSG0000(	0	0	0	5.992604	0	3.28786	-2.2293	0.097833	0.1722	RP11-452G	chr11	+	17249817	17250698	882
ENSG0000(	838.9914	740.6369	716.4417	1047.208	993.1461	1075.952	-0.43867	0.000622	0.001802	ABCB8	chr7	+	1.51E+08	1.51E+08	4683
ENSG0000(	7.250543	1.204288	0	0	14.72691	0	-0.3261	0.80735	0.87491	HIST1H3J	chr6	-	27858093	27860884	522
ENSG0000(	11061.22	10128.06	9458.877	4761.873	5231.735	4746.847	1.0546	1.35E-22	1.52E-21	SND1	chr7	+	1.27E+08	1.28E+08	3476
ENSG0000(	159.512	150.536	138.5384	94.38352	89.2819	112.6092	0.59483	0.01105	0.025443	ZNF785	chr16	-	30585061	30597092	3282
ENSG0000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	SULT1A2	chr16	-	28603264	28608430	1991
ENSG0000(	4.143168	14.45145	7.916483	0	3.681728	3.28786	1.6513	0.088173	0.15802	NEK5	chr13	-	52611093	52703214	2918
ENSG0000(	955.0001	912.8501	1006.713	2164.079	1805.888	1885.588	-1.025	1.01E-16	8.74E-16	PSMD12	chr17	-	65334032	65362743	4406
ENSG0000(	26.93059	50.58008	29.0271	23.22134	24.85166	27.94681	0.47219	0.28734	0.41089	BX936347.	chrX	-	1.54E+08	1.54E+08	255
ENSG0000(	2.071584	0	0	8.988907	9.20432	4.93179	-2.601	0.018833	0.041105	PIWIL2	chr8	+	22132810	22215076	5128
ENSG0000(	84.93494	102.3645	133.2608	0	0	0	7.8498	2.87E-15	2.30E-14	FLJ27365	chr22	+	46449749	46509808	4560
ENSG0000(	1005.754	967.043	1010.671	126.5938	164.7573	143.8439	2.7723	9.30E-74	4.31E-72	C20orf112	chr20	-	31030862	31172876	5991
ENSG0000(	40.39588	19.2686	29.0271	21.72319	40.49901	41.09825	-0.20372	0.65579	0.76078	C9orf169	chr9	+	1.4E+08	1.4E+08	1297
ENSG0000(	24.85901	37.33292	29.0271	18.72689	18.40864	26.30288	0.50508	0.27825	0.40022	SLC22A4	chr5	+	1.32E+08	1.32E+08	2201
ENSG0000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	ZSCAN5B	chr19	-	56700939	56709289	2059
ENSG0000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	TCEA1P1	chr9	+	99830031	99830910	880
ENSG0000(	921.8548	998.3545	1072.683	1668.94	2108.71	1671.877	-0.86276	1.66E-10	9.67E-10	ENTPD4	chr8	-	23243296	23315208	5861
ENSG0000(	217.5163	204.7289	216.3839	315.3608	237.4715	330.4299	-0.46692	0.014688	0.032861	C1D	chr2	-	68268262	68338080	2233
ENSG0000(	4673.493	4530.53	4249.832	1882.427	2373.794	2281.775	1.0396	4.83E-18	4.47E-17	TBC1D9B	chr5	-	1.79E+08	1.79E+08	5173
ENSG0000(	9.322127	15.65574	1.319414	6.74168	0.920432	8.219649	0.63167	0.48547	0.61462	HIST1H4J	chr6	+	27791884	27792257	374
ENSG0000(	5.17896	3.612863	0	0	0	0	2.4569	0.068737	0.12775	SLC2A7	chr1	-	9063359	9086404	1539
ENSG0000(	0	0	2.638828	31.46117	20.2495	18.90519	-4.139	6.42E-06	2.44E-05	FAM110D	chr1	+	26485511	26489119	1524
ENSG0000(	61.11172	33.72006	0	0.749076	10.12475	28.76877	0.84253	0.50907	0.63644	SERPINA1	chr14	-	94843084	94857030	3532
ENSG0000(	2341.925	2185.782	2323.488	650.9467	745.5499	632.091	1.7533	4.88E-48	1.27E-46	KANK2	chr19	-	11274943	11308467	5231
ENSG0000(	24.85901	42.15007	39.58241	2.996302	14.72691	13.9734	1.6808	0.00291	0.007531	EIF4BP6	chr7	+	1.04E+08	1.04E+08	1828
ENSG0000(	80.79177	97.54731	98.95603	232.2134	250.3575	251.5213	-1.3995	5.26E-11	3.18E-10	C6orf141	chr6	+	49518113	49529620	1820
ENSG0000(	699.1595	665.9711	647.8322	668.9245	628.6551	626.3373	0.065434	0.61762	0.73005	GTF2E2	chr8	-	30435835	30515768	1762
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	IL27	chr16	-	28510683	28523372	1044
ENSG0000(	35.21692	10.83859	38.263	128.0919	87.44104	115.8971	-1.9367	2.83E-07	1.24E-06	RAD54B	chr8	-	95384188	95487337	3068
ENSG0000(	10.35792	12.04288	6.597069	129.5901	80.07758	97.81383	-3.3113	5.60E-15	4.41E-14	ZNF165	chr6	+	28048753	28057341	2107

ENSG00000(	1619.979	1769.099	1493.576	692.8949	851.3996	1051.293	0.90924	3.33E-09	1.75E-08	SYNGAP1	chr6	+	33387847	33421466	5916
ENSG00000(	9.322127	7.225726	3.958241	0.749076	2.761296	4.93179	1.1085	0.24725	0.36401	RP11-589F	chr5	-	70070478	70074135	3658
ENSG00000(	3.107376	7.225726	1.319414	10.48706	3.681728	5.753754	-0.67036	0.47259	0.60167	RAMP2-AS1	chr17	-	40905932	40913275	3118
ENSG00000(	294.1649	297.4591	350.9641	131.8373	86.52061	120.0069	1.4636	3.66E-12	2.41E-11	FITM2	chr20	-	42931478	42939809	4597
ENSG00000(	78.72018	62.62296	93.67838	571.5446	550.4183	450.4368	-2.73	5.54E-41	1.17E-39	BLM	chr15	+	91260558	91358859	4555
ENSG00000(	216.4805	222.7932	295.5487	66.66772	100.3271	94.52597	1.481	3.63E-10	2.06E-09	RP11-366L	chr12	-	66245120	66275947	4617
ENSG00000(	221.6595	226.4061	258.6051	254.6857	312.0264	243.3016	-0.1962	0.29275	0.41701	ZNF720	chr16	+	31724550	31806190	5994
ENSG00000(	3.107376	0	0	50.93714	56.14635	68.22309	-5.1101	1.88E-11	1.17E-10	GATA3-AS1	chr10	-	8092413	8095447	2214
ENSG00000(	439.1758	461.2422	517.2102	791.0238	1178.153	947.7256	-1.0374	2.11E-10	1.22E-09	DDI2	chr1	+	15943995	15995539	10625
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC060834.	chr7	+	9765870	9767915	2032
ENSG00000(	2615.375	2403.758	3150.76	1409.76	2214.559	1511.593	0.66758	5.17E-05	0.000175	SVIL	chr10	-	29746267	30025710	7994
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	C17orf102	chr17	-	32901142	32906388	3997
ENSG00000(	577.9719	592.5096	786.3706	927.3555	913.0685	766.0713	-0.41395	0.007872	0.01875	TRIM33	chr1	-	1.15E+08	1.15E+08	8339
ENSG00000(	4755.321	4643.733	4524.27	1939.357	2085.699	2117.382	1.1792	4.88E-30	7.41E-29	LRP10	chr14	+	23340822	23350789	6886
ENSG00000(	252.7332	290.2333	257.2857	659.1865	786.9694	656.75	-1.389	5.48E-19	5.30E-18	PELI1	chr2	-	64319786	64371588	3750
ENSG00000(	3.107376	2.408575	2.638828	11.23613	3.681728	16.4393	-1.6982	0.05772	0.11007	ZNF833P	chr19	+	11750591	11797382	3381
ENSG00000(	3.107376	0	0	0	3.681728	0	-0.09374	0.94492	0.96694	AC032027.	chr8	+	57868647	57868875	228
ENSG00000(	1341.351	1462.005	1291.706	1187.285	1112.802	1004.441	0.3087	0.01309	0.029619	ZNF655	chr7	+	99156029	99205433	4886
ENSG00000(	733.3407	785.1956	624.0827	883.1601	711.4939	969.0966	-0.25795	0.093595	0.16607	MRPL21	chr11	-	68658744	68671303	2283
ENSG00000(	931.1769	939.3444	800.8842	128.0919	89.2819	101.1017	3.051	2.12E-70	9.25E-69	UAP1L1	chr9	+	1.4E+08	1.4E+08	4412
ENSG00000(	3.107376	8.430014	7.916483	0	0.920432	2.465895	2.0112	0.063064	0.11867	BNIP3P1	chr14	+	28733596	28735180	1585
ENSG00000(	1.035792	3.612863	2.638828	2.247227	0.920432	2.465895	0.26289	0.82252	0.88542	FBXL22	chr15	+	63889552	63894627	1526
ENSG00000(	100.4718	91.52587	97.63662	294.3867	259.5618	289.3317	-1.5329	5.46E-14	4.06E-13	ZNF786	chr7	-	1.49E+08	1.49E+08	3144
ENSG00000(	251.6974	240.8575	175.482	161.8003	126.0992	165.2149	0.55731	0.010923	0.025182	ZNF517	chr8	+	1.46E+08	1.46E+08	3191
ENSG00000(	102.5434	149.3317	108.1919	219.4791	202.495	188.23	-0.75761	0.000759	0.002172	ZNF675	chr19	-	23708433	23870022	4227
ENSG00000(	166.7625	96.34302	176.8014	277.907	255.8801	286.8658	-0.89354	8.46E-05	0.000279	SLC22A5	chr5	+	1.32E+08	1.32E+08	10435
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	OR8S1	chr12	+	48901137	48923680	2209
ENSG00000(	308.666	354.0606	356.2417	201.5013	286.2544	224.3964	0.51569	0.005771	0.014123	DACT3	chr19	-	47150869	47164395	3085
ENSG00000(	496.1443	452.8122	600.3333	258.4311	357.1276	318.1004	0.72831	3.64E-05	0.000126	ADARB1	chr21	+	46493768	46646478	7027
ENSG00000(	3.107376	3.612863	6.597069	44.19546	37.73771	27.94681	-2.9008	2.41E-06	9.57E-06	ZNF860	chr3	+	32023263	32033120	3098
ENSG00000(	2108.872	2071.375	2256.198	1985.799	3007.051	2534.94	-0.22501	0.11949	0.203	HTT	chr4	+	3076408	3245676	14438
ENSG00000(	38.3243	21.67718	19.79121	12.73428	15.64734	18.90519	0.73646	0.15762	0.25397	C5AR1	chr19	+	47793280	47825323	2311
ENSG00000(	4.143168	10.83859	14.51355	5.992604	3.681728	20.54912	-0.04696	0.95222	0.9715	DIO3	chr14	+	1.02E+08	1.02E+08	2102
ENSG00000(	69.39806	65.03154	76.526	9.737982	15.64734	9.863579	2.5308	7.57E-10	4.19E-09	HIST1H3D	chr6	-	26197068	26199521	865
ENSG00000(	17.60846	9.634302	26.38828	0.749076	4.60216	2.465895	2.5399	0.001303	0.00359	DCHS2	chr4	-	1.55E+08	1.55E+08	8912
ENSG00000(	99.43602	114.4073	96.31721	35.20655	22.09037	15.61733	2.0455	5.11E-09	2.63E-08	VEPH1	chr3	-	1.57E+08	1.57E+08	4202
ENSG00000(	62.14751	34.92434	48.81831	110.1141	89.2819	80.55256	-0.92279	0.003928	0.009942	SHPK	chr17	-	3511556	3539616	3838
ENSG00000(	0	0	0	1.498151	1.840864	1.64393	-1.5124	0.26495	NA	GGT3P	chr22	-	18761178	18830912	2340
ENSG00000(	328.346	314.3191	410.3377	253.9366	199.7337	226.0404	0.62518	0.000707	0.002033	IPP	chr1	-	46159996	46216322	3113
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	OR13G1	chr1	-	2.48E+08	2.48E+08	1046
ENSG00000(	11.39371	7.225726	18.47179	197.0069	226.4263	163.571	-3.9308	2.33E-28	3.33E-27	MAP3K5	chr6	-	1.37E+08	1.37E+08	5197
ENSG00000(	23.82321	14.45145	25.06886	36.7047	66.2711	48.49593	-1.2205	0.00499	0.012361	OGDHL	chr10	-	50942689	50970425	3704
ENSG00000(	5.17896	4.817151	2.638828	0	0	0	3.172	0.014447	0.032394	C16orf47	chr16	-	73160536	73178346	1308
ENSG00000(	1.035792	0	0	0	0	3.28786	-0.59917	0.65385	NA	CYP2F1	chr19	+	41620337	41634271	2080

ENSG00000(	1480.147	1387.339	1254.763	1276.425	937.9202	1071.02	0.32625	0.020643	0.044604	GSTK1	chr7	+	1.43E+08	1.43E+08	2692
ENSG00000(	2857.75	2567.541	2790.56	6162.645	7844.842	9054.766	-1.4851	3.73E-27	5.04E-26	HNRNPAB	chr5	+	1.78E+08	1.78E+08	1796
ENSG00000(	2097.479	1956.968	1708.641	1686.918	1600.631	1825.584	0.17278	0.1597	0.25688	STMN3	chr20	-	62271061	62284780	2255
ENSG00000(	15.53688	13.24716	15.83297	20.22504	48.7829	36.16646	-1.1863	0.019974	0.043318	HIST1H2BH	chr6	+	26251879	26252303	425
ENSG00000(	45.57484	57.80581	36.94359	257.682	189.609	205.4912	-2.1951	8.32E-17	7.21E-16	PDGFA	chr7	-	536895	559933	2305
ENSG00000(	3.107376	10.83859	6.597069	0	2.761296	0	2.2803	0.041888	0.083344	GYPE	chr4	-	1.45E+08	1.45E+08	1684
ENSG00000(	584.1866	566.0152	730.9552	172.2874	148.1896	125.7606	2.0639	2.70E-30	4.14E-29	COL13A1	chr10	+	71561644	71724031	3136
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	SPN	chr16	+	29674300	29682187	6854
ENSG00000(	10.35792	9.634302	5.277655	97.37982	72.71413	90.41614	-3.2544	1.81E-13	1.30E-12	ZNF695	chr1	-	2.47E+08	2.47E+08	3340
ENSG00000(	36.25272	21.67718	32.98534	5.992604	6.443024	6.575719	2.1552	0.000161	0.00051	PCDHB11	chr5	+	1.41E+08	1.41E+08	3271
ENSG00000(	321.0955	237.2447	217.7033	314.6117	283.4931	269.6045	-0.1569	0.41773	0.54844	ZNF628	chr19	+	55987699	55995854	3847
ENSG00000(	789.2734	803.2599	756.0241	30.7121	37.73771	32.05663	4.5291	7.80E-118	8.01E-116	SLC2A10	chr20	+	45338126	45364965	4368
ENSG00000(	4.143168	3.612863	2.638828	43.44638	46.94203	60.00344	-3.633	1.37E-09	7.41E-09	ZNF665	chr19	-	53662466	53696639	2352
ENSG00000(	384.2788	352.8563	364.1582	870.4258	638.7798	683.8748	-0.9907	5.50E-10	3.07E-09	RPF2	chr6	+	1.11E+08	1.11E+08	1531
ENSG00000(	2.071584	0	7.916483	2.996302	0	1.64393	0.76172	0.53431	0.65883	AL627171.	chr14	-	50300810	50311552	60
ENSG00000(	3.107376	0	0	2.247227	2.761296	4.93179	-1.13	0.35983	0.48944	SLC28A3	chr9	-	86890372	86955672	4887
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	FAM177B	chr1	+	2.23E+08	2.23E+08	1994
ENSG00000(	1507.077	1543.897	1124.141	1083.912	859.6835	1117.05	0.44671	0.003648	0.009287	MIB2	chr1	+	1550795	1565990	4247
ENSG00000(	1546.437	1329.534	1992.315	858.4406	1030.884	724.1511	0.89406	8.10E-08	3.74E-07	MYO5A	chr15	-	52599480	52821247	12225
ENSG00000(	13.46529	12.04288	27.70769	4.494453	4.60216	7.397684	1.5639	0.02348	0.050076	C5orf56	chr5	+	1.32E+08	1.32E+08	2025
ENSG00000(	0	1.204288	5.277655	0	0	1.64393	1.1002	0.41222	0.54272	GZMM	chr19	+	544034	549919	912
ENSG00000(	565.5424	490.1451	547.5567	330.3423	317.549	300.0172	0.75595	5.57E-07	2.37E-06	ATG7	chr3	+	11313995	11599139	4959
ENSG00000(	3.107376	4.817151	9.235896	5.243529	19.32907	18.08323	-1.2103	0.11554	0.19769	RP11-460N	chr9	+	69830288	69848759	3275
ENSG00000(	340.7755	344.4263	484.2249	955.0713	1001.43	856.4874	-1.2646	6.08E-15	4.78E-14	SIPA1L1	chr14	+	71787166	72207946	7831
ENSG00000(	100.4718	81.89156	145.1355	71.16218	98.48622	57.53754	0.52069	0.087863	0.15762	TTC30A	chr2	-	1.78E+08	1.78E+08	4669
ENSG00000(	50.7538	54.19295	32.98534	8.988907	6.443024	15.61733	2.0754	2.58E-05	9.08E-05	SSPO	chr7	+	1.49E+08	1.5E+08	15583
ENSG00000(	11.39371	3.612863	5.277655	0	0	0	3.9092	0.001601	0.004333	ELANE	chr19	+	851014	856242	1023
ENSG00000(	595.5803	599.7353	515.8908	456.9361	485.9881	491.535	0.25516	0.074438	0.13672	RAB40C	chr16	+	639357	679272	2717
ENSG00000(	439.1758	468.4679	509.2937	402.2536	380.1384	378.1039	0.2855	0.055675	0.10665	PIGN	chr18	-	59710800	59854351	5501
ENSG00000(	38.3243	37.33292	60.69303	706.3782	971.0558	960.055	-4.2588	1.99E-83	1.13E-81	COL4A6	chrX	-	1.07E+08	1.08E+08	6700
ENSG00000(	88.04231	46.96722	73.88717	44.19546	63.50981	46.03004	0.44158	0.19942	0.30702	ZNF624	chr17	-	16524051	16557170	4241
ENSG00000(	227.8742	251.6961	233.5362	214.9847	132.5422	165.2149	0.4692	0.029252	0.060809	HHLA3	chr1	+	70820488	70851022	898
ENSG00000(	0	1.204288	1.319414	0	9.20432	3.28786	-1.5899	0.20282	0.31073	RPS17P2	chr5	+	1.16E+08	1.16E+08	459
ENSG00000(	19.68005	12.04288	10.55531	2.247227	0	3.28786	2.5686	0.002958	0.007648	HOXA4	chr7	-	27168126	27170418	1747
ENSG00000(	264.1269	284.2119	374.7135	323.6006	358.9685	305.7709	-0.10058	0.58189	0.69958	TOPORS	chr9	-	32540542	32552551	4098
ENSG00000(	6.214751	10.83859	18.47179	0.749076	6.443024	1.64393	1.7875	0.041439	0.082549	BCO2	chr11	+	1.12E+08	1.12E+08	2930
ENSG00000(	12.4295	26.49433	15.83297	12.73428	11.04518	13.15144	0.53461	0.36485	0.49466	GPX1P1	chrX	-	13396854	13397459	606
ENSG00000(	6.214751	3.612863	7.916483	2.247227	1.840864	4.109825	0.94344	0.32779	0.45552	KCNMB2	chr3	+	1.78E+08	1.79E+08	2552
ENSG00000(	1810.564	1917.226	1612.324	1650.213	1686.231	1634.066	0.10372	0.37161	0.50216	ENTPD6	chr20	+	25176329	25207365	2766
ENSG00000(	268.2701	314.3191	262.5633	316.1099	342.4007	309.0588	-0.19388	0.25231	0.37008	ENPP1	chr6	+	1.32E+08	1.32E+08	7442
ENSG00000(	4.143168	14.45145	1.319414	5.992604	4.60216	9.041614	0.017818	0.98391	0.99083	CCDC154	chr16	-	1484384	1494557	2564
ENSG00000(	1013.004	1091.085	1608.365	1458.45	1497.543	1227.194	-0.17275	0.29966	0.4246	FAR1	chr11	+	13690217	13753893	5820
ENSG00000(	412.2452	392.5978	595.0556	203.7485	233.7897	204.6693	1.1176	5.41E-09	2.78E-08	C5orf42	chr5	-	37106330	37249530	11250
ENSG00000(	2.071584	0	1.319414	4.494453	0.920432	7.397684	-1.4096	0.23174	0.34526	AC022532.	chr10	+	72194585	72196314	1730

ENSG00000(	382.2072	419.0921	349.6447	164.0475	190.5294	235.9039	0.95953	3.31E-07	1.45E-06	ZNF841	chr19	-	52567719	52599018	3876
ENSG00000(	391.5293	461.2422	415.6153	2217.264	1602.472	1739.278	-2.1264	1.90E-45	4.60E-44	MFAP5	chr12	-	8789942	8815484	2845
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	MYH6	chr14	-	23851199	23877486	5941
ENSG00000(	141.9035	148.1274	157.0102	83.14739	67.19154	62.46933	1.0582	2.10E-05	7.50E-05	ZNF615	chr19	-	52494585	52511483	4122
ENSG00000(	197.8363	213.1589	150.4132	86.89276	119.6562	138.9121	0.69871	0.004313	0.010824	CXorf40A	chrX	+	1.49E+08	1.49E+08	2411
ENSG00000(	769.5934	690.0569	853.6607	1080.167	1414.704	1359.53	-0.73438	4.20E-07	1.81E-06	CDC42SE1	chr1	-	1.51E+08	1.51E+08	3181
ENSG00000(	70.43385	87.913	64.65128	5.992604	6.443024	4.93179	3.5736	1.13E-14	8.70E-14	SERPINB2	chr18	+	61538926	61571124	2155
ENSG00000(	156.4046	171.0089	159.6491	934.0972	943.4428	932.1082	-2.5213	1.73E-64	6.69E-63	DPP4	chr2	-	1.63E+08	1.63E+08	3904
ENSG00000(	0	0	0	3.745378	4.60216	0	-2.0709	0.12551	0.2113	SERPINB13	chr18	+	61254223	61271873	3114
ENSG00000(	0	0	5.277655	0	0	0.821965	1.1957	0.37766	0.50836	AC106870.	chr2	+	30122463	30130065	200
ENSG00000(	31.07376	43.35436	29.0271	13.48336	10.12475	3.28786	1.8526	0.000906	0.002557	PDCD1LG2	chr9	+	5510545	5571282	2363
ENSG00000(	20.71584	34.92434	11.87472	53.93344	58.90765	74.79881	-1.4329	0.00066	0.001904	ZNF433	chr19	-	12125547	12146556	2322
ENSG00000(	66.29068	74.66584	79.16483	8.239831	25.7721	4.109825	2.4678	3.14E-07	1.38E-06	DNAH10	chr12	+	1.24E+08	1.24E+08	14166
ENSG00000(	25.8948	6.021439	17.15238	12.73428	36.81728	18.08323	-0.42323	0.48692	0.61608	RP4-724E1	chr20	+	52169309	52191847	1947
ENSG00000(	19.68005	4.817151	18.47179	7.490755	9.20432	9.863579	0.65016	0.34691	0.47647	TBC1D3	chr17	-	36337711	36358166	3389
ENSG00000(	6991.595	6495.928	7276.567	5384.355	6046.318	5452.093	0.29816	0.004917	0.0122	SPTAN1	chr9	+	1.31E+08	1.31E+08	7872
ENSG00000(	143.9751	138.4931	108.1919	81.64923	57.06678	58.35951	0.9757	0.000355	0.001068	NMB	chr15	-	85198360	85201794	1017
ENSG00000(	15.53688	15.65574	6.597069	0.749076	9.20432	4.109825	1.3068	0.11236	0.19299	HIST1H2BE	chr6	+	26183958	26184454	497
ENSG00000(	30.03797	15.65574	40.90183	18.72689	34.97642	27.94681	0.083538	0.86336	0.91356	ZNF595	chr4	+	53179	88099	2908
ENSG00000(	2911.611	3043.235	3222.008	2332.621	2110.551	2075.461	0.49215	8.16E-06	3.06E-05	PARVA	chr11	+	12398732	12552348	4458
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	FRMPD2P1	chr10	-	48844036	48868504	1947
ENSG00000(	3.107376	14.45145	11.87472	29.21395	29.45382	8.219649	-1.1214	0.095031	0.16808	KLHL14	chr18	-	30252634	30353025	4312
ENSG00000(	3090.803	3154.03	2801.115	494.3899	584.4743	415.9142	2.592	4.73E-79	2.51E-77	FAM114A1	chr4	+	38869298	38947360	4050
ENSG00000(	651.5131	761.1098	825.953	806.0053	809.0597	855.6655	-0.14357	0.29429	0.41872	RPE	chr2	+	2.11E+08	2.11E+08	2569
ENSG00000(	163.6551	155.3531	232.2168	25.46857	102.168	61.64737	1.5223	1.56E-05	5.66E-05	ZNF460	chr19	+	57791419	57804937	3350
ENSG00000(	1.035792	1.204288	10.55531	5.992604	0	0	0.76074	0.52991	0.65467	HSPB9	chr17	+	40274756	40275371	616
ENSG00000(	594.5446	545.5423	589.778	343.8257	434.4439	348.5131	0.61813	6.53E-05	0.000218	PHF2	chr9	+	96338689	96441869	5565
ENSG00000(	3834.502	3552.649	2539.872	7304.236	5448.037	6301.183	-0.93725	1.13E-09	6.15E-09	RPS26	chr12	+	56435637	56438116	1204
ENSG00000(	0	0	1.319414	1.498151	0	0	-0.08979	0.94423	NA	C14orf178	chr14	+	78227173	78236085	642
ENSG00000(	31.07376	30.10719	30.34652	27.7158	22.09037	36.16646	0.08603	0.8434	0.90015	PTMAP2	chr5	+	1.18E+08	1.18E+08	327
ENSG00000(	23549.76	23505.29	23436.75	18006.28	16928.59	17567.03	0.42456	5.88E-06	2.24E-05	PSAP	chr10	-	73576055	73611126	2866
ENSG00000(	7534.35	7572.561	6429.503	8284.776	7485.873	8947.91	-0.19837	0.08639	0.1554	S100A10	chr1	-	1.52E+08	1.52E+08	1202
ENSG00000(	5.17896	4.817151	9.235896	4.494453	9.20432	9.041614	-0.22133	0.7849	0.85858	WDR96	chr10	-	1.06E+08	1.06E+08	5365
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	LHFPL5	chr6	+	35773070	35801651	2147
ENSG00000(	24738.85	25194.9	20216.06	12136.52	13406.09	15122.51	0.78507	2.28E-10	1.31E-09	RPL37A	chr2	+	2.17E+08	2.17E+08	3112
ENSG00000(	436.0684	368.512	292.9099	86.89276	78.23672	53.42772	2.312	1.57E-23	1.83E-22	HOXC6	chr12	+	54384408	54424607	2943
ENSG00000(	96.32865	71.05298	84.44248	83.14739	64.43024	61.64737	0.26403	0.36689	0.49692	TXNRD3	chr3	-	1.26E+08	1.26E+08	2950
ENSG00000(	106.6866	126.4502	72.56776	22.47227	13.80648	13.15144	2.5699	7.06E-12	4.54E-11	CFD	chr19	+	859453	863569	1330
ENSG00000(	4.143168	13.24716	1.319414	0.749076	1.840864	3.28786	1.3726	0.18913	0.2942	C9orf173	chr9	+	1.4E+08	1.4E+08	1206
ENSG00000(	9.322127	14.45145	10.55531	44.19546	29.45382	27.12484	-1.4999	0.004157	0.010469	MAP1LC3C	chr1	-	2.42E+08	2.42E+08	1182
ENSG00000(	655.6563	637.0682	732.2746	2071.194	1785.638	1674.343	-1.4473	5.30E-28	7.42E-27	MCMBP	chr10	-	1.22E+08	1.22E+08	4113
ENSG00000(	366.6703	328.7705	258.6051	129.5901	131.6218	253.1652	0.88483	0.000419	0.001245	EME2	chr16	+	1823208	1831709	5613
ENSG00000(	26.93059	74.66584	69.92893	8.239831	13.80648	9.863579	2.3464	1.85E-06	7.47E-06	KLHDC1	chr14	+	50159823	50219870	2691
ENSG00000(	65.25489	40.94578	98.95603	29.96302	61.66894	34.52253	0.68884	0.083632	0.15107	ZNF81	chrX	+	47696301	47861960	7933

ENSG00000(	666.0142	567.2195	687.4146	492.8917	436.2848	492.357	0.43211	0.003125	0.008047	TAF13	chr1	-	1.1E+08	1.1E+08	1076
ENSG00000(	184.371	221.5889	279.7157	202.9995	192.3703	129.8705	0.37847	0.10187	0.17806	ZNF780A	chr19	-	40575059	40596845	7500
ENSG00000(	1191.161	1080.246	899.8402	2221.758	1959.6	2262.047	-1.0192	2.35E-14	1.78E-13	ATAD3A	chr1	+	1447531	1470067	2612
ENSG00000(	302.4512	363.6949	357.5611	516.1131	449.1708	404.4067	-0.42077	0.011167	0.025689	FAM118B	chr11	+	1.26E+08	1.26E+08	2402
ENSG00000(	98.40023	127.6545	96.31721	68.16587	59.82808	53.42772	0.81878	0.003558	0.009074	ZNF461	chr19	-	37128094	37157755	3326
ENSG00000(	72.50543	77.07441	68.60952	8.239831	12.88605	15.61733	2.5185	6.06E-10	3.38E-09	CTC-301O7	chr19	-	49834874	49843865	573
ENSG00000(	24.85901	12.04288	25.06886	8.988907	21.16994	16.4393	0.4007	0.48388	0.61309	AC122129.	chr17	+	17761583	17762295	710
ENSG00000(	30.03797	54.19295	27.70769	20.97412	21.16994	18.08323	0.86762	0.059237	0.11242	CCDC180	chr9	+	1E+08	1E+08	7884
ENSG00000(	497.1801	498.5751	410.3377	256.1838	355.2868	332.8958	0.57476	0.001065	0.002975	SLC9A8	chr20	+	48429250	48508779	6303
ENSG00000(	1.035792	7.225726	1.319414	385.7739	413.274	308.2368	-6.6204	1.78E-40	3.74E-39	OCLN	chr5	+	68788119	68853931	6438
ENSG00000(	1.035792	6.021439	0	0	0	0	2.0906	0.12335	0.20852	AC061975.	chr17	-	26529824	26530831	150
ENSG00000(	5.17896	4.817151	5.277655	0	0	0	3.4819	0.006108	0.01488	C4orf22	chr4	+	81256874	81884910	3349
ENSG00000(	8.286335	2.408575	5.277655	9.737982	16.56778	3.28786	-0.77774	0.35504	0.48466	AC011385.	chr5	-	1.38E+08	1.38E+08	1363
ENSG00000(	104.615	90.32158	89.72014	14.98151	88.36147	62.46933	0.76795	0.070016	0.12981	HIST4H4	chr12	-	14920933	14924065	1918
ENSG00000(	101.5076	133.6759	93.67838	74.90755	68.11197	60.00344	0.68789	0.01303	0.029504	ZNF181	chr19	+	35225060	35233777	3589
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	AL358813.	chr1	+	1.5E+08	1.5E+08	486
ENSG00000(	9.322127	9.634302	7.916483	0.749076	24.85166	15.61733	-0.54645	0.4969	0.62537	HIST1H2BF	chr6	+	26199748	26200942	1195
ENSG00000(	14.50109	9.634302	13.19414	38.20285	34.97642	48.49593	-1.6453	0.000677	0.001949	SLC22A20	chr11	+	64981311	65010228	3196
ENSG00000(	1.035792	0	2.638828	0	0.920432	4.109825	-0.28862	0.82659	0.88831	POM121L6	chr6	+	26864126	26865739	1614
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	OR8G1	chr11	+	1.24E+08	1.24E+08	936
ENSG00000(	608.0098	568.4238	641.2351	322.8516	474.0225	408.5166	0.59202	0.000365	0.001096	FAM212B	chr1	-	1.12E+08	1.12E+08	5980
ENSG00000(	106.6866	99.95588	64.65128	198.505	205.2563	191.5178	-1.1175	3.06E-06	1.20E-05	ZNF44	chr19	-	12335501	12405702	3236
ENSG00000(	2972.723	3017.945	2396.055	2403.783	1950.395	2194.646	0.3561	0.006391	0.015506	GPAA1	chr8	+	1.45E+08	1.45E+08	2078
ENSG00000(	0	0	0	2.247227	13.80648	13.15144	-4.0521	0.000727	0.002087	ADAMTSL2	chr9	+	1.36E+08	1.36E+08	4270
ENSG00000(	230.9816	262.5347	386.5882	340.0803	277.05	269.6045	-0.0153	0.94163	0.9649	SGTB	chr5	-	64961755	65018862	5469
ENSG00000(	48.68222	103.5687	98.95603	71.16218	56.14635	80.55256	0.26102	0.43047	0.56032	ZNF790	chr19	-	37308330	37341689	3037
ENSG00000(	0	0	3.958241	0.749076	6.443024	5.753754	-1.2693	0.29269	0.41698	PRB3	chr12	-	11418857	11422739	1153
ENSG00000(	240.3037	244.4704	316.6593	73.4094	63.50981	62.46933	1.9889	8.72E-19	8.36E-18	FAM49A	chr2	-	16730727	16847599	4670
ENSG00000(	2796.638	2520.574	2717.992	2658.469	2757.614	2912.222	-0.05143	0.63362	0.74325	MYO1C	chr17	-	1367392	1396106	5145
ENSG00000(	0	0	0	2.996302	0.920432	7.397684	-2.6284	0.045605	0.089631	OR7E13P	chr11	-	86543582	86544491	910
ENSG00000(	138.7961	148.1274	145.1355	193.2615	115.9744	115.0751	0.022115	0.93032	0.95814	NKIRAS1	chr3	-	23933151	23988082	2391
ENSG00000(	0	0	0	2.996302	0.920432	0	-1.1048	0.40628	NA	UGT2B17	chr4	-	69402902	69434245	2077
ENSG00000(	2.071584	3.612863	0	11.23613	0	2.465895	-0.94388	0.42404	0.55456	MEIG1	chr10	+	15001438	15030049	625
ENSG00000(	447.4621	405.845	445.9619	98.87797	142.667	142.1999	1.7544	5.87E-20	5.93E-19	KIF13B	chr8	-	28924796	29120641	8745
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	NRAP	chr10	-	1.15E+08	1.15E+08	5600
ENSG00000(	3003.797	2989.042	3017.499	4340.144	3829.918	3968.447	-0.42946	4.41E-05	0.000151	ADH5	chr4	-	99992132	1E+08	2612
ENSG00000(	2627.804	2403.758	2041.133	2365.581	1779.195	1910.246	0.22362	0.1111	0.19101	HIST1H2BK	chr6	-	27106073	27114619	820
ENSG00000(	296.2365	285.4162	248.0498	889.9018	816.4232	849.0898	-1.6161	1.20E-28	1.73E-27	TEAD4	chr12	+	3068496	3149839	1690
ENSG00000(	1735.987	1855.807	1666.42	1468.937	1400.897	1671.877	0.21087	0.080483	0.1461	SPG7	chr16	+	89557325	89624176	3076
ENSG00000(	7.250543	15.65574	0	9.737982	3.681728	11.50751	-0.1047	0.90542	0.94157	HIST1H4K	chr6	-	27798952	27799305	354
ENSG00000(	0	3.612863	0	11.23613	30.37426	17.26126	-3.4705	0.000144	0.000459	HRNR	chr1	-	1.52E+08	1.52E+08	9623
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	IFNA1	chr9	+	21440440	21441315	876
ENSG00000(	51.7896	69.84869	51.45714	27.7158	23.93123	18.90519	1.2654	0.001113	0.003097	C2orf27A	chr2	+	1.32E+08	1.33E+08	1331
ENSG00000(	60.07593	48.17151	72.56776	214.2356	236.551	204.6693	-1.8459	3.03E-14	2.28E-13	ZNF677	chr19	-	53731577	53758151	8731

ENSG0000(	1838.531	2006.343	1979.121	1126.61	1035.486	951.0134	0.90133	5.58E-14	4.15E-13	ERO1L	chr14	-	53106634	53162618	5285
ENSG0000(	131.5456	138.4931	118.7472	250.9403	137.1444	151.2415	-0.47002	0.067732	0.12623	F8A1	chrX	+	1.54E+08	1.54E+08	1701
ENSG0000(	31.07376	21.67718	29.0271	144.5716	110.4518	131.5144	-2.208	3.09E-12	2.04E-11	ZNF823	chr19	-	11832080	11849824	2423
ENSG0000(	2.071584	4.817151	7.916483	0.749076	1.840864	0.821965	1.6617	0.13419	0.22317	AP001597.	chr21	+	27765954	27941571	3412
ENSG0000(	6.214751	3.612863	0	50.18806	76.39586	62.46933	-3.969	2.26E-11	1.40E-10	ZNF311	chr6	-	28962562	28973093	3027
ENSG0000(	61.11172	61.41867	83.12307	164.0475	175.8025	147.1317	-1.2378	9.88E-07	4.10E-06	ZNF347	chr19	-	53627325	53662328	4553
ENSG0000(	15.53688	34.92434	31.66593	37.45378	36.81728	34.52253	-0.40473	0.35932	0.48886	PLCG2	chr16	+	81772702	81991899	4308
ENSG0000(	413.281	517.8437	451.2395	116.1067	173.9616	184.9421	1.535	1.65E-14	1.27E-13	FCHSD1	chr5	-	1.41E+08	1.41E+08	4320
ENSG0000(	368.7419	401.0278	431.4483	407.4971	391.1836	377.2819	0.028796	0.85097	0.90506	ZNF71	chr19	+	57106632	57137849	5428
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AADACL2	chr3	+	1.51E+08	1.51E+08	4848
ENSG0000(	6235.467	6487.498	5310.64	633.7179	590.9173	927.1764	3.0565	2.78E-84	1.59E-82	S100A6	chr1	-	1.54E+08	1.54E+08	673
ENSG0000(	29947.85	30793.64	22938.01	18166.58	15633.54	19007.12	0.6626	4.22E-07	1.82E-06	RPL12	chr9	-	1.3E+08	1.3E+08	2275
ENSG0000(	29.00217	24.08575	21.11062	37.45378	37.73771	30.4127	-0.49008	0.25647	0.37482	DNM3	chr1	+	1.72E+08	1.72E+08	7643
ENSG0000(	335.5966	357.6735	273.1187	1048.706	968.2945	1004.441	-1.6379	3.79E-29	5.57E-28	ZNF121	chr19	-	9671029	9695209	2407
ENSG0000(	2125.445	1954.559	2268.072	4807.567	4704.328	4522.451	-1.143	4.90E-26	6.31E-25	MPZL1	chr1	+	1.68E+08	1.68E+08	5010
ENSG0000(	354.2408	269.7604	481.586	386.523	461.1364	364.1305	-0.13268	0.51065	0.63792	VPS13A	chr9	+	79792269	80036457	15320
ENSG0000(	51.7896	55.39724	54.09597	419.4823	348.8437	350.979	-2.7789	3.90E-37	7.43E-36	MBP	chr18	-	74690783	74845639	9797
ENSG0000(	1502.934	1449.962	1390.662	1123.613	1085.189	1286.375	0.31305	0.010343	0.023971	AKAP17A	chrX	+	1710486	1721407	3232
ENSG0000(	29.00217	33.72006	32.98534	154.3096	147.2691	119.1849	-2.1139	1.37E-12	9.29E-12	ELOVL2	chr6	-	10980992	11044547	3997
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	GOLGA6L9	chr15	+	82722223	82731338	4086
ENSG0000(	10.35792	12.04288	5.277655	7.490755	10.12475	4.93179	0.28128	0.71012	0.80403	LEKR1	chr3	+	1.57E+08	1.57E+08	2881
ENSG0000(	1022.327	1070.612	841.786	992.5251	746.4703	984.714	0.10723	0.48073	0.60986	C1orf122	chr1	+	38272651	38275126	2229
ENSG0000(	301.4154	343.222	233.5362	773.046	606.5647	949.3695	-1.3991	1.79E-13	1.29E-12	SNHG12	chr1	-	28905050	28909495	1903
ENSG0000(	2.071584	6.021439	7.916483	7.490755	12.88605	9.863579	-0.84463	0.29246	0.41667	PCDH20	chr13	-	61983818	62002220	6347
ENSG0000(	0	0	5.277655	0.749076	2.761296	0.821965	0.16608	0.89877	0.93723	CLEC9A	chr12	+	10183276	10218565	1673
ENSG0000(	1.035792	1.204288	3.958241	2.247227	2.761296	0.821965	0.051081	0.96599	0.98015	KEL	chr7	-	1.43E+08	1.43E+08	2812
ENSG0000(	557.256	550.3595	567.3479	696.6403	710.5735	582.7731	-0.24791	0.080168	0.14563	NOL8	chr9	-	95059640	95087918	4598
ENSG0000(	181.2636	145.7188	164.9267	214.9847	232.8693	227.6843	-0.45298	0.021184	0.045693	IRAK4	chr12	+	44152747	44183346	4147
ENSG0000(	13.46529	14.45145	2.638828	8.988907	0.920432	12.32947	0.40896	0.62762	0.73857	CCDC151	chr19	-	11531272	11546603	2448
ENSG0000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	DLGAP2	chr8	+	1449532	1656642	10132
ENSG0000(	632.8689	729.7984	741.5105	1146.835	945.2837	870.4608	-0.49368	0.000726	0.002083	MRPL42	chr12	+	93861264	93897545	3138
ENSG0000(	290.0217	193.8903	385.2688	250.9403	339.6394	238.3698	0.067621	0.77187	0.85002	ENTPD7	chr10	+	1.01E+08	1.01E+08	3550
ENSG0000(	2.071584	0	0	0.749076	0	0	0.47431	0.71145	NA	FCGR1B	chr1	-	1.21E+08	1.21E+08	1044
ENSG0000(	686.73	586.4881	517.2102	691.3967	531.0893	607.4321	-0.03059	0.84779	0.90301	ZNF335	chr20	-	44577292	44600833	4430
ENSG0000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	ZNF560	chr19	-	9577183	9609283	2654
ENSG0000(	22772.92	23358.36	18446.72	15223.46	11776.01	12936.08	0.69177	8.85E-08	4.08E-07	RPS4X	chrX	-	71475529	71497150	1820
ENSG0000(	36.25272	30.10719	26.38828	32.21025	23.93123	34.52253	0.033876	0.93709	0.96179	AGAP9	chr10	+	48189612	48237508	2410
ENSG0000(	77.68439	52.98866	67.2901	242.7005	227.3467	200.5594	-1.7424	3.67E-13	2.59E-12	ZNF273	chr7	+	64330550	64391344	3757
ENSG0000(	938.4275	952.5916	1009.352	499.6334	498.8741	499.7547	0.95041	7.16E-14	5.27E-13	ZNF84	chr12	+	1.34E+08	1.34E+08	7162
ENSG0000(	307.6302	314.3191	339.0893	799.2636	668.2336	650.9962	-1.1385	8.31E-14	6.10E-13	MAK16	chr8	+	33342268	33358778	3991
ENSG0000(	424.6747	381.7592	424.8512	382.0285	289.9361	324.6761	0.30229	0.069524	0.12899	SIRPA	chr20	+	1875154	1920543	3996
ENSG0000(	504.4307	384.1678	406.3794	1618.752	1298.73	1507.484	-1.7655	1.32E-32	2.19E-31	GRK6	chr5	+	1.77E+08	1.77E+08	2939
ENSG0000(	35.21692	40.94578	29.0271	381.2795	231.0284	263.8507	-3.0242	6.05E-28	8.44E-27	PRIM1	chr12	-	57125406	57146157	1393
ENSG0000(	661.871	757.497	770.5376	1018.743	952.6471	867.173	-0.37466	0.005261	0.012978	5-Mar	chr10	+	94050920	94113721	3926

ENSG00000(	9.322127	10.83859	10.55531	0	0.920432	4.109825	2.2278	0.019794	0.043	AKR1B10	chr7	+	1.34E+08	1.34E+08	1590
ENSG00000(	25.8948	46.96722	39.58241	37.45378	26.69253	29.59074	0.24725	0.55592	0.67653	SULT1C4	chr2	+	1.09E+08	1.09E+08	1860
ENSG00000(	13.46529	1.204288	6.597069	0	3.681728	0	1.9933	0.078003	0.14223	CYP2A7	chr19	-	41381344	41388657	2281
ENSG00000(	104.615	107.1816	104.2337	179.7781	208.9381	158.6392	-0.78573	0.000491	0.001445	ZBTB14	chr18	-	5289018	5297052	3528
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	KRTAP9-9	chr17	+	39411636	39412616	981
ENSG00000(	219.5879	230.019	336.4505	974.5473	1188.278	997.0434	-2.0031	9.68E-31	1.50E-29	CD2AP	chr6	+	47445525	47594999	5412
ENSG00000(	0	0	1.319414	43.44638	33.13555	32.05663	-5.29	2.68E-08	1.30E-07	NUP62CL	chrX	-	1.06E+08	1.06E+08	1755
ENSG00000(	254.8048	295.0505	184.7179	322.1025	351.605	355.0888	-0.48075	0.012654	0.028735	SFI1	chr22	+	31884674	32014572	5250
ENSG00000(	3.107376	0	1.319414	0.749076	0	1.64393	0.51931	0.698	0.79445	TMPRSS11F	chr4	-	68918916	68995598	2088
ENSG00000(	47.64643	62.62296	34.30476	90.63814	107.6905	115.8971	-1.1006	0.00038	0.001137	ZNF649	chr19	-	52392477	52408293	3197
ENSG00000(	0	2.408575	3.958241	0.749076	0	3.28786	0.41088	0.74975	0.83383	ADH4	chr4	-	1E+08	1E+08	2151
ENSG00000(	1.035792	0	1.319414	0	1.840864	2.465895	-0.49225	0.71368	0.80659	AL138751.	chr9	-	74576256	74576469	210
ENSG00000(	300.3797	309.5019	415.6153	143.8225	105.8497	154.5294	1.3302	3.53E-10	2.01E-09	ZNF248	chr10	-	38091751	38147034	5141
ENSG00000(	15.53688	15.65574	17.15238	9.737982	16.56778	7.397684	0.49806	0.41968	0.55042	SNX29P2	chr16	+	29262829	29519817	6046
ENSG00000(	370.8135	337.2006	398.463	64.4205	79.15715	67.40112	2.3809	2.39E-32	3.90E-31	CHSY3	chr5	+	1.29E+08	1.3E+08	3850
ENSG00000(	59.04014	50.58008	39.58241	48.68991	44.18074	78.08667	-0.1887	0.60117	0.71645	TOR4A	chr9	+	1.4E+08	1.4E+08	4148
ENSG00000(	1863.39	1820.883	2173.074	384.2758	364.4911	307.4149	2.4643	1.71E-71	7.64E-70	LPAR1	chr9	-	1.14E+08	1.14E+08	3637
ENSG00000(	313.8449	362.4906	354.9223	344.5748	324.9125	313.9906	0.066487	0.68015	0.78088	HIBCH	chr2	-	1.91E+08	1.91E+08	3383
ENSG00000(	233.0532	298.6634	204.5091	680.9097	506.2376	572.9095	-1.2518	8.83E-12	5.64E-11	ZNF544	chr19	+	58739960	58788815	4109
ENSG00000(	4.143168	0	0	4.494453	9.20432	3.28786	-1.5118	0.18083	0.28381	TMEM229B	chr14	-	67913801	68000456	4068
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP11-267J	chr12	+	12264097	12264423	327
ENSG00000(	305.5586	329.9748	328.534	373.7887	308.3447	401.1189	-0.16939	0.31561	0.44225	SOWAHC	chr2	+	1.1E+08	1.1E+08	4653
ENSG00000(	437.1042	375.7378	530.4043	373.7887	577.1109	416.7362	-0.02525	0.89499	0.93511	ZNF770	chr15	-	35270542	35280488	5439
ENSG00000(	21.75163	49.3758	23.74945	21.72319	21.16994	22.19305	0.52354	0.27718	0.39884	AC135178.	chr17	-	8261731	8263538	1808
ENSG00000(	20.71584	20.47289	13.19414	106.3687	100.3271	96.1699	-2.4225	1.33E-11	8.41E-11	ZNF876P	chr4	+	206399	249774	2598
ENSG00000(	12.4295	4.817151	6.597069	5.243529	2.761296	10.68554	0.31977	0.70076	0.79659	A-575C2.4	chr16	-	28353876	28374829	2016
ENSG00000(	135.6887	125.2459	102.9143	158.0549	131.6218	117.541	-0.15916	0.50775	0.63525	HMGN5	chrX	-	80369200	80457441	2126
ENSG00000(	420.5315	481.7151	529.0849	473.4157	516.3624	355.9108	0.087705	0.61484	0.72803	MIER1	chr1	+	67390578	67454302	4978
ENSG00000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	PPIAL4C	chr1	+	1.5E+08	1.5E+08	785
ENSG00000(	623.5467	620.2082	894.5625	600.7586	770.4016	630.4471	0.094122	0.58135	0.69924	MAN1A2	chr1	+	1.18E+08	1.18E+08	8576
ENSG00000(	47.64643	52.98866	38.263	443.4527	383.8201	481.6714	-3.2098	5.25E-47	1.32E-45	SVIP	chr11	-	22835345	22851845	4541
ENSG00000(	310.7376	402.2321	389.2271	113.8595	158.3143	151.2415	1.3741	5.81E-12	3.76E-11	ZNF251	chr8	-	1.46E+08	1.46E+08	2807
ENSG00000(	1042.007	977.8816	832.5501	706.3782	894.6599	1031.566	0.11665	0.46	0.58944	DDRGK1	chr20	-	3170996	3185331	1306
ENSG00000(	1563.01	1590.864	1576.699	3484.699	3195.74	3189.224	-1.0595	3.70E-23	4.24E-22	TFDP1	chr13	+	1.14E+08	1.14E+08	2648
ENSG00000(	92.18548	77.07441	96.31721	138.579	170.2799	164.393	-0.82586	0.000586	0.001703	ZNF607	chr19	-	38187264	38210691	4364
ENSG00000(	110.8297	102.3645	104.2337	101.1252	99.40666	104.3895	0.058309	0.8112	0.87758	ZNF334	chr20	-	45129701	45142198	3487
ENSG00000(	448.4979	484.1237	460.4754	147.5679	161.996	138.9121	1.6299	4.21E-22	4.65E-21	HSD17B11	chr4	-	88257762	88312538	1885
ENSG00000(	827.5977	936.9358	796.9259	339.3312	560.5431	475.9177	0.89489	3.36E-07	1.47E-06	SZT2	chr1	+	43855553	43918321	12281
ENSG00000(	18.64425	9.634302	13.19414	2.996302	7.363456	0.821965	1.7276	0.032086	0.065923	SULT1C2	chr2	+	1.09E+08	1.09E+08	6366
ENSG00000(	50.7538	61.41867	60.69303	53.18436	60.74851	52.60575	0.051681	0.87224	0.91976	ZXDA	chrX	-	57931864	57937067	5204
ENSG00000(	7.250543	4.817151	2.638828	74.90755	66.2711	76.44274	-3.7021	6.63E-13	4.60E-12	RPS6KL1	chr14	-	75370657	75390099	5456
ENSG00000(	4.143168	0	0	0	2.761296	0	0.32622	0.80997	0.87669	CACNA1E	chr1	+	1.81E+08	1.82E+08	16170
ENSG00000(	980.8949	1065.795	1109.627	1771.564	1707.401	1569.953	-0.67723	1.58E-08	7.81E-08	QRICH1	chr3	-	49067140	49131796	3549
ENSG00000(	16.57267	25.29004	10.55531	36.7047	47.86246	43.56414	-1.2444	0.007026	0.016913	MLLT4-AS1	chr6	-	1.68E+08	1.68E+08	2238

ENSG00000(	1.035792	3.612863	0	24.71949	8.283888	22.19305	-3.1098	0.000423	0.001258	CSF2RA	chrX	+	1387693	1429274	2291
ENSG00000(	10.35792	8.430014	10.55531	13.48336	6.443024	8.219649	0.048544	0.94546	0.96725	FKBP1C	chr6	+	63921351	63922929	1579
ENSG00000(	2507.652	2610.896	2735.145	2163.33	3016.256	2655.769	0.003592	0.97837	0.98741	DDX42	chr17	+	61850963	61896677	4337
ENSG00000(	4.143168	2.408575	6.597069	4.494453	4.60216	0	0.42607	0.69013	0.78851	RP11-98J2	chr5	+	69171098	69274436	633
ENSG00000(	1137.3	1052.547	1106.988	1010.503	849.5587	900.0516	0.25532	0.043554	0.086198	RPL23A	chr17	+	27046411	27051377	1562
ENSG00000(	102.5434	151.7403	112.1502	57.67882	56.14635	50.13986	1.1461	4.50E-05	0.000154	SLC29A3	chr10	+	73079015	73123142	2257
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTC-490E2	chr19	-	41414377	41416754	660
ENSG00000(	464.0348	357.6735	502.6967	512.3677	485.0677	394.5432	-0.07199	0.67907	0.78	STYX	chr14	+	53196898	53241716	4857
ENSG00000(	1010.933	944.1616	803.523	1007.507	953.5675	1440.083	-0.3003	0.07005	0.12984	UBL5	chr19	+	9938568	9940791	1450
ENSG00000(	1212.912	1140.46	1472.466	544.5779	844.9566	639.4887	0.91236	4.77E-08	2.26E-07	HELZ	chr17	-	65066554	65242105	13810
ENSG00000(	77.68439	75.87013	64.65128	104.1215	111.3723	105.2115	-0.54684	0.038556	0.077501	TMEM116	chr12	-	1.12E+08	1.12E+08	3640
ENSG00000(	489.9296	573.241	459.156	732.5959	554.1001	641.9546	-0.34091	0.030849	0.063694	UCKL1	chr20	-	62571186	62587769	1954
ENSG00000(	1.035792	0	0	337.084	323.0716	347.6912	-8.3073	2.22E-24	2.68E-23	CARD11	chr7	-	2945775	3083579	4366
ENSG00000(	61.11172	43.35436	62.01245	57.67882	46.0216	38.63235	0.22053	0.52889	0.65369	ZNF485	chr10	+	44101855	44113351	2054
ENSG00000(	2.071584	1.204288	0	0	0.920432	0.821965	0.49539	0.7148	NA	PEG3	chr19	-	57321445	57352096	8723
ENSG00000(	364.5988	405.845	500.0578	631.4707	541.214	440.5732	-0.34569	0.052136	0.10072	SDAD1	chr4	-	76862103	76912115	3080
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	SPDYE8P	chr7	-	72490260	72500313	2818
ENSG00000(	10.35792	12.04288	22.43003	12.73428	6.443024	10.68554	0.53331	0.41448	0.545	RP11-381C	chr9	+	66960613	66964189	885
ENSG00000(	161.5835	197.5032	385.2688	33.7084	126.0992	30.4127	1.83	0.008644	0.020396	ZKSCAN8	chr6	+	28109716	28124089	4215
ENSG00000(	737.4838	643.0896	526.4461	277.907	309.2652	358.3767	1.0102	3.51E-09	1.84E-08	FAM109A	chr12	-	1.12E+08	1.12E+08	3256
ENSG00000(	9.322127	0	3.958241	0	0	0	3.0694	0.020296	0.043956	TMEM239	chr20	+	2795614	2800930	3892
ENSG00000(	111.8655	78.2787	83.12307	239.7042	226.4263	203.8473	-1.2788	2.18E-08	1.07E-07	HYLS1	chr11	+	1.26E+08	1.26E+08	2061
ENSG00000(	0	2.408575	1.319414	86.14369	99.40666	106.0335	-5.8095	4.98E-16	4.18E-15	MYL4	chr17	+	45277812	45301045	920
ENSG00000(	44.53905	46.96722	32.98534	13.48336	92.0432	92.88204	-0.64336	0.19491	0.30125	HIST1H4I	chr6	+	27107076	27108418	1343
ENSG00000(	2.071584	2.408575	6.597069	18.72689	17.48821	16.4393	-2.0899	0.005246	0.012946	ZNF442	chr19	-	12460185	12476719	2797
ENSG00000(	103.5792	84.30014	97.63662	254.6857	266.0048	240.0138	-1.4032	2.56E-11	1.58E-10	ZNF813	chr19	+	53970989	54006950	6151
ENSG00000(	121.1877	101.1602	100.2754	17.97781	13.80648	21.37109	2.5558	8.01E-14	5.88E-13	HOXC4	chr12	+	54410715	54449814	1666
ENSG00000(	12.4295	9.634302	9.235896	4.494453	7.363456	8.219649	0.59803	0.41792	0.54863	DCAF12L2	chrX	-	1.25E+08	1.25E+08	1652
ENSG00000(	558.2918	525.0694	394.5047	794.7692	711.4939	650.9962	-0.54181	0.000814	0.002316	PIM3	chr22	+	50354161	50357728	2369
ENSG00000(	1998.043	1916.022	1632.115	1554.332	1425.749	1926.686	0.17655	0.20816	0.31763	ASNA1	chr19	+	12847953	12859137	1368
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	RP11-544M	chr1	+	1.61E+08	1.61E+08	2136
ENSG00000(	3893.542	4168.04	4955.718	1247.211	1392.614	1098.967	1.7955	5.47E-42	1.20E-40	ASPH	chr8	-	62413116	62627155	5153
ENSG00000(	1.035792	0	5.277655	0	1.840864	3.28786	0.19145	0.88066	0.92529	HIST1H3A	chr6	+	26020718	26021186	469
ENSG00000(	594.5446	539.5209	662.3457	586.5262	708.7326	572.9095	-0.05612	0.70892	0.80322	SPRED2	chr2	-	65537985	65659771	4097
ENSG00000(	485.7864	514.2309	473.6695	556.5631	654.4271	665.7916	-0.34704	0.016073	0.035651	WWP2	chr16	+	69796209	69975644	4515
ENSG00000(	0	0	0	0.749076	2.761296	0	-0.97685	0.45852	NA	HIST1H2AL	chr6	+	27833034	27833606	573
ENSG00000(	1529.865	1580.025	1932.941	1700.401	1895.169	1705.577	-0.07245	0.57138	0.69031	GFPT1	chr2	-	69546905	69614382	8695
ENSG00000(	229.9458	199.9118	277.0769	277.907	282.5726	210.423	-0.12564	0.53249	0.657	UVRAG	chr11	+	75526212	75854239	4123
ENSG00000(	0	0	3.958241	0.749076	2.761296	0	0.085807	0.94922	0.96942	TPTE2P3	chr13	+	53063128	53161222	2610
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC092291.	chr16	-	14548061	14548155	90
ENSG00000(	158.4762	160.1703	182.0791	151.3133	126.0992	184.1201	0.1139	0.60909	0.72313	ZNF26	chr12	+	1.34E+08	1.34E+08	4853
ENSG00000(	204.051	208.3418	255.9663	187.2689	208.0176	196.4496	0.17318	0.36997	0.50043	ITSN2	chr2	-	24425733	24583583	6300
ENSG00000(	5.17896	6.021439	2.638828	1.498151	5.522592	0	0.80081	0.46408	0.59328	NTRK1	chr1	+	1.57E+08	1.57E+08	3052
ENSG00000(	14.50109	9.634302	23.74945	34.45748	25.7721	62.46933	-1.3176	0.010021	0.0233	BZW1P2	chr3	-	1.16E+08	1.16E+08	826

ENSG00000(	1873.748	2055.719	2369.667	1673.435	1858.352	1665.301	0.27643	0.026967	0.056654	MGEA5	chr10	-	1.04E+08	1.04E+08	5146
ENSG00000(	10.35792	1.204288	2.638828	0	0	2.465895	1.8139	0.13485	0.22398	CTD-2173L	chr9	-	39443804	39464526	4037
ENSG00000(	108.7581	107.1816	63.33186	149.066	152.7917	230.1502	-0.91478	0.000803	0.002287	MT1F	chr16	+	56691606	56694610	1573
ENSG00000(	698.1237	679.2183	756.0241	437.4601	511.7602	500.5766	0.55618	7.39E-05	0.000245	FAM115A	chr7	-	1.44E+08	1.44E+08	5733
ENSG00000(	47.64643	31.31148	71.24834	129.5901	120.5766	152.8855	-1.4126	4.31E-06	1.67E-05	ZNF69	chr19	+	11998599	12025144	2010
ENSG00000(	1203.59	1259.685	1570.102	3402.301	3366.94	2798.791	-1.2441	4.61E-20	4.67E-19	TXNRD1	chr12	+	1.05E+08	1.05E+08	3974
ENSG00000(	5.17896	8.430014	23.74945	67.4168	37.73771	60.8254	-2.1047	3.97E-05	0.000137	NRARP	chr9	-	1.4E+08	1.4E+08	2621
ENSG00000(	148.1182	140.9017	145.1355	62.17327	61.66894	38.63235	1.4041	2.65E-07	1.17E-06	ZNF583	chr19	+	56909335	56947404	4916
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	KRTAP4-1	chr17	-	39340354	39341594	1241
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	F8A2	chrX	+	1.55E+08	1.55E+08	1701
ENSG00000(	71.46964	39.74149	73.88717	62.17327	57.98722	78.08667	-0.09769	0.77041	0.84909	ZNF568	chr19	+	37407231	37489602	3774
ENSG00000(	133.6172	144.5145	197.9121	96.63075	125.1788	99.45776	0.56123	0.02243	0.048055	ZXDB	chrX	+	57618269	57623906	5638
ENSG00000(	247.5543	266.1476	311.3817	364.7998	372.775	350.1571	-0.39962	0.017371	0.03826	ZNF480	chr19	+	52800430	52829175	4738
ENSG00000(	1169.409	1216.331	849.7025	1116.123	934.2385	1236.235	-0.02201	0.8899	0.9317	ZNF587	chr19	+	58361225	58376480	6882
ENSG00000(	13248.81	12950.91	10379.83	7955.182	8051.939	10337.85	0.47242	0.000469	0.001383	TPM2	chr9	-	35681989	35691017	2147
ENSG00000(	31.07376	38.53721	50.13772	41.19916	57.06678	66.57916	-0.45739	0.21949	0.33111	FLVCR1-AS1	chr1	-	2.13E+08	2.13E+08	2525
ENSG00000(	38.3243	33.72006	62.01245	41.94823	50.62376	25.48091	0.17578	0.66755	0.77083	ZNF280B	chr22	-	22838767	22863505	5726
ENSG00000(	185.4068	162.5788	153.052	1140.842	1075.065	941.1498	-2.6429	1.44E-63	5.46E-62	SH3BGRL2	chr6	+	80341000	80413372	4649
ENSG00000(	135.6887	124.0416	143.8161	167.7929	253.1188	209.6011	-0.63763	0.004317	0.010831	ZNF808	chr19	+	53030905	53067717	4233
ENSG00000(	222.6953	185.4603	224.3003	0	3.681728	0	7.0832	1.13E-29	1.70E-28	ANKRD35	chr1	+	1.46E+08	1.46E+08	3342
ENSG00000(	1826.101	1891.936	1947.455	2093.666	2331.454	2019.568	-0.18558	0.1009	0.17674	YTHDF2	chr1	+	29063133	29096287	2925
ENSG00000(	96.32865	105.9773	81.80365	124.3465	143.5874	125.7606	-0.46367	0.058025	0.11056	NBR2	chr17	+	41277627	41305688	1344
ENSG00000(	343.8829	328.7705	356.2417	537.0872	550.4183	543.3188	-0.6628	5.08E-06	1.95E-05	TMA16	chr4	+	1.64E+08	1.64E+08	1978
ENSG00000(	203.0152	213.1589	233.5362	155.0586	143.5874	130.6924	0.59224	0.003231	0.00831	ATL1	chr14	+	50999227	51099786	2853
ENSG00000(	0	0	1.319414	3.745378	8.283888	7.397684	-2.8131	0.0174	0.038316	CNGA1	chr4	-	47937994	48018689	2867
ENSG00000(	147.0825	180.6432	117.4278	239.7042	225.5058	326.3201	-0.82317	0.000268	0.000822	MAFK	chr7	+	1570350	1582679	3368
ENSG00000(	50.7538	19.2686	39.58241	11.98521	29.45382	18.08323	0.86195	0.087154	0.15664	HIST1H4E	chr6	+	26204858	26206266	1409
ENSG00000(	32.10955	55.39724	26.38828	11.98521	7.363456	11.50751	1.8057	0.00049	0.001442	C1orf228	chr1	+	45140364	45191263	2113
ENSG00000(	241.3395	292.6419	284.9934	841.2118	660.8702	655.106	-1.3949	2.74E-17	2.44E-16	ZNF43	chr19	-	21987752	22034927	5584
ENSG00000(	367.7061	404.6407	374.7135	769.3006	490.5903	505.5084	-0.62066	0.0008	0.002281	GPN1	chr2	+	27851114	27874375	2496
ENSG00000(	0	2.408575	1.319414	2.247227	0	2.465895	-0.23209	0.85977	0.91092	PLN	chr6	+	1.19E+08	1.19E+08	2001
ENSG00000(	4.143168	2.408575	0	11.23613	14.72691	20.54912	-2.4563	0.003784	0.009607	C2CD4A	chr15	+	62359176	62363116	3445
ENSG00000(	145.0109	154.1488	159.6491	275.6598	362.6502	352.623	-1.1054	1.13E-08	5.67E-08	ZNF28	chr19	-	53300662	53360853	5171
ENSG00000(	239.2679	160.1703	263.8828	0	6.443024	5.753754	5.281	2.62E-12	1.74E-11	ITGBL1	chr13	+	1.02E+08	1.02E+08	2494
ENSG00000(	120.1519	115.6116	105.5531	188.767	162.9165	197.2716	-0.68018	0.001908	0.0051	ZNF511	chr10	+	1.35E+08	1.35E+08	2004
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	C20orf203	chr20	-	31220661	31239680	3456
ENSG00000(	311.7734	321.5448	307.4234	256.9329	238.3919	203.0253	0.42762	0.015148	0.033781	ZNF627	chr19	+	11670189	11729950	2840
ENSG00000(	12.4295	13.24716	27.70769	6.74168	5.522592	14.79537	0.90732	0.16911	0.26902	KCNRG	chr13	+	50589390	50595058	1623
ENSG00000(	135.6887	184.256	216.3839	758.8135	710.5735	607.4321	-1.9505	6.25E-26	8.01E-25	WDHD1	chr14	-	55405668	55493823	5996
ENSG00000(	189.5499	201.116	217.7033	278.6561	304.663	320.5663	-0.57007	0.001448	0.003948	ZNF789	chr7	+	99070464	99101273	4253
ENSG00000(	3375.646	3396.091	3686.442	5866.011	6050.92	5170.981	-0.70733	1.25E-10	7.34E-10	CTNND1	chr11	+	57520715	57587018	6553
ENSG00000(	1819.886	1889.527	1560.867	1112.377	1166.187	1228.016	0.5872	1.85E-06	7.45E-06	DDX39B	chr6	-	31497996	31510225	5158
ENSG00000(	35.21692	24.08575	17.15238	6.74168	23.0108	20.54912	0.59291	0.29245	0.41667	SLC34A3	chr9	+	1.4E+08	1.4E+08	2162
ENSG00000(	0	0	0	5.243529	6.443024	5.753754	-3.3492	0.007167	0.017225	RD3	chr1	-	2.12E+08	2.12E+08	4266

ENSG00000(	2.071584	0	0	0.749076	0	0.821965	0.18163	0.8922	NA	SPANXC	chrX	-	1.4E+08	1.4E+08	387
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	SH2D1B	chr1	-	1.62E+08	1.62E+08	2523
ENSG00000(	25.8948	24.08575	19.79121	0.749076	1.840864	0	4.2081	9.08E-07	3.78E-06	ARC	chr8	-	1.44E+08	1.44E+08	3948
ENSG00000(	12.4295	18.06432	13.19414	0	2.761296	3.28786	2.5521	0.002797	0.007265	AC073343.	chr7	+	6713376	6715991	1170
ENSG00000(	2547.012	2410.984	2550.427	650.9467	780.5263	807.9915	1.7425	4.86E-45	1.16E-43	NUDT16	chr3	+	1.31E+08	1.31E+08	6117
ENSG00000(	340.7755	297.4591	435.4065	665.1791	769.4811	631.2691	-0.94212	2.39E-08	1.16E-07	TLK1	chr2	-	1.72E+08	1.72E+08	5730
ENSG00000(	391.5293	345.6306	522.4879	683.906	882.6943	753.7418	-0.87903	3.81E-07	1.65E-06	LRBA	chr4	-	1.51E+08	1.52E+08	10313
ENSG00000(	17.60846	15.65574	11.87472	5.992604	20.2495	10.68554	0.28829	0.65364	0.75938	C3orf35	chr3	+	37427760	37476988	1859
ENSG00000(	2.071584	3.612863	0	1.498151	1.840864	0	0.50213	0.6997	0.79573	ZNF536	chr19	+	30719197	31204445	4945
ENSG00000(	190.5857	134.8802	159.6491	194.7596	179.4842	178.3664	-0.18457	0.38525	0.51607	MMP17	chr12	+	1.32E+08	1.32E+08	2411
ENSG00000(	580.0435	507.0051	723.0388	976.7945	886.376	731.5488	-0.51897	0.001577	0.004274	BAZ1A	chr14	-	35221937	35344853	6010
ENSG00000(	2888.824	2799.969	3070.276	1456.203	1060.338	1218.974	1.2256	1.94E-20	2.00E-19	COPS8	chr2	+	2.38E+08	2.38E+08	4007
ENSG00000(	1629.301	1601.703	1622.879	1130.355	1365.001	1518.169	0.27402	0.037665	0.075945	PPIAP22	chr21	+	20230097	20230594	498
ENSG00000(	7.250543	8.430014	15.83297	99.62705	108.611	88.77221	-3.1847	1.45E-14	1.11E-13	CCDC69	chr5	-	1.51E+08	1.51E+08	3451
ENSG00000(	1096.904	1107.945	911.7149	1098.894	912.1481	1108.009	-0.00092	0.99467	0.99666	MDM4	chr1	+	2.04E+08	2.05E+08	10073
ENSG00000(	0	1.204288	2.638828	71.91125	90.20234	51.78379	-5.3548	5.91E-13	4.10E-12	RYR2	chr1	+	2.37E+08	2.38E+08	16562
ENSG00000(	1073.08	1107.945	1299.623	728.1014	886.376	708.5338	0.58181	3.72E-05	0.000128	KLHL9	chr9	-	21329670	21335379	5710
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	FAM3D	chr3	-	58619673	58652575	1319
ENSG00000(	896.9958	858.6571	1137.335	765.5552	1015.236	748.81	0.19294	0.22815	0.3414	NCOA6	chr20	-	33284722	33413452	9311
ENSG00000(	378.064	367.3078	445.9619	247.1949	264.164	216.1768	0.70802	3.87E-05	0.000133	STK39	chr2	-	1.69E+08	1.69E+08	3820
ENSG00000(	5.17896	3.612863	0	0.749076	4.60216	3.28786	0.047885	0.96646	0.98027	TAT	chr16	-	71599563	71611033	3983
ENSG00000(	1040.971	1104.332	980.3244	327.346	556.8614	349.3351	1.3377	2.36E-13	1.69E-12	C6orf89	chr6	+	36839646	36892331	2565
ENSG00000(	3137.414	3078.159	3404.088	7143.934	6697.984	6376.804	-1.0702	4.40E-24	5.26E-23	CALM1	chr14	+	90862846	90874605	4242
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	LPA	chr6	-	1.61E+08	1.61E+08	6490
ENSG00000(	8.286335	7.225726	9.235896	21.72319	23.0108	22.19305	-1.3637	0.022014	0.047267	FAM19A2	chr12	-	62102040	62672931	4128
ENSG00000(	1903.786	1773.916	2233.768	1104.137	1288.605	970.7406	0.81148	7.53E-09	3.82E-08	TTC37	chr5	-	94799599	94890711	5706
ENSG00000(	393.6009	287.8248	362.8388	381.2795	311.106	346.8692	0.006872	0.96893	0.98173	TUSC1	chr9	-	25676396	25678856	2461
ENSG00000(	1624.122	1558.348	1795.722	186.5198	149.11	156.9953	3.3242	2.38E-118	2.45E-116	PAPSS2	chr10	+	89419370	89507462	3949
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	C3orf27	chr3	-	1.28E+08	1.28E+08	2697
ENSG00000(	338.704	296.2548	439.3648	237.4569	256.8005	189.0519	0.64833	0.001103	0.003071	SLC9A6	chrX	+	1.35E+08	1.35E+08	4681
ENSG00000(	196.8005	254.1047	282.3545	200.7522	223.665	167.6808	0.30443	0.14235	0.2338	FAN1	chr15	+	31196055	31235311	4999
ENSG00000(	139.8319	149.3317	174.1626	86.14369	110.4518	85.48435	0.71074	0.003059	0.00789	ABCA4	chr1	-	94458393	94586688	7309
ENSG00000(	452.6411	493.758	438.0454	567.7993	517.2828	544.1408	-0.23455	0.10067	0.17642	EIF1AY	chrY	+	22737611	22755040	3148
ENSG00000(	10824.03	11346.8	10610.73	14679.63	9570.652	14094.23	-0.22558	0.11809	0.20124	MT-ND6	chrMT	-	14149	14673	525
ENSG00000(	1888.249	1777.529	1845.86	2599.292	2435.463	2034.363	-0.35829	0.003725	0.009468	IPO9	chr1	+	2.02E+08	2.02E+08	11435
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	GPX6	chr6	-	28471073	28495992	1712
ENSG00000(	456.7842	474.4894	507.9743	238.9551	263.2436	196.4496	1.0389	8.04E-10	4.44E-09	CEP290	chr12	-	88442793	88535993	7948
ENSG00000(	13.46529	6.021439	9.235896	0.749076	2.761296	6.575719	1.3362	0.13218	0.2203	C1orf191	chr1	+	54703710	54704736	1027
ENSG00000(	72845.17	73852.94	62706.46	115549.4	66394.44	75222.12	-0.29531	0.073972	0.13602	MT-CO2	chrMT	+	7586	8269	684
ENSG00000(	1322.706	1292.201	1051.573	576.7882	559.6227	586.883	1.0872	1.01E-15	8.30E-15	C1orf85	chr1	-	1.56E+08	1.56E+08	1604
ENSG00000(	254.8048	227.6104	358.8805	146.0697	181.3251	147.9537	0.81766	0.000161	0.000509	FAM179B	chr14	+	45431411	45543634	6375
ENSG00000(	15.53688	21.67718	14.51355	7.490755	31.29469	32.8786	-0.441	0.45281	0.58252	DLL1	chr6	-	1.71E+08	1.71E+08	3174
ENSG00000(	523.0749	504.5966	386.5882	277.907	305.5834	293.4415	0.6894	4.38E-05	0.00015	ANKRD13B	chr17	+	27916787	27941779	3214
ENSG00000(	258.948	308.2977	252.008	308.6191	231.0284	303.3051	-0.04262	0.82061	0.88422	ECI2	chr6	-	4115923	4135831	3870

ENSG00000(	257.9122	262.5347	286.3128	505.626	569.7474	511.2622	-0.97328	3.88E-10	2.19E-09	UNC13B	chr9	+	35161999	35405335	6303
ENSG00000(	5.17896	0	0	0	0	0.821965	1.2091	0.37233	0.50277	C19orf45	chr19	+	7557862	7573336	1679
ENSG00000(	56840.12	54793.89	48010.83	75116.55	52430.57	55348.65	-0.19565	0.1566	0.25262	MT-CYB	chrMT	+	14747	15887	1141
ENSG00000(	2076.763	2015.978	1928.983	1394.03	1654.937	1596.256	0.37441	0.001445	0.003939	LDB1	chr10	-	1.04E+08	1.04E+08	2285
ENSG00000(	1.035792	7.225726	1.319414	7.490755	6.443024	4.109825	-0.77693	0.43001	0.56003	PPP1R14C	chr6	+	1.5E+08	1.51E+08	2152
ENSG00000(	1059.615	1264.502	1256.082	1068.182	1213.129	950.1914	0.14715	0.28475	0.40779	CTR9	chr11	+	10772534	10801290	4586
ENSG00000(	0	1.204288	2.638828	15.73059	0	5.753754	-1.9203	0.094682	0.16758	SMOC1	chr14	+	70320848	70499083	3666
ENSG00000(	1.035792	1.204288	0	11.23613	18.40864	9.863579	-3.3509	0.000799	0.002277	F5	chr1	-	1.69E+08	1.7E+08	7039
ENSG00000(	796.524	783.9913	740.1911	510.1204	423.3987	466.8761	0.7261	1.81E-07	8.09E-07	MSRB1	chr16	-	1988211	1993327	1423
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	SMIM11P1	chr6	-	86444925	86445786	862
ENSG00000(	42.46747	34.92434	55.41538	2.996302	0.920432	0	4.6227	9.51E-11	5.64E-10	LRRTM3	chr10	+	68685764	68859588	4358
ENSG00000(	388.422	367.3078	372.0747	400.7554	368.1728	364.9524	-0.00776	0.95949	0.97632	ZNF652	chr17	-	47366568	47439835	5988
ENSG00000(	428.8178	373.3292	390.5465	654.692	696.767	603.3223	-0.70925	1.13E-06	4.65E-06	SMURF1	chr7	-	98625061	98741723	5737
ENSG00000(	1298.883	1224.761	2067.521	452.4416	550.4183	466.0541	1.6365	2.95E-19	2.89E-18	SLC5A3	chr21	+	35445870	35478559	11574
ENSG00000(	21.75163	30.10719	15.83297	47.94084	15.64734	27.12484	-0.41103	0.42552	0.5559	RP5-857K2	chr1	+	569756	570302	547
ENSG00000(	252.7332	208.3418	207.148	265.1727	284.4135	308.2368	-0.35575	0.051427	0.099525	GPATCH3	chr1	-	27216979	27226957	2123
ENSG00000(	30.03797	14.45145	19.79121	4.494453	10.12475	1.64393	1.8644	0.007191	0.017277	GATSL2	chr7	-	74807499	74867509	1264
ENSG00000(	2434.111	2332.705	2529.316	1569.313	2482.405	2121.491	0.24085	0.10974	0.18915	CDC42BPB	chr14	-	1.03E+08	1.04E+08	6758
ENSG00000(	493.0369	528.6823	431.4483	4.494453	3.681728	21.37109	5.2422	6.61E-15	5.19E-14	PLXNB3	chrX	+	1.53E+08	1.53E+08	6377
ENSG00000(	22314.06	21739.8	17093.01	14592.74	13476.04	14175.61	0.53253	9.36E-06	3.49E-05	RPL10A	chr6	+	35436185	35438562	1069
ENSG00000(	32.10955	30.10719	43.54065	95.13259	121.497	92.88204	-1.5319	1.73E-06	6.98E-06	COLGALT2	chr1	-	1.84E+08	1.84E+08	5177
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	EPS8L3	chr1	-	1.1E+08	1.1E+08	2325
ENSG00000(	5.17896	0	6.597069	15.73059	13.80648	12.32947	-1.6492	0.042281	0.083984	EGFL6	chrX	+	13587724	13651694	2398
ENSG00000(	28790.87	29880.79	25636.21	51901.2	32613.67	40014.07	-0.56109	0.00014	0.000446	MT-ND2	chrMT	+	4470	5511	1042
ENSG00000(	20.71584	22.88147	27.70769	5.992604	5.522592	11.50751	1.5423	0.009868	0.022982	APCDD1L	chr20	-	57034157	57090187	3426
ENSG00000(	0	0	0	2.247227	8.283888	5.753754	-3.2079	0.011103	0.025552	RCSD1	chr1	+	1.68E+08	1.68E+08	3135
ENSG00000(	10.35792	13.24716	25.06886	17.97781	6.443024	2.465895	0.77137	0.28668	0.41015	RASSF9	chr12	-	86198331	86230348	1826
ENSG00000(	29.00217	21.67718	52.77655	1051.702	1416.545	1048.005	-5.0684	3.44E-103	2.78E-101	FAM169A	chr5	-	74073399	74162776	5990
ENSG00000(	311.7734	230.019	241.4527	241.9514	238.3919	270.4265	0.063508	0.73675	0.82369	ZNF830	chr17	+	33288549	33290205	1657
ENSG00000(	4.143168	9.634302	10.55531	2.996302	20.2495	14.79537	-0.5908	0.44207	0.5718	GRIN3A	chr9	-	1.04E+08	1.05E+08	7770
ENSG00000(	35906.76	35220.6	36574.15	36976.62	30681.68	32477.48	0.10489	0.32141	0.44866	MT-ND5	chrMT	+	12337	14148	1812
ENSG00000(	931.1769	969.4516	1050.253	2253.968	1909.896	1791.062	-1.0116	5.29E-15	4.18E-14	CNOT7	chr8	-	17086737	17104387	2649
ENSG00000(	1397.283	1127.213	1183.514	853.9461	929.6363	895.9418	0.46875	0.000323	0.000978	TMEM184B	chr22	-	38615298	38669040	3667
ENSG00000(	556.2203	647.9068	877.4102	1149.082	1238.901	1138.421	-0.76002	2.22E-06	8.88E-06	MTOR	chr1	-	11166592	11322564	8677
ENSG00000(	140.8677	85.50443	118.7472	111.6123	113.2131	143.0219	-0.08841	0.73381	0.82196	SCAMP5	chr15	+	75249560	75313837	3427
ENSG00000(	1633.444	1616.154	1687.53	299.6302	282.5726	212.8889	2.6264	2.38E-72	1.08E-70	ZNF521	chr18	-	22641890	22932154	4871
ENSG00000(	170.9057	169.8046	250.6886	898.8907	869.8082	633.735	-2.0165	9.92E-26	1.26E-24	ALPK2	chr18	-	56148479	56296189	7303
ENSG00000(	0	0	0	2.247227	10.12475	3.28786	-3.1278	0.014003	0.031524	MAGEB3	chrX	+	30248553	30255607	2303
ENSG00000(	312.8092	301.0719	310.0622	271.1653	324.9125	240.8357	0.14362	0.41835	0.54898	LRIG2	chr1	+	1.14E+08	1.14E+08	5076
ENSG00000(	250308.4	254307	230529.3	319390.8	213479.5	217924.3	-0.03031	0.83343	0.89318	MT-CO1	chrMT	+	5904	7445	1542
ENSG00000(	240.3037	199.9118	199.2315	1045.709	651.6659	732.3707	-1.9151	1.04E-23	1.22E-22	PNP	chr14	+	20937113	20945253	2573
ENSG00000(	1.035792	3.612863	1.319414	12.73428	11.96562	4.109825	-1.945	0.040746	0.081388	PAX9	chr14	+	37126773	37148920	4514
ENSG00000(	62.14751	22.88147	56.73479	110.8632	115.9744	131.5144	-1.3139	7.48E-05	0.000248	GK	chrX	+	30671476	30748725	3707
ENSG00000(	744.7344	617.7996	790.3289	623.2309	741.8682	580.3072	0.14627	0.33824	0.46684	FOXJ3	chr1	-	42642210	42801548	5352

ENSG00000(	584.1866	482.9194	343.0476	296.6339	262.3231	217.8207	0.85729	2.53E-05	8.93E-05	ZNF358	chr19	+	7580178	7585912	1954
ENSG00000(	724.0185	687.6483	655.7486	629.2235	601.0421	737.3025	0.071633	0.60952	0.72336	SFT2D1	chr6	-	1.67E+08	1.67E+08	2576
ENSG00000(	0	0	0	4.494453	2.761296	10.68554	-3.3552	0.007383	0.017685	CD247	chr1	-	1.67E+08	1.67E+08	2922
ENSG00000(	0	2.408575	1.319414	2.247227	6.443024	4.93179	-1.4395	0.20976	0.31944	GRM3	chr7	+	86273230	86494200	4268
ENSG00000(	505.4664	428.7264	538.3208	969.3038	1006.032	812.9233	-0.91849	6.24E-10	3.47E-09	CHAMP1	chr13	+	1.15E+08	1.15E+08	3788
ENSG00000(	204.051	198.7075	241.4527	668.1754	639.7002	517.8379	-1.4991	1.62E-18	1.53E-17	INPP5F	chr10	+	1.21E+08	1.22E+08	4925
ENSG00000(	480.6074	411.8664	584.5003	1582.048	1931.066	1857.641	-1.858	1.71E-35	3.10E-34	ARHGAP11	chr15	+	32907345	32932150	5898
ENSG00000(	3227.528	3186.545	3157.357	5663.76	5537.319	6080.896	-0.85124	4.56E-17	4.01E-16	HMGN2	chr1	+	26798941	26802463	1496
ENSG00000(	2255.955	2124.364	1696.766	89.88907	87.44104	60.00344	4.6596	1.86E-158	3.19E-156	SELM	chr22	-	31500758	31516055	2070
ENSG00000(	1014.04	971.8602	1077.961	6257.028	5433.31	5209.614	-2.4594	1.22E-97	8.98E-96	UBE2J1	chr6	-	90036344	90062567	4290
ENSG00000(	77.68439	78.2787	50.13772	18.72689	22.09037	29.59074	1.5235	6.55E-05	0.000219	GJC2	chr1	+	2.28E+08	2.28E+08	2243
ENSG00000(	989.1813	979.0859	1124.141	1406.764	1242.583	1132.668	-0.29066	0.027765	0.058082	OPA1	chr3	+	1.93E+08	1.93E+08	6492
ENSG00000(	776.8439	762.3141	707.2058	830.7248	919.5116	844.9799	-0.20669	0.10585	0.18376	DENND4B	chr1	-	1.54E+08	1.54E+08	5706
ENSG00000(	29.00217	28.90291	30.34652	82.39831	138.0648	104.3895	-1.8489	3.55E-08	1.70E-07	RYR3	chr15	+	33603163	34158303	15559
ENSG00000(	408.102	363.6949	402.4212	244.1986	217.222	166.0369	0.89927	1.35E-06	5.53E-06	ZNF277	chr7	+	1.12E+08	1.12E+08	2218
ENSG00000(	11074.69	11850.19	11800.84	11099.8	11459.38	17156.87	-0.19316	0.19604	0.30268	MT-ND3	chrMT	+	10059	10404	346
ENSG00000(	216.4805	177.0303	149.0938	209.7412	161.996	163.571	0.021563	0.92231	0.95297	KTI12	chr1	-	52497775	52499488	1714
ENSG00000(	0	0	0	30.7121	53.38506	42.74218	-6.2105	3.19E-09	1.68E-08	DUSP27	chr1	+	1.67E+08	1.67E+08	4164
ENSG00000(	894.9242	832.1628	1043.656	1724.372	1519.633	1506.662	-0.77709	3.45E-09	1.81E-08	SELT	chr3	+	1.5E+08	1.5E+08	3469
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	ARHGEF15	chr17	+	8213559	8225829	4154
ENSG00000(	217.5163	252.9004	246.7304	120.6012	135.3035	111.7872	0.95844	2.39E-06	9.51E-06	TOX	chr8	-	59717977	60031767	4131
ENSG00000(	2.071584	0	0	0	3.681728	3.28786	-0.99366	0.4545	0.58422	CES1	chr16	-	55836763	55867249	2178
ENSG00000(	769.5934	764.7227	785.0512	423.9768	440.8869	385.5015	0.88937	6.67E-11	4.00E-10	RUSC2	chr9	+	35490124	35561895	5636
ENSG00000(	60.07593	61.41867	54.09597	35.95563	70.87326	39.45432	0.26615	0.46192	0.59116	FICD	chr12	+	1.09E+08	1.09E+08	3347
ENSG00000(	5033.949	5220.587	4482.049	2518.392	2375.635	2447.812	1.0036	2.23E-20	2.29E-19	OSTC	chr4	+	1.1E+08	1.1E+08	1077
ENSG00000(	22.78742	9.634302	18.47179	5.243529	9.20432	7.397684	1.153	0.082805	0.1498	HSD3BP5	chr1	+	1.2E+08	1.2E+08	1132
ENSG00000(	1287.489	1286.179	1091.155	953.5732	822.8662	892.6539	0.45647	0.000444	0.001314	R3HDM4	chr19	-	896503	913240	1815
ENSG00000(	211.3015	215.5675	265.2022	887.6545	724.38	790.7303	-1.7931	5.65E-29	8.25E-28	TSEN15	chr1	+	1.84E+08	1.84E+08	1960
ENSG00000(	442.2831	474.4894	649.1516	614.2419	622.212	412.6264	-0.07594	0.69247	0.79018	LTN1	chr21	-	30300466	30365277	7756
ENSG00000(	315.9165	266.1476	317.9787	385.0248	343.3211	356.7328	-0.26922	0.10358	0.18058	RUNDC1	chr17	+	41132582	41145707	3828
ENSG00000(	0	1.204288	1.319414	0	0.920432	1.64393	-0.02084	0.98774	NA	CCDC152	chr5	+	42756903	42802462	3431
ENSG00000(	72.50543	52.98866	50.13772	18.72689	17.48821	15.61733	1.7237	2.02E-05	7.23E-05	C9orf96	chr9	+	1.36E+08	1.36E+08	2825
ENSG00000(	310.7376	302.2762	286.3128	141.5753	161.996	160.2832	0.95289	2.03E-07	9.05E-07	GRK5	chr10	+	1.21E+08	1.21E+08	2654
ENSG00000(	270.3417	263.739	257.2857	385.7739	312.0264	327.964	-0.37346	0.028934	0.060226	TYW1	chr7	+	66460160	66704501	3348
ENSG00000(	526.1823	552.7681	577.9032	954.3222	945.2837	898.4077	-0.75519	4.48E-09	2.32E-08	DCAF12	chr9	-	34086385	34127397	3667
ENSG00000(	107.7224	93.93444	104.2337	183.5235	289.9361	200.5594	-1.1278	2.33E-06	9.28E-06	SFMBT2	chr10	-	7200586	7453450	7922
ENSG00000(	11.39371	30.10719	29.0271	43.44638	53.38506	55.07165	-1.0908	0.012186	0.02778	ITPRIPL1	chr2	+	96991069	96994091	2156
ENSG00000(	85881.65	87958.77	80510.63	161738.1	93908.92	110945.5	-0.52556	0.000907	0.002558	MT-ND4	chrMT	+	10760	12137	1378
ENSG00000(	1101.047	1146.482	1401.217	704.8801	808.1393	609.898	0.77876	1.68E-07	7.53E-07	SMC5	chr9	+	72873937	72969804	5921
ENSG00000(	46496.7	46203.7	39166.8	78136.07	52035.7	60605.12	-0.53134	0.000178	0.000559	MT-ND1	chrMT	+	3307	4262	956
ENSG00000(	1.035792	0	1.319414	21.72319	17.48821	17.26126	-3.8637	3.91E-05	0.000135	DCAF12L1	chrX	-	1.26E+08	1.26E+08	3379
ENSG00000(	404.9946	392.5978	469.7113	602.2567	601.9625	544.9627	-0.46485	0.00167	0.004507	PRMT6	chr1	+	1.08E+08	1.08E+08	2639
ENSG00000(	482.679	429.9307	414.2959	49.43899	48.7829	78.90863	2.8865	1.94E-40	4.06E-39	SHISA4	chr1	+	2.02E+08	2.02E+08	1341
ENSG00000(	148.1182	191.4817	232.2168	265.9218	296.3791	206.3132	-0.42751	0.051544	0.099726	KIAA1737	chr14	+	77564440	77583630	4486

ENSG00000(	1477.039	1600.498	1634.754	1600.774	1373.285	1314.322	0.13493	0.27716	0.39884	CAPZA2	chr7	+	1.16E+08	1.17E+08	2394
ENSG00000(	33617.66	33687.54	32325.64	62392.75	35500.14	49142.82	-0.55963	0.000374	0.001122	MT-ATP6	chrMT	+	8527	9207	681
ENSG00000(	1691.448	1641.444	2016.064	2074.939	2430.861	2077.927	-0.29925	0.018746	0.040936	TOP1	chr20	+	39657458	39753127	3738
ENSG00000(	486.8222	485.328	596.375	1401.52	1476.373	1335.693	-1.4238	3.25E-26	4.22E-25	PRC1	chr15	-	91509270	91538859	4087
ENSG00000(	174.013	157.7617	145.1355	94.38352	82.83888	72.33291	0.92754	0.000109	0.000355	BHLHB9	chrX	+	1.02E+08	1.02E+08	5130
ENSG00000(	633.9046	643.0896	757.3435	396.261	543.9753	526.8795	0.47029	0.00356	0.009076	MAP3K3	chr17	+	61699775	61773663	4818
ENSG00000(	39.36009	26.49433	38.263	1695.158	1728.571	1846.133	-5.6268	2.57E-177	5.75E-175	L1CAM	chrX	-	1.53E+08	1.53E+08	5113
ENSG00000(	5559.095	5257.92	5425.429	3317.656	3501.323	3443.211	0.66168	3.07E-11	1.89E-10	SREBF2	chr22	+	42229109	42303312	5699
ENSG00000(	342.8471	299.8676	246.7304	728.1014	552.2592	655.106	-1.1148	9.94E-11	5.89E-10	C1orf174	chr1	-	3805689	3816857	3499
ENSG00000(	43.50326	21.67718	54.09597	0	0	0	6.5205	6.87E-10	3.81E-09	POU3F3	chr2	+	1.05E+08	1.05E+08	4961
ENSG00000(	4.143168	2.408575	6.597069	44.94453	47.86246	36.98842	-3.1496	9.78E-08	4.49E-07	RASGEF1A	chr10	-	43689983	43762367	4104
ENSG00000(	366.6703	388.9849	372.0747	519.1094	637.8594	700.3141	-0.71684	6.22E-06	2.36E-05	C9orf114	chr9	-	1.32E+08	1.32E+08	4286
ENSG00000(	6924.269	7953.116	6991.574	3565.6	3687.251	5290.988	0.79953	5.01E-08	2.36E-07	RPL39	chrX	-	1.19E+08	1.19E+08	1915
ENSG00000(	299.3439	337.2006	337.7699	534.0909	525.5667	401.9408	-0.58401	0.000533	0.001559	DZIP3	chr3	+	1.08E+08	1.08E+08	5350
ENSG00000(	407.0662	479.3065	455.1978	453.1907	503.4763	419.2021	-0.03672	0.81116	0.87758	KIAA0753	chr17	-	6481468	6544247	4859
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-290L	chr12	+	76357812	76358780	198
ENSG00000(	45.57484	59.0101	60.69303	261.4274	289.0156	216.1768	-2.202	1.30E-19	1.29E-18	DCLRE1A	chr10	-	1.16E+08	1.16E+08	4464
ENSG00000(	1811.6	1676.369	1746.904	1005.259	827.4684	747.1661	1.0178	5.36E-14	3.99E-13	ATG9A	chr2	-	2.2E+08	2.2E+08	5245
ENSG00000(	19.68005	9.634302	25.06886	10.48706	26.69253	35.34449	-0.39426	0.4925	0.62151	NOS1AP	chr1	+	1.62E+08	1.62E+08	5559
ENSG00000(	1866.497	1902.775	1479.063	1680.926	1356.717	1671.877	0.15603	0.2619	0.38127	APRT	chr16	-	88875747	88878352	947
ENSG00000(	110.8297	150.536	166.2461	32.21025	46.0216	55.89361	1.6528	2.60E-08	1.26E-07	GPRASP1	chrX	+	1.02E+08	1.02E+08	5980
ENSG00000(	513.7528	529.8866	399.7824	383.5267	286.2544	482.4934	0.32329	0.098367	0.173	TBKBP1	chr17	+	45771447	45789416	4121
ENSG00000(	31.07376	21.67718	27.70769	62.17327	82.83888	58.35951	-1.3063	0.000454	0.001343	MAGEE1	chrX	+	75648046	75651744	3699
ENSG00000(	245.4827	275.7819	191.315	367.7961	340.5598	372.3501	-0.59636	0.001051	0.002937	CCDC167	chr6	-	37450696	37467698	619
ENSG00000(	119243.5	115729.6	96145.68	147931.2	128951.6	126227.5	-0.28328	0.015945	0.035398	MT-CO3	chrMT	+	9207	9990	784
ENSG00000(	16.57267	22.88147	27.70769	13.48336	7.363456	9.041614	1.0976	0.059078	0.11225	ZFP2	chr5	+	1.78E+08	1.78E+08	2429
ENSG00000(	1.035792	2.408575	0	30.7121	49.70333	43.56414	-4.5996	6.21E-09	3.18E-08	SOWAHA	chr5	+	1.32E+08	1.32E+08	3456
ENSG00000(	454.7126	440.7693	509.2937	335.5858	414.1944	358.3767	0.34152	0.030589	0.063228	L3MBTL3	chr6	+	1.3E+08	1.3E+08	4518
ENSG00000(	36.25272	57.80581	77.84541	125.8447	176.7229	167.6808	-1.4447	1.12E-06	4.63E-06	DMD	chrX	-	31137336	33357558	13956
ENSG00000(	25.8948	43.35436	67.2901	50.18806	75.47542	64.11326	-0.47447	0.21352	0.32383	MFAP3L	chr4	-	1.71E+08	1.71E+08	6318
ENSG00000(	588.3298	643.0896	649.1516	255.4348	254.9597	226.0404	1.3477	4.73E-19	4.59E-18	NAGA	chr22	-	42454358	42466846	3694
ENSG00000(	1942.11	1879.893	1756.14	3519.906	3558.39	3690.622	-0.94713	4.15E-19	4.03E-18	SMG5	chr1	-	1.56E+08	1.56E+08	4559
ENSG00000(	474.3927	460.0379	550.1955	766.3043	733.5843	590.1708	-0.49299	0.001421	0.003879	KIAA1279	chr10	+	70748487	70776738	2534
ENSG00000(	54.89697	10.83859	26.38828	1773.062	1290.446	1409.67	-5.3196	8.32E-20	8.36E-19	TGM2	chr20	-	36756863	36794980	3996
ENSG00000(	11.39371	6.021439	7.916483	296.6339	353.4459	363.3085	-5.2029	3.16E-48	8.28E-47	ARMCX6	chrX	-	1.01E+08	1.01E+08	1928
ENSG00000(	2638.162	2796.356	3419.921	1164.812	1372.364	997.8654	1.321	6.66E-20	6.71E-19	PJA2	chr5	-	1.09E+08	1.09E+08	4889
ENSG00000(	0	0	2.638828	2.996302	6.443024	4.93179	-1.8322	0.12283	0.20788	RORB	chr9	+	77112281	77302117	3567
ENSG00000(	223.7311	237.2447	222.9809	274.9107	235.6306	233.438	-0.12195	0.50187	0.62993	SGMS1	chr10	-	52065360	52384795	3744
ENSG00000(	1.035792	2.408575	0	0	0.920432	4.109825	-0.32753	0.80401	0.87283	RP11-47J1	chr11	-	12942733	12944472	566
ENSG00000(	1.035792	0	0	0	6.443024	13.15144	-2.7047	0.029965	0.062109	AL356475.	chr1	-	1.7E+08	1.7E+08	790
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-560A	chr20	+	55689971	55697148	770
ENSG00000(	7.250543	21.67718	7.916483	14.23244	2.761296	1.64393	0.86276	0.29933	0.42429	AL353898.	chr1	-	54498816	54500553	1737
ENSG00000(	2.071584	6.021439	5.277655	8.988907	9.20432	9.863579	-0.97384	0.23793	0.35274	RP11-498P	chr9	-	1E+08	1E+08	578
ENSG00000(	2.071584	3.612863	1.319414	0.749076	6.443024	7.397684	-0.84344	0.4302	0.56016	CTA-221G9	chr22	-	25498407	25508659	950

ENSG00000(	0	0	0	0	1.840864	2.465895	-1.2108	0.36631	NA	AL590489.	chr6	-	1.08E+08	1.08E+08	243
ENSG00000(	0	0	2.638828	0	1.840864	0	0.2163	0.87177	NA	AL591516.	chr6	+	1.08E+08	1.08E+08	255
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AL591516.	chr6	+	1.08E+08	1.08E+08	234
ENSG00000(	4.143168	1.204288	5.277655	1.498151	0	0	1.8495	0.14281	0.23442	AL365202.	chr9	-	3452305	3469181	312
ENSG00000(	0	0	1.319414	0.749076	0.920432	0	-0.15244	0.90808	NA	RP11-98D1	chr1	+	1.52E+08	1.52E+08	992
ENSG00000(	3.107376	1.204288	9.235896	2.247227	0.920432	0	1.5416	0.18848	0.29344	AL590822.	chr1	-	2143360	2145620	2261
ENSG00000(	7.250543	10.83859	3.958241	13.48336	2.761296	0.821965	0.31024	0.7367	0.82369	AP001007.	chr11	+	1.25E+08	1.25E+08	2033
ENSG00000(	9.322127	6.021439	2.638828	4.494453	4.60216	8.219649	0.063012	0.94232	0.96521	AC015815.	chr17	+	75087901	75088024	123
ENSG00000(	3.107376	1.204288	5.277655	4.494453	3.681728	4.109825	-0.30693	0.76272	0.84327	RP11-197P	chr9	+	77567884	77611209	719
ENSG00000(	4.143168	8.430014	1.319414	8.239831	2.761296	2.465895	0.033781	0.97253	0.984	RP11-277A	chr1	-	32517892	32539075	624
ENSG00000(	40.39588	26.49433	46.17948	175.2837	171.2004	180.0103	-2.1978	3.05E-15	2.44E-14	ZNF525	chr19	+	53868946	53895470	6107
ENSG00000(	14.50109	10.83859	14.51355	5.243529	13.80648	1.64393	0.87891	0.24705	0.36383	AC012358.	chr2	-	55441523	55443262	916
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC006019.	chr7	-	1.54E+08	1.54E+08	2470
ENSG00000(	0	1.204288	1.319414	0	0	0.821965	0.59385	0.65509	NA	RP11-296A	chr1	-	51660767	51700768	2366
ENSG00000(	60.07593	49.3758	55.41538	154.3096	172.1208	187.408	-1.6225	1.97E-10	1.14E-09	RP3-337H4	chr6	-	43555967	43559099	990
ENSG00000(	1.035792	0	1.319414	0	2.761296	1.64393	-0.50913	0.70413	0.79928	AC131568.	chr8	+	1.31E+08	1.31E+08	246
ENSG00000(	53.86118	55.39724	26.38828	12.73428	15.64734	17.26126	1.5319	0.000972	0.00273	AC105020.	chr15	+	75970672	75973093	2422
ENSG00000(	0	0	1.319414	1.498151	0	0	-0.08979	0.94423	NA	AP001187.	chr11	-	64657298	64657758	459
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	AC009061.	chr16	+	67466595	67468931	2334
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	BTBD7P1	chr10	-	13198684	13200136	1453
ENSG00000(	0	3.612863	0	0.749076	2.761296	0.821965	-0.15482	0.90702	0.94269	AC016734.	chr2	-	63745026	63746647	1621
ENSG00000(	0	0	1.319414	0.749076	0	0.821965	-0.12362	0.92519	NA	AC140061.	chr12	+	50711462	50711558	93
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	AC140061.	chr12	-	50710653	50710749	93
ENSG00000(	0	3.612863	1.319414	1.498151	0	7.397684	-0.60403	0.62881	0.73916	AC140061.	chr12	+	50707798	50707894	93
ENSG00000(	0	1.204288	0	0	0	2.465895	-0.37534	0.77612	NA	AC140061.	chr12	-	50698425	50698530	102
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	AC140061.	chr12	+	50697570	50697669	96
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC008147.	chr12	-	50683977	50684073	93
ENSG00000(	0	1.204288	0	3.745378	0	0	-0.68738	0.60971	NA	AC008147.	chr12	-	50678449	50678545	93
ENSG00000(	3.107376	2.408575	0	4.494453	0	0	0.17998	0.89137	0.93258	RP11-163F	chr10	-	1.1E+08	1.1E+08	575
ENSG00000(	11.39371	2.408575	3.958241	1.498151	0	0	2.5591	0.02995	0.062083	AC104600.	chr2	-	1.97E+08	1.97E+08	1422
ENSG00000(	0	1.204288	0	0	0.920432	0.821965	-0.17164	0.89643	NA	RP11-820K	chr12	+	31617996	31618776	781
ENSG00000(	1.035792	1.204288	6.597069	11.23613	16.56778	12.32947	-1.979	0.019532	0.042482	LINC00449	chr13	-	1E+08	1E+08	872
ENSG00000(	2.071584	1.204288	0	0.749076	0	4.109825	-0.33197	0.80192	0.87107	AC092964.	chr3	+	1.72E+08	1.72E+08	198
ENSG00000(	2.071584	3.612863	2.638828	0	0.920432	0	1.9512	0.13592	0.22522	AC004988.	chr7	-	40577726	40586527	1771
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC068896.	chr10	+	1.26E+08	1.26E+08	219
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AL359697.	chr10	+	22183277	22183445	165
ENSG00000(	4.143168	7.225726	11.87472	7.490755	4.60216	4.93179	0.3847	0.64094	0.7487	RP11-77K1	chr16	+	75509794	75529305	573
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC105036.	chr15	-	75830020	75830438	183
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC061975.	chr17	+	26547062	26547215	150
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	AC100852.	chr17	-	26496027	26496180	150
ENSG00000(	2714.811	2419.414	1965.927	2873.454	2582.732	2955.786	-0.24344	0.068004	0.12662	INF2	chr14	+	1.05E+08	1.05E+08	4672
ENSG00000(	6.214751	25.29004	15.83297	6.74168	12.88605	20.54912	0.21645	0.74405	0.8295	PDCD4-AS1	chr10	-	1.13E+08	1.13E+08	778
ENSG00000(	2.071584	1.204288	0	370.0433	390.2632	327.964	-7.6472	5.25E-31	8.25E-30	RP11-429J	chr8	+	1.45E+08	1.45E+08	5239
ENSG00000(	1.035792	0	1.319414	0.749076	2.761296	1.64393	-0.69626	0.5958	0.71157	AC131571.	chr11	+	31705636	31707478	1841

ENSG00000(	1.035792	2.408575	0	2.247227	12.88605	2.465895	-1.7818	0.11574	0.19798	RBMS3-AS2	chr3	-	29657466	29684300	865
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	AC103801.	chr11	+	22766126	22768414	2288
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	AL353662.	chr9	-	34201271	34201513	237
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AL353662.	chr9	+	34195642	34195883	240
ENSG00000(	0	0	0	1.498151	3.681728	0.821965	-1.734	0.20077	0.30831	AL353662.	chr9	+	34169687	34169934	246
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AL023807.	chr6	+	17894075	17894300	225
ENSG00000(	18.64425	10.83859	13.19414	0	0	0	5.0827	7.80E-06	2.93E-05	TAS2R2P	chr7	+	12530721	12531630	910
ENSG00000(	0	0	1.319414	2.996302	0.920432	0	-0.79043	0.56007	NA	AL353671.	chr9	-	32548215	32548487	264
ENSG00000(	0	4.817151	0	2.996302	0	0.821965	0.1828	0.89115	0.93243	RP11-176H	chr14	-	31803518	31926647	3860
ENSG00000(	0	3.612863	1.319414	0	0.920432	1.64393	0.55906	0.67461	0.77652	AL135901.	chr13	+	50243040	50243254	213
ENSG00000(	9.322127	1.204288	0	0.749076	1.840864	1.64393	0.98629	0.41295	0.54346	AC138951.	chr5	+	21493692	21494062	369
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP13-259N	chr10	+	33973683	33975992	452
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	AC090519.	chr15	+	44589782	44590272	174
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC090519.	chr15	+	44575957	44576117	159
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	OR1F2P	chr16	+	3265562	3266546	983
ENSG00000(	7.250543	9.634302	2.638828	2.996302	13.80648	16.4393	-0.67734	0.40222	0.53345	IGBP1-AS1	chrX	-	69383692	69385056	542
ENSG00000(	7.250543	25.29004	11.87472	4.494453	4.60216	4.109825	1.5972	0.034259	0.069837	RP5-886K2	chr1	-	24032291	24033424	1134
ENSG00000(	1.035792	0	0	2.247227	2.761296	0	-1.0704	0.42984	0.55987	RP5-1096D	chr12	+	2113832	2120558	629
ENSG00000(	3.107376	1.204288	1.319414	4.494453	2.761296	1.64393	-0.49551	0.66506	0.76874	AL137059.	chr13	-	28008286	28008752	465
ENSG00000(	1.035792	0	0	2.996302	1.840864	2.465895	-1.587	0.22968	0.34296	AC004832.	chr22	+	30831531	30832231	699
ENSG00000(	8.286335	22.88147	6.597069	1.498151	0	9.041614	1.5927	0.081174	0.14725	AL512652.	chr13	+	21286570	21288285	1714
ENSG00000(	1.035792	0	1.319414	0.749076	2.761296	6.575719	-1.4422	0.24633	0.36299	AC069200.	chr4	-	56277189	56277313	123
ENSG00000(	13.46529	10.83859	23.74945	3.745378	6.443024	12.32947	1.014	0.14347	0.23527	AL136531.	chr20	-	1316228	1317555	1328
ENSG00000(	1.035792	20.47289	0	0.749076	0	4.93179	1.4445	0.21377	0.32407	AC007690.	chr3	+	1.87E+08	1.87E+08	1845
ENSG00000(	0	0	0	3.745378	11.96562	7.397684	-3.7467	0.002049	0.005451	AC144450.	chr2	-	1624282	1629191	1641
ENSG00000(	6.214751	12.04288	9.235896	114.6086	80.99802	68.22309	-3.1856	1.08E-12	7.39E-12	AC083799.	chr3	-	1.3E+08	1.3E+08	906
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	LINC00501	chr3	+	1.77E+08	1.77E+08	2046
ENSG00000(	5.17896	2.408575	0	0	10.12475	0	-0.26107	0.83475	0.8942	AC106827.	chr3	-	65994445	65994875	429
ENSG00000(	0	0	2.638828	0	0.920432	1.64393	0.005124	0.99699	NA	AC007618.	chr12	+	2769103	2770135	732
ENSG00000(	0	0	0	5.992604	0	0	-1.4779	0.2718	0.39245	RP4-562J1	chrX	+	1.18E+08	1.18E+08	2290
ENSG00000(	3.107376	1.204288	3.958241	0	0	0.821965	1.9651	0.13492	0.22408	AC099048.	chr3	+	30030355	30031951	1596
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	OR2L2	chr1	+	2.48E+08	2.48E+08	1134
ENSG00000(	0	0	0	0	2.761296	1.64393	-1.2339	0.35779	NA	OR2W5	chr1	+	2.48E+08	2.48E+08	1341
ENSG00000(	59.04014	55.39724	83.12307	226.2208	185.0068	196.4496	-1.6149	8.00E-11	4.77E-10	EFCAB2	chr1	+	2.45E+08	2.45E+08	6167
ENSG00000(	39.36009	30.10719	47.4989	15.73059	36.81728	42.74218	0.29072	0.51777	0.64403	COX20	chr1	+	2.45E+08	2.45E+08	2631
ENSG00000(	367.7061	370.9206	527.7655	652.4448	708.7326	554.0044	-0.59645	0.000636	0.001838	CHML	chr1	-	2.42E+08	2.42E+08	7078
ENSG00000(	0	0	3.958241	0	1.840864	5.753754	-0.61969	0.63474	0.74395	C1orf148	chr1	-	2.28E+08	2.28E+08	594
ENSG00000(	26.93059	26.49433	26.38828	0	1.840864	0	4.7644	9.51E-08	4.37E-07	C1orf95	chr1	+	2.27E+08	2.27E+08	7705
ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	RP11-351J	chr6	-	1.68E+08	1.68E+08	2557
ENSG00000(	9.322127	3.612863	11.87472	6.74168	15.64734	6.575719	-0.19865	0.79472	0.86586	AC092811.	chr1	+	2.26E+08	2.26E+08	1637
ENSG00000(	0	0	1.319414	6.74168	7.363456	3.28786	-2.6586	0.026765	0.056275	CAPN8	chr1	-	2.24E+08	2.24E+08	2596
ENSG00000(	203.0152	150.536	122.7055	156.5568	116.8949	93.704	0.37408	0.15768	0.25402	TATDN3	chr1	+	2.13E+08	2.13E+08	2389
ENSG00000(	34.18113	22.88147	25.06886	59.17697	77.31629	72.33291	-1.3118	0.000345	0.001041	SERTAD4-A	chr1	-	2.1E+08	2.1E+08	726
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	C1orf132	chr1	-	2.08E+08	2.08E+08	3197

ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CR1	chr1	+	2.08E+08	2.08E+08	7470
ENSG0000(	2.071584	6.021439	0	8.988907	7.363456	11.50751	-1.5279	0.10111	0.17704	C6orf99	chr6	+	1.59E+08	1.59E+08	1018
ENSG0000(	1.035792	6.021439	13.19414	1.498151	0	6.575719	1.0561	0.31919	0.44629	LINC00862	chr1	-	2E+08	2E+08	1417
ENSG0000(	3.107376	7.225726	10.55531	0	0	3.28786	2.0758	0.060772	0.11489	RAET1G	chr6	-	1.5E+08	1.5E+08	1107
ENSG0000(	108.7581	114.4073	110.8308	26.96672	21.16994	23.01502	2.1953	3.46E-12	2.29E-11	C1orf53	chr1	+	1.98E+08	1.98E+08	588
ENSG0000(	696.0522	661.154	740.1911	1184.288	1247.185	998.6874	-0.70806	1.78E-07	7.98E-07	SAMD5	chr6	+	1.48E+08	1.48E+08	6089
ENSG0000(	0	0	1.319414	2.247227	1.840864	1.64393	-1.2384	0.35415	0.48398	TEDDM1	chr1	-	1.82E+08	1.82E+08	2500
ENSG0000(	5.17896	3.612863	6.597069	12.73428	9.20432	10.68554	-0.99386	0.19826	0.30553	ECT2L	chr6	+	1.39E+08	1.39E+08	4319
ENSG0000(	0	1.204288	1.319414	1.498151	0.920432	0	0.014559	0.99143	NA	GPR52	chr1	+	1.74E+08	1.74E+08	1472
ENSG0000(	34.18113	14.45145	22.43003	28.46487	23.93123	32.05663	-0.23393	0.62767	0.73859	RP11-296C	chr1	-	1.73E+08	1.73E+08	1815
ENSG0000(	0	0	0	5.243529	0.920432	1.64393	-2.0997	0.11845	0.2017	METTL11B	chr1	+	1.7E+08	1.7E+08	992
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	TMEM244	chr6	-	1.3E+08	1.3E+08	568
ENSG0000(	124.295	97.54731	92.35896	584.2789	559.6227	562.224	-2.423	6.88E-41	1.45E-39	CENPW	chr6	+	1.27E+08	1.27E+08	750
ENSG0000(	14.50109	51.78437	31.66593	21.72319	28.53339	21.37109	0.43144	0.38763	0.51843	MSTO2P	chr1	+	1.56E+08	1.56E+08	2045
ENSG0000(	97.36444	86.70872	88.40072	117.6049	99.40666	92.88204	-0.18377	0.47661	0.6059	SPRN	chr10	-	1.35E+08	1.35E+08	3172
ENSG0000(	190.5857	232.4275	155.6908	49.43899	23.93123	46.03004	2.2418	1.65E-14	1.26E-13	FAM229B	chr6	+	1.12E+08	1.12E+08	2543
ENSG0000(	107.7224	84.30014	87.08131	66.66772	70.87326	101.1017	0.22637	0.43025	0.56018	FANK1	chr10	+	1.28E+08	1.28E+08	1583
ENSG0000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	LOR	chr1	+	1.53E+08	1.53E+08	1230
ENSG0000(	0	0	0	4.494453	11.96562	7.397684	-3.8038	0.001649	0.004456	PRR9	chr1	+	1.53E+08	1.53E+08	1229
ENSG0000(	0	0	0	11.23613	2.761296	17.26126	-4.1678	0.000458	0.001352	SPRR2E	chr1	-	1.53E+08	1.53E+08	692
ENSG0000(	71.46964	95.13873	64.65128	104.8706	88.36147	126.5826	-0.46335	0.10018	0.17576	METTL10	chr10	-	1.26E+08	1.26E+08	3587
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	FAM24A	chr10	+	1.25E+08	1.25E+08	596
ENSG0000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	DDO	chr6	-	1.11E+08	1.11E+08	2130
ENSG0000(	4.143168	22.88147	3.958241	2.996302	5.522592	1.64393	1.4109	0.11808	0.20122	CCDC162P	chr6	+	1.1E+08	1.1E+08	2943
ENSG0000(	2.071584	0	2.638828	0.749076	1.840864	0	0.52207	0.69496	0.79211	LINC00222	chr6	+	1.09E+08	1.09E+08	1785
ENSG0000(	3.107376	4.817151	1.319414	0	0	1.64393	1.6298	0.20248	0.3103	C1orf138	chr1	-	1.51E+08	1.51E+08	490
ENSG0000(	517.896	544.338	530.4043	441.9546	350.6846	305.7709	0.53253	0.001457	0.003969	PPAPDC1A	chr10	+	1.22E+08	1.22E+08	1521
ENSG0000(	2.071584	1.204288	0	0.749076	0.920432	3.28786	-0.36301	0.77986	0.85498	BVES-AS1	chr6	+	1.06E+08	1.06E+08	1716
ENSG0000(	0	0	0	2.996302	3.681728	1.64393	-2.2168	0.097064	0.1711	LINC00577	chr6	-	1.05E+08	1.05E+08	575
ENSG0000(	2.071584	0	0	0	0.920432	0.821965	0.13309	0.92108	NA	HIST2H3C	chr1	-	1.5E+08	1.5E+08	1656
ENSG0000(	9.322127	6.021439	5.277655	1.498151	1.840864	5.753754	1.0235	0.27554	0.39702	HIST2H2AA	chr1	+	1.5E+08	1.5E+08	549
ENSG0000(	91.14969	73.46155	69.92893	39.701	42.33987	44.38611	0.8833	0.005312	0.013093	HIST1H3H	chr6	+	27777842	27778314	473
ENSG0000(	27.96638	9.634302	36.94359	9.737982	55.22592	42.74218	-0.5025	0.38359	0.51422	HIST2H2BF	chr1	-	1.5E+08	1.5E+08	1047
ENSG0000(	1.035792	2.408575	1.319414	6.74168	0	0	-0.34663	0.78743	0.86075	AL358813.	chr1	+	1.5E+08	1.5E+08	632
ENSG0000(	0	0	0	4.494453	7.363456	5.753754	-3.3585	0.007002	0.016868	FAM72C	chr1	-	1.49E+08	1.49E+08	1243
ENSG0000(	9.322127	4.817151	15.83297	2.996302	4.60216	9.863579	0.69897	0.3861	0.51697	HIST2H2BC	chr1	-	1.5E+08	1.5E+08	580
ENSG0000(	30.03797	31.31148	48.81831	18.72689	11.96562	9.041614	1.4079	0.004841	0.012025	NBPF16	chr1	+	1.49E+08	1.49E+08	3830
ENSG0000(	190.5857	198.7075	221.6615	98.87797	69.0324	72.33291	1.3308	1.47E-08	7.26E-08	NBPF20	chr1	-	1.48E+08	1.48E+08	15690
ENSG0000(	13.46529	15.65574	9.235896	0.749076	10.12475	2.465895	1.3922	0.093801	0.16637	NBPF24	chr1	-	1.48E+08	1.48E+08	5152
ENSG0000(	5.17896	3.612863	2.638828	0	0	0	3.0137	0.021287	0.045877	PFN1P2	chr1	-	1.45E+08	1.45E+08	418
ENSG0000(	13.46529	8.430014	7.916483	5.243529	2.761296	0	1.6376	0.075001	0.13763	RP11-417J	chr1	-	1.43E+08	1.43E+08	5786
ENSG0000(	1.035792	2.408575	0	0.749076	0.920432	0	0.55135	0.68416	NA	HIST2H3A	chr1	+	1.5E+08	1.5E+08	1656
ENSG0000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	HSD3BP4	chr1	+	1.2E+08	1.2E+08	1120
ENSG0000(	0	0	0	3.745378	0	0.821965	-1.2809	0.34031	NA	HSD3B1	chr1	+	1.2E+08	1.2E+08	1680

ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	HSD3BP2	chr1	+	1.2E+08	1.2E+08	1118
ENSG00000(	0	3.612863	0	5.992604	7.363456	1.64393	-1.5348	0.19018	0.29552	AL079342.	chr6	+	89674246	89676685	2440
ENSG00000(	10.35792	15.65574	7.916483	6.74168	24.85166	8.219649	-0.2018	0.7719	0.85002	ATP1A1OS	chr1	-	1.17E+08	1.17E+08	1011
ENSG00000(	22.78742	16.86003	14.51355	36.7047	66.2711	36.16646	-1.3075	0.00442	0.011065	RBM20	chr10	+	1.12E+08	1.13E+08	7233
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	SMIM9	chrX	-	1.54E+08	1.54E+08	904
ENSG00000(	15.53688	8.430014	10.55531	5.243529	6.443024	5.753754	0.91452	0.2155	0.32621	C6orf164	chr6	+	88106840	88109467	1560
ENSG00000(	10.35792	2.408575	11.87472	15.73059	18.40864	6.575719	-0.6655	0.36429	0.49411	C6orf163	chr6	+	88054571	88075181	1296
ENSG00000(	7446.308	7567.744	6012.569	3716.913	3424.927	4779.726	0.81647	7.36E-09	3.74E-08	SNHG5	chr6	-	86370710	86388451	1029
ENSG00000(	12.4295	16.86003	7.916483	0	1.840864	5.753754	2.0143	0.024516	0.052054	RP11-451M	chr10	-	1.12E+08	1.12E+08	1063
ENSG00000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	RIPPLY2	chr6	+	84562985	84567234	664
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CHIAP2	chr1	+	1.12E+08	1.12E+08	2829
ENSG00000(	3430.543	3174.502	2872.364	2358.839	2158.413	2435.482	0.44632	0.000115	0.000371	GDI1	chrX	+	1.54E+08	1.54E+08	4069
ENSG00000(	505.4664	514.2309	548.8761	291.3904	256.8005	318.9224	0.85066	5.61E-08	2.64E-07	PCMTD2	chr20	+	62887048	62926855	3843
ENSG00000(	40.39588	9.634302	26.38828	2.996302	8.283888	1.64393	2.3965	0.00079	0.002253	SOX18	chr20	-	62679076	62680994	1723
ENSG00000(	0	0	1.319414	0.749076	1.840864	1.64393	-0.92219	0.49549	NA	C1orf146	chr1	+	92683497	92711370	871
ENSG00000(	19.68005	7.225726	9.235896	0.749076	2.761296	1.64393	2.4813	0.005676	0.013912	RP1-177G6	chrX	+	1.4E+08	1.4E+08	1381
ENSG00000(	4.143168	3.612863	6.597069	6.74168	5.522592	5.753754	-0.29826	0.73428	0.82224	SAMD13	chr1	+	84764049	84855640	1565
ENSG00000(	1426.285	1193.449	1081.919	1524.369	1020.759	1057.047	0.039244	0.8132	0.87873	FAM127B	chrX	-	1.34E+08	1.34E+08	1244
ENSG00000(	10.35792	6.021439	9.235896	56.18067	46.0216	23.83698	-2.1971	5.52E-05	0.000186	CCDC160	chrX	+	1.33E+08	1.33E+08	1790
ENSG00000(	120.1519	124.0416	143.8161	76.40571	72.71413	65.75719	0.8426	0.000884	0.0025	EFCAB7	chr1	+	63989043	64038364	3795
ENSG00000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	RP11-188C	chr9	-	1.41E+08	1.41E+08	3222
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RHOXF2B	chrX	-	1.19E+08	1.19E+08	1690
ENSG00000(	210.2658	225.2018	178.1209	226.9699	254.9597	291.7975	-0.33071	0.088385	0.15834	C9orf37	chr9	-	1.41E+08	1.41E+08	1424
ENSG00000(	7.250543	4.817151	2.638828	131.0882	123.3379	127.4046	-4.5085	5.60E-22	6.14E-21	ZYG11A	chr1	+	53308183	53360670	4469
ENSG00000(	2.071584	0	2.638828	0	0	0	1.5584	0.24658	NA	RP11-290F	chr20	+	48909257	48931459	2281
ENSG00000(	14.50109	25.29004	14.51355	11.23613	8.283888	9.041614	0.87182	0.15578	0.2517	COL5A1-AS	chr9	-	1.38E+08	1.38E+08	336
ENSG00000(	26.93059	26.49433	14.51355	35.95563	28.53339	24.65895	-0.37355	0.4295	0.55967	TRABD2B	chr1	-	48231308	48462567	1926
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	LIPK	chr10	+	90484301	90512543	1230
ENSG00000(	2.071584	0	0	1.498151	0.920432	0	-0.08493	0.94997	NA	LIPJ	chr10	+	90346510	90366733	3575
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	LRIT2	chr10	-	85980254	85985345	3081
ENSG00000(	1.035792	0	0	12.73428	1.840864	3.28786	-2.7078	0.026786	0.056314	AL359195.	chr10	+	82009466	82013395	3930
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-465L	chr20	-	44642141	44650712	1955
ENSG00000(	4.143168	2.408575	6.597069	4.494453	5.522592	4.109825	-0.09383	0.92031	0.95154	AL391421.	chr10	+	79626633	79629368	1922
ENSG00000(	38.3243	44.55865	22.43003	3.745378	4.60216	10.68554	2.3524	5.31E-05	0.00018	LRRC73	chr6	-	43474707	43478424	2121
ENSG00000(	181.2636	151.7403	97.63662	61.42419	77.31629	101.9236	0.83542	0.00401	0.010133	RP11-492E	chr9	+	1.32E+08	1.32E+08	2003
ENSG00000(	5.17896	8.430014	7.916483	6.74168	14.72691	12.32947	-0.60067	0.41279	0.54332	RP11-247A	chr9	+	1.32E+08	1.32E+08	2047
ENSG00000(	0	7.225726	0	26.96672	20.2495	17.26126	-2.8297	0.000657	0.001896	FOXO6	chr1	+	41827594	41849262	2398
ENSG00000(	0	4.817151	0	0.749076	1.840864	6.575719	-0.65018	0.60147	0.71666	TCEAL5	chrX	-	1.03E+08	1.03E+08	1168
ENSG00000(	488.8938	460.0379	469.7113	608.2493	446.4095	412.6264	-0.04938	0.7728	0.85077	SYS1	chr20	+	43990577	44005438	2915
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	TCEAL6	chrX	-	1.01E+08	1.01E+08	1106
ENSG00000(	0	0	0	2.996302	4.60216	4.93179	-2.8359	0.028065	0.058606	RP4-545K1	chrX	+	1.01E+08	1.01E+08	655
ENSG00000(	371.8493	417.8878	370.7553	483.9028	453.773	525.2356	-0.33358	0.027717	0.058008	INPP5B	chr1	-	38326369	38412729	4694
ENSG00000(	1.035792	1.204288	0	2.247227	5.522592	9.041614	-2.1416	0.063505	0.11934	RPA4	chrX	+	96138907	96140446	1540
ENSG00000(	2.071584	1.204288	5.277655	0	0	0	2.519	0.060242	0.11408	TDRG1	chr6	+	40302693	40347624	1165

ENSG00000(	3.107376	1.204288	0	0	0	0	1.4526	0.27741	NA	RP11-552E	chr6	-	40312083	40313890	554
ENSG00000(	1.035792	1.204288	0	0	0	2.465895	-0.0579	0.9659	NA	NEU4	chr2	+	2.43E+08	2.43E+08	3142
ENSG00000(	10491.54	9727.032	10482.74	961.0639	1256.39	1041.43	3.2303	1.69E-156	2.80E-154	MAFB	chr20	-	39314488	39317880	3393
ENSG00000(	358.384	314.3191	312.7011	276.4089	316.6286	315.6345	0.11887	0.47625	0.60557	TRAF3IP1	chr2	+	2.39E+08	2.39E+08	4279
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	BMP2KL	chrX	+	73405764	73406990	1225
ENSG00000(	160.5477	199.9118	215.0644	86.14369	84.67974	87.12828	1.1464	5.31E-07	2.27E-06	CHIC1	chrX	+	72783036	72906937	6797
ENSG00000(	0	0	0	16.47966	8.283888	10.68554	-4.4164	0.000132	0.000425	NAP1L6	chrX	-	72345876	72347919	2044
ENSG00000(	993.3244	893.5815	1194.069	731.0977	1014.316	798.1279	0.2759	0.081315	0.14742	GIGYF2	chr2	+	2.34E+08	2.34E+08	7878
ENSG00000(	1.035792	0	1.319414	0.749076	3.681728	3.28786	-1.1333	0.37296	0.50348	AC068134.	chr2	-	2.33E+08	2.33E+08	1742
ENSG00000(	18.64425	15.65574	11.87472	156.5568	251.2779	247.4114	-3.7492	1.44E-28	2.08E-27	C2orf72	chr2	+	2.32E+08	2.32E+08	3657
ENSG00000(	383.243	384.1678	419.5736	270.4163	268.7661	218.6427	0.64422	0.000133	0.000426	RUFY2	chr10	-	70100864	70167051	4512
ENSG00000(	100.4718	103.5687	174.1626	24.71949	56.14635	31.23467	1.7309	7.07E-07	2.98E-06	NHSL2	chrX	+	71130938	71363424	3978
ENSG00000(	5.17896	4.817151	1.319414	11.98521	5.522592	4.109825	-0.80047	0.38304	0.51363	GGTA1P	chr9	-	1.24E+08	1.24E+08	3478
ENSG00000(	819.3114	944.1616	903.7984	1308.635	1350.274	1189.383	-0.5283	2.55E-05	9.01E-05	PHACTR4	chr1	+	28696114	28826881	6190
ENSG00000(	31.07376	42.15007	29.0271	62.17327	57.06678	65.75719	-0.84093	0.018391	0.040234	ASAH2B	chr10	+	52499078	52576255	3715
ENSG00000(	206.1226	217.9761	179.4403	383.5267	277.05	304.949	-0.67467	0.000486	0.001433	AGAP6	chr10	+	51748078	51770259	2703
ENSG00000(	0	0	0	3.745378	0	3.28786	-1.8467	0.17329	0.27459	CTGLF11P	chr10	+	47708307	47730235	2419
ENSG00000(	6.214751	10.83859	14.51355	8.988907	12.88605	13.15144	-0.14944	0.82469	0.88676	TIMM23B	chr10	+	51371390	51387768	784
ENSG00000(	663.9426	631.0468	567.3479	1272.679	1158.824	1241.167	-0.97647	2.84E-14	2.14E-13	ZDHHC18	chr1	+	27153201	27184093	3135
ENSG00000(	49.71801	103.5687	25.06886	52.43529	61.66894	87.95025	-0.17304	0.67672	0.77834	BMS1P5	chr10	-	48901102	48950972	4074
ENSG00000(	0	0	0	12.73428	2.761296	2.465895	-3.3267	0.008341	0.019731	CXorf65	chrX	-	70323837	70326561	766
ENSG00000(	48.68222	66.23582	29.0271	68.91495	49.70333	83.01846	-0.47491	0.19641	0.30314	AGAP7	chr10	-	51464162	51486327	2420
ENSG00000(	4.143168	7.225726	7.916483	8.988907	6.443024	1.64393	0.1435	0.87033	0.91851	AGAP10	chr10	-	47191844	47239738	5005
ENSG00000(	22.78742	26.49433	19.79121	6.74168	2.761296	4.93179	2.1074	0.001069	0.002986	LRRC37A5P	chr9	-	1.14E+08	1.14E+08	1103
ENSG00000(	2.071584	2.408575	0	0	0	0.821965	1.1627	0.39146	NA	NPY4R	chr10	+	47083534	47088320	1956
ENSG00000(	0	1.204288	0	5.992604	9.20432	14.79537	-3.4504	0.002061	0.005481	GPRIN2	chr10	+	46994087	47005643	7718
ENSG00000(	37.28851	30.10719	27.70769	56.18067	48.7829	88.77221	-1.0015	0.008579	0.020251	SYT15	chr10	-	46955444	46971400	3537
ENSG00000(	9.322127	14.45145	9.235896	2.247227	0.920432	3.28786	2.0622	0.017944	0.039363	BMS1P1	chr10	-	46737612	46761205	4073
ENSG00000(	847.2778	892.3772	827.2724	528.8473	518.2032	480.0275	0.74752	1.22E-08	6.08E-08	TMEM57	chr1	+	25757388	25826700	3917
ENSG00000(	1.035792	1.204288	6.597069	0	0	0	2.5314	0.059212	0.1124	GDF5OS	chr20	+	34020827	34023248	1734
ENSG00000(	198.872	213.1589	261.2439	112.3613	125.1788	79.7306	1.0767	3.90E-06	1.52E-05	ZDBF2	chr2	+	2.07E+08	2.07E+08	10282
ENSG00000(	0	2.408575	0	0	1.840864	0	0.16879	0.89944	NA	TXNDC8	chr9	-	1.13E+08	1.13E+08	1787
ENSG00000(	1.035792	1.204288	0	1.498151	0	0.821965	-0.02548	0.98502	NA	RPL12P1	chr6	-	33367836	33368333	498
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	AWAT1	chrX	+	69454505	69460477	1365
ENSG00000(	989.1813	965.8388	898.5208	1644.97	1388.011	1404.738	-0.63555	4.52E-07	1.94E-06	DAXX	chr6	-	33286335	33297046	2613
ENSG00000(	982.9665	1077.838	1472.466	590.2715	724.38	524.4136	0.93791	4.47E-08	2.12E-07	BMPR2	chr2	+	2.03E+08	2.03E+08	11461
ENSG00000(	97.36444	144.5145	97.63662	11.23613	33.13555	20.54912	2.3558	3.19E-10	1.82E-09	TCEA3	chr1	-	23707554	23751233	1559
ENSG00000(	717.8038	741.8412	592.4168	416.486	755.6747	1338.159	-0.28202	0.53921	0.66288	PFDN6	chr6	+	33257079	33266178	1915
ENSG00000(	677.4079	724.9812	675.5399	481.6556	491.5107	650.9962	0.35421	0.022065	0.047363	RING1	chr6	+	33176272	33180499	1752
ENSG00000(	30.03797	19.2686	25.06886	75.65663	53.38506	55.89361	-1.2837	0.00097	0.002725	HSD17B8	chr6	+	33172419	33174608	990
ENSG00000(	1175.624	1038.096	1066.086	296.6339	333.1964	402.7628	1.6633	9.38E-29	1.36E-27	RXRB	chr6	-	33161365	33168630	2908
ENSG00000(	191.6215	187.8689	174.1626	209.7412	192.3703	197.2716	-0.1134	0.55544	0.67608	OXLD1	chr17	-	79632066	79633665	1600
ENSG00000(	0	2.408575	0	2.247227	0	4.93179	-0.95812	0.4688	0.59801	RP11-713P	chr11	+	1.34E+08	1.34E+08	2206
ENSG00000(	95.29286	79.48299	73.88717	14.23244	18.40864	21.37109	2.1684	3.30E-09	1.73E-08	COL11A2	chr6	-	33130458	33160276	6425

ENSG00000(	1.035792	0	0	2.247227	1.840864	0	-0.86384	0.52422	NA	HLA-DOA	chr6	-	32971955	32977389	3489
ENSG00000(	56.96855	49.3758	50.13772	51.68621	80.99802	65.75719	-0.33182	0.31269	0.43916	AC019178.	chr2	+	1.91E+08	1.91E+08	881
ENSG00000(	4092.414	3887.441	3674.567	3161.848	3306.192	3311.697	0.25295	0.014916	0.03333	BRD2	chr6	+	32936437	32949282	4898
ENSG00000(	31.07376	50.58008	25.06886	26.21764	28.53339	11.50751	0.66711	0.17156	0.27242	HLA-DMA	chr6	-	32916390	32936871	1735
ENSG00000(	5.17896	1.204288	0	0	0	0	1.9695	0.14647	0.23926	XXbac-BPG	chr6	+	32811863	32814272	1267
ENSG00000(	31844.39	32465.19	35207.24	6500.478	8678.753	6886.422	2.1687	8.09E-69	3.45E-67	COL5A2	chr2	-	1.9E+08	1.9E+08	6949
ENSG00000(	125.3308	110.7945	114.789	24.71949	14.72691	23.83698	2.4258	1.21E-13	8.84E-13	PSMB8	chr6	-	32808494	32812480	1351
ENSG00000(	70.43385	101.1602	108.1919	56.92974	55.22592	53.42772	0.74244	0.012823	0.029067	TAP2	chr6	-	32789610	32806557	5684
ENSG00000(	95.29286	92.73015	106.8725	50.93714	71.7937	49.3179	0.77136	0.008128	0.019276	SPIN3	chrX	-	57002803	57021970	1670
ENSG00000(	765.4502	809.2813	622.7633	514.6149	424.3192	456.1905	0.65333	2.05E-05	7.34E-05	RP11-622K	chrX	+	56755692	56844813	1529
ENSG00000(	6.214751	13.24716	7.916483	0.749076	0	0	3.7198	0.001025	0.002869	RP11-219G	chr17	-	76257430	76274573	2934
ENSG00000(	0	1.204288	1.319414	92.13629	89.2819	91.23811	-6.0819	8.94E-15	6.96E-14	RP11-153A	chr17	-	76103479	76107880	3192
ENSG00000(	276.5564	246.879	237.4945	25.46857	32.21512	25.48091	3.1728	7.76E-36	1.43E-34	COL15A1	chr9	+	1.02E+08	1.02E+08	5491
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	C6orf10	chr6	-	32256303	32339684	2173
ENSG00000(	7.250543	7.225726	5.277655	6.74168	17.48821	21.37109	-1.1059	0.12266	0.20763	NOTCH4	chr6	-	32162620	32191844	6745
ENSG00000(	1555.759	1742.604	1402.537	1397.026	2079.256	2692.757	-0.38993	0.034009	0.069383	PBX2	chr6	-	32151966	32157963	3757
ENSG00000(	43.50326	33.72006	22.43003	53.93344	53.38506	61.64737	-0.73615	0.051316	0.099317	AGER	chr6	-	32148745	32152101	1597
ENSG00000(	726.0901	767.1313	631.9992	872.673	807.2189	966.6307	-0.31518	0.023299	0.049726	RNF5	chr6	+	32146131	32151930	1325
ENSG00000(	944.6422	829.7542	728.3164	1136.348	1055.736	955.1232	-0.32842	0.019294	0.042018	AGPAT1	chr6	-	32135989	32145873	2496
ENSG00000(	21.75163	21.67718	21.11062	19.47596	27.61296	21.37109	-0.07813	0.87293	0.92025	DFNB59	chr2	+	1.79E+08	1.79E+08	1942
ENSG00000(	33.14534	36.12863	21.11062	19.47596	11.96562	13.9734	0.9555	0.057584	0.10984	PRRT1	chr6	-	32116136	32122150	2782
ENSG00000(	125.3308	110.7945	64.65128	184.2726	192.3703	210.423	-0.94854	0.000165	0.000523	FKBPL	chr6	-	32096484	32098068	1345
ENSG00000(	12.4295	22.88147	23.74945	21.72319	19.32907	26.30288	-0.19311	0.70773	0.80239	MRPL38	chr17	-	73894724	73905899	1888
ENSG00000(	59.04014	48.17151	59.37362	3.745378	10.12475	17.26126	2.3471	1.73E-06	6.98E-06	SMIM5	chr17	+	73629514	73637484	4344
ENSG00000(	3.107376	0	5.277655	9.737982	7.363456	1.64393	-0.96546	0.34939	0.47909	ERICH2	chr2	+	1.72E+08	1.72E+08	601
ENSG00000(	6.214751	2.408575	0	8.988907	8.283888	2.465895	-0.96174	0.34119	0.47005	SP5	chr2	+	1.72E+08	1.72E+08	2033
ENSG00000(	1.035792	1.204288	1.319414	0	0.920432	0.821965	0.58234	0.66567	NA	CYP21A1P	chr6	+	31973413	31976228	1971
ENSG00000(	339.7397	320.3405	292.9099	177.5309	226.4263	235.082	0.57678	0.001832	0.004918	STK19	chr6	+	31938868	31950598	1894
ENSG00000(	165.7267	195.0946	204.5091	244.1986	178.5638	236.7259	-0.22525	0.2759	0.39742	DOM3Z	chr6	-	31937587	31940069	2093
ENSG00000(	1100.011	1191.041	1048.934	976.7945	1072.303	1227.194	0.028075	0.83181	0.89232	SKIV2L	chr6	+	31926857	31937532	4507
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	C9orf129	chr9	-	96080481	96108696	1154
ENSG00000(	1271.952	1170.568	1026.504	1318.373	1171.71	1296.239	-0.1253	0.3301	0.45788	NELFE	chr6	-	31919864	31926887	1855
ENSG00000(	3.107376	4.817151	1.319414	0	2.761296	0	1.2159	0.33532	0.46345	NXPE2	chr11	+	1.15E+08	1.15E+08	2273
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	RP11-380J	chr1	+	17516278	17524112	4676
ENSG00000(	0	0	0	2.247227	2.761296	2.465895	-2.0693	0.1234	0.20854	C10orf126	chr10	+	29135337	29170827	2149
ENSG00000(	157.4404	143.3102	167.5656	98.1289	142.667	183.2982	0.14315	0.57016	0.68915	ZBTB12	chr6	-	31867384	31869769	1875
ENSG00000(	296.2365	319.1362	336.4505	460.6815	397.6266	439.7512	-0.44833	0.004554	0.011375	SDHD	chr11	+	1.12E+08	1.12E+08	1439
ENSG00000(	1532.972	1495.725	1298.303	1605.269	1559.212	1883.122	-0.22122	0.083521	0.15091	EHMT2	chr6	-	31847536	31865464	4129
ENSG00000(	29.00217	32.51577	14.51355	10.48706	12.88605	23.83698	0.6644	0.22779	0.34098	C1orf134	chr1	-	16555368	16556038	252
ENSG00000(	5.17896	0	5.277655	7.490755	13.80648	4.109825	-1.0932	0.24443	0.36062	AC005042.	chr2	-	1.6E+08	1.6E+08	4067
ENSG00000(	1052.365	1073.02	1079.28	936.3444	662.711	661.6818	0.50057	0.001089	0.003037	LAYN	chr11	+	1.11E+08	1.11E+08	2172
ENSG00000(	6.214751	3.612863	3.958241	0.749076	0	2.465895	1.5988	0.16203	0.25976	SLC44A4	chr6	-	31830969	31846823	2634
ENSG00000(	1253.308	1212.718	1208.583	1391.782	1036.406	1066.91	0.071477	0.60798	0.72215	NEU1	chr6	-	31825436	31830683	4616
ENSG00000(	3771.318	3797.119	3427.837	1590.287	1502.145	2273.555	1.0319	5.23E-12	3.41E-11	C6orf48	chr6	+	31802385	31807541	1053

ENSG00000(	647.3699	546.7466	577.9032	746.8283	1029.043	936.218	-0.61033	6.81E-05	0.000227	HSPA1B	chr6	+	31795512	31798031	2520
ENSG00000(	313.8449	308.2977	325.8952	250.1912	311.106	320.5663	0.10492	0.54428	0.66652	HSPA1A	chr6	+	31783291	31785717	2427
ENSG00000(	26.93059	43.35436	31.66593	23.97042	35.89685	13.15144	0.46903	0.3264	0.4541	HSPA1L	chr6	-	31777396	31783437	2544
ENSG00000(	628.7257	615.391	535.682	1456.203	1036.406	1281.443	-1.0807	8.71E-13	5.99E-12	LSM2	chr6	-	31765173	31774761	876
ENSG00000(	2962.365	2693.992	2859.17	4436.025	3803.225	3795.012	-0.49816	1.04E-05	3.85E-05	VARS	chr6	-	31745295	31763730	4312
ENSG00000(	6.214751	7.225726	11.87472	12.73428	9.20432	18.08323	-0.62872	0.36086	0.49042	VWA7	chr6	-	31733367	31745108	2942
ENSG00000(	391.5293	360.082	442.0036	122.0993	171.2004	110.1433	1.5592	1.50E-14	1.15E-13	MBD5	chr2	+	1.49E+08	1.49E+08	8489
ENSG00000(	63.18331	79.48299	55.41538	71.16218	81.91845	74.79881	-0.19738	0.50749	0.63499	MSH5	chr6	+	31707725	31732622	3986
ENSG00000(	6.214751	2.408575	9.235896	11.23613	4.60216	12.32947	-0.6034	0.45755	0.5872	C6orf25	chr6	+	31686371	31694491	2396
ENSG00000(	1.035792	0	0	2.247227	2.761296	9.863579	-2.472	0.046668	0.091398	LY6G6C	chr6	-	31686425	31689622	992
ENSG00000(	5.17896	14.45145	6.597069	1.498151	3.681728	11.50751	0.57611	0.50675	0.63443	ABHD16A	chr6	-	31654726	31671221	2260
ENSG00000(	12.4295	8.430014	11.87472	39.701	19.32907	48.49593	-1.6457	0.002364	0.006221	LY6G5C	chr6	-	31644461	31651817	1428
ENSG00000(	34.18113	45.76293	39.58241	41.19916	32.21512	52.60575	-0.07941	0.8366	0.89558	CSNK2B	chr6	+	31633013	31638120	1792
ENSG00000(	283.807	275.7819	277.0769	297.383	341.4803	360.8426	-0.2548	0.12955	0.21662	GPANK1	chr6	-	31629006	31634060	2793
ENSG00000(	317.9881	338.4048	249.3692	259.1801	319.3899	327.964	0.001602	0.9931	0.9956	C6orf47	chr6	-	31626075	31628549	2475
ENSG00000(	96.32865	90.32158	113.4696	33.7084	40.49901	36.98842	1.4153	3.21E-06	1.26E-05	FAM155A	chr13	-	1.08E+08	1.09E+08	2043
ENSG00000(	34.18113	57.80581	26.38828	30.7121	21.16994	30.4127	0.5079	0.24851	0.36559	APOM	chr6	+	31620193	31625987	1184
ENSG00000(	4.143168	9.634302	7.916483	5.243529	0	3.28786	1.1134	0.25449	0.37255	C9orf170	chr9	+	89763559	89774471	3239
ENSG00000(	0	0	0	1.498151	2.761296	0	-1.199	0.3707	NA	TRIM49C	chr11	+	89764274	89806558	2163
ENSG00000(	4980.087	4825.581	4596.838	4949.891	4839.631	5280.303	-0.06514	0.52371	0.64899	BAG6	chr6	-	31606805	31620482	3881
ENSG00000(	1.035792	0	0	0	0	2.465895	-0.37334	0.77636	NA	C1orf195	chr1	-	15490840	15497813	441
ENSG00000(	0	0	0	4.494453	5.522592	2.465895	-2.8237	0.028992	0.060335	DGKK	chrX	-	50108408	50213737	7406
ENSG00000(	10603.4	10430.34	10028.86	6871.27	11261.49	10937.07	0.095466	0.53926	0.66292	PRRC2A	chr6	+	31588497	31605548	6893
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AIF1	chr6	+	31582961	31584798	1180
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	NCR3	chr6	-	31556672	31560762	1097
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	PRAMEF14	chr1	-	13668269	13673511	2100
ENSG00000(	0	10.83859	0	0.749076	0	0	2.0645	0.12247	0.20739	LST1	chr6	+	31553901	31556686	1832
ENSG00000(	495.1085	409.4578	323.2564	216.4828	194.2112	290.1536	0.80582	8.90E-05	0.000292	NFKBIL1	chr6	+	31514647	31526606	1478
ENSG00000(	3.107376	3.612863	3.958241	1.498151	1.840864	0.821965	1.0531	0.35233	0.48206	MCCD1	chr6	+	31496494	31498009	955
ENSG00000(	396.7083	492.5537	358.8805	365.5489	311.106	393.7212	0.22026	0.20772	0.31699	ZNF814	chr19	-	58360099	58400442	3146
ENSG00000(	183.3352	185.4603	259.9245	282.4015	226.4263	228.5062	-0.23321	0.25902	0.37776	MICB	chr6	+	31462658	31478901	2446
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	AADACL4	chr1	+	12704566	12727097	1575
ENSG00000(	162.6193	169.8046	143.8161	229.9662	223.665	206.3132	-0.46683	0.017848	0.039184	ZNF551	chr19	+	58193337	58202022	4564
ENSG00000(	533.4328	505.8008	397.1435	333.3386	327.6738	303.3051	0.5746	0.000513	0.001506	MICA	chr6	+	31371356	31383092	1386
ENSG00000(	39.36009	14.45145	42.22124	19.47596	22.09037	24.65895	0.51919	0.29121	0.41531	ZNF805	chr19	+	57751973	57766503	2413
ENSG00000(	321.0955	308.2977	273.1187	268.9181	261.4027	316.4565	0.092837	0.59439	0.71042	HLA-C	chr6	-	31236526	31239907	1880
ENSG00000(	4.143168	0	0	0	0.920432	0	0.95689	0.47805	NA	PSORS1C3	chr6	-	31141512	31145676	593
ENSG00000(	0	0	2.638828	0	3.681728	7.397684	-1.3833	0.28008	0.40231	POU5F1	chr6	-	31130253	31148508	3262
ENSG00000(	0	0	0	2.996302	0.920432	0	-1.1048	0.40628	NA	ZSCAN5C	chr19	+	56713670	56720821	1892
ENSG00000(	24.85901	12.04288	26.38828	3.745378	20.2495	18.90519	0.53828	0.39365	0.52449	AC024580.	chr19	-	56662314	56663250	717
ENSG00000(	313.8449	309.5019	242.7721	348.3201	384.7406	441.3952	-0.43483	0.013928	0.031376	CCHCR1	chr6	-	31110216	31126015	2958
ENSG00000(	5.17896	1.204288	3.958241	3.745378	1.840864	1.64393	0.41082	0.70596	0.80075	PSORS1C2	chr6	-	31105313	31107127	1150
ENSG00000(	5.17896	2.408575	1.319414	0	0	0	2.6031	0.051514	0.099677	CDSN	chr6	-	31082867	31088223	2552
ENSG00000(	53.86118	72.25726	44.86007	5.243529	4.60216	6.575719	3.2555	9.65E-11	5.73E-10	PSORS1C1	chr6	+	31082527	31107869	3827

ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	C6orf15	chr6	-	31079000	31080336	1140
ENSG0000(	6.214751	1.204288	6.597069	8.239831	6.443024	4.93179	-0.42486	0.6358	0.74472	CTD-2514C	chr20	+	25999468	26001320	353
ENSG0000(	702.2669	612.9824	616.1662	1010.503	943.4428	983.892	-0.60276	3.30E-06	1.29E-05	DHX16	chr6	-	30620896	30640814	3445
ENSG0000(	92.18548	80.68728	87.08131	209.7412	142.667	193.9837	-1.0639	1.29E-05	4.74E-05	C6orf136	chr6	+	30614816	30620987	1978
ENSG0000(	1078.259	1158.525	926.2285	1330.358	1189.198	1252.675	-0.25319	0.050759	0.098385	MRPS18B	chr6	+	30585486	30594172	1610
ENSG0000(	1434.572	1271.728	1504.132	1232.978	1312.536	1197.603	0.16946	0.16323	0.26118	PPP1R10	chr6	-	30568177	30586389	4525
ENSG0000(	1784.669	1731.766	1669.058	2849.483	2473.201	2468.361	-0.58626	2.88E-07	1.27E-06	ABCF1	chr6	+	30539153	30564956	3481
ENSG0000(	433.9968	490.1451	494.7802	408.9952	335.9577	342.7594	0.3799	0.016228	0.035948	PRR3	chr6	+	30524663	30531500	3429
ENSG0000(	11.39371	13.24716	7.916483	11.98521	14.72691	15.61733	-0.35063	0.57906	0.69739	LILRB3	chr19	-	54720147	54746602	2848
ENSG0000(	963.2865	828.55	781.093	2435.245	2828.488	3265.667	-1.7231	4.88E-35	8.74E-34	DDR1	chr6	+	30844198	30867933	4148
ENSG0000(	5.17896	4.817151	2.638828	18.72689	11.96562	13.15144	-1.6322	0.03022	0.062588	RP11-304F	chr17	+	47923272	47926199	2100
ENSG0000(	3.107376	8.430014	7.916483	1.498151	0.920432	8.219649	0.72706	0.45537	0.58508	AC013268.	chr2	+	1.11E+08	1.11E+08	2436
ENSG0000(	2080.906	2226.728	1943.497	1298.897	1432.192	1463.92	0.57481	8.79E-07	3.67E-06	GNL1	chr6	-	30509154	30524951	7490
ENSG0000(	4836.112	4808.721	4272.262	904.1342	899.2621	1002.797	2.3062	9.72E-92	6.36E-90	HLA-E	chr6	+	30457244	30461982	2601
ENSG0000(	169.8699	146.9231	130.622	144.5716	168.4391	198.0935	-0.18671	0.404	0.53496	TRIM39	chr6	+	30294256	30311506	3535
ENSG0000(	158.4762	173.4174	147.7743	344.5748	335.9577	295.9074	-1.02	3.52E-08	1.69E-07	ZNF468	chr19	-	53341261	53360902	4407
ENSG0000(	221.6595	216.7718	263.8828	183.5235	195.1316	197.2716	0.28349	0.13462	0.2237	ZNF616	chr19	-	52616344	52643175	4335
ENSG0000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	TRIM31	chr6	-	30070674	30080883	2043
ENSG0000(	53.86118	63.82725	59.37362	8.988907	12.88605	4.93179	2.6515	9.09E-09	4.57E-08	RNF39	chr6	-	30038043	30043664	2206
ENSG0000(	893.8884	942.9573	853.6607	804.5071	655.3476	711.8216	0.30762	0.022296	0.047793	PPP1R11	chr6	+	30034486	30038110	1731
ENSG0000(	5.17896	8.430014	5.277655	0	7.363456	6.575719	0.38378	0.69224	0.79004	AC115618.	chrX	-	48431482	48433275	1794
ENSG0000(	2.071584	0	1.319414	0	0	4.109825	-0.14984	0.91143	0.94564	HLA-J	chr6	+	29974360	29977733	1306
ENSG0000(	149.154	143.3102	134.5802	92.13629	69.95283	83.01846	0.7925	0.00119	0.003295	ZNRD1-AS1	chr6	-	29968788	30029417	9771
ENSG0000(	19.68005	15.65574	6.597069	3.745378	6.443024	6.575719	1.2336	0.092386	0.16424	PTCHD2	chr1	+	11539223	11597641	5215
ENSG0000(	2.071584	3.612863	0	0	0	0.821965	1.4184	0.29471	0.41906	HCG9	chr6	+	29942889	29946183	659
ENSG0000(	42901.46	43102.66	34153.03	27968.98	21154.29	22335.25	0.74791	2.14E-08	1.05E-07	GNB2L1	chr5	-	1.81E+08	1.81E+08	1651
ENSG0000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	HLA-G	chr6	+	29794744	29798902	1578
ENSG0000(	204.051	203.5246	221.6615	297.383	351.605	341.1154	-0.65131	0.000214	0.000665	TBC1D8	chr2	-	1.02E+08	1.02E+08	3803
ENSG0000(	2.071584	0	2.638828	0	0	0.821965	1.2046	0.37464	NA	HLA-F	chr6	+	29690552	29706305	1622
ENSG0000(	0	0	0	5.992604	0.920432	4.93179	-2.7088	0.038388	0.077236	ZFP57	chr6	-	29640169	29648887	1980
ENSG0000(	54.89697	91.52587	55.41538	286.8959	251.2779	310.7027	-2.0581	1.85E-17	1.66E-16	CRHR1-IT1	chr17	+	43697694	43725582	2609
ENSG0000(	1.035792	0	0	2.247227	0.920432	1.64393	-1.098	0.41621	NA	RPS26P8	chr17	+	43685909	43686349	441
ENSG0000(	12.4295	12.04288	2.638828	0	3.681728	7.397684	1.1196	0.24116	0.35658	ASPDH	chr19	-	51014857	51017947	1040
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	MOG	chr6	+	29624758	29640149	2499
ENSG0000(	2.071584	4.817151	1.319414	0	0	0.821965	1.9524	0.138	0.22811	OR2H2	chr6	+	29555683	29556745	1063
ENSG0000(	2.071584	6.021439	0	0	0	0.821965	1.8322	0.17001	0.27017	CBY3	chr5	-	1.79E+08	1.79E+08	785
ENSG0000(	3.107376	0	0	1.498151	0	4.109825	-0.48197	0.71735	0.80968	C5orf60	chr5	-	1.79E+08	1.79E+08	3245
ENSG0000(	0	7.225726	0	0	0.920432	0	1.5108	0.26454	0.38438	CTD-2126E	chr19	+	50553846	50570050	1525
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	C9orf57	chr9	-	74666292	74687733	1502
ENSG0000(	3402.576	3150.417	2686.326	2250.972	2103.187	2248.896	0.48406	5.58E-05	0.000188	AKT1S1	chr19	-	50372295	50381716	3640
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	FAM153C	chr5	+	1.77E+08	1.77E+08	1510
ENSG0000(	1007.826	1051.343	1067.406	555.065	523.7258	646.8864	0.85463	2.02E-10	1.17E-09	GABBR1	chr6	-	29523406	29601753	4527
ENSG0000(	548.9697	463.6508	440.6842	855.4443	762.1177	800.5938	-0.73084	3.57E-07	1.55E-06	C10orf114	chr10	-	21781587	21786191	3801
ENSG0000(	1.035792	4.817151	0	2.247227	0.920432	0	0.55101	0.67407	0.77612	C10orf113	chr10	-	21414692	21435488	614

ENSG00000(	88.04231	60.21439	71.24834	67.4168	62.58938	68.22309	0.14814	0.62154	0.73369	AC012307.	chr2	+	96874154	96908359	1721
ENSG00000(	40.39588	36.12863	48.81831	14.23244	19.32907	18.08323	1.2468	0.004596	0.011471	RP11-195E	chr9	-	72700732	72790804	2097
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	C6orf100	chr6	+	28911654	28912314	466
ENSG00000(	2.071584	3.612863	1.319414	0	0	0	2.2408	0.097211	0.17127	SPDYC	chr11	+	64937625	64940715	991
ENSG00000(	5.17896	0	1.319414	3.745378	4.60216	11.50751	-1.284	0.2179	0.32923	C9orf135	chr9	+	72435709	72521148	873
ENSG00000(	1080.331	1112.762	1134.696	1855.46	1686.231	1617.627	-0.63195	7.04E-08	3.28E-07	TRIM27	chr6	-	28870779	28891766	7006
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	AC073464.	chr2	-	95461553	95472197	534
ENSG00000(	0	0	0	1.498151	0	2.465895	-1.1271	0.39798	NA	C10orf112	chr10	+	19492779	20079330	4661
ENSG00000(	52.82539	25.29004	32.98534	92.13629	66.2711	51.78379	-0.89414	0.019172	0.041781	AC083899.	chr2	+	87352513	87423770	3819
ENSG00000(	4.143168	8.430014	11.87472	6.74168	14.72691	12.32947	-0.43989	0.5473	0.66903	CTC-308K2	chr5	-	1.72E+08	1.72E+08	2067
ENSG00000(	60.07593	57.80581	63.33186	214.9847	289.0156	245.7675	-2.0326	6.92E-18	6.34E-17	RANBP17	chr5	+	1.7E+08	1.71E+08	4739
ENSG00000(	59.04014	21.67718	97.63662	3.745378	0.920432	2.465895	4.3121	3.48E-11	2.13E-10	FAM196B	chr5	-	1.69E+08	1.69E+08	2999
ENSG00000(	0	0	0	2.996302	0.920432	2.465895	-1.8353	0.17499	0.27674	CTD-3232M	chr8	+	1.45E+08	1.45E+08	3778
ENSG00000(	1.035792	1.204288	0	0	7.363456	2.465895	-1.3671	0.28518	0.40829	KM-PA-2	chr8	-	1.45E+08	1.45E+08	1969
ENSG00000(	7.250543	6.021439	5.277655	11.23613	1.840864	12.32947	-0.40937	0.62505	0.73646	RP11-15J1(	chr9	-	70181520	70216621	655
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	FOXD4L5	chr9	-	70175707	70178815	3109
ENSG00000(	2.071584	2.408575	0	30.7121	25.7721	19.72716	-3.6148	7.61E-06	2.87E-05	ZNF204P	chr6	-	27325604	27339304	4006
ENSG00000(	70.43385	86.70872	56.73479	170.0401	127.0196	140.556	-1.0222	0.000121	0.000389	CBWD6	chr9	-	69204538	69269662	3334
ENSG00000(	2.071584	4.817151	0	0	4.60216	5.753754	-0.42124	0.72339	0.81419	CTD-3065J:	chr8	+	1.45E+08	1.45E+08	1390
ENSG00000(	0	0	1.319414	5.992604	4.60216	4.93179	-2.513	0.038469	0.077379	AC104135.	chr2	+	75145275	75165545	3662
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	FOXD4L6	chr9	-	69199480	69202204	2725
ENSG00000(	1.035792	3.612863	6.597069	0	2.761296	4.93179	0.41811	0.7118	0.80524	PGM5P1	chr9	-	68741234	68809906	2259
ENSG00000(	1.035792	12.04288	6.597069	2.247227	0	0.821965	2.0495	0.065558	0.12267	RP11-111F	chr9	-	46685429	46688137	2541
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AL953889.	chr9	-	45727440	45727852	381
ENSG00000(	8.286335	6.021439	9.235896	7.490755	10.12475	6.575719	-0.03339	0.9648	0.97969	FAM27E4	chr9	+	44997777	44999352	1401
ENSG00000(	0	0	0	2.247227	0	1.64393	-1.1086	0.40518	NA	FAM27E2	chr9	+	45733559	45734896	1338
ENSG00000(	18.64425	24.08575	19.79121	11.23613	12.88605	9.041614	0.87389	0.12372	0.20888	TTC25	chr17	+	40086888	40117648	1752
ENSG00000(	39.36009	34.92434	43.54065	39.701	46.94203	41.92021	-0.12308	0.73954	0.82557	MRPL53	chr2	-	74699085	74700449	1162
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	ST8SIA6-AS	chr10	+	17428935	17455502	1811
ENSG00000(	17.60846	8.430014	32.98534	56.92974	44.18074	29.59074	-1.1187	0.0244	0.05186	RP11-204M	chr9	-	41961615	42019580	1890
ENSG00000(	65.25489	86.70872	36.94359	98.87797	71.7937	108.4994	-0.55216	0.096439	0.17025	MROH6	chr8	-	1.45E+08	1.45E+08	3469
ENSG00000(	705.3743	688.8526	729.6358	993.2742	943.4428	867.173	-0.40024	0.001754	0.004721	ATXN2	chr12	-	1.12E+08	1.12E+08	4702
ENSG00000(	4050.982	3847.699	4364.621	2089.921	2601.141	2520.966	0.76458	2.29E-10	1.32E-09	DCTN1	chr2	-	74588281	74619214	5414
ENSG00000(	16.57267	39.74149	22.43003	3.745378	16.56778	7.397684	1.4362	0.021703	0.046667	PNMAL2	chr19	-	46990163	46999755	5308
ENSG00000(	660.8352	667.1754	547.5567	268.169	248.5166	299.1952	1.1971	4.36E-14	3.26E-13	TCTN1	chr12	+	1.11E+08	1.11E+08	4209
ENSG00000(	218.5521	227.6104	208.4674	185.0217	131.6218	154.5294	0.46921	0.023311	0.049747	FAM216A	chr12	+	1.11E+08	1.11E+08	1679
ENSG00000(	415.3526	370.9206	292.9099	310.8664	332.276	395.3651	0.057973	0.74939	0.83352	ZBTB48	chr1	+	6640061	6649340	2484
ENSG00000(	0	0	0	17.97781	23.93123	9.041614	-4.9271	1.11E-05	4.10E-05	FAM201A	chr9	+	38620471	38624987	3437
ENSG00000(	6.214751	9.634302	1.319414	18.72689	10.12475	10.68554	-1.0885	0.15698	0.25307	IGFL2	chr19	+	46646363	46664556	1920
ENSG00000(	10.35792	13.24716	1.319414	13.48336	16.56778	29.59074	-1.1552	0.093226	0.1655	IGFL4	chr19	-	46543006	46580376	2719
ENSG00000(	5.17896	2.408575	6.597069	0	0	0	3.3418	0.009254	0.021687	GPR20	chr8	-	1.42E+08	1.42E+08	1515
ENSG00000(	0	2.408575	0	0	2.761296	1.64393	-0.46918	0.72831	0.81801	KRT40	chr17	-	39133968	39143387	2102
ENSG00000(	335.5966	355.2649	343.0476	886.1564	904.7847	868.8169	-1.3601	7.42E-24	8.79E-23	MZT1	chr13	-	73282495	73301825	2299
ENSG00000(	1.035792	0	0	10.48706	11.04518	8.219649	-3.4861	0.001833	0.004919	CXorf31	chrX	-	46746852	46759138	521

ENSG00000(	5.17896	0	2.638828	5.992604	0.920432	1.64393	-0.09714	0.93354	0.96015	SPINK9	chr5	+	1.48E+08	1.48E+08	604
ENSG00000(	74.57702	85.50443	64.65128	28.46487	19.32907	16.4393	1.7665	2.25E-06	8.97E-06	ZNF155	chr19	+	44472014	44502477	2596
ENSG00000(	51.7896	46.96722	31.66593	56.92974	44.18074	32.8786	-0.03434	0.92905	0.95729	C11orf83	chr11	+	62437745	62441159	2288
ENSG00000(	13.46529	27.69862	13.19414	17.97781	25.7721	18.08323	-0.17611	0.74659	0.83147	FBXO48	chr2	-	68689486	68694390	2731
ENSG00000(	6.214751	4.817151	2.638828	0	0	0	3.2951	0.010503	0.024303	AC074391.	chr2	+	65663864	66126649	1266
ENSG00000(	0	0	0	1.498151	1.840864	0.821965	-1.2806	0.34348	NA	FAM221B	chr9	-	35816388	35828744	3763
ENSG00000(	8.286335	2.408575	10.55531	38.20285	29.45382	34.52253	-2.1615	0.000195	0.000608	ATP6V0E2-/	chr7	-	1.5E+08	1.5E+08	2974
ENSG00000(	0	0	0	28.46487	39.57858	20.54912	-5.7201	9.52E-08	4.38E-07	CD177	chr19	+	43857825	43867480	2483
ENSG00000(	5.17896	0	0	34.45748	38.65814	45.20807	-4.0071	5.39E-08	2.53E-07	PSG5	chr19	-	43670408	43690688	2145
ENSG00000(	341.8113	373.3292	341.7282	218.7301	199.7337	243.3016	0.67172	9.48E-05	0.00031	ZNF783	chr7	+	1.49E+08	1.49E+08	4452
ENSG00000(	132.5814	125.2459	133.2608	71.16218	81.91845	102.7456	0.60799	0.016363	0.036223	ZNF425	chr7	-	1.49E+08	1.49E+08	3220
ENSG00000(	2.071584	3.612863	0	28.46487	37.73771	27.94681	-3.6622	9.47E-07	3.94E-06	LRRC10B	chr11	+	61276272	61278482	2211
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	FBXO47	chr17	-	37092685	37123655	2302
ENSG00000(	107.7224	143.3102	139.8579	143.8225	113.2131	160.2832	-0.09852	0.68288	0.78312	C12orf73	chr12	-	1.04E+08	1.04E+08	1738
ENSG00000(	11.39371	9.634302	1.319414	8.988907	0.920432	0.821965	0.87899	0.37891	0.50967	PCDHGA1	chr5	+	1.41E+08	1.41E+08	4602
ENSG00000(	13.46529	3.612863	10.55531	26.96672	22.09037	20.54912	-1.254	0.039365	0.078884	AC006486.	chr19	+	42746927	42749125	2199
ENSG00000(	29.00217	34.92434	22.43003	33.7084	96.64536	111.7872	-1.4436	0.000776	0.002218	RP4-798C1	chr7	-	1.44E+08	1.44E+08	5045
ENSG00000(	18.64425	37.33292	10.55531	4.494453	14.72691	8.219649	1.214	0.062407	0.11755	PCDHA9	chr5	+	1.4E+08	1.4E+08	6388
ENSG00000(	9.322127	18.06432	17.15238	26.96672	10.12475	7.397684	-0.01384	0.98297	0.99027	PCDHA8	chr5	+	1.4E+08	1.4E+08	5260
ENSG00000(	13.46529	4.817151	6.597069	15.73059	12.88605	31.23467	-1.1705	0.076729	0.14022	PCDHA7	chr5	+	1.4E+08	1.4E+08	5221
ENSG00000(	8.286335	3.612863	10.55531	4.494453	7.363456	10.68554	-0.00482	0.99519	0.99693	PCDHA5	chr5	+	1.4E+08	1.4E+08	5218
ENSG00000(	97.36444	102.3645	129.3026	103.3724	126.0992	87.95025	0.049885	0.84793	0.90301	PCDHA4	chr5	+	1.4E+08	1.4E+08	5251
ENSG00000(	128.4382	84.30014	204.5091	25.46857	23.93123	15.61733	2.6295	4.75E-13	3.33E-12	PCDHA2	chr5	+	1.4E+08	1.4E+08	5254
ENSG00000(	5.17896	8.430014	3.958241	3.745378	9.20432	3.28786	0.11134	0.9	0.9378	PCDHA1	chr5	+	1.4E+08	1.4E+08	5260
ENSG00000(	412.2452	438.3607	350.9641	519.1094	362.6502	396.1871	-0.08909	0.61631	0.72914	TRIM13	chr13	+	50570024	50594617	7249
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	C19orf69	chr19	+	41949063	41950670	946
ENSG00000(	0	0	0	1.498151	3.681728	0	-1.4292	0.2903	NA	PRSS3P4	chr9	-	33613846	33614007	162
ENSG00000(	133.6172	109.5902	106.8725	193.2615	244.8349	272.8924	-1.0106	5.43E-06	2.08E-05	SPIRE2	chr16	+	89884587	89937727	3235
ENSG00000(	0	1.204288	2.638828	0.749076	2.761296	2.465895	-0.44973	0.72296	0.81382	AC139712.	chr2	+	52797786	52799660	1875
ENSG00000(	33.14534	34.92434	15.83297	34.45748	49.70333	32.8786	-0.4557	0.30163	0.42673	AARD	chr8	+	1.18E+08	1.18E+08	2299
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-830F	chr16	+	89006197	89017932	1812
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	PABPN1L	chr16	-	88928034	88933068	1272
ENSG00000(	1.035792	3.612863	7.916483	0	0.920432	1.64393	1.6684	0.16323	0.26118	RP11-863P	chr16	-	88121647	88134591	3468
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	PKHD1L1	chr8	+	1.1E+08	1.11E+08	13076
ENSG00000(	113.9371	79.48299	58.05421	5.243529	44.18074	13.9734	1.9357	0.000129	0.000415	CTC-425O2	chr19	-	40779396	40781386	1462
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	SLFN12L	chr17	-	33791268	33864880	3119
ENSG00000(	42.46747	50.58008	58.05421	31.46117	80.99802	68.22309	-0.25113	0.51266	0.63966	FLJ00104	chr16	-	87731749	87739290	6938
ENSG00000(	18.64425	19.2686	13.19414	0	0	0	5.3543	1.62E-06	6.58E-06	AC009236.	chr2	-	45392009	45550434	2226
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	RP11-693J	chr12	+	92860227	92885867	10626
ENSG00000(	474.3927	529.8866	671.5816	594.766	600.1217	509.6182	-0.02642	0.8708	0.91876	SLC35B4	chr7	-	1.34E+08	1.34E+08	6797
ENSG00000(	49.71801	20.47289	15.83297	20.97412	46.94203	46.852	-0.38376	0.44103	0.57084	SYCE1L	chr16	+	77233294	77247112	858
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	CXorf30	chrX	+	36246735	36403431	2860
ENSG00000(	210.2658	213.1589	191.315	142.3244	105.8497	120.0069	0.7329	0.000618	0.001792	TMEM231	chr16	-	75572015	75590184	2991
ENSG00000(	29.00217	26.49433	23.74945	37.45378	18.40864	26.30288	-0.05399	0.90803	0.94343	FAM71F2	chr7	+	1.28E+08	1.28E+08	2147

ENSG00000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	C2orf91	chr2	-	42162508	42181406	3721
ENSG00000(	0	0	0	5.992604	6.443024	8.219649	-3.6084	0.003158	0.008131	CCNI2	chr5	+	1.32E+08	1.32E+08	2355
ENSG00000(	126.3666	107.1816	98.95603	36.7047	27.61296	42.74218	1.6121	1.51E-07	6.81E-07	TMEM240	chr1	-	1470554	1475833	718
ENSG00000(	2.071584	7.225726	5.277655	0	0	0	3.3712	0.008579	0.020251	FRG2	chr4	-	1.91E+08	1.91E+08	2100
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	COX17P1	chr13	+	47064997	47065397	401
ENSG00000(	3.107376	1.204288	0	0	0	0	1.4526	0.27741	NA	CTD-2210P	chr11	+	45792983	45793909	649
ENSG00000(	2.071584	15.65574	17.15238	0	1.840864	2.465895	2.5479	0.009316	0.021814	FAM205A	chr9	-	34723052	34729464	4225
ENSG00000(	2.071584	0	3.958241	2.996302	0	1.64393	0.23402	0.85446	0.90742	CDKL4	chr2	-	39402787	39456729	1567
ENSG00000(	3.107376	4.817151	1.319414	10.48706	11.96562	13.9734	-1.758	0.033829	0.069036	TMEM88B	chr1	+	1361508	1363167	492
ENSG00000(	46.61064	85.50443	36.94359	11.23613	8.283888	17.26126	2.1263	7.92E-06	2.98E-05	C4orf47	chr4	+	1.86E+08	1.86E+08	1134
ENSG00000(	189.5499	196.2989	228.2586	154.3096	160.1552	97.81383	0.56968	0.014631	0.032756	TRIQK	chr8	-	93895758	94029901	3672
ENSG00000(	245.4827	221.5889	145.1355	220.9773	276.1296	249.0554	-0.27814	0.20075	0.30831	SDHAF1	chr19	+	36486090	36487220	1131
ENSG00000(	3.107376	4.817151	1.319414	0	0.920432	0	2.0818	0.10915	0.18834	ARID3C	chr9	-	34621376	34628104	1411
ENSG00000(	7.250543	15.65574	10.55531	2.996302	1.840864	7.397684	1.2951	0.1135	0.19465	AC016586.	chr19	-	4041127	4043154	2028
ENSG00000(	2.071584	0	3.958241	0	0	0	1.8862	0.16413	0.26236	AC016251.	chr15	-	96831280	96831660	381
ENSG00000(	30.03797	40.94578	43.54065	17.22874	20.2495	50.96182	0.35749	0.45039	0.58016	PSENEN	chr19	+	36236015	36237911	1152
ENSG00000(	0	0	7.916483	0	0	1.64393	1.232	0.35995	0.48954	C11orf91	chr11	-	33719807	33722347	811
ENSG00000(	3.107376	0	0	0	0	0.821965	0.7418	0.57612	NA	LINC00654	chr20	-	5476713	5485259	6113
ENSG00000(	502.3591	517.8437	599.0139	623.2309	724.38	592.6367	-0.26079	0.078541	0.14308	ZBTB10	chr8	+	81397854	81438500	10132
ENSG00000(	362.5272	454.0165	407.6989	764.8061	595.5195	590.9928	-0.6721	3.59E-05	0.000124	C4orf46	chr4	-	1.6E+08	1.6E+08	3521
ENSG00000(	14.50109	7.225726	10.55531	5.243529	15.64734	9.041614	0.11664	0.86973	0.91824	SCGB2B2	chr19	-	35084234	35166604	2505
ENSG00000(	0	0	0	5.243529	9.20432	9.863579	-3.8469	0.00138	0.003783	CCDC144N	chr17	-	20739760	20799453	2806
ENSG00000(	497.1801	509.4137	583.1809	450.9435	566.0657	383.0357	0.18284	0.28212	0.40479	LGR4	chr11	-	27387508	27494322	5206
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC015818.	chr17	-	20422625	20432000	2334
ENSG00000(	2.071584	1.204288	0	11.98521	7.363456	10.68554	-2.5989	0.009294	0.02177	FAM106B	chr17	+	20320741	20322363	1623
ENSG00000(	51.7896	61.41867	48.81831	27.7158	30.37426	27.94681	0.89741	0.015473	0.034434	PSMB10	chr16	-	67968405	67970990	1218
ENSG00000(	7.250543	0	0	53.93344	62.58938	60.00344	-3.7337	0.00026	0.000798	VIT	chr2	+	36923833	37041935	2810
ENSG00000(	125.3308	119.2245	116.1084	66.66772	83.75931	114.2531	0.44409	0.10029	0.17588	SPDYE2	chr7	+	1.02E+08	1.02E+08	1742
ENSG00000(	1.035792	2.408575	1.319414	0	0	0	1.6865	0.21314	NA	OR7E36P	chr13	-	42005425	42006446	1022
ENSG00000(	277.5922	354.0606	248.0498	399.2573	285.3339	393.7212	-0.29308	0.13398	0.22287	RPSAP58	chr19	+	23945807	24010937	1397
ENSG00000(	959.1433	1066.999	798.2453	1795.534	1488.339	1603.654	-0.78869	1.57E-08	7.74E-08	E2F4	chr16	+	67226072	67232821	2615
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	AL353997.	chr17	+	18319042	18328411	2552
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	DGAT2L7P	chr7	-	1.01E+08	1.01E+08	744
ENSG00000(	266.1985	338.4048	347.0058	761.8098	789.7307	646.8864	-1.2065	6.45E-14	4.77E-13	PDE7A	chr8	-	66629745	66754557	3673
ENSG00000(	14.50109	19.2686	40.90183	67.4168	85.60018	64.11326	-1.522	0.000187	0.000586	TMEM170B	chr6	+	11537938	11583757	8362
ENSG00000(	0	2.408575	5.277655	0	4.60216	4.109825	-0.14324	0.9052	0.94142	RP11-152F	chr15	+	83128128	83145983	4893
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	TRBV20OR9	chr9	+	33617760	33618504	416
ENSG00000(	1.035792	2.408575	7.916483	0.749076	0.920432	2.465895	1.0899	0.34627	0.47581	RP13-608F	chr15	-	82970479	82988374	4926
ENSG00000(	0	7.225726	2.638828	4.494453	6.443024	4.109825	-0.51275	0.6206	0.73278	MUC12	chr7	+	1.01E+08	1.01E+08	16737
ENSG00000(	1.035792	0	1.319414	2.247227	0.920432	0	-0.23628	0.86136	NA	RP11-1112	chr8	+	58890917	58896685	2109
ENSG00000(	1117.619	1135.643	1048.934	1862.202	1650.335	1564.199	-0.61917	3.78E-07	1.64E-06	SNX2	chr5	+	1.22E+08	1.22E+08	2128
ENSG00000(	46.61064	27.69862	18.47179	44.19546	48.7829	38.63235	-0.47732	0.26048	0.37953	NT5M	chr17	+	17206649	17250977	1617
ENSG00000(	0	0	0	0.749076	0.920432	0.821965	-0.73223	0.57364	NA	GCNT6	chr6	+	10633993	10647501	1176
ENSG00000(	83.89914	83.09585	116.1084	53.18436	33.13555	54.24968	0.98784	0.00196	0.005227	SARNP	chr12	-	56146247	56211540	2242

ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	AC005863.	chr17	-	14670900	14683520	2998
ENSG00000(	2.071584	21.67718	6.597069	2.247227	3.681728	2.465895	1.6072	0.080649	0.14639	AC074091.	chr2	-	27928653	27938599	2860
ENSG00000(	23.82321	26.49433	31.66593	535.589	609.326	614.0078	-4.4001	1.91E-77	9.79E-76	GPR56	chr16	+	57644564	57698944	4042
ENSG00000(	3816.893	3901.892	4707.668	5136.411	5616.476	4829.866	-0.32613	0.006653	0.016072	IPO7	chr11	+	9406169	9469673	6191
ENSG00000(	548.9697	569.6281	519.849	665.9282	544.8957	715.1095	-0.23301	0.11959	0.20315	PRR13	chr12	+	53835389	53840429	1375
ENSG00000(	465.0706	527.478	489.5025	297.383	280.7318	332.0738	0.70002	7.15E-06	2.70E-05	TECPR1	chr7	-	97843936	97881563	6564
ENSG00000(	0	0	0	24.71949	16.56778	13.15144	-5.0418	5.56E-06	2.13E-05	MT1H	chr16	+	56703726	56705041	697
ENSG00000(	10.35792	6.021439	2.638828	7.490755	5.522592	1.64393	0.33865	0.71002	0.80396	SLCO6A1	chr5	-	1.02E+08	1.02E+08	2689
ENSG00000(	9.322127	10.83859	18.47179	0.749076	3.681728	0	2.7266	0.003206	0.008248	MT1A	chr16	+	56672578	56673999	396
ENSG00000(	42.46747	19.2686	34.30476	32.21025	37.73771	12.32947	0.22093	0.6585	0.7631	C15orf59	chr15	-	74032141	74045088	2204
ENSG00000(	5.17896	0	0	9.737982	6.443024	9.041614	-1.816	0.077614	0.14164	MT1M	chr16	+	56666145	56667898	829
ENSG00000(	279.6638	309.5019	324.5758	0	0.920432	1.64393	7.8786	7.07E-33	1.18E-31	CFI	chr4	-	1.11E+08	1.11E+08	2366
ENSG00000(	89.0781	109.5902	106.8725	5.243529	2.761296	3.28786	4.5765	1.11E-21	1.21E-20	SAMD9	chr7	-	92728829	92747336	6852
ENSG00000(	36.25272	24.08575	19.79121	0.749076	7.363456	3.28786	2.6553	0.000119	0.000383	RP11-401P	chr16	-	50639987	50647595	2469
ENSG00000(	0	0	0	8.988907	2.761296	4.93179	-3.2587	0.009646	0.022514	KRT6A	chr12	-	52880958	52887041	2310
ENSG00000(	311.7734	337.2006	238.8139	338.5821	279.8113	313.1686	-0.06819	0.71115	0.80477	CNEP1R1	chr16	+	50058321	50070999	2965
ENSG00000(	7.250543	18.06432	5.277655	0	1.840864	0	3.2703	0.002204	0.00583	AL592528.	chr21	-	47247875	47256333	3466
ENSG00000(	17.60846	10.83859	14.51355	5.243529	4.60216	2.465895	1.6554	0.026167	0.055177	KRT81	chr12	-	52679697	52685318	1929
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	EXOC3L4	chr14	+	1.04E+08	1.04E+08	2341
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	KRTAP10-7	chr21	+	46020497	46022091	1595
ENSG00000(	52.82539	40.94578	46.17948	46.44268	37.73771	34.52253	0.2334	0.52471	0.64968	ATP6AP1L	chr5	+	81575281	81682796	3524
ENSG00000(	58.00435	52.98866	65.97069	563.3048	846.7974	825.2528	-3.6379	3.49E-64	1.34E-62	CCDC85C	chr14	-	99977603	1E+08	5307
ENSG00000(	6.214751	9.634302	11.87472	5.243529	9.20432	20.54912	-0.31675	0.66404	0.76804	AC007000.	chr7	-	76682095	76688757	939
ENSG00000(	108.7581	102.3645	72.56776	77.90386	80.99802	77.2647	0.26665	0.33557	0.46378	AC004980.	chr7	+	76178677	76257299	2667
ENSG00000(	8.286335	9.634302	10.55531	0.749076	2.761296	0	2.5549	0.010004	0.023266	AC013472.	chr2	-	27207644	27237480	1966
ENSG00000(	2.071584	0	1.319414	2.247227	2.761296	3.28786	-0.90326	0.46059	0.59001	C2CD4B	chr15	-	62455734	62457482	1579
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC006014.	chr7	+	74966356	74974606	2034
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC004878.	chr7	+	74936533	74944219	1369
ENSG00000(	0	0	0	0	0	4.93179	-1.2404	0.35057	NA	AC004878.	chr7	+	74910311	74918380	1850
ENSG00000(	1.035792	0	1.319414	0	0.920432	0	0.55201	0.67753	NA	AC138783.	chr7	+	74696066	74704116	1850
ENSG00000(	0	0	0	265.9218	208.9381	334.5397	-8.6038	3.24E-19	3.16E-18	RGL3	chr19	-	11495017	11530018	2542
ENSG00000(	2562.549	2374.855	2464.665	3859.237	3305.271	3554.176	-0.5333	1.38E-06	5.62E-06	NAP1L4	chr11	-	2965667	3013607	2511
ENSG00000(	53.86118	40.94578	39.58241	39.701	67.19154	50.96182	-0.21878	0.54834	0.66994	RP11-345J	chr16	-	29538889	29606395	4221
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-89H1	chr12	+	48276432	48295308	1287
ENSG00000(	54635.95	52354	41589.24	46930.33	38499.83	46912.83	0.16659	0.19621	0.30292	TMSB4X	chrX	+	12993227	12995346	1702
ENSG00000(	21.75163	39.74149	26.38828	18.72689	14.72691	15.61733	0.80565	0.10516	0.18274	TMEM256	chr17	-	7306294	7307456	511
ENSG00000(	0	2.408575	1.319414	0	0	0	1.2548	0.34239	NA	C9orf92	chr9	-	16203933	16276311	379
ENSG00000(	6.214751	14.45145	19.79121	4.494453	11.96562	18.90519	0.17301	0.80406	0.87283	CTA-384D8	chr22	+	51021455	51022306	578
ENSG00000(	0	0	2.638828	3.745378	2.761296	11.50751	-2.1169	0.068653	0.12764	CPT1B	chr22	-	51007290	51017899	2933
ENSG00000(	1.035792	3.612863	2.638828	2.996302	5.522592	0.821965	-0.28329	0.80053	0.87004	RP11-497E	chr14	-	85991477	85996332	1747
ENSG00000(	4.143168	2.408575	1.319414	0	2.761296	0	1.0313	0.4214	0.55206	RP11-497H	chr5	+	69803906	69808422	4335
ENSG00000(	58.00435	85.50443	72.56776	154.3096	134.3831	150.4196	-1.0189	7.45E-05	0.000247	SMN2	chr5	+	69345350	69374349	1573
ENSG00000(	27.96638	20.47289	35.62417	22.47227	25.7721	36.98842	-0.02169	0.96227	0.97817	SERF1B	chr5	+	69321074	69338940	1889
ENSG00000(	36.25272	45.76293	34.30476	20.22504	43.2603	39.45432	0.17786	0.67371	0.7758	POM121B	chr7	+	72707497	72716496	3067

ENSG00000(	1.035792	3.612863	7.916483	3.745378	2.761296	8.219649	-0.21761	0.82462	0.88676	DYNLL1P1	chr14	-	81712638	81712907	270
ENSG00000(	5127.17	5197.706	5140.436	7081.76	7954.373	8601.041	-0.61098	1.97E-08	9.69E-08	HMGN1	chr21	-	40714241	40721573	4299
ENSG00000(	85.97073	63.82725	69.92893	104.8706	119.6562	177.5444	-0.85813	0.002657	0.006931	STAG3L1	chr7	+	74988448	75024657	1818
ENSG00000(	0	0	2.638828	2.247227	0	0	0.077345	0.95422	NA	AC005488.	chr7	+	72440345	72442258	468
ENSG00000(	0	7.225726	5.277655	47.19176	55.22592	57.53754	-3.5377	2.92E-09	1.54E-08	MUC19	chr12	+	40787197	40964632	19569
ENSG00000(	237.1963	175.826	164.9267	20.22504	38.65814	66.57916	2.1758	6.00E-11	3.60E-10	DENND6B	chr22	-	50750392	50765489	2450
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AREGB	chr4	+	75480629	75490486	1239
ENSG00000(	100.4718	116.8159	139.8579	179.0291	80.07758	130.6924	-0.13161	0.65016	0.75641	EIF3CL	chr16	-	28390900	28415200	3096
ENSG00000(	6.214751	4.817151	6.597069	0	0.920432	0	3.0315	0.011276	0.025915	RP4-610C1	chr20	-	29513582	29521213	3328
ENSG00000(	516.8602	504.5966	498.7384	859.9387	703.21	752.0979	-0.60573	1.58E-05	5.75E-05	LCMT1	chr16	+	25123050	25189552	1529
ENSG00000(	11.39371	7.225726	11.87472	5.243529	3.681728	2.465895	1.2719	0.11923	0.20267	MFSD2B	chr2	+	24232951	24286191	2834
ENSG00000(	0	0	1.319414	0	0	1.64393	-0.1317	0.91874	NA	VCX3B	chrX	+	8432871	8434550	1171
ENSG00000(	224.7668	237.2447	180.7597	173.7855	142.667	116.719	0.56565	0.010977	0.025292	CDPF1	chr22	-	46639908	46646576	1875
ENSG00000(	0	0	0	3.745378	1.840864	4.109825	-2.4456	0.064342	0.12065	CTD-2375G	chr5	+	64711180	64712049	870
ENSG00000(	64.2191	68.6444	101.5949	241.9514	185.0068	207.1352	-1.4323	7.80E-09	3.95E-08	LIN52	chr14	+	74551499	74667936	2774
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-706C	chrX	-	3809479	3838787	2194
ENSG00000(	211.3015	220.3847	215.0644	370.0433	306.5039	309.8808	-0.60779	0.000584	0.001697	RP11-706C	chrX	-	3735569	3761898	922
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	ARSH	chrX	+	2924654	2951612	1875
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	ACOT6	chr14	+	74077649	74086592	1004
ENSG00000(	192.6573	217.9761	200.5509	157.3059	179.4842	204.6693	0.17402	0.38664	0.51749	SMIM11	chr21	+	35747779	35780164	1857
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	TECRL	chr4	-	65140975	65275186	3573
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-798L	chr4	-	62285964	62293939	2079
ENSG00000(	439.1758	375.7378	453.8783	12.73428	6.443024	22.19305	4.8665	6.38E-65	2.48E-63	DPF3	chr14	-	73086004	73360809	3755
ENSG00000(	0	3.612863	0	0	3.681728	1.64393	-0.32775	0.80548	0.87389	MANSC4	chr12	-	27915671	27924209	1023
ENSG00000(	20.71584	14.45145	19.79121	20.22504	15.64734	24.65895	-0.13478	0.79818	0.86851	CYP2D7P1	chr22	-	42536214	42540576	1738
ENSG00000(	3.107376	10.83859	5.277655	3.745378	9.20432	9.863579	-0.22225	0.79002	0.86254	LINC00634	chr22	+	42348169	42354937	1510
ENSG00000(	105.6508	136.0845	118.7472	114.6086	81.91845	78.08667	0.38433	0.14569	0.23834	LYRM5	chr12	+	25348150	25362579	1138
ENSG00000(	15.53688	4.817151	5.277655	0.749076	0.920432	0	3.0926	0.004446	0.011124	C17orf107	chr17	+	4802713	4806227	3199
ENSG00000(	0	3.612863	2.638828	0	0	0	1.93	0.15472	0.25026	AC007248.	chr2	-	1.03E+08	1.03E+08	399
ENSG00000(	2569.8	2720.486	3092.706	1471.933	1509.508	1419.533	0.92756	1.59E-15	1.29E-14	ITSN1	chr21	+	35014706	35272165	17015
ENSG00000(	1036.828	1038.096	1192.75	559.5594	626.8142	578.6633	0.88644	1.45E-11	9.10E-11	ITPRIPL2	chr16	+	19125254	19132946	7693
ENSG00000(	7.250543	1.204288	0	3.745378	6.443024	0	-0.17092	0.88544	0.92848	AL359878.	chr10	-	1017097	1034281	1875
ENSG00000(	6.214751	0	0	147.5679	191.4499	318.1004	-5.4796	4.64E-08	2.20E-07	DENND1C	chr19	-	6467218	6482568	2933
ENSG00000(	182.2994	217.9761	197.9121	44.19546	90.20234	91.23811	1.3971	3.15E-07	1.38E-06	RP11-1212	chr16	-	18428257	18488396	6405
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	CRLF2	chrX	-	1314890	1331616	1035
ENSG00000(	424.6747	405.845	411.6571	413.4897	385.661	387.9674	0.065119	0.66069	0.76504	CRYZL1	chr21	-	34961647	35016232	2558
ENSG00000(	217.5163	219.1804	175.482	146.8188	135.3035	129.8705	0.56925	0.006211	0.015097	RP9P	chr7	-	32956427	32982788	1303
ENSG00000(	656.6921	632.2511	874.7713	891.3999	888.2169	746.3441	-0.22401	0.15095	0.24531	C5orf51	chr5	+	41904290	41921738	5241
ENSG00000(	10.35792	14.45145	9.235896	6.74168	3.681728	4.109825	1.1128	0.14596	0.23861	CATSPER2P	chr15	-	44019116	44039292	1653
ENSG00000(	10.35792	7.225726	6.597069	0	10.12475	8.219649	0.36379	0.68918	0.78771	AC005594.	chr19	+	4679294	4685960	3071
ENSG00000(	12.4295	15.65574	18.47179	6.74168	0.920432	7.397684	1.4737	0.047815	0.093348	LOH12CR2	chr12	-	12508342	12510001	1538
ENSG00000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	RP11-333E	chr4	-	40044537	40058819	1613
ENSG00000(	77.68439	73.46155	58.05421	5.243529	1.840864	3.28786	4.1304	4.49E-15	3.56E-14	CYS1	chr2	-	10196907	10221071	2738
ENSG00000(	90.1139	73.46155	83.12307	148.317	133.4626	110.9653	-0.66377	0.009493	0.022194	PPAPDC2	chr9	+	4662298	4665256	2959

ENSG00000(	0	0	0	1.498151	1.840864	0	-0.93652	0.47589	NA	KLRC3	chr12	-	10564911	10573194	1028
ENSG00000(	7.250543	19.2686	17.15238	23.97042	14.72691	39.45432	-0.81452	0.15618	0.25219	RP1-59D14	chr17	-	2308856	2319379	2644
ENSG00000(	0	0	0	2.247227	5.522592	0	-1.9602	0.14787	0.24097	TPTE2P6	chr13	+	25141011	25171814	1710
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	AC024132.	chr4	-	27209127	27220026	2509
ENSG00000(	3.107376	4.817151	1.319414	2.247227	1.840864	0	0.8649	0.47072	0.59975	C16orf96	chr16	+	4606491	4650715	3823
ENSG00000(	0	0	5.277655	4.494453	9.20432	8.219649	-1.6971	0.11255	0.19327	GMNC	chr3	-	1.91E+08	1.91E+08	3422
ENSG00000(	12.4295	12.04288	9.235896	12.73428	11.96562	6.575719	0.10458	0.87671	0.92282	TTC23L	chr5	+	34838938	34899561	3410
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CLEC6A	chr12	+	8608522	8630926	1682
ENSG00000(	0	0	0	4.494453	3.681728	2.465895	-2.5888	0.048324	0.094201	OR7E91P	chr2	+	71256158	71256736	579
ENSG00000(	6.214751	0	2.638828	3.745378	1.840864	2.465895	0.11625	0.91853	0.9507	RFPL3S	chr22	-	32755893	32778039	1295
ENSG00000(	0	0	2.638828	3.745378	2.761296	2.465895	-1.2373	0.32605	0.45372	C1QTNF9B-	chr13	+	24463028	24471402	805
ENSG00000(	0	0	3.958241	2.247227	0	2.465895	-0.1793	0.89292	0.93378	C1QTNF9B	chr13	-	24465238	24476794	1111
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	KRTAP5-6	chr11	+	1718425	1718985	561
ENSG00000(	0	0	0	14.98151	4.60216	13.9734	-4.3093	0.000231	0.000715	KRTAP5-1	chr11	-	1605572	1606513	942
ENSG00000(	0	0	2.638828	0	0	0.821965	0.55859	0.66971	NA	RPS3AP47	chr15	-	43407897	43408691	792
ENSG00000(	89.0781	128.8588	110.8308	189.5161	174.8821	179.1884	-0.72438	0.001479	0.004025	AC130352.	chr8	+	12294626	12424423	2501
ENSG00000(	0	0	1.319414	2.247227	3.681728	5.753754	-2.1071	0.09461	0.16748	FAM90A2P	chr8	-	12029711	12036084	2423
ENSG00000(	111.8655	114.4073	93.67838	47.94084	120.5766	147.1317	0.023336	0.94471	0.96693	C1RL-AS1	chr12	+	7260648	7275097	5272
ENSG00000(	0	0	2.638828	5.992604	10.12475	15.61733	-2.9475	0.004967	0.012309	RP11-473N	chr16	+	3082482	3089134	3061
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	OR7E136P	chr7	-	6906289	6907303	1015
ENSG00000(	0	0	5.277655	0.749076	1.840864	0.821965	0.37281	0.77728	0.85333	RP11-3B12	chr7	-	1.25E+08	1.25E+08	574
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	BHLHA9	chr17	+	1173853	1174754	902
ENSG00000(	772.7008	739.4327	694.0116	418.7332	693.0853	635.3789	0.33692	0.056362	0.10779	ZNF316	chr7	+	6676953	6694242	3015
ENSG00000(	17.60846	14.45145	17.15238	14.23244	24.85166	13.9734	-0.09691	0.86276	0.91313	SRRM2-AS1	chr16	-	2787077	2802601	3523
ENSG00000(	80.79177	99.95588	69.92893	44.94453	64.43024	63.2913	0.53507	0.082925	0.14998	PDPK2	chr16	-	2666122	2693297	2387
ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	ONECUT3	chr19	+	1752372	1780987	8318
ENSG00000(	10.35792	1.204288	2.638828	0	0.920432	2.465895	1.5709	0.17891	0.28158	C21orf62	chr21	-	34162985	34186053	3889
ENSG00000(	13.46529	9.634302	11.87472	8.239831	11.04518	9.863579	0.25159	0.70618	0.80093	C21orf49	chr21	+	34144411	34266043	2453
ENSG00000(	1879.962	1876.28	1754.82	2725.137	2456.633	2906.468	-0.55245	1.37E-06	5.60E-06	RNPS1	chr16	-	2303117	2318413	3337
ENSG00000(	0	8.430014	1.319414	1.498151	2.761296	0.821965	0.6873	0.56759	0.68671	HSP90AB2I	chr4	+	13335038	13340281	2176
ENSG00000(	0	1.204288	1.319414	2.247227	0	3.28786	-0.71064	0.59122	0.7076	HSP90AA5I	chr3	+	1.84E+08	1.84E+08	2192
ENSG00000(	10.35792	10.83859	7.916483	8.988907	0.920432	12.32947	0.34278	0.67165	0.77391	RP11-689P	chr4	+	8483997	8514337	3204
ENSG00000(	0	1.204288	5.277655	0	5.522592	1.64393	-0.1088	0.93073	0.95831	AC074389.	chr7	-	1732446	1733961	1423
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-404K	chr5	-	7299887	7306705	2465
ENSG00000(	2407.18	2437.478	2427.721	217.2319	342.4007	262.2068	3.1394	1.06E-94	7.38E-93	NYNRIN	chr14	+	24867992	24888494	7857
ENSG00000(	310.7376	295.0505	213.745	495.888	396.7062	498.9327	-0.75787	3.88E-05	0.000134	DNAJC19	chr3	-	1.81E+08	1.81E+08	1630
ENSG00000(	0	8.430014	5.277655	0	0.920432	1.64393	1.7242	0.15658	0.2526	IFITM5	chr11	-	298200	299526	736
ENSG00000(	4.143168	6.021439	6.597069	0	0	0	3.6229	0.003983	0.010073	SMIM21	chr18	-	73121431	73139658	2554
ENSG00000(	5.17896	14.45145	21.11062	4.494453	6.443024	13.15144	0.68707	0.34824	0.47789	AC005841.	chr12	-	2958397	2966213	939
ENSG00000(	71.46964	60.21439	79.16483	30.7121	23.93123	24.65895	1.3815	0.000103	0.000336	DOK6	chr18	+	67068291	67516323	8890
ENSG00000(	1268.845	1389.748	1366.913	4938.655	4351.802	4465.735	-1.7704	3.38E-57	1.11E-55	HN1L	chr16	+	1728257	1752281	3718
ENSG00000(	0	6.021439	0	0	0	1.64393	0.96324	0.47712	0.6063	IGLL3P	chr22	+	25714223	25716047	434
ENSG00000(	2.071584	0	0	0	0	1.64393	0.14412	0.91322	NA	SERPINB11	chr18	+	61314813	61391127	1918
ENSG00000(	9.322127	10.83859	11.87472	0	0	0	4.6503	6.90E-05	0.00023	SERPINB4	chr18	-	61304493	61311532	1749

ENSG00000(	0	0	1.319414	1.498151	0	8.219649	-1.725	0.19125	0.29687	SERPINB5	chr18	+	61143994	61172318	2783
ENSG00000(	1.035792	2.408575	1.319414	0	0	3.28786	0.32144	0.80824	0.87555	ZDHHC11B	chr5	-	710475	767067	2733
ENSG00000(	0	0	0	2.247227	1.840864	1.64393	-1.6991	0.21004	NA	AC010507.	chr19	-	197124	205076	1478
ENSG00000(	1.035792	1.204288	2.638828	0	0	0	1.7123	0.20641	NA	RP11-503N	chr4	+	2420701	2430972	2790
ENSG00000(	8.286335	3.612863	2.638828	5.992604	13.80648	4.93179	-0.65205	0.4497	0.5795	EGFEM1P	chr3	+	1.68E+08	1.69E+08	2327
ENSG00000(	2.071584	1.204288	6.597069	0	0	1.64393	1.6859	0.18629	0.2909	GOLGA8O	chr15	-	32737307	32747835	1997
ENSG00000(	14.50109	3.612863	7.916483	7.490755	5.522592	6.575719	0.37915	0.6343	0.74375	CTD-2008L	chr18	-	53670844	53858493	2558
ENSG00000(	6.214751	9.634302	10.55531	30.7121	24.85166	34.52253	-1.7061	0.002205	0.005833	TMEM191C	chr22	+	21820712	21825558	2593
ENSG00000(	2.071584	3.612863	0	0	0	0	1.8175	0.17961	NA	P2RX6P	chr22	-	21389532	21399306	468
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	RP11-106A	chr9	+	6639139	6639604	466
ENSG00000(	271.3775	234.8361	314.0205	179.0291	159.2347	186.586	0.63863	0.001004	0.002814	HERC2P9	chr15	+	28834638	28930410	5187
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RNASE13	chr14	-	21500979	21502944	1607
ENSG00000(	2.071584	7.225726	0	35.20655	39.57858	33.70056	-3.2888	1.17E-06	4.83E-06	GYG2P1	chrY	-	14475147	14532255	944
ENSG00000(	5.17896	4.817151	3.958241	2.996302	0	1.64393	1.2321	0.26444	0.38438	Z69890.1	chr16	+	281133	281471	339
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	HBA1	chr16	+	226679	227521	674
ENSG00000(	4.143168	2.408575	0	14.98151	14.72691	25.48091	-2.6985	0.000985	0.002765	AC023490.	chr22	+	20378814	20380440	788
ENSG00000(	0	2.408575	1.319414	1.498151	1.840864	0	0.085203	0.9491	0.96942	TCEB3B	chr18	-	44558943	44561988	3046
ENSG00000(	22.78742	21.67718	17.15238	20.22504	6.443024	14.79537	0.53673	0.35538	0.48497	ATP10A	chr15	-	25922420	26110317	6766
ENSG00000(	25.8948	39.74149	30.34652	8.988907	12.88605	2.465895	1.8896	0.001221	0.003375	AP000525.	chr22	-	16147979	16193004	4136
ENSG00000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	ANKUB1	chr3	-	1.49E+08	1.5E+08	2471
ENSG00000(	2.071584	2.408575	3.958241	1.498151	2.761296	6.575719	-0.29904	0.7791	0.85466	HNRNPA1P	chr8	-	83203859	83204614	756
ENSG00000(	2.071584	1.204288	6.597069	0	0.920432	0	2.1384	0.098988	0.17393	AP000525.	chr22	-	16157306	16157938	633
ENSG00000(	73.54123	68.6444	87.08131	73.4094	99.40666	85.48435	-0.16979	0.54875	0.67027	C3orf72	chr3	+	1.39E+08	1.39E+08	3538
ENSG00000(	8.286335	7.225726	7.916483	6.74168	4.60216	3.28786	0.60459	0.46562	0.5948	HCP5	chr6	+	31368479	31445283	2658
ENSG00000(	1.035792	1.204288	1.319414	0.749076	0	4.109825	-0.29373	0.82153	0.88465	HLA-H	chr6	+	29855350	29858259	1366
ENSG00000(	6.214751	0	1.319414	5.243529	2.761296	4.93179	-0.59462	0.587	0.70417	HCG27	chr6	+	31165537	31171745	1720
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-93O1	chr5	-	98858015	98861166	3152
ENSG00000(	1.035792	2.408575	3.958241	161.0512	205.2563	182.4762	-5.9642	5.50E-26	7.06E-25	COL6A6	chr3	+	1.3E+08	1.3E+08	9581
ENSG00000(	18.64425	18.06432	22.43003	23.97042	23.93123	40.27628	-0.56058	0.24823	0.36522	H1FX-AS1	chr3	+	1.29E+08	1.29E+08	2600
ENSG00000(	392.5651	335.9963	386.5882	380.5304	453.773	459.4784	-0.21242	0.18561	0.29005	RAB12	chr18	+	8609443	8639379	2137
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	LRRC30	chr18	+	7231123	7232045	923
ENSG00000(	281.7354	219.1804	259.9245	114.6086	152.7917	78.08667	1.1333	3.43E-06	1.34E-05	TMEM200C	chr18	-	5889419	5895954	3290
ENSG00000(	2.071584	6.021439	1.319414	0	4.60216	0	0.74496	0.54911	0.67064	PPIAP30	chr10	-	15196801	15197319	519
ENSG00000(	774.7723	870.7	655.7486	33.7084	36.81728	57.53754	4.1431	5.09E-85	2.96E-83	HLA-A	chr6	+	29909037	29913661	1868
ENSG00000(	1176.66	1038.096	1419.689	1286.912	1338.308	1077.596	-0.0273	0.85146	0.90523	PTPLB	chr3	-	1.23E+08	1.23E+08	4257
ENSG00000(	217.5163	193.8903	246.7304	65.16957	59.82808	46.03004	1.9267	1.54E-15	1.26E-14	WDR52	chr3	-	1.13E+08	1.13E+08	10259
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	CD200R1L	chr3	-	1.13E+08	1.13E+08	1597
ENSG00000(	126.3666	127.6545	159.6491	76.40571	57.06678	76.44274	0.96402	0.000215	0.000669	RP11-553A	chr3	-	1.11E+08	1.11E+08	856
ENSG00000(	38.3243	37.33292	44.86007	42.69731	32.21512	37.81039	0.089493	0.81433	0.87947	LNP1	chr3	+	1E+08	1E+08	2210
ENSG00000(	554.1487	578.0581	675.5399	458.4342	666.3928	535.0992	0.12296	0.45948	0.58903	VGLL3	chr3	-	86987119	87040269	10400
ENSG00000(	0	0	0	1.498151	1.840864	0	-0.93652	0.47589	NA	PRSS50	chr3	-	46753605	46854064	2958
ENSG00000(	0	1.204288	0	1250.207	2268.865	1369.394	-10.365	2.67E-41	5.71E-40	TRIM71	chr3	+	32859510	32938323	7690
ENSG00000(	31.07376	10.83859	11.87472	6.74168	6.443024	3.28786	1.5918	0.024677	0.052355	ZCWPW2	chr3	+	28390637	28579613	1716
ENSG00000(	702.2669	728.5941	853.6607	668.1754	853.2405	682.2309	0.051721	0.72874	0.81829	ANKRD28	chr3	-	15708743	15901278	6564

ENSG00000(	47.64643	22.88147	36.94359	5.992604	14.72691	12.32947	1.648	0.001928	0.005152	COLQ	chr3	-	15491640	15563258	3147
ENSG00000(	306.5944	338.4048	216.3839	265.1727	196.9724	254.8091	0.26365	0.20519	0.31373	METTL6	chr3	-	15422782	15482073	4020
ENSG00000(	22.78742	38.53721	21.11062	59.92604	57.06678	59.18147	-1.0739	0.005476	0.013455	AC022007.	chr3	-	10048102	10052893	1897
ENSG00000(	270.3417	225.2018	211.1062	441.9546	362.6502	369.8842	-0.72767	4.57E-05	0.000156	SETD5-AS1	chr3	-	9391373	9440263	3253
ENSG00000(	0	0	0	34.45748	94.8045	38.63235	-6.5367	3.93E-10	2.22E-09	XKR4	chr8	+	56014949	56438714	3981
ENSG00000(	79.75598	61.41867	54.09597	103.3724	103.0884	133.1583	-0.78333	0.005667	0.013894	GPX3	chr5	+	1.5E+08	1.5E+08	1636
ENSG00000(	11.39371	14.45145	15.83297	17.22874	21.16994	14.79537	-0.33894	0.55258	0.67344	DIO2	chr14	-	80663873	80854100	6367
ENSG00000(	351.1335	427.5221	398.463	466.6741	404.0696	559.7581	-0.28194	0.096152	0.16983	C11orf31	chr11	+	57508825	57510986	1454
ENSG00000(	27.96638	12.04288	10.55531	6.74168	17.48821	20.54912	0.18323	0.77184	0.85002	GNRHR2	chr1	-	1.46E+08	1.46E+08	1599
ENSG00000(	9.322127	8.430014	9.235896	4.494453	2.761296	4.109825	1.1108	0.18061	0.28356	DIO1	chr1	+	54356912	54376759	1861
ENSG00000(	39.36009	9.634302	13.19414	11.23613	11.04518	6.575719	1.0519	0.10791	0.18669	AKR7L	chr1	-	19592476	19600688	2115
ENSG00000(	492.0012	479.3065	610.8886	631.4707	654.4271	544.9627	-0.21122	0.17045	0.27079	STK38L	chr12	+	27396901	27478892	5068
ENSG00000(	488.8938	404.6407	580.5421	716.1162	767.6403	636.2008	-0.52317	0.001155	0.003208	SACM1L	chr3	+	45730548	45786916	4661
ENSG00000(	1246.058	1229.578	1319.414	2045.725	2004.701	1978.47	-0.66703	1.33E-09	7.21E-09	TSN	chr2	+	1.22E+08	1.23E+08	3420
ENSG00000(	101.5076	131.2674	134.5802	207.4939	208.0176	257.275	-0.8716	6.55E-05	0.000219	SLC48A1	chr12	+	48147699	48176536	3010
ENSG00000(	4.143168	0	1.319414	3.745378	0	0	0.32344	0.80779	0.87527	IGLV5-52	chr22	+	22673082	22673581	379
ENSG00000(	0	0	3.958241	1.498151	5.522592	2.465895	-0.91258	0.46113	0.59054	IGLV1-51	chr22	+	22676828	22677336	400
ENSG00000(	1.035792	0	0	4.494453	1.840864	0	-1.3255	0.32605	0.45372	IGLV1-50	chr22	+	22681658	22682172	405
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	TRGV9	chr7	-	38356618	38358462	1735
ENSG00000(	0	2.408575	2.638828	0	0	0	1.6365	0.22501	NA	TRBV9	chr7	-	1.42E+08	1.42E+08	390
ENSG00000(	0	0	0	2.996302	1.840864	0	-1.3549	0.31496	NA	TRBV20-1	chr7	+	1.42E+08	1.42E+08	413
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	TRBJ2-4	chr7	+	1.42E+08	1.42E+08	50
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	TRBJ2-6	chr7	+	1.42E+08	1.42E+08	53
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	TRBJ2-7	chr7	+	1.42E+08	1.42E+08	47
ENSG00000(	216.4805	270.9647	230.8974	471.1685	342.4007	368.2403	-0.71717	0.000118	0.00038	TRBC2	chr7	+	1.42E+08	1.43E+08	758
ENSG00000(	0	0	0	5.992604	1.840864	0.821965	-2.2375	0.09467	0.16757	TRAV8-1	chr14	+	22265459	22266058	473
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	TRAV8-2	chr14	+	22314719	22315403	566
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	TRAV8-3	chr14	+	22320735	22321183	341
ENSG00000(	2.071584	3.612863	2.638828	4.494453	1.840864	4.93179	-0.36735	0.72606	0.8163	TRAV13-1	chr14	+	22337020	22337546	360
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	TRAJ32	chr14	+	22978325	22978390	66
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	TSSK1B	chr5	-	1.13E+08	1.13E+08	2478
ENSG00000(	5.17896	26.49433	11.87472	53.18436	37.73771	65.75719	-1.7935	0.000424	0.00126	PRR22	chr19	-	5782971	5784776	1640
ENSG00000(	6.214751	2.408575	6.597069	4.494453	2.761296	4.93179	0.2718	0.77256	0.85055	TAS2R19	chr12	-	11174218	11175219	1002
ENSG00000(	9.322127	1.204288	7.916483	4.494453	7.363456	3.28786	0.25767	0.77758	0.85348	TAS2R15	chr12	-	11117024	11117951	928
ENSG00000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	TAS2R50	chr12	-	11138512	11139511	1000
ENSG00000(	22.78742	37.33292	26.38828	18.72689	26.69253	15.61733	0.48875	0.31278	0.43921	TAS2R14	chr12	-	11090005	11324172	1858
ENSG00000(	0	2.408575	2.638828	0	0	2.465895	0.5704	0.67147	0.77389	TAS2R13	chr12	-	11060525	11062161	1637
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	RP1-122K4	chrX	-	13998185	14006939	544
ENSG00000(	9.322127	15.65574	19.79121	13.48336	6.443024	20.54912	0.12256	0.84772	0.90301	RP11-592N	chr15	-	71633466	71634086	580
ENSG00000(	24.85901	19.2686	19.79121	32.95932	35.89685	21.37109	-0.47631	0.3129	0.43931	AL161915.	chr1	+	54569968	54571750	1783
ENSG00000(	3.107376	10.83859	9.235896	5.243529	4.60216	6.575719	0.43192	0.60477	0.71965	AL136115.	chr1	+	32379174	32380745	1572
ENSG00000(	111.8655	134.8802	65.97069	167.7929	141.7465	216.9987	-0.74056	0.007005	0.016871	AC084018.	chr12	-	1.22E+08	1.22E+08	1603
ENSG00000(	2.071584	1.204288	0	0	0.920432	0	0.824	0.54141	NA	RP11-134K	chr9	+	8713311	8713841	531
ENSG00000(	0	0	0	4.494453	1.840864	0	-1.6936	0.21189	0.32187	CTAGE1	chr18	-	19993564	19997878	4306

ENSG0000(	557.256	580.4667	651.7904	348.3201	414.1944	392.8992	0.62924	2.76E-05	9.71E-05	C17orf51	chr17	-	21428051	21477781	7914
ENSG0000(	2.071584	3.612863	6.597069	2.247227	3.681728	1.64393	0.56354	0.59074	0.70729	KRTAP4-9	chr17	+	39261584	39262740	1157
ENSG0000(	11.39371	9.634302	14.51355	81.64923	26.69253	40.27628	-1.9944	0.000128	0.000412	KRTAP2-3	chr17	-	39215495	39216344	850
ENSG0000(	0	9.634302	0	0	0.920432	0.821965	1.5054	0.25298	0.37081	DKFZP667F	chr10	+	6392278	6394723	2446
ENSG0000(	733.3407	658.7454	748.1076	582.0317	421.5579	403.5848	0.60125	0.000272	0.000833	FAM127C	chrX	-	1.34E+08	1.34E+08	2017
ENSG0000(	0	0	1.319414	11.23613	9.20432	1.64393	-2.9463	0.012566	0.028563	LINC00277	chr15	+	69365266	69388160	2498
ENSG0000(	0	0	2.638828	1.498151	0.920432	3.28786	-0.71787	0.58578	0.70318	ST13P5	chr11	+	18283529	18284638	1110
ENSG0000(	172.9772	184.256	166.2461	113.8595	89.2819	161.1051	0.51724	0.036182	0.073274	RPL15P3	chr6	+	12514342	12515006	615
ENSG0000(	1.035792	0	1.319414	0	1.840864	1.64393	-0.30298	0.82242	NA	OR2A42	chr7	-	1.44E+08	1.44E+08	933
ENSG0000(	1.035792	1.204288	0	1.498151	1.840864	2.465895	-0.8575	0.50907	0.63644	RPS26P3	chr9	+	9090876	9091311	436
ENSG0000(	40.39588	37.33292	11.87472	77.90386	47.86246	51.78379	-0.95071	0.027934	0.058383	RNF208	chr9	-	1.4E+08	1.4E+08	1127
ENSG0000(	2.071584	0	1.319414	53.18436	21.16994	23.83698	-4.2525	3.63E-07	1.58E-06	KRTAP3-1	chr17	-	39164773	39175576	656
ENSG0000(	6432.268	6815.064	9878.451	5113.939	7004.487	5782.523	0.36809	0.021864	0.04698	MT-ND4L	chrMT	+	10470	10766	297
ENSG0000(	54.89697	51.78437	44.86007	91.38722	49.70333	36.16646	-0.22351	0.55974	0.6803	MAP10	chr1	+	2.33E+08	2.33E+08	5450
ENSG0000(	0	1.204288	0	0.749076	0	0	0.1572	0.90001	NA	RPL23AP4	chr21	+	48110676	48111157	463
ENSG0000(	1.035792	0	0	0	0	4.109825	-0.79743	0.55418	NA	RP11-211N	chr9	-	46842616	46844326	1711
ENSG0000(	107.7224	109.5902	88.40072	225.4717	148.1896	194.8057	-0.8876	0.000224	0.000695	AC016747.	chr2	-	61368732	61372104	2346
ENSG0000(	0	1.204288	0	24.71949	11.96562	27.94681	-4.5486	7.49E-06	2.82E-05	POU5F1B	chr8	+	1.28E+08	1.28E+08	5357
ENSG0000(	6.214751	7.225726	1.319414	9.737982	8.283888	11.50751	-0.88457	0.27923	0.40144	RPS26P6	chr8	+	1.02E+08	1.02E+08	414
ENSG0000(	10.35792	7.225726	3.958241	1.498151	1.840864	4.109825	1.323	0.16281	0.26081	AC023632.	chr8	+	95558771	95560630	1860
ENSG0000(	7.250543	8.430014	11.87472	0.749076	11.04518	4.109825	0.71582	0.40848	0.53922	RBM12B-AS	chr8	+	94752349	94753001	653
ENSG0000(	1.035792	1.204288	0	0.749076	0	0	0.55357	0.6746	NA	BTF3P12	chr8	+	71185604	71186072	469
ENSG0000(	0	2.408575	0	0.749076	0.920432	0	0.23282	0.86283	NA	VN2R17P	chr19	-	56828546	56829377	832
ENSG0000(	616.2962	619.0039	455.1978	641.2087	384.7406	472.6298	0.1726	0.37129	0.50186	ZNF580	chr19	+	56146382	56154835	1418
ENSG0000(	2.071584	7.225726	0	2.996302	7.363456	4.93179	-0.57793	0.5788	0.69719	AL590762.	chrX	-	70639933	70640364	432
ENSG0000(	240.3037	219.1804	192.6344	667.4263	740.0273	729.0829	-1.7026	1.37E-27	1.89E-26	ZNF611	chr19	-	53206066	53238326	4796
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	SYT3	chr19	-	51124564	51171651	2915
ENSG0000(	1122.798	1130.826	940.742	2568.58	1974.327	2114.094	-1.0563	1.32E-14	1.02E-13	NUP62	chr19	-	50410082	50433020	3590
ENSG0000(	1.035792	0	2.638828	0	4.60216	2.465895	-0.62262	0.62796	0.73871	COX20P1	chr10	+	70392128	70392484	357
ENSG0000(	0	0	0	2.996302	0.920432	0	-1.1048	0.40628	NA	RP11-108F	chr1	-	2.3E+08	2.3E+08	906
ENSG0000(	1.035792	0	1.319414	0	0.920432	0	0.55201	0.67753	NA	AURKAPS1	chr1	-	2.2E+08	2.2E+08	1212
ENSG0000(	1.035792	2.408575	0	0	1.840864	3.28786	-0.34609	0.79225	0.86423	RP11-365D	chr1	-	2.15E+08	2.15E+08	575
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-383G	chr1	+	2.05E+08	2.05E+08	552
ENSG0000(	3.107376	0	3.958241	2.247227	0	0	0.97799	0.45988	0.58936	EEF1A1P32	chr1	+	1.98E+08	1.98E+08	1347
ENSG0000(	56.96855	59.0101	52.77655	66.66772	85.60018	45.20807	-0.2198	0.51388	0.64083	DENND1B	chr1	-	1.97E+08	1.98E+08	6960
ENSG0000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	OR5S1P	chr2	+	2.41E+08	2.41E+08	951
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-436I9	chr12	-	9180128	9181685	950
ENSG0000(	0	0	0	0.749076	1.840864	0.821965	-1.0455	0.43461	NA	TPM3P1	chr7	-	1.17E+08	1.17E+08	747
ENSG0000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP4-635A2	chr1	-	1.85E+08	1.85E+08	893
ENSG0000(	1.035792	2.408575	0	0	0	1.64393	0.52159	0.70059	NA	AC064852.	chr2	-	2.34E+08	2.34E+08	676
ENSG0000(	4.143168	3.612863	14.51355	7.490755	2.761296	4.93179	0.46256	0.59897	0.7143	C1orf220	chr1	+	1.79E+08	1.79E+08	2595
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP4-765C7	chr1	+	1.78E+08	1.78E+08	357
ENSG0000(	4.143168	0	0	0	0	1.64393	0.64085	0.63628	NA	RP4-612B1	chr1	+	1.72E+08	1.72E+08	423
ENSG0000(	1.035792	0	0	0	3.681728	1.64393	-1.1227	0.40737	0.53818	PFN1P11	chr10	-	1.05E+08	1.05E+08	389

ENSG00000(	0	1.204288	2.638828	8.988907	2.761296	5.753754	-1.7597	0.11137	0.19144	AL021068.	chr1	+	1.69E+08	1.69E+08	1463
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-375F	chr1	+	1.69E+08	1.69E+08	457
ENSG00000(	176.0846	214.3632	281.0351	153.5605	257.721	167.6808	0.21173	0.38276	0.5134	SFT2D2	chr1	+	1.68E+08	1.68E+08	1155
ENSG00000(	340.7755	351.652	378.6718	789.5256	576.1904	657.5719	-0.91645	1.15E-08	5.76E-08	FGFR1OP	chr6	+	1.67E+08	1.67E+08	3871
ENSG00000(	0	0	0	3.745378	0	4.93179	-2.136	0.11352	0.19465	RP11-277B	chr1	-	1.67E+08	1.67E+08	415
ENSG00000(	0	1.204288	1.319414	0.749076	0	0	0.61214	0.64459	NA	KRT8P40	chr2	+	1.78E+08	1.78E+08	563
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	HMGB3P6	chr1	+	1.64E+08	1.64E+08	598
ENSG00000(	9.322127	1.204288	11.87472	15.73059	5.522592	16.4393	-0.69015	0.37553	0.50606	LPAL2	chr6	-	1.61E+08	1.61E+08	2368
ENSG00000(	81.82756	89.11729	77.84541	17.22874	44.18074	62.46933	0.98975	0.011326	0.026006	RP11-288H	chr6	+	1.61E+08	1.61E+08	3131
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	yR211F11.2	chr6	-	1.59E+08	1.59E+08	580
ENSG00000(	0	0	1.319414	0	0.920432	0.821965	-0.17431	0.89516	NA	FAM106A	chr17	-	18427880	18430160	2281
ENSG00000(	540.6834	480.5108	654.4292	423.9768	621.2916	447.1489	0.16686	0.35453	0.48427	SCAF8	chr6	+	1.55E+08	1.55E+08	5055
ENSG00000(	1.035792	0	1.319414	10.48706	4.60216	14.79537	-2.93	0.005366	0.01321	RP11-312J1	chr1	+	1.61E+08	1.61E+08	1097
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	PPP1R14BI	chr2	+	2.09E+08	2.09E+08	444
ENSG00000(	25.8948	3.612863	14.51355	27.7158	26.69253	23.01502	-0.76074	0.19701	0.30392	CCDC19	chr1	-	1.6E+08	1.6E+08	1976
ENSG00000(	0	1.204288	0	18.72689	9.20432	29.59074	-4.3675	2.46E-05	8.70E-05	DARC	chr1	+	1.59E+08	1.59E+08	1902
ENSG00000(	12.4295	15.65574	27.70769	8.239831	7.363456	11.50751	0.97141	0.12126	0.20564	PDCL3P5	chr6	+	1.51E+08	1.51E+08	722
ENSG00000(	8.286335	4.817151	3.958241	0.749076	0.920432	2.465895	1.6647	0.11538	0.19745	AC007256.	chr2	-	2.02E+08	2.02E+08	2765
ENSG00000(	179.192	270.9647	294.2293	291.3904	320.3103	272.8924	-0.25125	0.21908	0.33064	ZNF254	chr19	+	24216276	24312654	3967
ENSG00000(	1.035792	7.225726	1.319414	5.243529	0.920432	4.93179	-0.18283	0.86592	0.9154	NPM1P46	chr2	-	1.98E+08	1.98E+08	865
ENSG00000(	0	2.408575	3.958241	0	0.920432	1.64393	0.81551	0.53355	0.65808	RP11-55K2	chr6	-	1.37E+08	1.37E+08	1297
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC019178.	chr2	-	1.91E+08	1.91E+08	440
ENSG00000(	4.143168	3.612863	1.319414	0	0	0	2.6368	0.048148	0.09393	COX5BP2	chr6	-	1.36E+08	1.36E+08	1125
ENSG00000(	0	0	0	2.996302	0	0.821965	-1.0802	0.41594	NA	AC104131.	chr2	+	1.89E+08	1.89E+08	1194
ENSG00000(	45.57484	32.51577	29.0271	44.94453	49.70333	41.09825	-0.3261	0.39458	0.52548	TCTEX1D2	chr3	-	1.96E+08	1.96E+08	800
ENSG00000(	8.286335	12.04288	14.51355	2.247227	8.283888	6.575719	0.94327	0.21785	0.3292	YWHAZP4	chr6	+	1.28E+08	1.28E+08	708
ENSG00000(	5.17896	18.06432	6.597069	5.243529	20.2495	13.15144	-0.33962	0.6423	0.74983	AC022498.	chr3	+	1.88E+08	1.88E+08	2268
ENSG00000(	3.107376	0	0	0	1.840864	0	0.36193	0.78835	NA	PPP1R14BI	chr6	-	1.27E+08	1.27E+08	435
ENSG00000(	11.39371	16.86003	5.277655	7.490755	6.443024	11.50751	0.37169	0.60658	0.72109	AC015815.	chr17	-	75085986	75087063	123
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	ARF1P2	chr12	-	1.21E+08	1.21E+08	538
ENSG00000(	568.6498	455.2208	455.1978	16.47966	28.53339	23.01502	4.4229	2.34E-73	1.08E-71	CRYGS	chr3	-	1.86E+08	1.86E+08	1536
ENSG00000(	1.035792	0	1.319414	1.498151	11.96562	2.465895	-2.0039	0.090163	0.16102	RP11-64B1	chr12	+	1.2E+08	1.2E+08	545
ENSG00000(	6.214751	3.612863	0	0	0	3.28786	1.0575	0.40821	0.53902	CRIP1	chr14	+	1.06E+08	1.06E+08	2241
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RPL23AP6(	chr10	+	1.36E+08	1.36E+08	454
ENSG00000(	7.250543	12.04288	9.235896	9.737982	6.443024	3.28786	0.49368	0.52402	0.64914	CNN2P9	chr6	+	1.11E+08	1.11E+08	909
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-346C	chr6	+	1.11E+08	1.11E+08	860
ENSG00000(	0	4.817151	1.319414	0	0.920432	0	1.4368	0.28779	0.41144	RPL7AP60	chr12	-	1.13E+08	1.13E+08	794
ENSG00000(	122.2234	139.6974	159.6491	456.187	532.9301	421.668	-1.7382	1.06E-20	1.10E-19	KLHL23	chr2	+	1.71E+08	1.71E+08	4077
ENSG00000(	8.286335	9.634302	22.43003	0	0	0	4.9599	1.65E-05	5.96E-05	RP11-81B1	chr10	+	1.28E+08	1.28E+08	594
ENSG00000(	0	3.612863	2.638828	0	2.761296	1.64393	0.3366	0.79254	0.86444	RPL13P6	chr14	+	1.04E+08	1.04E+08	626
ENSG00000(	37.28851	49.3758	32.98534	29.96302	27.61296	60.00344	0.024222	0.95431	0.97285	RP11-641D	chr3	-	1.69E+08	1.69E+08	410
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RPL36AP48	chr17	+	65220844	65221157	314
ENSG00000(	176.0846	169.8046	222.9809	512.3677	567.9065	519.4818	-1.4887	3.01E-18	2.81E-17	TRIM59	chr3	-	1.6E+08	1.6E+08	4615
ENSG00000(	1.035792	3.612863	7.916483	2.996302	4.60216	3.28786	0.15572	0.87765	0.92357	YBX1P4	chr7	+	1.52E+08	1.52E+08	808

ENSG00000(	6.214751	1.204288	6.597069	12.73428	7.363456	10.68554	-1.0201	0.21538	0.32607	BTF3L4P2	chr2	+	1.6E+08	1.6E+08	712
ENSG00000(	924.9622	973.0645	910.3955	1125.861	963.6923	910.7371	-0.09557	0.4671	0.59636	MLLT11	chr1	+	1.51E+08	1.51E+08	4072
ENSG00000(	20.71584	16.86003	19.79121	0.749076	6.443024	3.28786	2.2834	0.002017	0.005373	AC012066.	chr2	+	1.53E+08	1.53E+08	694
ENSG00000(	14.50109	21.67718	35.62417	50.18806	26.69253	29.59074	-0.56677	0.23886	0.35385	ASIC3	chr7	+	1.51E+08	1.51E+08	2232
ENSG00000(	23.82321	25.29004	25.06886	23.22134	29.45382	29.59074	-0.1437	0.75105	0.83481	C6orf165	chr6	+	88117701	88221352	2580
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	STRADBP1	chr7	-	1.5E+08	1.5E+08	1281
ENSG00000(	8.286335	13.24716	5.277655	2.247227	9.20432	18.08323	-0.11934	0.88034	0.92524	NCLP1	chr9	-	1.4E+08	1.4E+08	1963
ENSG00000(	35.21692	72.25726	47.4989	29.21395	38.65814	55.89361	0.31526	0.43027	0.56018	KIAA1984	chr9	+	1.4E+08	1.4E+08	4244
ENSG00000(	10.35792	20.47289	10.55531	105.6197	185.9273	184.1201	-3.4542	1.00E-19	9.99E-19	ARHGEF35	chr7	-	1.44E+08	1.44E+08	2431
ENSG00000(	0	0	1.319414	0	1.840864	0.821965	-0.46629	0.72905	NA	RP11-355C	chr9	-	1.26E+08	1.26E+08	381
ENSG00000(	7.250543	4.817151	6.597069	3.745378	0	1.64393	1.4444	0.16412	0.26236	DNLZ	chr9	-	1.39E+08	1.39E+08	2934
ENSG00000(	65.25489	60.21439	54.09597	9.737982	16.56778	13.15144	2.1439	3.57E-07	1.55E-06	AC093724.	chr2	-	1.32E+08	1.32E+08	1027
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC018804.	chr2	+	1.31E+08	1.31E+08	2235
ENSG00000(	2.071584	2.408575	5.277655	2.996302	3.681728	3.28786	-0.03648	0.97201	0.98377	RPL12P38	chr17	-	58511039	58513357	2319
ENSG00000(	0	0	1.319414	0	0	1.64393	-0.1317	0.91874	NA	ST13P10	chr11	-	1.12E+08	1.12E+08	1082
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	EEF1A1P16	chr12	+	17143604	17145017	1414
ENSG00000(	0	2.408575	0	0.749076	6.443024	7.397684	-1.846	0.12797	0.21462	YWHAZP2	chr2	-	1.27E+08	1.27E+08	728
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	NPM1P32	chr2	-	1.22E+08	1.22E+08	604
ENSG00000(	495.1085	508.2094	713.8029	56.18067	98.48622	70.68898	2.9163	1.78E-39	3.64E-38	NOTCH2NL	chr1	+	1.45E+08	1.45E+08	5036
ENSG00000(	0	0	0	0.749076	2.761296	0	-0.97685	0.45852	NA	HIST2H3DP	chr1	+	1.21E+08	1.21E+08	416
ENSG00000(	239.2679	283.0076	294.2293	650.1976	431.6826	554.0044	-1.0013	4.62E-08	2.19E-07	SUPT4H1	chr17	-	56422539	56430454	1643
ENSG00000(	8.286335	6.021439	3.958241	0.749076	3.681728	0.821965	1.5108	0.14301	0.23464	RBMS2P1	chr12	-	94817520	94818745	1226
ENSG00000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	RP11-819N	chr11	-	1.07E+08	1.07E+08	1499
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	CTC-250I14	chr19	-	13268773	13269602	499
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	YWHAZP5	chr10	+	1.07E+08	1.07E+08	730
ENSG00000(	4.143168	4.817151	7.916483	7.490755	7.363456	3.28786	-0.10149	0.90668	0.94247	AC093106.	chr7	-	1.31E+08	1.31E+08	673
ENSG00000(	0	1.204288	0	0.749076	2.761296	0	-0.67728	0.61696	NA	TSGA13	chr7	-	1.3E+08	1.3E+08	2046
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-613N	chr12	+	76993451	76994250	800
ENSG00000(	2.071584	0	0	0	1.840864	0	0.093542	0.94384	NA	IFITM9P	chr11	-	69070879	69071274	396
ENSG00000(	2.071584	2.408575	2.638828	2.247227	1.840864	10.68554	-0.86063	0.41563	0.54624	MARCKSL1I	chr10	+	1.05E+08	1.05E+08	541
ENSG00000(	1.035792	1.204288	3.958241	2.996302	0	0	0.63126	0.6294	0.73967	RP11-212P	chr7	-	1.28E+08	1.28E+08	448
ENSG00000(	1767.061	1700.454	1870.929	2514.647	2436.383	2097.654	-0.40039	0.000718	0.002062	NRAS	chr1	-	1.15E+08	1.15E+08	4449
ENSG00000(	0	1.204288	0	0	0.920432	0.821965	-0.17164	0.89643	NA	AC009237.	chr2	+	96191093	96192968	1427
ENSG00000(	1.035792	0	1.319414	0	1.840864	0	0.17192	0.89859	NA	PGK1P2	chr19	+	12670385	12671919	1214
ENSG00000(	17.60846	37.33292	15.83297	15.73059	25.7721	55.07165	-0.42932	0.4253	0.55568	RP11-642N	chr3	+	75263782	75264787	1006
ENSG00000(	3.107376	3.612863	2.638828	0	0.920432	2.465895	1.0699	0.3764	0.50698	CTC-398G3	chr19	+	11634251	11634646	396
ENSG00000(	2.071584	3.612863	0	1.498151	0.920432	7.397684	-0.57717	0.62546	0.7369	CTC-398G3	chr19	+	11632783	11633313	531
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-3L10	chr7	+	1.21E+08	1.21E+08	316
ENSG00000(	1.035792	1.204288	0	0	0.920432	0	0.54457	0.68095	NA	CTD-3035D	chr14	+	91232875	91233333	459
ENSG00000(	17.60846	12.04288	19.79121	28.46487	13.80648	27.12484	-0.47519	0.38034	0.51098	RPS7P11	chr17	-	44798948	44799533	586
ENSG00000(	56.96855	25.29004	35.62417	68.91495	39.57858	38.63235	-0.30819	0.45743	0.58711	ANKRD39	chr2	-	97502348	97523832	4965
ENSG00000(	883.5305	893.5815	622.7633	728.1014	539.3732	752.0979	0.24822	0.15365	0.24902	QTRT1	chr19	+	10812106	10824113	2034
ENSG00000(	277.5922	316.7277	394.5047	469.6704	508.9989	438.1073	-0.51958	0.002425	0.006369	CHUK	chr10	-	1.02E+08	1.02E+08	4845
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	PCNPP3	chr12	-	66039772	66040242	471

ENSG00000(	193.6931	215.5675	170.2044	216.4828	254.0392	258.097	-0.32661	0.091839	0.16346	MXD3	chr5	-	1.77E+08	1.77E+08	2279
ENSG00000(	0	0	0	1.498151	1.840864	0	-0.93652	0.47589	NA	GAPDHP44	chr12	+	63149007	63150013	1007
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	AC092933.	chr3	-	1.96E+08	1.96E+08	945
ENSG00000(	0	0	1.319414	0	9.20432	0	-1.5172	0.25935	0.37814	RP4-778K6	chr7	+	1.05E+08	1.05E+08	319
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AP000593.	chr11	+	71991195	71992222	712
ENSG00000(	389.4578	375.7378	335.1311	28.46487	23.0108	36.16646	3.6176	1.07E-52	3.15E-51	GSTM2	chr1	+	1.1E+08	1.1E+08	4321
ENSG00000(	2.071584	0	2.638828	0	4.60216	0.821965	-0.11863	0.92702	0.95608	ST13P11	chr11	+	94646212	94646931	720
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	GAPDHP71	chr5	+	1.74E+08	1.74E+08	1003
ENSG00000(	378.064	417.8878	369.4359	457.6852	447.33	518.6599	-0.28801	0.059037	0.11219	COG8	chr16	-	69354043	69373570	4247
ENSG00000(	1.035792	0	1.319414	1.498151	1.840864	1.64393	-0.67375	0.60745	0.7217	AC104297.	chr3	-	17913221	17914090	870
ENSG00000(	3.107376	3.612863	5.277655	3.745378	0	7.397684	0.072334	0.94555	0.96725	RP11-577H	chr7	+	1.02E+08	1.02E+08	794
ENSG00000(	299.3439	244.4704	277.0769	534.0909	529.2484	501.3986	-0.9262	3.82E-09	1.99E-08	ARHGAP19	chr10	-	98978996	99052413	5525
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-66N1	chrX	+	1.53E+08	1.53E+08	372
ENSG00000(	11.39371	13.24716	10.55531	4.494453	23.93123	10.68554	-0.12913	0.85259	0.90604	HAUS7	chrX	-	1.53E+08	1.53E+08	2124
ENSG00000(	147.0825	150.536	72.56776	217.2319	163.8369	233.438	-0.71965	0.00701	0.01688	LCAT	chr16	-	67973653	67978034	1507
ENSG00000(	0	1.204288	3.958241	0.749076	0	1.64393	0.63468	0.63346	0.74321	AC022210.	chr2	+	85142910	85143789	876
ENSG00000(	7.250543	10.83859	6.597069	8.239831	4.60216	20.54912	-0.40205	0.59422	0.71029	PTPRCAP	chr11	-	67202981	67205538	1292
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CISD1P1	chr2	+	20026010	20026336	327
ENSG00000(	2.071584	2.408575	1.319414	0	0	0.821965	1.5294	0.25509	0.37325	ANXA2P1	chr4	-	1.54E+08	1.54E+08	926
ENSG00000(	0	0	0	1.498151	6.443024	3.28786	-2.637	0.044147	0.087167	RP11-658F	chr11	-	66529046	66529870	825
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC009951.	chr2	+	1.45E+08	1.45E+08	306
ENSG00000(	0	3.612863	2.638828	3.745378	0.920432	1.64393	-0.03514	0.97695	0.98658	RBM22P2	chr13	-	31113734	31117598	1814
ENSG00000(	0	0	0	39.701	43.2603	46.03004	-6.2477	2.19E-09	1.17E-08	HNRNPA1P	chr10	-	47133338	47133898	561
ENSG00000(	12.4295	9.634302	9.235896	2.247227	2.761296	1.64393	1.9809	0.022291	0.047787	PVRIG	chr7	+	99815864	99819113	1583
ENSG00000(	0	0	0	5.243529	0	0	-1.3189	0.32312	NA	KRTAP4-12	chr17	-	39279343	39280419	1077
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	KRTAP2-4	chr17	-	39221369	39222131	763
ENSG00000(	184.371	175.826	203.1897	99.62705	127.94	138.0901	0.62055	0.005151	0.012735	GPC2	chr7	-	99767229	99774995	2532
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RBMX2P2	chrX	-	1.4E+08	1.4E+08	946
ENSG00000(	12.4295	9.634302	2.638828	11.23613	4.60216	13.15144	-0.20045	0.79603	0.86688	HSPD1P1	chr5	+	21882694	21884421	1726
ENSG00000(	0	4.817151	3.958241	1.498151	0	3.28786	0.59758	0.62841	0.73907	RP11-54C4	chr5	-	1.51E+08	1.51E+08	520
ENSG00000(	0	0	1.319414	1.498151	0	0.821965	-0.38347	0.77483	NA	VTI1BP2	chr4	+	1.84E+08	1.84E+08	696
ENSG00000(	4.143168	1.204288	1.319414	1.498151	0	0	1.2798	0.33281	0.46082	RP11-47G1	chr10	+	1.26E+08	1.26E+08	760
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	OR5AC1	chr3	+	97783316	97784240	925
ENSG00000(	1.035792	0	3.958241	1.498151	6.443024	0	-0.46297	0.71337	0.80636	H2AFZP1	chr21	-	45466228	45466922	395
ENSG00000(	218.5521	231.2232	141.1773	183.5235	117.8153	240.0138	0.12579	0.63473	0.74395	RPL18AP3	chr12	+	1.05E+08	1.05E+08	563
ENSG00000(	11.39371	13.24716	14.51355	14.98151	7.363456	24.65895	-0.25664	0.68366	0.78355	RP11-75L1	chr12	+	9847980	9848823	844
ENSG00000(	641.1552	528.6823	513.252	451.6926	491.5107	493.179	0.23015	0.12519	0.21087	SIPA1	chr11	+	65405568	65418401	3628
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-88K1	chr3	-	77365903	77366749	847
ENSG00000(	3.107376	3.612863	5.277655	14.23244	1.840864	7.397684	-0.85969	0.34737	0.47699	FTH1P3	chr2	-	27615651	27616234	584
ENSG00000(	90.1139	74.66584	155.6908	54.68252	76.39586	60.00344	0.7337	0.021691	0.046646	ERV3-1	chr7	-	64451187	64467121	2719
ENSG00000(	259.9838	249.2876	232.2168	310.1173	264.164	271.2484	-0.1884	0.28419	0.40715	SYNJ2BP	chr14	-	70838148	70883778	2080
ENSG00000(	421.5673	410.6621	278.3963	374.5378	266.9253	314.8126	0.21551	0.27669	0.39827	ARL2	chr11	+	64781585	64789656	1228
ENSG00000(	62.14751	22.88147	43.54065	48.68991	77.31629	99.45776	-0.78462	0.046535	0.091192	RP11-453F	chrX	-	1.31E+08	1.31E+08	2928
ENSG00000(	0	0	0	5.243529	0.920432	8.219649	-2.9861	0.020508	0.044338	TTLL13	chr15	+	90792762	90808199	2738

ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	EIF4A1P8	chr10	+	93896632	93898127	1190
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTB-85P21	chr5	+	1.44E+08	1.44E+08	513
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	ACTN4P1	chr4	+	1.18E+08	1.18E+08	1451
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CCL14	chr17	-	34310327	34329100	3265
ENSG00000(	0	0	1.319414	1.498151	1.840864	0.821965	-0.90829	0.50213	NA	PPIAP16	chr3	+	57927545	57928031	487
ENSG00000(	7.250543	6.021439	1.319414	2.996302	18.40864	27.94681	-1.5546	0.057762	0.11013	RP13-39P1	chr10	-	79540095	79541634	1540
ENSG00000(	1.035792	0	0	8.239831	4.60216	1.64393	-2.446	0.04931	0.095918	RP11-428P	chr10	+	79490524	79494527	3711
ENSG00000(	205.0868	242.0618	304.7846	404.5008	399.4675	374.816	-0.64992	0.000352	0.00106	RBMXL1	chr1	-	89445139	89458643	5084
ENSG00000(	1.035792	0	0	1.498151	0	0.821965	-0.37092	0.78098	NA	AC132008.	chr3	-	1.97E+08	1.97E+08	286
ENSG00000(	0	0	0	3.745378	0.920432	0	-1.3029	0.33256	NA	RAC1P5	chr4	-	1.08E+08	1.08E+08	576
ENSG00000(	854.5283	805.6685	763.9406	912.374	761.1973	849.0898	-0.05731	0.66606	0.76962	SRA1	chr5	-	1.4E+08	1.4E+08	2165
ENSG00000(	0	0	1.319414	1.498151	0	0	-0.08979	0.94423	NA	RP11-432F	chr9	+	1.15E+08	1.15E+08	403
ENSG00000(	2.071584	1.204288	1.319414	0	3.681728	1.64393	-0.12396	0.92214	0.95285	TMEM110	chr3	-	52870235	52931612	4769
ENSG00000(	2.071584	1.204288	2.638828	0	1.840864	0	1.0349	0.43502	0.56479	KRT8P41	chr11	+	9115910	9117737	1828
ENSG00000(	0	2.408575	0	0	0.920432	0.821965	0.212	0.87508	NA	RP11-486G	chr1	+	84551424	84551916	493
ENSG00000(	1.035792	4.817151	2.638828	2.996302	4.60216	1.64393	-0.10244	0.92509	0.9546	RP11-467H	chr7	-	76744716	76745509	794
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC005077.	chr7	-	75742344	75742718	375
ENSG00000(	78.72018	116.8159	84.44248	164.7966	155.553	101.1017	-0.58551	0.032929	0.067383	DNAJC9	chr10	-	74943120	75008620	3032
ENSG00000(	120.1519	156.5574	130.622	132.5864	93.88406	204.6693	-0.08367	0.76389	0.84398	RPLP0P6	chr2	+	38708920	38710012	954
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP11-240E	chr9	+	1.11E+08	1.11E+08	380
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-115A	chr1	-	80916768	80917689	922
ENSG00000(	745.7702	646.7025	597.6944	397.7591	336.8781	399.475	0.80905	1.39E-07	6.27E-07	C8orf82	chr8	-	1.46E+08	1.46E+08	2476
ENSG00000(	2.071584	0	0	0	2.761296	0	-0.15346	0.90925	NA	RP13-383K	chrX	+	1.06E+08	1.06E+08	611
ENSG00000(	5862.582	5940.751	5748.686	6415.832	5556.648	5631.282	-0.00434	0.96718	0.98074	VDAC1	chr5	-	1.33E+08	1.33E+08	1953
ENSG00000(	214.4089	222.7932	209.7868	441.2055	423.3987	443.0391	-1.0116	3.67E-10	2.08E-09	ZBTB9	chr6	+	33422356	33425325	2716
ENSG00000(	2.071584	1.204288	6.597069	6.74168	0.920432	9.863579	-0.71213	0.4832	0.6125	RP11-229P	chr9	+	1.4E+08	1.4E+08	1322
ENSG00000(	0	2.408575	3.958241	0	0	0	1.9515	0.15023	0.24432	AP000662.	chr11	-	57485516	57486002	487
ENSG00000(	1089.653	1142.869	1005.393	1677.18	1398.136	1412.958	-0.47013	0.000231	0.000715	TMX2	chr11	+	57480072	57508445	1697
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-112J	chr14	+	59261372	59261747	376
ENSG00000(	13.46529	20.47289	6.597069	0.749076	8.283888	8.219649	1.1309	0.15691	0.25298	U73169.1	chr3	+	50277054	50277416	359
ENSG00000(	1.035792	0	0	0.749076	1.840864	0	-0.44174	0.74166	NA	KRT18P19	chr2	-	1.9E+08	1.9E+08	705
ENSG00000(	2.071584	2.408575	7.916483	4.494453	0	0	1.0374	0.38686	0.51775	SLC25A14P	chr4	+	84398677	84399577	901
ENSG00000(	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	RP11-170N	chr10	-	65662211	65663005	795
ENSG00000(	1.035792	0	1.319414	8.239831	23.93123	5.753754	-3.2349	0.001641	0.004438	FAM220CP	chr9	+	99883941	99884771	831
ENSG00000(	13.46529	4.817151	10.55531	1.498151	2.761296	3.28786	1.7077	0.054279	0.10439	RP11-380G	chr10	+	89705259	89705781	523
ENSG00000(	118.0803	143.3102	137.219	134.8336	91.12277	120.0069	0.19772	0.4206	0.55131	HEXA	chr15	-	72635775	72668817	6909
ENSG00000(	958.1075	973.0645	856.2995	1074.174	899.2621	1072.664	-0.12772	0.33447	0.46244	NDUFS3	chr11	+	47586888	47606114	1769
ENSG00000(	5.17896	6.021439	2.638828	5.243529	0.920432	5.753754	0.17787	0.85653	0.90907	RPSAP54	chr13	+	21535449	21536334	886
ENSG00000(	1229.485	1334.351	1267.957	1573.059	1436.794	1342.269	-0.18377	0.12572	0.21159	LEPROT	chr1	+	65886270	65901690	4622
ENSG00000(	332.4892	325.1577	426.1707	194.7596	382.8997	326.3201	0.26102	0.24494	0.36127	LBH	chr2	+	30454397	30546596	2933
ENSG00000(	71.46964	49.3758	50.13772	211.2393	201.5746	192.3398	-1.7993	5.68E-13	3.95E-12	ADAT3	chr19	+	1905377	1913444	1618
ENSG00000(	2710.667	2781.905	2914.585	3136.379	2629.674	2505.349	0.023028	0.84751	0.90293	PPP1CB	chr2	+	28974506	29025806	4893
ENSG00000(	0	1.204288	0	3.745378	3.681728	5.753754	-2.3059	0.063617	0.11949	RP11-797H	chr7	+	64323377	64324748	880
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-132J	chr14	+	56010119	56010887	769

ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	SULT1A4	chr16	+	29467127	29476300	2369
ENSG00000(	38.3243	50.58008	34.30476	259.1801	235.6306	240.0138	-2.5533	2.47E-24	2.98E-23	GPSM3	chr6	-	32158543	32163300	1476
ENSG00000(	306.5944	302.2762	252.008	507.1241	460.216	503.8645	-0.76876	1.44E-06	5.89E-06	NCKIPSD	chr3	-	48701364	48723797	2989
ENSG00000(	1507.077	1536.671	1402.537	1161.816	1050.213	1099.789	0.4241	0.000293	0.000892	ATF6B	chr6	-	32065953	32096030	2624
ENSG00000(	0	1.204288	1.319414	0.749076	0.920432	3.28786	-0.62081	0.63729	0.74586	AC002056.	chr22	-	51193096	51193862	762
ENSG00000(	97.36444	101.1602	94.99779	107.8669	91.12277	97.81383	-0.0172	0.9456	0.96726	TREX1	chr3	+	48506445	48509044	2197
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP11-513D	chr1	-	2.43E+08	2.43E+08	510
ENSG00000(	23.82321	13.24716	11.87472	23.22134	23.93123	12.32947	-0.2564	0.65121	0.7573	SEC14L1P1	chr11	+	43919006	43921186	2181
ENSG00000(	853.4925	738.2284	836.5083	795.5182	791.5715	705.2459	0.083161	0.53188	0.65642	S1PR3	chr9	+	91606362	91619925	8505
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RPS7P14	chrX	+	73629353	73629935	583
ENSG00000(	1074.116	904.4201	874.7713	1068.182	971.9762	1080.884	-0.12818	0.33249	0.4606	SLC35F6	chr2	+	26987152	27004099	3898
ENSG00000(	44.53905	54.19295	63.33186	4.494453	10.12475	7.397684	2.7976	9.62E-09	4.82E-08	RPL17P50	chr10	-	74765591	74766353	546
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	RP5-849H1	chr1	-	63106793	63107338	546
ENSG00000(	0	1.204288	0	5.992604	2.761296	3.28786	-2.1806	0.083119	0.15029	AL590762.	chrX	+	70572268	70572838	571
ENSG00000(	17.60846	38.53721	14.51355	66.66772	57.98722	77.2647	-1.48	0.000335	0.001011	HMGB1P1(	chr22	+	26956492	26957054	563
ENSG00000(	96.32865	90.32158	105.5531	65.91865	94.8045	89.59418	0.22301	0.41381	0.54422	PIGCP1	chr11	-	33097112	33098006	895
ENSG00000(	1.035792	1.204288	1.319414	0.749076	0	4.109825	-0.29373	0.82153	0.88465	FAM209B	chr20	+	55108302	55111576	694
ENSG00000(	6127.745	5831.161	5504.594	10248.1	7903.75	9381.086	-0.65553	4.14E-08	1.97E-07	CLIC1	chr6	-	31698358	31707540	1560
ENSG00000(	6.214751	0	2.638828	2.996302	0	4.109825	0.23636	0.84383	0.90048	HMGN2P3(	chr7	+	42152964	42153219	256
ENSG00000(	1468.753	1451.167	1403.856	1056.197	1051.133	1360.352	0.31762	0.017937	0.039352	DDAH2	chr6	-	31694815	31698394	1688
ENSG00000(	5.17896	0	0	1.498151	7.363456	1.64393	-0.69113	0.56927	0.68843	RAB5CP1	chr10	-	76183193	76183772	580
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	ANAPC10P:	chr1	+	52719293	52719848	556
ENSG00000(	1.035792	1.204288	6.597069	1.498151	1.840864	7.397684	-0.24481	0.82406	0.88639	SERBP1P1	chrX	+	68003315	68004909	1160
ENSG00000(	3308.319	4018.708	3206.175	2494.422	3422.166	3542.669	0.15493	0.28894	0.41256	RPS29	chr14	-	50043390	50065408	1374
ENSG00000(	30.03797	26.49433	32.98534	14.23244	13.80648	5.753754	1.3475	0.012062	0.027527	RP4-694B1	chr20	+	25604681	25658710	4666
ENSG00000(	0	0	0	0	2.761296	3.28786	-1.6293	0.2296	0.34285	RPS10P14	chr7	+	37415125	37415626	502
ENSG00000(	930.1411	853.84	787.69	787.2784	742.7886	730.7268	0.18627	0.15324	0.24846	RPL23AP7:	chr19	+	59084870	59111168	3282
ENSG00000(	0	1.204288	0	0.749076	0.920432	0.821965	-0.45539	0.73631	NA	RP11-284B	chrX	-	63524927	63526613	1436
ENSG00000(	0	0	1.319414	0	0	1.64393	-0.1317	0.91874	NA	RP11-342F	chr5	+	78806257	78806742	486
ENSG00000(	6.214751	6.021439	3.958241	2.996302	2.761296	4.109825	0.61735	0.51406	0.64092	CTC-451P1	chr5	-	78579955	78580741	787
ENSG00000(	47.64643	21.67718	21.11062	3.745378	10.12475	11.50751	1.7578	0.00323	0.008307	ATP6V1G2	chr6	-	31512239	31516204	1588
ENSG00000(	0	0	0	3.745378	1.840864	0	-1.5327	0.25777	NA	MT1P1	chr9	-	98175549	98175731	183
ENSG00000(	279.6638	292.6419	278.3963	224.7227	247.5962	208.7791	0.32032	0.068366	0.12716	ZNF134	chr19	+	58125601	58134724	3547
ENSG00000(	2.071584	0	2.638828	0.749076	0.920432	0	0.84278	0.53072	0.6555	ACTBP2	chr5	+	77080705	77081827	1123
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-385J:	chr2	-	9411421	9411757	337
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC010904.	chr2	-	7464879	7465193	315
ENSG00000(	0	0	0	4.494453	1.840864	4.109825	-2.5551	0.051964	0.10042	CTD-2224J!	chr19	+	54006646	54015941	887
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP11-452G	chr11	+	17215036	17215855	454
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	GTF2H4	chr6	+	30875961	30881883	1735
ENSG00000(	17.60846	8.430014	23.74945	19.47596	6.443024	18.90519	0.13226	0.83305	0.89318	DDX47	chr12	+	12966250	12982915	2689
ENSG00000(	1.035792	6.021439	3.958241	1.498151	0	0	1.8837	0.13485	0.22398	OLA1P1	chr22	-	42503769	42504957	1189
ENSG00000(	9.322127	2.408575	7.916483	7.490755	11.04518	9.863579	-0.47411	0.54454	0.66676	ZNF888	chr19	-	53418449	53426723	551
ENSG00000(	87.00652	93.93444	116.1084	162.5494	165.6778	138.9121	-0.65219	0.006123	0.01491	ZNF845	chr19	+	53837002	53858122	4311
ENSG00000(	3.107376	0	3.958241	0	2.761296	0	0.8516	0.51855	0.64488	AC017028.	chr2	-	2.4E+08	2.4E+08	264

ENSG0000(	1.035792	0	0	2.247227	0	1.64393	-0.82311	0.54382	NA	CFL1P5	chr5	-	68609198	68609699	502
ENSG0000(	114.9729	79.48299	118.7472	95.13259	114.1336	74.79881	0.1413	0.61176	0.72543	RP11-3J10.	chr9	+	37885680	37886387	708
ENSG0000(	8.286335	4.817151	2.638828	0.749076	0	4.109825	1.3371	0.2268	0.3398	SUGT1P2	chr3	+	32794402	32795393	992
ENSG0000(	21.75163	48.17151	43.54065	2.247227	3.681728	0.821965	3.8055	1.77E-08	8.73E-08	AC098614.	chr3	+	27674467	27675211	745
ENSG0000(	112.9013	119.2245	101.5949	1026.983	1018.918	1126.092	-3.2353	7.69E-92	5.05E-90	EMP2	chr16	-	10622279	10674555	5197
ENSG0000(	0	0	0	0	1.840864	2.465895	-1.2108	0.36631	NA	CNN2P6	chr3	-	31223243	31224142	900
ENSG0000(	0	0	0	1.498151	1.840864	0	-0.93652	0.47589	NA	VDAC1P2	chrX	-	49397103	49397952	850
ENSG0000(	321.0955	331.1791	221.6615	102.6234	141.7465	156.1733	1.1218	7.59E-07	3.19E-06	KCTD11	chr17	+	7255208	7258258	3051
ENSG0000(	8.286335	6.021439	1.319414	5.243529	1.840864	9.863579	-0.09007	0.92342	0.95368	RPL21P75	chr7	+	20042346	20042909	564
ENSG0000(	1.035792	2.408575	2.638828	1.498151	0.920432	0	0.85166	0.50963	0.63692	CTD-2270N	chr15	-	48022341	48023132	792
ENSG0000(	2.071584	0	0	3.745378	0	0	-0.39189	0.77243	NA	XX-C2158C	chr6	+	1.71E+08	1.71E+08	758
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	EEF1B2P2	chr5	-	67455046	67455721	676
ENSG0000(	87.00652	121.6331	102.9143	50.18806	46.0216	64.11326	0.94393	0.001326	0.00365	C8orf44	chr8	+	67579850	67597799	1835
ENSG0000(	30.03797	26.49433	17.15238	17.97781	17.48821	18.90519	0.42947	0.39279	0.52351	YBX1P10	chr9	-	35971341	35972315	975
ENSG0000(	0	3.612863	1.319414	0	0	0	1.6005	0.2346	NA	TAF9BP1	chr3	+	25796416	25797161	746
ENSG0000(	0	0	1.319414	0	4.60216	3.28786	-1.489	0.26401	0.38386	AC092798.	chr3	+	25790979	25791387	409
ENSG0000(	13.46529	12.04288	17.15238	29.96302	11.96562	22.19305	-0.57084	0.3174	0.44424	NPM1P6	chr8	+	62114909	62115779	871
ENSG0000(	5.17896	7.225726	0	0.749076	0	0.821965	2.0168	0.10572	0.18357	RPL13AP7	chr21	+	26734135	26734745	611
ENSG0000(	33.14534	45.76293	42.22124	35.20655	54.30549	53.42772	-0.23469	0.53226	0.65675	AC005003.	chr22	+	31742875	31744670	1796
ENSG0000(	8.286335	9.634302	5.277655	0.749076	8.283888	5.753754	0.58898	0.50688	0.6345	PPM1N	chr19	+	45992035	46005768	1953
ENSG0000(	3.107376	2.408575	7.916483	0	4.60216	0.821965	1.0268	0.36642	0.49642	RPL3P6	chr5	-	60686495	60687698	1204
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-546N	chr5	-	59725730	59726103	374
ENSG0000(	40.39588	51.78437	36.94359	14.98151	7.363456	21.37109	1.5043	0.001718	0.004628	SLC23A3	chr2	-	2.2E+08	2.2E+08	4222
ENSG0000(	70.43385	69.84869	51.45714	98.87797	67.19154	85.48435	-0.38563	0.20357	0.31172	LTB4R	chr14	+	24780656	24787242	4110
ENSG0000(	9.322127	1.204288	0	5.243529	7.363456	0	-0.17258	0.88058	0.92529	CTB-50E14.	chr19	+	42901280	43156507	2383
ENSG0000(	2.071584	15.65574	11.87472	4.494453	9.20432	13.9734	0.078809	0.92007	0.95145	LTB4R2	chr14	+	24774940	24781259	3092
ENSG0000(	1.035792	0	0	0	0.920432	0.821965	-0.16752	0.89839	NA	AC008279.	chr2	-	2.15E+08	2.15E+08	815
ENSG0000(	444.3547	426.3179	390.5465	271.1653	340.5598	309.0588	0.45482	0.005443	0.013378	DNASE1	chr16	+	3661729	3730144	4731
ENSG0000(	1.035792	9.634302	2.638828	2.247227	0.920432	0.821965	1.3212	0.24523	0.36164	AC011500.	chr19	+	39930212	39932082	468
ENSG0000(	3637.701	3568.305	2944.932	3250.239	3044.789	3381.564	0.069202	0.56008	0.6806	CSNK1E	chr22	-	38686697	38794527	2791
ENSG0000(	17.60846	28.90291	7.916483	6.74168	12.88605	18.08323	0.50671	0.42684	0.55705	IRF9	chr14	+	24630262	24635774	1838
ENSG0000(	73.54123	77.07441	63.33186	71.16218	51.54419	70.68898	0.14255	0.63977	0.74777	GALT	chr9	+	34638130	34651032	2566
ENSG0000(	0	0	1.319414	16.47966	10.12475	9.863579	-3.7311	0.000578	0.001683	HBE1	chr11	-	5289582	5526847	906
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AC092610.	chr7	-	4905063	4905435	373
ENSG0000(	0	0	0	25.46857	25.7721	28.76877	-5.5977	1.86E-07	8.31E-07	CLDN9	chr16	+	3062457	3064506	2050
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	SEPHS1P6	chr2	+	2.01E+08	2.01E+08	1179
ENSG0000(	0	0	2.638828	0.749076	0.920432	1.64393	-0.20682	0.87815	0.92389	RP11-314A	chr17	-	4608111	4608512	402
ENSG0000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	KRT18P17	chr3	-	12828892	12830170	1279
ENSG0000(	1377.603	1315.082	2027.939	849.4517	943.4428	737.3025	0.89578	8.93E-08	4.12E-07	ITGA1	chr5	+	52083730	52252327	8044
ENSG0000(	4.143168	0	2.638828	3.745378	0	0	0.52713	0.68764	0.7865	AC018867.	chr2	+	1.87E+08	1.87E+08	57
ENSG0000(	11.39371	16.86003	2.638828	20.22504	19.32907	23.01502	-0.94824	0.13231	0.22049	AC074286.	chr2	-	1.78E+08	1.78E+08	5202
ENSG0000(	2.071584	1.204288	6.597069	0	0	0	2.7266	0.040427	0.080799	CHCHD4P4	chr3	-	11275942	11276268	327
ENSG0000(	93.22127	75.87013	77.84541	137.0808	135.3035	139.734	-0.72947	0.002928	0.007577	NUDT19	chr19	+	33182867	33204702	2967
ENSG0000(	6.214751	4.817151	2.638828	128.841	137.1444	117.541	-4.6157	4.86E-22	5.35E-21	ZNF726	chr19	+	24097678	24127961	2473

ENSG00000(	0	0	0	0.749076	0.920432	2.465895	-1.2662	0.34855	NA	RP11-264F	chr12	-	4433538	4433977	440
ENSG00000(	48.68222	28.90291	10.55531	143.0734	109.5314	131.5144	-2.0598	3.76E-08	1.80E-07	RP11-15H2	chr19	-	23442708	23457053	2651
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP3-522P1	chr6	-	25272428	25273979	927
ENSG00000(	9.322127	7.225726	14.51355	64.4205	106.7701	61.64737	-2.8317	4.44E-10	2.50E-09	CTD-2561J	chr19	+	21565667	21569979	1764
ENSG00000(	17.60846	13.24716	9.235896	5.243529	6.443024	10.68554	0.79083	0.2562	0.37453	TAX1BP3	chr17	-	3566196	3571976	1377
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RPL7AP14	chr20	-	36073135	36073936	802
ENSG00000(	147.0825	125.2459	96.31721	292.1395	281.6522	301.6611	-1.2342	2.64E-09	1.39E-08	AP1G2	chr14	-	24028774	24037279	3298
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC078899.	chr19	+	20368529	20370227	1185
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-399E	chr1	-	41730222	41730534	313
ENSG00000(	11.39371	10.83859	10.55531	232.9625	229.1876	278.6461	-4.4208	3.47E-38	6.82E-37	ZNF90	chr19	+	20188803	20237885	2310
ENSG00000(	0	3.612863	1.319414	2.247227	0	0	0.60342	0.65453	0.75999	RP11-414H	chr10	-	6239575	6244656	438
ENSG00000(	416.3883	384.1678	423.5318	403.0026	499.7946	410.1605	-0.09959	0.52827	0.65296	CARKD	chr13	+	1.11E+08	1.11E+08	2659
ENSG00000(	5.17896	4.817151	0	5.243529	3.681728	4.93179	-0.37239	0.71663	0.8091	TM6SF2	chr19	-	19375173	19384200	1829
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	MEF2B	chr19	-	19256377	19281098	1683
ENSG00000(	1.035792	3.612863	7.916483	4.494453	9.20432	8.219649	-0.72047	0.42835	0.55849	AL353671.	chr9	+	32556904	32557921	267
ENSG00000(	135.6887	174.6217	124.0249	126.5938	88.36147	112.6092	0.40104	0.10713	0.18569	GANC	chr15	+	42565431	42645864	4512
ENSG00000(	0	4.817151	1.319414	0.749076	0	0	1.5049	0.26613	0.38615	RP6-105D1	chrX	+	44600333	44601210	878
ENSG00000(	4.143168	0	2.638828	0	0.920432	0	1.5854	0.23844	0.35335	RRM2P3	chrX	-	44168560	44169722	1163
ENSG00000(	467.1421	531.0909	431.4483	182.0254	174.8821	235.082	1.2663	1.69E-12	1.14E-11	TTLL3	chr3	+	9849770	9896822	5282
ENSG00000(	790.3092	626.2296	633.3186	3888.451	3613.616	3736.653	-2.4477	8.69E-85	5.03E-83	REPIN1	chr7	+	1.5E+08	1.5E+08	3292
ENSG00000(	1313.384	1178.998	868.1743	1500.398	1255.469	1329.939	-0.27998	0.070137	0.12992	MRPL23	chr11	+	1968508	2005752	919
ENSG00000(	105.6508	116.8159	85.7619	31.46117	49.70333	50.13986	1.2211	8.84E-05	0.00029	ZNF891	chr12	-	1.34E+08	1.34E+08	4118
ENSG00000(	1.035792	3.612863	1.319414	0.749076	1.840864	0.821965	0.56257	0.65381	0.75954	PGAM1P4	chr3	+	9390071	9390952	882
ENSG00000(	4.143168	3.612863	0	0	0	0	2.2704	0.093695	0.16623	RP5-944M2	chr12	+	1.27E+08	1.27E+08	2458
ENSG00000(	601.7951	658.7454	485.5443	644.205	510.8398	642.7766	-0.04178	0.79609	0.8669	SMIM7	chr19	-	16741562	16771253	2776
ENSG00000(	0	0	0	249.4422	173.9616	170.9687	-8.2154	3.66E-17	3.24E-16	UCA1	chr19	+	15939757	15947130	2313
ENSG00000(	26.93059	31.31148	17.15238	44.19546	47.86246	59.18147	-0.97448	0.016876	0.037268	FBXO16	chr8	-	28205804	28347835	2983
ENSG00000(	3.107376	1.204288	0	0.749076	0.920432	0	0.7699	0.56818	0.68732	RP11-1E1.1	chr4	-	78003556	78004279	724
ENSG00000(	2760.385	2476.016	2105.784	1172.303	1041.929	1330.761	1.0479	3.45E-14	2.59E-13	TSPAN4	chr11	+	842808	867116	2777
ENSG00000(	2.071584	4.817151	13.19414	4.494453	0	1.64393	1.3545	0.19823	0.30551	CPSF1P1	chr22	+	32665368	32669097	3730
ENSG00000(	0	0	0	1.498151	2.761296	0	-1.199	0.3707	NA	GNAQP1	chr2	-	1.32E+08	1.32E+08	1067
ENSG00000(	3218.205	3108.267	2675.771	1913.888	1533.44	1820.652	0.77123	1.36E-09	7.38E-09	CPNE1	chr20	-	34213953	34252878	2204
ENSG00000(	679.4795	593.7138	559.4314	780.5367	564.2248	670.7234	-0.13664	0.3856	0.51644	ARL16	chr17	-	79648204	79650954	2343
ENSG00000(	5.17896	0	0	2.247227	0	0	0.62904	0.64254	0.75004	RP11-247I1	chr22	+	31955469	31955925	457
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	SMCO1	chr3	-	1.96E+08	1.96E+08	1846
ENSG00000(	1.035792	3.612863	0	2.247227	0	0	0.55949	0.67862	0.77969	WEE2	chr7	+	1.41E+08	1.41E+08	3061
ENSG00000(	42.46747	37.33292	26.38828	17.22874	21.16994	22.19305	0.79415	0.078375	0.14284	AC093726.	chr7	+	1.55E+08	1.55E+08	2121
ENSG00000(	3.107376	3.612863	1.319414	2.247227	1.840864	8.219649	-0.49064	0.64459	0.75173	AC008686.	chr19	-	13890884	13900972	384
ENSG00000(	67.32647	104.773	114.789	62.92235	65.35067	53.42772	0.64569	0.032902	0.067341	LDHAP4	chr9	-	14921335	14922332	998
ENSG00000(	668.0858	597.3267	529.0849	720.6107	511.7602	652.6401	-0.07055	0.6651	0.76874	LYRM4	chr6	-	5108653	5261172	1489
ENSG00000(	114.9729	169.8046	122.7055	528.0983	369.0932	435.6414	-1.7023	2.95E-16	2.50E-15	MYCBP	chr1	-	39328636	39347289	3231
ENSG00000(	1.035792	3.612863	1.319414	3.745378	0.920432	8.219649	-0.88269	0.42619	0.55653	PP12708	chr7	+	1.39E+08	1.39E+08	1921
ENSG00000(	2.071584	1.204288	3.958241	0.749076	3.681728	2.465895	0.054875	0.96213	0.97812	TDPX2	chr9	-	12972842	12973437	596
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	TMEM213	chr7	+	1.38E+08	1.39E+08	4167

ENSG00000(	269.3059	248.0833	283.674	299.6302	298.22	271.2484	-0.11756	0.49104	0.62012	AC024560.	chr3	-	1.97E+08	1.97E+08	1552
ENSG00000(	52.82539	59.0101	42.22124	3.745378	12.88605	3.28786	2.8634	7.80E-08	3.62E-07	PRCD	chr17	+	74523668	74549660	3372
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	AC073842.	chr7	-	99737252	99738305	735
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-513G	chr3	-	1.94E+08	1.94E+08	2880
ENSG00000(	950.857	873.1086	711.164	1215.001	902.0234	894.2978	-0.24695	0.12303	0.20813	ALG3	chr3	-	1.84E+08	1.84E+08	1697
ENSG00000(	197.8363	186.6646	189.9956	86.14369	63.50981	80.55256	1.3063	1.66E-08	8.18E-08	AMZ2P1	chr17	-	62962668	62971694	3425
ENSG00000(	317.9881	287.8248	303.4652	126.5938	211.6994	212.8889	0.72086	0.00083	0.002357	PLEKHM1P	chr17	-	62775377	62833272	5014
ENSG00000(	7.250543	7.225726	14.51355	25.46857	11.04518	28.76877	-1.1222	0.073196	0.13476	PTMAP5	chr13	+	82264203	82264535	333
ENSG00000(	12.4295	16.86003	15.83297	5.992604	12.88605	2.465895	1.0092	0.15673	0.25275	AC012487.	chr2	-	1.09E+08	1.09E+08	574
ENSG00000(	8.286335	16.86003	6.597069	2.996302	1.840864	0.821965	2.1533	0.017576	0.038665	XPOTP1	chr20	-	32801301	32803698	2398
ENSG00000(	4.143168	3.612863	0	3.745378	10.12475	9.041614	-1.2901	0.18547	0.28988	ST7-OT4	chr7	+	1.17E+08	1.17E+08	1576
ENSG00000(	1.035792	0	1.319414	6.74168	7.363456	12.32947	-2.7696	0.009222	0.021617	ZNF788	chr19	+	12203078	12248050	3774
ENSG00000(	0	0	1.319414	0	0	4.93179	-0.89929	0.50711	0.63465	RP11-12D2	chr9	-	5418373	5418976	604
ENSG00000(	1.035792	1.204288	1.319414	2.996302	0	1.64393	-0.26148	0.84044	0.89784	UBE2V1P2	chr3	-	1.75E+08	1.75E+08	440
ENSG00000(	331.4534	472.0808	237.4945	164.7966	183.166	235.082	0.83126	0.000428	0.001272	SH3D21	chr1	+	36771988	36790484	3179
ENSG00000(	626.6541	625.0253	548.8761	856.9424	747.3908	800.5938	-0.41605	0.002221	0.005871	AC073346.	chr7	-	1.13E+08	1.13E+08	1070
ENSG00000(	18.64425	38.53721	13.19414	9.737982	11.04518	12.32947	1.0362	0.077981	0.1422	RP11-642P	chr12	-	1.04E+08	1.04E+08	3963
ENSG00000(	19.68005	18.06432	11.87472	5.243529	9.20432	1.64393	1.5151	0.036203	0.073312	EEF1A1P12	chr2	-	1.07E+08	1.07E+08	1346
ENSG00000(	2.071584	1.204288	0	3.745378	2.761296	4.109825	-1.2183	0.3048	0.43015	RP11-135F	chr12	-	1E+08	1E+08	787
ENSG00000(	1.035792	1.204288	6.597069	0	3.681728	0	0.86219	0.49714	0.62558	CTAGE14P	chr2	-	1.69E+08	1.69E+08	2403
ENSG00000(	3.107376	0	1.319414	1.498151	1.840864	5.753754	-0.73688	0.54027	0.66364	C19orf38	chr19	+	10947251	10980466	1223
ENSG00000(	6.214751	0	5.277655	0	0	0	2.854	0.032276	0.066256	IQCJ	chr3	+	1.59E+08	1.59E+08	1460
ENSG00000(	0	3.612863	1.319414	1.498151	0	0	0.87932	0.51595	0.64256	TUBBP2	chr13	-	41958909	41959319	411
ENSG00000(	68.36227	60.21439	56.73479	47.19176	58.90765	76.44274	0.02539	0.93784	0.96232	HNRNPA1P	chr19	-	11776884	11777845	962
ENSG00000(	70.43385	52.98866	48.81831	77.90386	63.50981	67.40112	-0.26981	0.3922	0.52309	C17orf67	chr17	-	54869274	54916134	2013
ENSG00000(	2.071584	2.408575	17.15238	0	3.681728	3.28786	1.3283	0.20855	0.31805	AL591025.	chr6	+	1.59E+08	1.59E+08	66
ENSG00000(	0	0	2.638828	0.749076	5.522592	0	-0.73982	0.57992	0.69813	AC004980.	chr7	-	76279718	76280214	497
ENSG00000(	2.071584	3.612863	7.916483	0	0	0.821965	2.6404	0.034677	0.070562	AC010336.	chr19	-	7963689	7968427	4739
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	CTAGE11P	chr13	-	75812080	75814432	2353
ENSG00000(	1609.621	1534.263	1352.399	1014.997	966.4536	1364.462	0.42534	0.004336	0.010872	FIS1	chr7	-	1.01E+08	1.01E+08	1005
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC136896.	chr15	-	27453236	27453782	547
ENSG00000(	156.4046	126.4502	244.0915	72.66033	201.5746	129.8705	0.37915	0.23525	0.34956	ANKRD36B	chr1	-	1.68E+08	1.68E+08	1779
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-356J!	chr11	+	1.12E+08	1.12E+08	1166
ENSG00000(	154.333	114.4073	204.5091	107.8669	212.6198	196.4496	-0.12546	0.652	0.75788	SNURF	chr15	+	25200133	25245423	3210
ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	AGGF1P1	chr4	+	1.91E+08	1.91E+08	2073
ENSG00000(	11.39371	8.430014	13.19414	8.988907	8.283888	13.15144	0.10739	0.87395	0.92079	ANG	chr14	+	21152336	21167130	1222
ENSG00000(	6.214751	7.225726	10.55531	0	0	0	4.191	0.000526	0.00154	CTD-2228K	chr5	-	403846	404661	816
ENSG00000(	80.79177	91.52587	65.97069	1.498151	12.88605	7.397684	3.3753	2.83E-12	1.88E-11	RP11-108K	chr10	+	1.35E+08	1.35E+08	4904
ENSG00000(	1.035792	2.408575	10.55531	0	1.840864	0.821965	1.7665	0.13735	0.22723	KRT8P14	chrX	-	45491537	45492978	1442
ENSG00000(	2.071584	0	2.638828	2.996302	0	0.821965	0.17411	0.89452	0.93475	RP11-85F1	chr3	-	1.37E+08	1.37E+08	1001
ENSG00000(	2.071584	0	2.638828	0	4.60216	2.465895	-0.38937	0.75797	0.83987	PDCL3P3	chr3	-	17918947	17919661	715
ENSG00000(	1.035792	0	0	0.749076	0.920432	0	-0.14603	0.91115	NA	RPL39P5	chr3	-	1.34E+08	1.34E+08	449
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	C11orf93	chr11	+	1.11E+08	1.11E+08	1414
ENSG00000(	67.32647	91.52587	93.67838	102.6234	129.7809	125.7606	-0.50267	0.056839	0.10859	RSBN1L-AS:	chr7	-	77286977	77325582	2029

ENSG00000(	63.18331	92.73015	62.01245	75.65663	105.8497	69.04505	-0.19639	0.52308	0.64835	SPDYE3	chr7	+	99905325	99919819	3185
ENSG00000(	32.10955	34.92434	21.11062	23.22134	18.40864	32.05663	0.2527	0.58786	0.7051	MBLAC1	chr7	+	99724317	99726118	1499
ENSG00000(	3.107376	0	0	0	0	0.821965	0.7418	0.57612	NA	AC025287.	chr16	-	75728367	75734089	456
ENSG00000(	80.79177	55.39724	44.86007	39.701	33.13555	36.16646	0.72347	0.047542	0.092892	RP11-252A	chr16	-	74366300	74402138	2355
ENSG00000(	1.035792	0	0	43.44638	108.611	60.00344	-6.1836	1.16E-11	7.38E-11	FOXI3	chr2	-	88747726	88752131	1340
ENSG00000(	6.214751	7.225726	5.277655	8.239831	8.283888	9.041614	-0.40719	0.60042	0.71585	SOGA3	chr6	-	1.28E+08	1.28E+08	11818
ENSG00000(	13.46529	0	0	0.749076	0	2.465895	1.4071	0.26524	0.38513	CTB-180A7	chr19	+	6393820	6412415	644
ENSG00000(	25.8948	18.06432	23.74945	5.243529	11.04518	7.397684	1.4495	0.015984	0.035472	RP11-394B	chr16	+	70789001	70807154	4853
ENSG00000(	3.107376	1.204288	0	0	0	0	1.4526	0.27741	NA	AC133644.	chr2	-	87865347	87866283	937
ENSG00000(	43.50326	37.33292	42.22124	8.239831	15.64734	15.61733	1.5971	0.000717	0.002058	NEURL1B	chr5	+	1.72E+08	1.72E+08	6424
ENSG00000(	3.107376	3.612863	6.597069	2.996302	0.920432	0	1.3306	0.24367	0.35965	RPL18P10	chr13	+	50673467	50674004	538
ENSG00000(	2.071584	1.204288	0	0	3.681728	0	-0.06447	0.96194	0.97801	EFCAB9	chr5	+	1.72E+08	1.72E+08	702
ENSG00000(	165.7267	187.8689	213.745	341.5785	284.4135	313.9906	-0.72928	9.77E-05	0.000319	HAUS3	chr4	-	2229191	2243891	5620
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	AC009967.	chr2	+	1.71E+08	1.71E+08	793
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RPLP2P1	chr6	+	27932953	27933292	340
ENSG00000(	0	3.612863	2.638828	1.498151	11.04518	10.68554	-1.5721	0.12877	0.21559	VSTM5	chr11	-	93551398	93583697	2969
ENSG00000(	94.25706	93.93444	75.20659	80.90016	53.38506	98.63579	0.17435	0.56366	0.68319	RPS3AP26	chr7	-	98015113	98015896	784
ENSG00000(	4.143168	0	2.638828	8.988907	3.681728	2.465895	-0.92215	0.39158	0.52228	RP11-121L	chr11	+	90015728	90017340	1613
ENSG00000(	9.322127	19.2686	6.597069	17.22874	10.12475	15.61733	-0.27353	0.67391	0.77598	KANSL1-AS	chr17	+	44270942	44274089	666
ENSG00000(	8.286335	15.65574	3.958241	0	0	0	4.3942	0.000247	0.000761	LCNL1	chr9	+	1.4E+08	1.4E+08	3706
ENSG00000(	327.3102	321.5448	298.1875	187.2689	190.5294	184.1201	0.75103	1.59E-05	5.75E-05	BBIP1	chr10	-	1.13E+08	1.13E+08	4712
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	KRT18P13	chr9	+	1E+08	1E+08	1290
ENSG00000(	29.00217	21.67718	14.51355	44.19546	45.10117	50.13986	-1.0561	0.013132	0.029709	LRRC37A4P	chr17	-	43578685	43627701	4939
ENSG00000(	0	0	0	2.996302	0.920432	0	-1.1048	0.40628	NA	AC064872.	chr2	-	78639919	78640220	302
ENSG00000(	4.143168	7.225726	2.638828	0.749076	3.681728	3.28786	0.72219	0.48509	0.61423	AC068831.	chr15	+	91565849	91579841	2159
ENSG00000(	4.143168	8.430014	5.277655	0	4.60216	13.15144	0.007813	0.99363	0.996	AC091167.	chr15	+	90835194	90838915	779
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	AS3MT	chr10	+	1.05E+08	1.05E+08	2404
ENSG00000(	8.286335	3.612863	9.235896	5.243529	8.283888	9.863579	-0.1296	0.87038	0.91851	FAM185BP	chr7	-	76713203	76751433	716
ENSG00000(	266.1985	215.5675	236.1751	124.3465	182.2455	171.7907	0.58608	0.005844	0.014277	RCN1P2	chr13	-	45964486	45965402	915
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	PLIN5	chr19	-	4522543	4535236	2470
ENSG00000(	0	0	0	2.247227	5.522592	1.64393	-2.3809	0.072827	0.13414	RP11-76H1	chr6	+	87680184	87680911	728
ENSG00000(	6.214751	1.204288	2.638828	0	1.840864	0	1.6728	0.18738	0.29205	SMARCE1P	chr2	+	26372073	26373600	1216
ENSG00000(	0	0	3.958241	0	0	1.64393	0.57053	0.67342	NA	AL139333.	chr6	+	83782692	83782854	54
ENSG00000(	163.6551	163.7831	196.5927	143.0734	86.52061	193.9837	0.30023	0.26278	0.38241	CTB-13H5.1	chr5	+	1.49E+08	1.49E+08	760
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	SEC14L6	chr22	-	30920465	30942669	1713
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	SPINK13	chr5	+	1.48E+08	1.48E+08	1022
ENSG00000(	1.035792	0	0	1.498151	0.920432	0.821965	-0.68763	0.61221	NA	HIGD1C	chr12	+	51347705	51364289	371
ENSG00000(	2.071584	0	0	0	0	2.465895	-0.09123	0.94581	NA	NOTO	chr2	+	73429386	73439641	2749
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	KRT42P	chr17	-	39782579	39796451	2895
ENSG00000(	1458.395	1360.845	1442.119	2919.896	1966.043	1989.155	-0.68824	6.60E-06	2.50E-05	PPME1	chr11	+	73882144	73965748	4055
ENSG00000(	1.035792	3.612863	0	0	1.840864	0	0.72975	0.58976	0.70665	AC130709.	chr2	-	68755373	68756584	1212
ENSG00000(	252.7332	210.7504	182.0791	675.6661	578.9517	570.4437	-1.4893	4.55E-18	4.21E-17	STARD10	chr11	-	72465774	72505213	1963
ENSG00000(	1.035792	3.612863	3.958241	0	2.761296	0	1.116	0.38079	0.51146	ZNF705E	chr11	-	71518637	71532594	3442
ENSG00000(	4.143168	3.612863	0	0	0	1.64393	1.3494	0.30751	0.43325	RPS15AP1	chr20	-	21146846	21147236	391

ENSG00000(	2.071584	0	1.319414	2.996302	0.920432	0	-0.12336	0.92626	0.95558	GTF2IRD2P	chr7	-	72656902	72694143	3010
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC087491.	chr17	+	37775866	37778766	616
ENSG00000(	13.46529	2.408575	5.277655	0.749076	0.920432	3.28786	1.7337	0.092137	0.1639	MEG3	chr14	+	1.01E+08	1.01E+08	4867
ENSG00000(	0	0	0	4.494453	7.363456	3.28786	-3.1175	0.013969	0.031454	LRRC37A11	chr17	+	37183530	37209458	3717
ENSG00000(	7.250543	0	6.597069	2.247227	0.920432	0.821965	1.3575	0.23903	0.35399	RP11-74E2	chr6	+	66011354	66014960	3237
ENSG00000(	0	0	0	0	1.840864	6.575719	-2.0608	0.12767	0.2142	RP11-323J	chr4	-	99172839	99182781	397
ENSG00000(	22.78742	22.88147	18.47179	47.94084	48.7829	49.3179	-1.1555	0.004596	0.011471	NUTM2D	chr10	+	89117425	89130452	5543
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	GAPDHP15	chr6	-	58293965	58294939	975
ENSG00000(	10.35792	28.90291	19.79121	0	0	0	5.5294	6.55E-07	2.77E-06	CPEB1	chr15	-	83211951	83317612	4882
ENSG00000(	5.17896	2.408575	0	0.749076	0.920432	2.465895	0.63781	0.60553	0.72022	HMGN2P15	chr17	-	40904898	40905817	270
ENSG00000(	0	2.408575	0	0	2.761296	0	-0.08034	0.95255	NA	RP11-65N1	chr9	-	1.28E+08	1.28E+08	246
ENSG00000(	31.07376	10.83859	32.98534	5.992604	14.72691	7.397684	1.3482	0.028994	0.060335	EML6	chr2	+	54950636	55199157	8320
ENSG00000(	0	0	0	6.74168	0.920432	3.28786	-2.5891	0.049331	0.095941	TMEM249	chr8	-	1.46E+08	1.46E+08	1763
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	NPM1P36	chr6	-	55804588	55805422	835
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	SLC6A10P	chr16	-	32888790	32896822	3846
ENSG00000(	3.107376	0	0	0.749076	2.761296	0	-0.06371	0.96243	0.97823	POLR3DP1	chr10	+	76414714	76415889	1176
ENSG00000(	0	0	3.958241	0	1.840864	1.64393	0.09058	0.94635	0.96756	RP11-506B	chr10	+	76131293	76132174	882
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	DEFB133	chr6	-	49913814	49917157	186
ENSG00000(	2.071584	0	0	0	0	2.465895	-0.09123	0.94581	NA	RP11-114H	chr15	-	78232253	78236924	602
ENSG00000(	9.322127	16.86003	13.19414	0.749076	0.920432	10.68554	1.4751	0.087957	0.15774	RP11-83B2	chr12	+	1.25E+08	1.25E+08	1282
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	RP11-477J	chr9	-	1.24E+08	1.24E+08	1463
ENSG00000(	1.035792	0	0	0.749076	2.761296	7.397684	-2.0405	0.11376	0.19496	HNRNPA3P	chrX	+	1.39E+08	1.39E+08	1137
ENSG00000(	29.00217	27.69862	30.34652	82.39831	75.47542	101.9236	-1.5539	4.75E-06	1.83E-05	RP11-27I1.	chr9	+	1.24E+08	1.24E+08	1017
ENSG00000(	1249.165	1178.998	1329.969	453.1907	571.5883	716.7534	1.1062	6.82E-12	4.39E-11	ZSWIM8	chr10	+	75545340	75561551	6075
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	KRT8P26	chr11	+	65494410	65495685	1276
ENSG00000(	0	0	0	4.494453	0	0	-1.1446	0.38559	NA	RPL6P12	chr4	+	1.7E+08	1.7E+08	846
ENSG00000(	3.107376	2.408575	1.319414	0	4.60216	2.465895	-0.013	0.99132	0.99488	RPL9P16	chr4	+	1.7E+08	1.7E+08	567
ENSG00000(	2.071584	2.408575	3.958241	0	0	0	2.5267	0.059095	0.11225	C10orf105	chr10	-	73471458	73497581	4837
ENSG00000(	24.85901	13.24716	14.51355	8.988907	7.363456	4.93179	1.2285	0.061501	0.116	ARHGEF33	chr2	+	39117021	39202590	4484
ENSG00000(	0	3.612863	0	2.247227	0	4.93179	-0.6325	0.62862	0.73909	C12orf71	chr12	-	27233991	27235447	957
ENSG00000(	833.8125	933.323	811.4395	1600.025	1381.568	1440.905	-0.77691	7.35E-10	4.07E-09	IFRD2	chr3	-	50325163	50330349	2275
ENSG00000(	2.071584	2.408575	3.958241	0.749076	1.840864	3.28786	0.39765	0.72836	0.81801	AC090616.	chr17	-	30468245	30470154	1599
ENSG00000(	3.107376	0	1.319414	5.243529	0	1.64393	-0.42447	0.73909	0.82527	CAPN14	chr2	-	31395924	31456724	3820
ENSG00000(	374.9567	384.1678	386.5882	374.5378	497.0333	483.3154	-0.24006	0.14214	0.23366	ZBED1	chrX	-	2404455	2419008	4510
ENSG00000(	193.6931	195.0946	170.2044	325.8479	247.5962	274.5363	-0.59825	0.001874	0.00502	AC005562.	chr17	+	28903482	28999807	4740
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTD-2574D	chr16	+	29874914	29879371	756
ENSG00000(	1.035792	4.817151	0	2.247227	10.12475	10.68554	-1.6122	0.1194	0.20291	RP11-429J	chr8	+	1.45E+08	1.45E+08	699
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-54I5.	chrX	+	55987641	55988915	1275
ENSG00000(	1229.485	1123.6	1232.332	1045.709	1160.665	1292.951	0.035281	0.78293	0.85707	HNRNPUL2	chr11	-	62480102	62494821	5106
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AC004870.	chr7	+	47092391	47093272	882
ENSG00000(	176.0846	118.0202	143.8161	168.542	150.0304	201.3814	-0.24374	0.29164	0.4157	METTL12	chr11	+	62432781	62435968	2870
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RPL21P1	chr12	+	1.23E+08	1.23E+08	507
ENSG00000(	0	0	0	2.247227	0	2.465895	-1.3312	0.32317	NA	HNRNPA1P	chr9	+	1.28E+08	1.28E+08	960
ENSG00000(	189.5499	180.6432	228.2586	205.2467	156.4734	158.6392	0.19672	0.35197	0.48177	SEPT7P2	chr7	-	45763379	45808617	3006

ENSG00000(	1.035792	7.225726	9.235896	8.988907	14.72691	8.219649	-0.80159	0.32296	0.45029	RP11-544I2	chr14	-	64796149	64805317	1751
ENSG00000(	4.143168	0	2.638828	0	1.840864	4.93179	0.013362	0.99139	0.9949	RP11-174G	chr12	+	14818589	14910897	657
ENSG00000(	2.071584	0	2.638828	1.498151	3.681728	3.28786	-0.61863	0.60469	0.71962	RP11-717D	chr3	-	47643205	47646167	1428
ENSG00000(	4.143168	3.612863	3.958241	31.46117	16.56778	22.19305	-2.4022	0.000507	0.001488	RP11-726G	chr12	+	9620148	9728864	7863
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	MS4A18	chr11	+	60496789	60511685	969
ENSG00000(	128.4382	127.6545	120.0667	120.6012	138.0648	187.408	-0.24266	0.31497	0.44164	POLR2J4	chr7	-	43980494	44058774	6466
ENSG00000(	1.035792	1.204288	2.638828	2.247227	3.681728	1.64393	-0.4805	0.68479	0.78423	AC010468.	chr5	-	1.11E+08	1.11E+08	817
ENSG00000(	0	0	0	2.996302	0	1.64393	-1.3112	0.33001	NA	MS4A4E	chr11	-	59968726	60010561	1125
ENSG00000(	29.00217	26.49433	25.06886	400.0063	309.2652	401.1189	-3.7455	1.60E-47	4.10E-46	RP11-480I1	chr1	-	2.03E+08	2.03E+08	1835
ENSG00000(	4.143168	3.612863	5.277655	0	0	0	3.2229	0.012581	0.028587	RP11-37N2	chr8	-	1.25E+08	1.25E+08	1195
ENSG00000(	0	1.204288	0	0	0	1.64393	-0.12916	0.91993	NA	CYCSP55	chr6	+	34187216	34187843	311
ENSG00000(	81.82756	95.13873	93.67838	0	0.920432	1.64393	6.1752	6.83E-18	6.26E-17	FER1L6	chr8	+	1.25E+08	1.25E+08	6051
ENSG00000(	20.71584	13.24716	5.277655	7.490755	2.761296	10.68554	0.83407	0.26842	0.38872	MPRIPP1	chr3	-	44621430	44622518	1089
ENSG00000(	0	0	0	10.48706	11.04518	31.23467	-4.955	1.07E-05	3.96E-05	KRT16P3	chr17	-	20404826	20415670	1939
ENSG00000(	55.93276	86.70872	88.40072	252.4385	267.8457	377.2819	-1.9493	2.63E-15	2.12E-14	DDX12P	chr12	-	9570309	9600825	3929
ENSG00000(	1.035792	6.021439	21.11062	21.72319	23.93123	8.219649	-0.88108	0.24356	0.35955	MTCP1	chrX	-	1.54E+08	1.54E+08	2274
ENSG00000(	4.143168	8.430014	14.51355	6.74168	3.681728	9.041614	0.41162	0.60647	0.72101	UPF3AP2	chr17	-	20278682	20280153	1132
ENSG00000(	5.17896	8.430014	22.43003	7.490755	6.443024	6.575719	0.72768	0.33389	0.46199	RP11-261C	chr1	-	2.43E+08	2.43E+08	774
ENSG00000(	3.107376	3.612863	13.19414	0	0	0	3.8341	0.002127	0.005642	RAD51AP2	chr2	-	17691851	17699706	3724
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	ZFYVE9P2	chr2	+	17465559	17466162	604
ENSG00000(	0	0	0	0	3.681728	4.109825	-1.9686	0.14605	0.23869	RP11-115L	chr4	-	15732585	15733250	666
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	LINC00612	chr12	-	9208182	9217666	2213
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	APOC1P1	chr19	+	45430061	45434643	731
ENSG00000(	0	0	0	12.73428	19.32907	13.15144	-4.7772	2.21E-05	7.84E-05	KRT16P1	chr17	+	18335365	18346209	1958
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	SHFM1P1	chr5	+	81188309	81188540	209
ENSG00000(	2.071584	7.225726	0	7.490755	14.72691	14.79537	-1.742	0.047364	0.092616	SRSF9P1	chr21	-	37667471	37668000	530
ENSG00000(	0	0	0	2.996302	0	2.465895	-1.5141	0.2635	NA	AC004540.	chr7	+	26438213	26538594	3202
ENSG00000(	2.071584	0	1.319414	0.749076	0.920432	0	0.5396	0.69058	NA	AC005082.	chr7	+	23210760	23234503	258
ENSG00000(	2.071584	0	0	2.247227	0	3.28786	-0.77521	0.56359	0.68317	SMTNL1	chr11	+	57308979	57318108	2062
ENSG00000(	0	0	1.319414	0	0	2.465895	-0.38078	0.77353	NA	MED28P1	chr10	+	70750893	70751463	571
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	TMEM14D	chr10	-	70304246	70304590	345
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	FAM177A1	chr4	+	99877133	99877918	473
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	USP8P1	chr6	+	31243349	31246531	3183
ENSG00000(	15.53688	10.83859	11.87472	2.996302	8.283888	3.28786	1.2925	0.088617	0.1587	LINC00243	chr6	-	30766431	30798436	2052
ENSG00000(	3.107376	2.408575	3.958241	8.988907	14.72691	7.397684	-1.5229	0.074205	0.13635	C14orf182	chr14	-	50448430	50474238	4279
ENSG00000(	0	0	0	0	0	7.397684	-1.7322	0.20085	0.30837	DUTP8	chr4	+	98969706	98970194	489
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	XX-FW802(	chrX	+	1.51E+08	1.51E+08	482
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	AC104472.	chr3	-	1.55E+08	1.55E+08	1583
ENSG00000(	6.214751	6.021439	6.597069	0	0	0.821965	3.1592	0.007822	0.018637	HLA-F-AS1	chr6	-	29694378	29716826	2835
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-1212	chr16	-	18411799	18441131	4540
ENSG00000(	186.4425	162.5788	122.7055	358.0581	276.1296	298.3733	-0.97356	2.95E-06	1.16E-05	ZSWIM7	chr17	-	15879874	15903031	2008
ENSG00000(	48.68222	51.78437	59.37362	0	1.840864	9.863579	3.5683	6.78E-09	3.46E-08	ARHGEF28	chr5	+	72921983	73237818	8285
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	TBC1D26	chr17	+	15635561	15649476	3772
ENSG00000(	7.250543	14.45145	14.51355	28.46487	35.89685	24.65895	-1.2564	0.018918	0.041276	LRRC69	chr8	+	92114060	92231464	1861

ENSG00000(	3.107376	2.408575	3.958241	0.749076	1.840864	2.465895	0.70353	0.53621	0.66031	AP000318.	chr21	+	35445892	35732332	805
ENSG00000(	22.78742	28.90291	29.0271	27.7158	49.70333	44.38611	-0.57848	0.17544	0.27718	ISPD	chr7	-	16130817	16460947	1859
ENSG00000(	0	2.408575	2.638828	0	0	0	1.6365	0.22501	NA	CTC-297N7	chr17	+	10286449	10527201	2272
ENSG00000(	0	0	0	0.749076	2.761296	0	-0.97685	0.45852	NA	CHCHD3P3	chr1	-	27527325	27527964	640
ENSG00000(	19.68005	18.06432	13.19414	28.46487	12.88605	23.01502	-0.32384	0.55254	0.67343	PPIAP29	chr6	+	24976647	24977210	499
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-274J	chr4	+	85165156	85166641	1486
ENSG00000(	68.36227	42.15007	87.08131	56.18067	84.67974	65.75719	-0.06281	0.85245	0.90594	PARGP1	chr10	+	51623417	51732824	2455
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AL591516.	chr6	-	1.08E+08	1.08E+08	201
ENSG00000(	1.035792	0	0	1.498151	2.761296	0	-0.89883	0.50763	NA	RPL7AP26	chr4	-	83411976	83412788	813
ENSG00000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	AKAP16BP	chrX	-	1.18E+08	1.18E+08	2719
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC006465.	chr7	-	7948931	7950080	1150
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC129492.	chr17	+	7982800	7984883	1804
ENSG00000(	2.071584	1.204288	1.319414	2.996302	0	0	0.35656	0.78848	0.86154	ACSM4	chr12	+	7456880	7481320	2142
ENSG00000(	477.5001	488.9408	471.0307	1300.395	1296.889	1268.292	-1.4241	8.48E-31	1.32E-29	C22orf29	chr22	-	19833661	19842419	6785
ENSG00000(	12.4295	10.83859	2.638828	6.74168	16.56778	11.50751	-0.37018	0.6168	0.72942	AL645728.	chr1	+	1510355	1511373	1019
ENSG00000(	10.35792	10.83859	19.79121	0	1.840864	1.64393	3.0906	0.000785	0.00224	COL28A1	chr7	-	7395834	7575484	4277
ENSG00000(	4629.99	4570.272	3892.271	5620.314	4483.424	5029.603	-0.2085	0.089109	0.15946	PHB2	chr12	-	7074490	7079988	1518
ENSG00000(	2.071584	2.408575	0	0	2.761296	0	0.41595	0.75748	0.83961	AC114730.	chr2	-	2.43E+08	2.43E+08	739
ENSG00000(	33.14534	30.10719	29.0271	24.71949	23.0108	34.52253	0.16255	0.70992	0.80395	RPL13P12	chr17	-	17286691	17287326	636
ENSG00000(	1.035792	0	2.638828	5.243529	0.920432	0.821965	-0.65184	0.60637	0.721	GNL3LP1	chr5	-	60187762	60189404	1643
ENSG00000(	0	0	0	4.494453	2.761296	0	-1.8787	0.16586	0.26454	AL603965.	chr10	+	47746962	47770871	1970
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	FDPSP5	chrX	-	44335273	44336668	1057
ENSG00000(	14.50109	18.06432	21.11062	8.239831	11.04518	1.64393	1.2658	0.067863	0.12641	CD27-AS1	chr12	-	6548167	6560733	2364
ENSG00000(	145.0109	149.3317	167.5656	140.0771	216.3015	246.5895	-0.38114	0.10887	0.18798	NEURL4	chr17	-	7218947	7232712	5200
ENSG00000(	6.214751	3.612863	0	6.74168	13.80648	25.48091	-1.941	0.021535	0.046338	GRID2IP	chr7	-	6537093	6591067	3636
ENSG00000(	4.143168	0	0	0	1.840864	0.821965	0.3781	0.77965	0.85491	PRDX2P1	chr13	+	30870284	30870872	589
ENSG00000(	0	2.408575	0	0	0	1.64393	0.21935	0.86915	NA	DUSP8P4	chr10	+	47254247	47256007	1761
ENSG00000(	6.214751	7.225726	7.916483	1.498151	6.443024	3.28786	0.82378	0.35985	0.48944	C9orf38	chr9	-	6467618	6470375	2758
ENSG00000(	29.00217	28.90291	40.90183	17.22874	34.05598	26.30288	0.34097	0.45183	0.58151	AC027763.	chr17	-	6779954	6915668	1730
ENSG00000(	117.0445	126.4502	120.0667	5.992604	15.64734	17.26126	3.1794	9.12E-18	8.31E-17	AC025171.	chr5	+	43041677	43045492	2423
ENSG00000(	0	1.204288	0	2.247227	0	0	-0.3239	0.80512	NA	NPM1P24	chr10	-	74677399	74678292	894
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RPS5P3	chr21	-	34853887	34854502	616
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP13-138P	chrX	+	91714669	91715951	1283
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	EEF1A1P29	chrX	-	85415268	85416363	1096
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	IFITM8P	chr8	+	64321622	64322015	394
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	TERF1P4	chrX	-	83003833	83004947	1115
ENSG00000(	5.17896	4.817151	1.319414	1.498151	3.681728	3.28786	0.36046	0.73192	0.82072	RP11-217H	chrX	-	79528830	79565669	500
ENSG00000(	20.71584	20.47289	43.54065	65.16957	53.38506	32.8786	-0.82757	0.058864	0.11192	TTC3P1	chrX	-	74960541	74966749	6081
ENSG00000(	321.0955	316.7277	341.7282	629.2235	559.6227	472.6298	-0.76058	2.58E-06	1.02E-05	UBXN2B	chr8	+	59323823	59364060	5068
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	AL590763.	chrX	-	70747664	70750075	1545
ENSG00000(	3.107376	6.021439	1.319414	7.490755	4.60216	4.109825	-0.53696	0.57819	0.69656	CBWD7	chr9	+	42668608	42714962	3326
ENSG00000(	0	3.612863	1.319414	0.749076	0	0	1.2665	0.35059	NA	C16orf90	chr16	-	3543484	3545480	929
ENSG00000(	1.035792	0	0	4.494453	4.60216	1.64393	-2.0627	0.1072	0.18574	RP11-292B	chr9	-	40491622	40633282	1477
ENSG00000(	180.2278	189.0732	172.8432	118.3539	157.3939	148.7757	0.3533	0.099689	0.17501	AC141586.	chr16	+	2653351	2680495	2748

ENSG00000(	45.57484	40.94578	43.54065	11.98521	84.67974	46.03004	-0.1217	0.80633	0.87431	RP11-1023	chr5	+	34190161	34193758	3598
ENSG00000(	73.54123	98.75159	88.40072	43.44638	41.41944	87.12828	0.58772	0.08502	0.15333	RP11-1023	chr5	-	34164803	34244901	5001
ENSG00000(	3.107376	1.204288	17.15238	0.749076	0	0.821965	2.7627	0.01671	0.036925	RP11-629N	chr12	+	65153301	65173098	589
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	OR7E122P	chr3	+	8729829	8730845	1017
ENSG00000(	0	0	0	2.247227	0.920432	1.64393	-1.4644	0.28023	NA	LINC00269	chrX	+	68399400	68429767	2173
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-403F	chr9	+	38478468	38479347	880
ENSG00000(	0	3.612863	0	0	0.920432	0	0.81649	0.54246	NA	RP13-487C	chrX	-	57703500	57706693	3194
ENSG00000(	4.143168	3.612863	0	0.749076	4.60216	0.821965	0.27035	0.82223	0.88524	RP11-8L18	chr10	-	34964563	34964969	407
ENSG00000(	3.107376	2.408575	1.319414	0.749076	1.840864	0	0.95667	0.45276	0.58252	FAM166B	chr9	-	35561828	35563896	971
ENSG00000(	183.3352	157.7617	138.5384	140.8262	135.3035	103.5676	0.33742	0.14726	0.24027	LINC00680	chr6	-	58272352	58287779	2622
ENSG00000(	1159.051	1091.085	1056.85	1256.2	1168.949	1313.5	-0.17635	0.1412	0.2324	PEX26	chr22	+	18560689	18613905	4519
ENSG00000(	39.36009	39.74149	15.83297	0	2.761296	5.753754	3.2344	6.24E-06	2.37E-05	AC091878.	chr5	-	17130137	17217156	2941
ENSG00000(	9.322127	2.408575	1.319414	0.749076	2.761296	0.821965	1.2634	0.26506	0.38497	RP11-316C	chr12	-	65812511	65813807	1297
ENSG00000(	7.250543	19.2686	11.87472	0.749076	5.522592	11.50751	1.0026	0.21738	0.32862	C5orf49	chr5	-	7830491	7851603	2385
ENSG00000(	2.071584	2.408575	2.638828	23.22134	15.64734	21.37109	-2.8063	0.000285	0.000869	UBE2QL1	chr5	+	6448736	6495022	4317
ENSG00000(	3.107376	1.204288	3.958241	0.749076	3.681728	0.821965	0.50543	0.66716	0.77059	UBA52P6	chr9	+	22012154	22012535	382
ENSG00000(	0	3.612863	6.597069	2.247227	0	0	1.3786	0.28461	0.40765	CYP51P3	chr6	+	1.49E+08	1.49E+08	1428
ENSG00000(	0	1.204288	0	3.745378	2.761296	0	-1.313	0.32934	0.45707	RP11-54D1	chr9	+	14993310	15019727	1188
ENSG00000(	11.39371	7.225726	11.87472	5.992604	7.363456	8.219649	0.46201	0.52739	0.65215	RP11-266K	chr12	+	8388011	8395160	795
ENSG00000(	1.035792	4.817151	1.319414	2.996302	4.60216	3.28786	-0.48239	0.65725	0.76213	AL137145.	chr10	+	6319650	6377938	3080
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-43F1	chr5	-	987295	997423	3482
ENSG00000(	257.9122	217.9761	286.3128	444.9509	555.9409	468.52	-0.94311	5.08E-08	2.40E-07	FASTKD5	chr20	-	3127165	3140543	2874
ENSG00000(	254.8048	251.6961	244.0915	291.3904	248.5166	304.949	-0.17057	0.33333	0.46141	GOLGA8B	chr15	-	34817408	34880704	6488
ENSG00000(	92.18548	93.93444	125.3443	44.19546	58.90765	52.60575	0.98853	0.000753	0.002158	DHRS4-AS1	chr14	-	24407940	24458048	2852
ENSG00000(	2.071584	4.817151	7.916483	0	0	0	3.3897	0.00816	0.019342	LA16c-60H	chr22	+	16122720	16123768	1049
ENSG00000(	44.53905	62.62296	34.30476	103.3724	88.36147	98.63579	-1.0219	0.001124	0.003127	HOMEZ	chr14	-	23743250	23755326	3352
ENSG00000(	2.071584	2.408575	0	0	0	0	1.5041	0.26224	NA	GAGE10	chrX	+	49160148	49176323	538
ENSG00000(	14.50109	7.225726	15.83297	20.97412	15.64734	8.219649	-0.24318	0.70387	0.79912	C14orf164	chr14	+	23654525	23742686	1670
ENSG00000(	1.035792	7.225726	5.277655	11.23613	6.443024	6.575719	-0.76289	0.38469	0.51551	HMGB3P24	chr9	-	36303496	36304921	622
ENSG00000(	0	0	0	9.737982	2.761296	5.753754	-3.3933	0.006542	0.015832	TMCO5B	chr15	-	33527753	33539822	1568
ENSG00000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	RP11-62E1	chr9	-	3364329	3364792	464
ENSG00000(	3172.631	2938.462	3821.022	5279.484	5978.206	4773.15	-0.68926	1.36E-07	6.17E-07	DDX3X	chrX	+	41192651	41223725	5334
ENSG00000(	46.61064	37.33292	35.62417	10.48706	23.93123	7.397684	1.477	0.003532	0.009011	CTD-3092A	chr15	+	30762982	30799826	1502
ENSG00000(	2.071584	0	3.958241	0	0.920432	0	1.4353	0.28803	0.41168	RP13-395E	chr15	-	32691157	32727434	1097
ENSG00000(	647.3699	637.0682	635.9574	343.0766	276.1296	289.3317	1.0748	1.11E-12	7.62E-12	VPS16	chr20	+	2821349	2847378	2750
ENSG00000(	0	0	2.638828	0	0	4.93179	-0.48536	0.72032	0.81178	AL135998.	chr14	-	23286463	23291750	66
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	NPM1P12	chr7	+	1.49E+08	1.49E+08	834
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-98L4	chrX	-	9786279	9787509	1231
ENSG00000(	5.17896	4.817151	14.51355	0	2.761296	0.821965	2.2893	0.028053	0.05859	ASS1P10	chr5	+	1.45E+08	1.45E+08	1244
ENSG00000(	18.64425	8.430014	14.51355	2.996302	9.20432	8.219649	0.96288	0.1809	0.2839	AF131215.	chr8	-	10983980	10987745	2179
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	TMED11P	chr4	-	1108985	1147514	690
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RPL37P3	chr21	-	19266510	19266802	293
ENSG00000(	0	0	1.319414	0.749076	1.840864	0	-0.44914	0.73845	NA	FAM66B	chr8	-	7159133	7212876	1432
ENSG00000(	156.4046	196.2989	91.03955	71.16218	52.46462	89.59418	1.0438	0.000667	0.001924	MYL5	chr4	+	667369	675822	2956

ENSG00000(	43.50326	32.51577	47.4989	2.247227	0	0.821965	4.7718	1.89E-10	1.10E-09	LINC00478	chr21	+	17442842	17999716	3475
ENSG00000(	1.035792	3.612863	9.235896	4.494453	16.56778	1.64393	-0.6173	0.52029	0.64615	ACTG1P3	chr20	+	1141228	1142341	1114
ENSG00000(	6.214751	4.817151	0	0	0	0.821965	2.2571	0.083308	0.15059	LINC00516	chr14	+	19889386	19904890	783
ENSG00000(	6.214751	0	0	0	0	0	1.7844	0.18526	0.28968	SCRT2	chr20	-	642240	656823	3577
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	LL22NC01-	chr22	+	37361289	37364213	992
ENSG00000(	0	7.225726	3.958241	0.749076	0	1.64393	1.5114	0.22566	0.33835	PSMA6P1	chrY	+	15398518	15399258	741
ENSG00000(	19.68005	31.31148	43.54065	140.0771	116.8949	135.6242	-2.0432	2.40E-10	1.38E-09	MIR17HG	chr13	+	92000074	92006833	2845
ENSG00000(	315.9165	266.1476	370.7553	240.4533	298.22	207.9571	0.35037	0.07642	0.13986	ZNF407	chr18	+	72265106	72777627	7948
ENSG00000(	83.89914	83.09585	112.1502	86.89276	76.39586	57.53754	0.32991	0.2563	0.37463	MCM3AP-A	chr21	+	47649131	47679304	2539
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC015989.	chr18	+	60491423	60492724	81
ENSG00000(	50.7538	74.66584	68.60952	23.22134	47.86246	42.74218	0.7578	0.042406	0.084209	NPEPL1	chr20	+	57264187	57294294	4684
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CTAGE12P	chr9	-	27608380	27610743	2364
ENSG00000(	149.154	175.826	201.8703	16.47966	84.67974	85.48435	1.4126	0.025311	0.053558	BX322557.	chr21	+	46707967	46711653	1460
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP5-890O1	chr20	-	45789477	45790339	863
ENSG00000(	2.071584	4.817151	5.277655	12.73428	23.0108	27.12484	-2.2071	0.00209	0.005549	RP5-981L2	chr20	-	45042867	45087915	2722
ENSG00000(	20.71584	25.29004	14.51355	5.992604	15.64734	10.68554	0.87115	0.14879	0.24233	AP001053.	chr21	-	45225639	45232448	4598
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AL136218.	chr13	-	50007495	50020554	225
ENSG00000(	2.071584	0	0	0	2.761296	0.821965	-0.3653	0.78771	NA	RPL27AP	chr20	+	42281163	42281931	435
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	SKOR2	chr18	-	44746293	44775554	3006
ENSG00000(	0	0	0	15.73059	22.09037	4.93179	-4.64	5.39E-05	0.000182	SIAH3	chr13	-	46354405	46425871	4030
ENSG00000(	0	0	0	2.996302	4.60216	13.15144	-3.5623	0.003964	0.010027	CES5AP1	chr22	-	23701790	23729918	1016
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	BCRP3	chr22	+	25028882	25046799	1457
ENSG00000(	6.214751	0	0	0	1.840864	0	0.95738	0.47927	0.60833	CALM2P3	chr13	-	41744836	41745284	449
ENSG00000(	0	2.408575	0	2.247227	0.920432	0	-0.20772	0.87831	NA	LINC00598	chr13	-	41025131	41055143	702
ENSG00000(	1.035792	1.204288	2.638828	2.996302	0.920432	0.821965	0.007804	0.99501	0.99688	HNRNPA1P	chr18	-	29991471	29993167	1538
ENSG00000(	21.75163	26.49433	29.0271	12.73428	26.69253	13.15144	0.53967	0.29884	0.42381	XXbac-B56	chr22	+	20804409	20806111	1703
ENSG00000(	2.071584	10.83859	9.235896	3.745378	0	10.68554	0.50788	0.60211	0.71729	AP000974.	chr11	-	85563600	85565986	2387
ENSG00000(	0	0	0	18.72689	22.09037	21.37109	-5.2431	1.63E-06	6.61E-06	TPTE2P4	chrY	+	28654360	28725837	1605
ENSG00000(	117.0445	151.7403	59.37362	230.7153	150.9508	218.6427	-0.85849	0.003057	0.007886	PI4KAP1	chr22	-	20383524	20427835	2637
ENSG00000(	0	2.408575	0	1.498151	0.920432	1.64393	-0.43801	0.74404	0.8295	IFIT1P1	chr13	+	32958797	32960245	1449
ENSG00000(	0	1.204288	0	2.996302	0	3.28786	-1.2837	0.34063	0.46936	AP005482.	chr18	+	12658042	12658892	471
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	EFCAB8	chr20	+	31446729	31549006	1281
ENSG00000(	79.75598	71.05298	71.24834	48.68991	59.82808	36.98842	0.60536	0.060589	0.11461	RP11-764K	chr9	-	68427861	68455375	931
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	ANKRD20A	chr21	-	15281895	15352758	3717
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	AP003041.	chr11	+	1.3E+08	1.3E+08	261
ENSG00000(	3.107376	1.204288	3.958241	0	6.443024	0.821965	0.15527	0.89636	0.93579	GRK6P1	chr13	+	21893231	21895005	1711
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	BCORP1	chrY	-	21617317	21665039	5093
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP5-836E8	chr20	-	7812445	7812969	525
ENSG00000(	1.035792	0	3.958241	30.7121	37.73771	55.89361	-4.2763	1.32E-08	6.57E-08	HMX1	chr4	-	8847802	8873543	1893
ENSG00000(	7.250543	12.04288	27.70769	8.988907	11.96562	13.9734	0.38906	0.5516	0.67269	GUSBP9	chr5	-	70435716	70585611	1211
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	GCGR	chr17	+	79762008	79771889	2051
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC114730.	chr2	-	2.43E+08	2.43E+08	472
ENSG00000(	1.035792	4.817151	9.235896	1.498151	0	1.64393	1.6905	0.14059	0.23167	CELA2B	chr1	+	15792404	15817895	923
ENSG00000(	268.2701	329.9748	240.1333	325.0988	263.2436	338.6495	-0.14481	0.44089	0.57069	TMEM242	chr6	-	1.58E+08	1.58E+08	1799

ENSG00000(	755.0923	649.1111	783.7318	394.0137	393.9449	332.0738	0.96306	1.38E-10	8.11E-10	TMEM167B	chr1	+	1.1E+08	1.1E+08	2798
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP1-21O18	chr1	-	15518324	15519341	710
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP13-996F	chr15	-	82930438	82939159	4353
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	TAF9BP2	chr10	+	1.17E+08	1.17E+08	499
ENSG00000(	17.60846	28.90291	10.55531	0.749076	8.283888	9.863579	1.4811	0.04473	0.088146	hsa-mir-60	chr17	-	62745781	62778117	2861
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	LRRC37A14	chr22	-	41585731	41586192	462
ENSG00000(	4.143168	9.634302	5.277655	71.16218	64.43024	67.40112	-3.3051	2.62E-11	1.62E-10	FAM72D	chr1	-	1.44E+08	1.44E+08	2393
ENSG00000(	0	2.408575	1.319414	4.494453	0.920432	3.28786	-0.89503	0.4651	0.59417	CFL1P6	chr1	-	11051035	11051854	494
ENSG00000(	164.6909	209.5461	154.3714	47.19176	62.58938	43.56414	1.7731	1.77E-11	1.11E-10	TNFRSF25	chr1	-	6521211	6526255	3483
ENSG00000(	119.1161	85.50443	122.7055	50.18806	53.38506	42.74218	1.1491	8.85E-05	0.000291	SLC35E2	chr1	-	1656277	1677431	2078
ENSG00000(	2.071584	10.83859	11.87472	0	2.761296	1.64393	2.0642	0.045231	0.088977	RP11-488L	chr1	-	2.47E+08	2.47E+08	1670
ENSG00000(	0	4.817151	1.319414	0	5.522592	0	0.10423	0.93656	0.96168	RP11-551G	chr1	+	2.47E+08	2.47E+08	1231
ENSG00000(	232.0174	245.6747	315.3399	112.3613	97.56579	111.7872	1.2895	1.13E-09	6.17E-09	RP11-371I	chr1	-	2.39E+08	2.39E+08	1537
ENSG00000(	0	0	0	0.749076	0	3.28786	-1.135	0.39451	NA	BTNL10	chr1	-	2.29E+08	2.29E+08	869
ENSG00000(	36.25272	21.67718	36.94359	0.749076	2.761296	3.28786	3.5533	2.62E-07	1.15E-06	ZC3H11B	chr1	-	2.2E+08	2.2E+08	3237
ENSG00000(	2.071584	0	1.319414	0	6.443024	0.821965	-0.68494	0.59731	0.71301	RP11-9L18	chr1	-	1.66E+08	1.66E+08	1969
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-122G	chr1	+	1.61E+08	1.61E+08	884
ENSG00000(	1.035792	0	0	130.3391	115.054	132.3364	-7.0013	4.43E-16	3.73E-15	TSTD1	chr1	-	1.61E+08	1.61E+08	813
ENSG00000(	11.39371	27.69862	22.43003	4.494453	7.363456	0.821965	2.1059	0.003885	0.009845	WI2-1896C	chr1	-	1.45E+08	1.45E+08	377
ENSG00000(	11.39371	15.65574	19.79121	12.73428	15.64734	5.753754	0.42636	0.50246	0.63044	RP11-495P	chr1	-	1.48E+08	1.48E+08	2210
ENSG00000(	1.035792	3.612863	2.638828	83.14739	37.73771	50.13986	-4.2802	1.12E-10	6.64E-10	RP11-426L	chr1	-	1.13E+08	1.13E+08	1819
ENSG00000(	5.17896	6.021439	1.319414	0	0.920432	3.28786	1.2009	0.30144	0.42656	RP4-773A1	chr1	-	1.12E+08	1.12E+08	1254
ENSG00000(	0	0	0	17.22874	7.363456	10.68554	-4.4029	0.000144	0.000459	ST13P20	chr1	+	82187378	82188753	1065
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	MARCKSL1	chr6	-	1.39E+08	1.39E+08	976
ENSG00000(	27.96638	72.25726	32.98534	50.93714	36.81728	47.67397	-0.0283	0.94549	0.96725	CYB5RL	chr1	-	54638009	54665709	5643
ENSG00000(	0	4.817151	0	3.745378	0.920432	1.64393	-0.27197	0.83125	0.89192	RP4-635E8	chr1	+	41564310	41564808	499
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-334L	chr1	+	39174603	39176562	1960
ENSG00000(	1.035792	2.408575	1.319414	8.239831	11.04518	15.61733	-2.478	0.00737	0.01766	ZBTB8B	chr1	+	32930670	32953461	4008
ENSG00000(	0	0	0	0	5.522592	0	-1.3606	0.30939	NA	AL353354.	chr1	-	28527013	28527152	66
ENSG00000(	362.5272	360.082	303.4652	277.907	289.0156	378.9258	0.11829	0.51395	0.64086	CROCCP2	chr1	-	16944751	16971178	2763
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	C1orf167	chr1	+	11821844	11849642	4560
ENSG00000(	8.286335	8.430014	6.597069	5.992604	6.443024	1.64393	0.65069	0.44639	0.57603	TTC34	chr1	-	2567415	2718286	3737
ENSG00000(	12.4295	2.408575	3.958241	2.996302	0	0.821965	1.7975	0.10126	0.17728	MMP23A	chr1	+	1631369	1633249	1124
ENSG00000(	19.68005	3.612863	15.83297	25.46857	12.88605	21.37109	-0.57328	0.36212	0.49176	ATAD3C	chr1	+	1385069	1405538	3859
ENSG00000(	11.39371	30.10719	15.83297	17.97781	16.56778	23.01502	-0.01124	0.98379	0.99079	RP11-490H	chr12	+	1.04E+08	1.04E+08	765
ENSG00000(	3.107376	1.204288	0	0	0	0	1.4526	0.27741	NA	RP3-400B1	chr6	+	4189350	4190040	691
ENSG00000(	1.035792	3.612863	3.958241	5.992604	0	3.28786	-0.10928	0.92353	0.9537	RP3-354N1	chr6	-	1.2E+08	1.2E+08	582
ENSG00000(	31.07376	42.15007	34.30476	3.745378	8.283888	0.821965	2.9164	2.71E-06	1.07E-05	HIST1H1PS	chr6	+	26195794	26195999	206
ENSG00000(	3.107376	0	1.319414	1.498151	4.60216	0	-0.28149	0.82679	0.8884	RP1-182O1	chr6	-	5817654	5818599	946
ENSG00000(	0	0	0	0	0.920432	6.575719	-1.8834	0.16495	0.26344	MRPL42P2	chr6	+	16171837	16172262	426
ENSG00000(	2.071584	0	0	2.996302	0.920432	0	-0.45533	0.73695	0.82369	RPSAP43	chr6	-	1.14E+08	1.14E+08	625
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	IGSF23	chr19	+	45116940	45140081	989
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP3-391O2	chr6	+	34584315	34585035	721
ENSG00000(	1.035792	1.204288	1.319414	1.498151	0	1.64393	0.09671	0.94175	0.9649	RP3-355L5	chr6	+	1.06E+08	1.06E+08	747

ENSG00000(	3.107376	0	0	0	0	0.821965	0.7418	0.57612	NA	RP3-406P2	chr6	+	3978296	3979333	1038
ENSG00000(	0	0	0	5.243529	3.681728	3.28786	-2.8004	0.030496	0.063065	NUDT19P3	chr6	-	1.14E+08	1.14E+08	555
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	HMGA1P7	chr6	-	1.34E+08	1.34E+08	502
ENSG00000(	653.5847	622.6168	730.9552	312.3645	287.1748	227.6843	1.2731	7.73E-15	6.04E-14	RP1-152L7	chr6	+	52529946	52533953	3039
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP1-290I1(	chr6	-	10365826	10366815	675
ENSG00000(	2.071584	0	6.597069	5.243529	0.920432	0	0.325	0.79238	0.86431	RP11-390P	chr6	-	1.39E+08	1.39E+08	748
ENSG00000(	10.35792	2.408575	21.11062	2.247227	12.88605	2.465895	0.8458	0.32854	0.45624	RP11-57K1	chr6	-	1.19E+08	1.19E+08	2524
ENSG00000(	0	6.021439	0	0	6.443024	4.109825	-0.55893	0.65412	0.75975	RP11-812I;	chr6	+	47530358	47530754	397
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	R3HDM2P2	chr6	-	1.04E+08	1.04E+08	2116
ENSG00000(	1.035792	0	0	2.247227	2.761296	0.821965	-1.3048	0.33068	0.45853	TUBB2BP1	chr6	-	3177278	3179998	871
ENSG00000(	0	1.204288	2.638828	0	0	0	1.2853	0.33195	NA	RPL17P26	chr6	+	56735989	56736541	553
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	LY86-AS1	chr6	-	6346698	6622977	2819
ENSG00000(	27.96638	14.45145	14.51355	23.97042	9.20432	15.61733	0.21303	0.71503	0.80769	RPS2P55	chrX	-	40794198	40795117	883
ENSG00000(	6.214751	0	1.319414	0	9.20432	4.109825	-0.58617	0.61669	0.72942	AC114776.	chr2	+	1.11E+08	1.11E+08	387
ENSG00000(	31.07376	27.69862	23.74945	39.701	44.18074	53.42772	-0.71288	0.074085	0.13615	AC009403.	chr7	-	1.55E+08	1.55E+08	1008
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AL022393.	chr6	+	28143966	28144452	487
ENSG00000(	5.17896	3.612863	1.319414	0.749076	0	0	2.2702	0.079211	0.14412	RP11-350J2	chr6	+	1.5E+08	1.5E+08	2176
ENSG00000(	10.35792	8.430014	3.958241	2.247227	4.60216	0	1.4752	0.13729	0.22721	AC131097.	chr2	-	2.43E+08	2.43E+08	595
ENSG00000(	16.57267	13.24716	18.47179	12.73428	10.12475	9.041614	0.56243	0.35663	0.48619	CCDC7	chr10	+	32735068	32863492	3998
ENSG00000(	0	0	0	2.247227	0	2.465895	-1.3312	0.32317	NA	RPL21P65	chr6	+	1.07E+08	1.07E+08	466
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CYP2AC1P	chr6	-	49533637	49547879	1173
ENSG00000(	2.071584	4.817151	0	1.498151	0	3.28786	0.35817	0.77634	0.85303	RP3-329A5	chr6	-	35246954	35247596	328
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RPL10P1	chr21	-	28792699	28793342	644
ENSG00000(	6.214751	0	0	0	0	1.64393	1.0148	0.45353	0.58322	RP1-83M4.	chr6	-	1.45E+08	1.45E+08	519
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	RP11-346C	chr6	+	1.11E+08	1.11E+08	339
ENSG00000(	0	0	6.597069	0	2.761296	4.93179	-0.16655	0.89596	0.93558	AC007401.	chr2	-	36758948	36779411	430
ENSG00000(	0	0	2.638828	0.749076	1.840864	2.465895	-0.59121	0.65582	0.76078	RP1-13D10	chr6	-	16163608	16163993	386
ENSG00000(	4.143168	7.225726	5.277655	2.996302	6.443024	3.28786	0.34186	0.70884	0.80322	PPIAP31	chr10	-	32477251	32477745	495
ENSG00000(	689.8374	687.6483	808.8006	403.7517	396.7062	380.5698	0.88491	5.14E-10	2.88E-09	FNIP1	chr5	-	1.31E+08	1.31E+08	6393
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	RP3-375P9	chr6	+	34711953	34712450	498
ENSG00000(	5.17896	0	3.958241	0.749076	0	0.821965	1.6224	0.20768	0.31698	LARP1P1	chr6	+	26164300	26164591	292
ENSG00000(	22.78742	46.96722	34.30476	9.737982	14.72691	5.753754	1.714	0.00156	0.00423	ANKRD18E	chr6	+	39078097	39080728	2632
ENSG00000(	0	0	0	2.247227	5.522592	2.465895	-2.5145	0.056285	0.10767	RP11-360C	chr6	-	10574982	10575460	479
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP1-319M7	chr6	+	38555099	38556305	1207
ENSG00000(	7.250543	1.204288	7.916483	29.96302	39.57858	32.8786	-2.498	4.32E-05	0.000148	SP9	chr2	+	1.75E+08	1.75E+08	2554
ENSG00000(	1.035792	4.817151	1.319414	1.498151	4.60216	0	0.17678	0.8846	0.92798	CBX3P9	chr6	-	1.17E+08	1.17E+08	552
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC007249.	chr2	+	10592445	10595678	494
ENSG00000(	6.214751	4.817151	2.638828	0	0.920432	0	2.6502	0.032702	0.066989	RP1-34B20	chr6	+	26202384	26202882	499
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	UQCRFS1P3	chr6	-	19638271	19639039	385
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	OR2W2P	chr6	+	28001725	28002633	909
ENSG00000(	0	4.817151	0	1.498151	0	3.28786	-0.00266	0.9984	0.99905	PRELID1P1	chr6	+	1.27E+08	1.27E+08	903
ENSG00000(	7.250543	7.225726	0	6.74168	4.60216	4.93179	-0.12993	0.89231	0.9334	SSXP10	chr6	+	1.19E+08	1.19E+08	565
ENSG00000(	1.035792	1.204288	0	1.498151	1.840864	3.28786	-1.0006	0.43632	0.56592	ISCA1P1	chr5	-	62072704	62073090	387
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	SYCE3	chr22	-	50989541	51001334	448

ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP3-366N2	chr6	+	1.68E+08	1.68E+08	582
ENSG00000(	3.107376	16.86003	5.277655	0.749076	0	2.465895	2.3847	0.023572	0.050263	RP11-474L	chr6	-	76320674	76321661	831
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP1-95L4.2	chr6	-	1.44E+08	1.44E+08	785
ENSG00000(	5.17896	2.408575	0	0.749076	4.60216	0	0.3791	0.76252	0.84321	RP11-477E	chr6	-	79777409	79777855	447
ENSG00000(	4.143168	4.817151	7.916483	0	0.920432	3.28786	1.5895	0.14592	0.2386	RPS16P5	chr6	-	53201741	53202144	404
ENSG00000(	27.96638	28.90291	21.11062	16.47966	16.56778	16.4393	0.6366	0.19997	0.30774	CKLF	chr16	+	66586466	66600331	669
ENSG00000(	94.25706	77.07441	73.88717	69.66403	69.95283	51.78379	0.35667	0.23045	0.34385	RP11-64P1	chr13	-	52741844	52865692	3796
ENSG00000(	3.107376	3.612863	6.597069	2.247227	3.681728	1.64393	0.67083	0.51371	0.64073	RP11-204C	chrX	-	41535013	41535747	735
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	PTGES3P2	chr2	+	26045338	26045819	482
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP4-803A2	chr1	+	33445543	33446073	531
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	HIST1H2BP	chr6	-	27831840	27832179	340
ENSG00000(	11.39371	24.08575	13.19414	52.43529	37.73771	42.74218	-1.412	0.002413	0.00634	RP1-95L4.4	chr6	+	1.44E+08	1.44E+08	1138
ENSG00000(	0	0	2.638828	2.247227	0	0	0.077345	0.95422	NA	RP11-63K6	chr6	+	90524428	90525182	755
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-65C6	chr6	+	1.41E+08	1.41E+08	734
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	MGC10955	chr2	+	74361599	74362521	923
ENSG00000(	2.071584	3.612863	9.235896	3.745378	0	1.64393	1.1251	0.30799	0.4338	RPS10P3	chr9	+	90631215	90631708	494
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	CCT7P1	chr6	+	1.5E+08	1.5E+08	1611
ENSG00000(	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	RP11-160A	chr6	+	71444206	71444665	460
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	RP11-76H1	chr6	+	87606836	87607139	304
ENSG00000(	2.071584	3.612863	2.638828	0	0	0.821965	1.9865	0.12972	0.21685	LDHAL6FP	chr6	-	1.58E+08	1.58E+08	1082
ENSG00000(	20.71584	18.06432	32.98534	10.48706	20.2495	18.08323	0.53382	0.31912	0.44626	RP11-465B	chr1	+	995114	1004735	1220
ENSG00000(	1.035792	0	0	1.498151	2.761296	0	-0.89883	0.50763	NA	RP6-159A1	chrX	-	65176131	65177038	908
ENSG00000(	0	0	2.638828	0	0	0.821965	0.55859	0.66971	NA	HIST1H4PS	chr6	+	27774853	27775117	265
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP11-66N1	chrX	-	1.53E+08	1.53E+08	852
ENSG00000(	3.107376	0	0	1.498151	8.283888	4.109825	-1.5178	0.20313	0.31116	ZNF839P1	chrY	+	21147061	21148284	861
ENSG00000(	0	0	2.638828	2.247227	2.761296	4.109825	-1.253	0.31947	0.44661	RP11-420K	chr1	-	39769966	39770570	288
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP1-24O22	chr6	-	142272	145083	2812
ENSG00000(	65.25489	42.15007	15.83297	82.39831	100.3271	94.52597	-1.1291	0.003309	0.008495	PAM16	chr16	-	4381550	4405608	806
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	ZNF192P2	chr6	+	28155828	28157210	1383
ENSG00000(	0	1.204288	0	0	0.920432	6.575719	-1.4355	0.28512	0.40822	RP4-800J2:	chr20	-	55959216	55968118	1540
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-157J:	chr6	-	1513933	1515524	1592
ENSG00000(	41.43168	32.51577	35.62417	0	0	0	6.4391	1.01E-09	5.56E-09	RP11-561C	chr15	-	85798600	85873565	3611
ENSG00000(	0	0	0	8.239831	11.96562	1.64393	-3.6185	0.003394	0.008696	RP1-13D10	chr6	+	16161157	16161642	486
ENSG00000(	0	0	0	0	5.522592	0	-1.3606	0.30939	NA	DNAJA1P4	chr6	-	1.15E+08	1.15E+08	1166
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	KRT18P22	chr6	-	1.17E+08	1.17E+08	1347
ENSG00000(	5.17896	8.430014	5.277655	8.239831	0.920432	10.68554	-0.07311	0.93421	0.96038	AC016739.	chr2	-	1.77E+08	1.77E+08	345
ENSG00000(	5.17896	0	0	0	0	0	1.5469	0.24589	NA	POM121L1	chr6	+	58263736	58265293	1558
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RPS20P32	chr13	-	27591688	27592046	356
ENSG00000(	1.035792	3.612863	0	0	0	0	1.5346	0.25314	NA	RP11-367G	chr6	+	1.14E+08	1.14E+08	447
ENSG00000(	35.21692	61.41867	32.98534	13.48336	26.69253	13.15144	1.25	0.008441	0.019949	TATDN2P2	chr6	-	1.59E+08	1.59E+08	2226
ENSG00000(	0	7.225726	3.958241	5.992604	3.681728	2.465895	-0.11506	0.91327	0.94688	RP11-889L	chr5	+	1.77E+08	1.77E+08	591
ENSG00000(	0	0	3.958241	3.745378	1.840864	3.28786	-0.85323	0.49174	0.62078	NEPNP	chr6	+	1.18E+08	1.18E+08	1371
ENSG00000(	9.322127	0	0	0	0	0	2.3486	0.083387	0.15069	RP11-501I:	chr6	+	13521498	13522277	780
ENSG00000(	286.9144	292.6419	271.7992	185.7707	266.0048	180.8323	0.4292	0.031415	0.064726	MORF4L1P	chr1	+	2.2E+08	2.2E+08	967

ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC006024.	chr7	+	48959361	48965612	1719
ENSG00000(	5.17896	2.408575	7.916483	1.498151	1.840864	4.109825	0.8757	0.3877	0.5185	RP11-393I2	chr6	-	87883086	87884021	936
ENSG00000(	2454.827	2490.467	2905.349	2333.37	3146.037	2559.599	-0.03408	0.80022	0.86983	TENM3	chr4	+	1.83E+08	1.84E+08	10896
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	VN1R14P	chr6	-	26630782	26632007	929
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	LYPLA1P3	chr6	+	71874779	71875473	695
ENSG00000(	3.107376	1.204288	0	3.745378	1.840864	0.821965	-0.37548	0.76386	0.84398	RAET1K	chr6	-	1.5E+08	1.5E+08	1883
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-14H3	chr6	+	17582265	17582536	272
ENSG00000(	2.071584	1.204288	0	2.996302	4.60216	0	-0.77728	0.54362	0.66609	AC012078.	chrY	-	3719265	3720910	1646
ENSG00000(	23.82321	6.021439	14.51355	97.37982	124.2583	157.8173	-3.0061	3.63E-14	2.72E-13	AC110619.	chr2	-	2.41E+08	2.41E+08	2017
ENSG00000(	4.143168	8.430014	5.277655	7.490755	6.443024	9.041614	-0.33409	0.68028	0.78097	RP11-296E	chr6	-	80774003	80779916	5914
ENSG00000(	17.60846	12.04288	2.638828	20.97412	34.05598	47.67397	-1.5607	0.007741	0.018465	AC016773.	chr4	+	1741078	1743830	2751
ENSG00000(	152.2614	140.9017	117.4278	82.39831	75.47542	127.4046	0.52151	0.052054	0.10057	RP11-475C	chr6	-	1.54E+08	1.54E+08	447
ENSG00000(	2.071584	0	2.638828	1.498151	1.840864	0	0.309	0.81459	0.87959	NIP7P3	chr6	-	1.16E+08	1.16E+08	515
ENSG00000(	9.322127	0	1.319414	2.996302	0	0	1.191	0.354	0.48384	RPS27P15	chr6	+	74328069	74328320	252
ENSG00000(	0	1.204288	0	1.498151	2.761296	4.109825	-1.7009	0.19277	0.29861	H2AFZP3	chr13	-	99867626	99868012	387
ENSG00000(	165.7267	146.9231	134.5802	198.505	153.7121	194.8057	-0.2878	0.18298	0.28669	LINC00339	chr1	+	22351681	22357716	1054
ENSG00000(	2.071584	7.225726	0	0	2.761296	3.28786	0.4603	0.70465	0.79966	RP11-420A	chr6	-	37970608	37971089	482
ENSG00000(	5.17896	21.67718	3.958241	0.749076	1.840864	2.465895	2.2258	0.020331	0.04402	AP000350.	chr22	-	24236613	24241117	1476
ENSG00000(	0	0	0	2.247227	1.840864	1.64393	-1.6991	0.21004	NA	RP1-253B1	chr6	-	87439426	87439826	401
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RP1-256G2	chr6	-	5609460	5610428	969
ENSG00000(	3.107376	1.204288	5.277655	0	7.363456	3.28786	-0.11069	0.92123	0.95228	RP11-2J18.	chr6	+	1.57E+08	1.57E+08	378
ENSG00000(	0	0	1.319414	0	0	1.64393	-0.1317	0.91874	NA	RP3-395C1	chr6	-	1.58E+08	1.58E+08	616
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-425D	chr6	-	1.1E+08	1.1E+08	740
ENSG00000(	3.107376	3.612863	3.958241	0	3.681728	0	1.1268	0.35596	0.48557	BRD7P4	chr6	+	1.12E+08	1.12E+08	1522
ENSG00000(	0	0	0	2.247227	1.840864	0.821965	-1.4859	0.2733	NA	AC010150.	chr2	-	26079330	26079835	506
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP3-341I1(	chr6	-	1.3E+08	1.3E+08	815
ENSG00000(	0	0	0	0	1.840864	3.28786	-1.4188	0.29365	NA	HIST1H2AP	chr6	-	26272421	26272768	348
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	ST13P16	chr6	-	88154113	88154893	781
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP1-34L19	chr6	-	53071396	53073495	2100
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RP11-174C	chr6	+	1.3E+08	1.3E+08	1295
ENSG00000(	16.57267	4.817151	5.277655	19.47596	15.64734	13.9734	-0.80086	0.23558	0.34993	AC007390.	chr2	+	37423631	37440868	3158
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP3-340B1	chr6	+	35575405	35575711	307
ENSG00000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	RP3-472M2	chr6	-	1.55E+08	1.55E+08	547
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-207F	chr6	+	86578671	86579182	512
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-331C	chr6	+	1.54E+08	1.54E+08	692
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	PAPOLB	chr7	-	4897364	4901625	4262
ENSG00000(	0	3.612863	0	0	1.840864	0	0.45719	0.73538	NA	RP11-249L	chr6	-	1.09E+08	1.09E+08	338
ENSG00000(	1035.792	955.0002	723.0388	894.3962	735.4252	766.8933	0.17952	0.24998	0.36731	ZNF579	chr19	-	56088899	56092211	2136
ENSG00000(	0	0	1.319414	1.498151	0.920432	0	-0.40849	0.76088	NA	TUBB8P2	chr6	+	1.44E+08	1.44E+08	495
ENSG00000(	2.071584	0	2.638828	0	0	0	1.5584	0.24658	NA	FTH1P15	chr6	+	56869318	56869597	280
ENSG00000(	0	3.612863	1.319414	0.749076	0.920432	0.821965	0.60217	0.64738	0.75397	RP1-99E18	chr6	+	1.51E+08	1.51E+08	599
ENSG00000(	0	0	5.277655	0	6.443024	0.821965	-0.30514	0.81472	0.87963	CTA-299D3	chr22	-	48934712	48943199	3012
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP3-340B1	chr6	+	35523650	35524041	392
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	RPS3AP2	chr16	+	1527831	1528584	754

ENSG00000(	3.107376	0	0	0	4.60216	0.821965	-0.42981	0.74801	0.83249	NPM1P37	chr6	-	70415179	70416052	874
ENSG00000(	3.107376	0	5.277655	0	2.761296	3.28786	0.34212	0.77933	0.85472	RP1-167A1	chr1	-	54440642	54441704	1063
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-203F	chr1	-	2.04E+08	2.04E+08	483
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-569A	chr6	-	1.11E+08	1.11E+08	204
ENSG00000(	2.071584	8.430014	0	0.749076	1.840864	0	1.392	0.26803	0.38839	FTH1P19	chrX	+	37351274	37351801	528
ENSG00000(	3.107376	0	0	0	0	2.465895	0.17171	0.89908	NA	CACYBPP3	chr6	-	1.59E+08	1.59E+08	625
ENSG00000(	0	1.204288	0	0	1.840864	2.465895	-0.87156	0.52062	NA	RNASEK	chr17	+	6915736	6917851	952
ENSG00000(	32.10955	36.12863	38.263	19.47596	38.65814	33.70056	0.21184	0.62145	0.73365	RP11-181C	chr1	-	78276507	78277621	1115
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AMZ2P2	chr6	-	1.59E+08	1.59E+08	1057
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	PIP5K1P1	chr6	+	7986730	7988425	1656
ENSG00000(	1.035792	6.021439	2.638828	11.23613	0.920432	0.821965	-0.35487	0.74648	0.83142	RPL31P52	chr12	-	1.21E+08	1.21E+08	367
ENSG00000(	2.071584	1.204288	2.638828	2.247227	0	2.465895	0.21516	0.86274	0.91313	RP11-250B	chr6	-	81179788	81180145	358
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-69L1	chr6	-	7331519	7331909	391
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-491H	chr6	+	45126607	45127248	642
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	ATF1P1	chr6	-	93596969	93598299	927
ENSG00000(	1.035792	3.612863	1.319414	2.996302	0.920432	9.863579	-0.95824	0.38697	0.51775	RP1-265C2	chr6	+	28083406	28084329	924
ENSG00000(	14.50109	19.2686	13.19414	16.47966	6.443024	9.041614	0.51305	0.42095	0.55162	HSPA8P15	chr6	-	1.52E+08	1.52E+08	786
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-524C	chr6	-	22213535	22214466	604
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-106E	chr6	+	1.45E+08	1.45E+08	794
ENSG00000(	4.143168	4.817151	5.277655	2.996302	5.522592	2.465895	0.32387	0.7357	0.8232	RP4-761J14	chr12	+	6772426	6781235	723
ENSG00000(	3.107376	3.612863	0	1.498151	0	1.64393	0.7195	0.5759	0.69426	RP11-350J2	chr6	+	1.5E+08	1.5E+08	676
ENSG00000(	10.35792	2.408575	3.958241	28.46487	21.16994	27.12484	-2.032	0.001816	0.004878	FAM19A5	chr22	+	48885272	49246724	2638
ENSG00000(	0	3.612863	0	0	2.761296	2.465895	-0.31438	0.81324	0.87873	RP11-193H	chr6	-	1.58E+08	1.58E+08	5191
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RPL23P8	chr7	+	20866945	20867372	428
ENSG00000(	9.322127	3.612863	10.55531	6.74168	3.681728	8.219649	0.29392	0.71915	0.81074	RP3-337H4	chr6	-	43506559	43507440	882
ENSG00000(	877.3157	918.8715	924.9091	399.2573	361.7298	369.0622	1.2636	2.93E-21	3.13E-20	NBPF1	chr1	-	16888814	16940057	5932
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-365H	chr6	-	1.49E+08	1.49E+08	664
ENSG00000(	6.214751	14.45145	6.597069	5.992604	4.60216	2.465895	0.94343	0.25936	0.37814	FTH1P8	chrX	+	1.47E+08	1.47E+08	514
ENSG00000(	128.4382	108.3859	143.8161	134.0845	111.3723	94.52597	0.1591	0.52242	0.64784	AC006465.	chr7	+	7680342	8043689	2111
ENSG00000(	1.035792	4.817151	2.638828	2.247227	0	0	1.2295	0.3372	0.4657	RPL17P25	chr6	-	81083732	81084286	555
ENSG00000(	12.4295	0	0	0	3.681728	0.821965	1.0297	0.4145	0.545	ZNF259P1	chr6	-	1.09E+08	1.09E+08	4912
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-132N	chr6	-	85399010	85399147	138
ENSG00000(	31.07376	14.45145	25.06886	3.745378	0.920432	4.109825	2.7609	0.000106	0.000345	PPP1R3G	chr6	+	5085720	5087455	1736
ENSG00000(	0	0	6.597069	0.749076	0	0	1.463	0.28083	0.40315	HIGD1AP1(	chr20	+	34466398	34466655	258
ENSG00000(	51.7896	36.12863	59.37362	16.47966	18.40864	17.26126	1.4607	0.000604	0.001752	FAM228B	chr2	+	24299396	24392509	2616
ENSG00000(	0	0	3.958241	0	2.761296	0	0.25703	0.84975	0.90441	BMPR1APS	chr6	-	1.29E+08	1.29E+08	1598
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	GCNT1P4	chr6	+	64567334	64567662	329
ENSG00000(	73.54123	73.46155	81.80365	74.15848	43.2603	82.19649	0.18891	0.55292	0.67382	CTD-2006C	chr19	+	12098432	12157090	4000
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-174C	chr6	-	1.3E+08	1.3E+08	277
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP3-425P1	chr6	+	25140212	25141649	1438
ENSG00000(	0	1.204288	1.319414	1.498151	3.681728	5.753754	-1.5261	0.21029	0.32007	RP11-262H	chr9	+	66544359	66545745	292
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	PTCHD3P3	chr6	-	1.1E+08	1.1E+08	906
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-532F	chr6	-	669081	670307	1227
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	XXbac-BPG	chr6	-	27528601	27529523	572

ENSG00000(	0	2.408575	0	5.992604	3.681728	7.397684	-2.1165	0.067769	0.12628	RP1-292B1	chr6	+	1.51E+08	1.51E+08	405
ENSG00000(	1.035792	2.408575	1.319414	1.498151	0	0.821965	0.62171	0.63707	0.74574	RP1-199J3.	chr6	+	1E+08	1E+08	745
ENSG00000(	4.143168	0	0	0	0	0.821965	0.9919	0.46158	NA	OSTCP6	chr6	-	56840404	56840860	457
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	XX-C2158C	chr6	+	1.71E+08	1.71E+08	460
ENSG00000(	0	0	0	0	4.60216	0.821965	-1.4643	0.27877	NA	GAPDHP42	chr6	+	70455763	70456743	981
ENSG00000(	13.46529	9.634302	3.958241	24.71949	17.48821	22.19305	-1.1643	0.059606	0.11306	ZSCAN12P1	chr6	+	28058932	28061442	1657
ENSG00000(	2.071584	2.408575	2.638828	0.749076	4.60216	1.64393	0.030803	0.97871	0.98763	RPL35P3	chr6	-	1.06E+08	1.06E+08	371
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RPL12P8	chr10	+	69634090	69634672	580
ENSG00000(	3.107376	0	0	0	3.681728	0	-0.09374	0.94492	0.96694	RP11-378G	chr6	+	84102135	84103128	994
ENSG00000(	4.143168	0	3.958241	0.749076	3.681728	0	0.61644	0.62373	0.73538	RP11-420L	chr6	+	3754333	3755074	436
ENSG00000(	1.035792	2.408575	1.319414	0	0	0	1.6865	0.21314	NA	LINGO3	chr19	-	2289774	2308156	2241
ENSG00000(	19.68005	12.04288	11.87472	15.73059	8.283888	2.465895	0.66408	0.35265	0.48242	RP11-17M1	chr18	+	74207477	74210045	2077
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	LAP3P1	chr6	-	83634548	83634841	294
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-307I1	chr9	-	4781475	4782078	604
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-46B1	chr6	-	79987822	79988144	323
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	HNRNPA1P	chr5	-	79654899	79655859	961
ENSG00000(	10.35792	10.83859	5.277655	15.73059	17.48821	12.32947	-0.72339	0.2696	0.38994	RP1-37N7.1	chr17	+	18314473	18317694	1871
ENSG00000(	5.17896	3.612863	2.638828	14.98151	8.283888	14.79537	-1.5582	0.049546	0.096311	ZGLP1	chr19	-	10415479	10420556	2303
ENSG00000(	737.4838	839.3885	680.8175	379.7813	365.4115	411.8044	0.96166	4.63E-11	2.80E-10	VAMP2	chr17	-	8062467	8066864	2153
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	RPS24P12	chr6	+	1.08E+08	1.08E+08	394
ENSG00000(	7.250543	6.021439	11.87472	0	4.60216	7.397684	0.92585	0.32202	0.44933	RP1-56L9.3	chr6	-	1.6E+08	1.6E+08	1185
ENSG00000(	7.250543	2.408575	13.19414	4.494453	5.522592	3.28786	0.68284	0.43743	0.56711	HIST2H2BD	chr1	+	1.5E+08	1.5E+08	493
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP3-431A1	chr6	+	36704827	36705763	937
ENSG00000(	0	1.204288	0	1.498151	0	0	-0.08768	0.94524	NA	KRT8P42	chr6	-	1.35E+08	1.35E+08	1399
ENSG00000(	8.286335	2.408575	9.235896	0	0	0	3.8663	0.001868	0.005007	FCF1P5	chr6	+	1.12E+08	1.12E+08	482
ENSG00000(	0	0	0	7.490755	3.681728	13.15144	-3.8254	0.001575	0.004268	RP11-95M1	chr6	-	1.38E+08	1.38E+08	1779
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP3-520B1	chr6	-	5291263	5291621	359
ENSG00000(	1.035792	4.817151	0	6.74168	2.761296	4.93179	-1.0313	0.34827	0.47789	RP11-69L1	chr6	-	7339072	7339801	730
ENSG00000(	5.17896	12.04288	13.19414	0	0.920432	0	3.8233	0.000594	0.001726	YAP1P1	chr6	+	1.48E+08	1.48E+08	1393
ENSG00000(	3.107376	6.021439	6.597069	5.243529	7.363456	7.397684	-0.31719	0.70998	0.80395	RP3-415N1	chr6	-	1.12E+08	1.12E+08	654
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	PGAM1P10	chr6	+	73764820	73765580	761
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	ASS1P1	chr6	-	25023475	25024711	1237
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP1-177A1	chr6	-	1.28E+08	1.28E+08	418
ENSG00000(	15.53688	19.2686	15.83297	3.745378	1.840864	4.109825	2.1795	0.003045	0.007856	PKMP3	chr6	-	86369610	86370324	715
ENSG00000(	10.35792	1.204288	3.958241	10.48706	2.761296	0.821965	0.12136	0.90444	0.94085	RPL35P2	chr6	-	34231088	34231450	363
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	DDX18P6	chr10	+	92812808	92814804	1997
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-480N	chr6	+	43295872	43296214	343
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	KRASP1	chr6	+	54635381	54635932	552
ENSG00000(	0	0	0	2.996302	1.840864	0	-1.3549	0.31496	NA	RP3-391O2	chr6	+	34654379	34654883	280
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP3-406A7	chr6	+	1.37E+08	1.37E+08	543
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RCC2P7	chr6	-	56296748	56298011	1264
ENSG00000(	0	0	1.319414	4.494453	13.80648	4.109825	-2.9857	0.010724	0.024753	RP11-530A	chr6	-	5066029	5067216	1188
ENSG00000(	11.39371	8.430014	3.958241	0	1.840864	4.109825	1.6887	0.091475	0.16298	AC011498.	chr19	+	4477048	4479576	1846
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP3-403A1	chr6	+	1.28E+08	1.28E+08	554

ENSG00000(	1.035792	8.430014	1.319414	0	4.60216	1.64393	0.60393	0.60798	0.72215	RP1-121G1	chr6	+	1.01E+08	1.01E+08	777
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	OR1F12	chr6	+	28041094	28042011	918
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP11-277I2	chr6	-	1.45E+08	1.45E+08	392
ENSG00000(	1.035792	3.612863	2.638828	0.749076	1.840864	1.64393	0.57116	0.63504	0.74409	RP3-351K2	chr6	+	1.28E+08	1.28E+08	891
ENSG00000(	27.96638	43.35436	31.66593	46.44268	23.0108	40.27628	-0.09676	0.82083	0.88422	RPL21P28	chr1	-	2.12E+08	2.12E+08	543
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP3-322L4	chr6	+	21602359	21602614	256
ENSG00000(	7.250543	7.225726	11.87472	0	0	0	4.3371	0.000288	0.000879	RP3-334F4	chr6	+	54489403	54490286	884
ENSG00000(	30.03797	31.31148	25.06886	72.66033	93.88406	84.66239	-1.5095	1.01E-05	3.73E-05	MTMR9LP	chr1	-	32697259	32707221	2624
ENSG00000(	5.17896	1.204288	2.638828	0	0	3.28786	0.99983	0.42723	0.55743	RPL21P119	chr16	-	9250219	9250761	543
ENSG00000(	4.143168	10.83859	3.958241	6.74168	11.96562	10.68554	-0.57373	0.46402	0.59324	AC093642.	chr2	+	2.43E+08	2.43E+08	1235
ENSG00000(	91.14969	97.54731	68.60952	88.39091	57.98722	106.8554	0.022475	0.94107	0.96455	RP11-572P	chr10	-	1.22E+08	1.22E+08	542
ENSG00000(	16.57267	14.45145	17.15238	7.490755	7.363456	13.9734	0.69728	0.2695	0.38988	RPS18P9	chr6	+	1.5E+08	1.5E+08	460
ENSG00000(	4.143168	7.225726	6.597069	0	0	0.821965	3.0794	0.010146	0.023557	RP3-403L1	chr6	+	1.58E+08	1.58E+08	275
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	MRPL35P1	chr6	+	13949326	13949897	572
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	DNAJC19P6	chr6	+	90507317	90507596	280
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	MESTP1	chr6	-	1.29E+08	1.29E+08	994
ENSG00000(	4.143168	2.408575	0	0	0	2.465895	0.85513	0.51943	0.64554	RP3-525L6	chr6	+	17953803	17954161	359
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	OSTCP4	chr4	+	1.14E+08	1.14E+08	449
ENSG00000(	1.035792	0	1.319414	2.247227	4.60216	0	-0.95302	0.46694	0.59623	IGBP1-AS2	chrX	-	69368432	69369504	513
ENSG00000(	0	0	1.319414	3.745378	0	1.64393	-1.0885	0.42102	0.55162	RP11-125K	chr9	-	4944670	4945902	928
ENSG00000(	5.17896	2.408575	11.87472	14.23244	23.93123	26.30288	-1.6287	0.01597	0.035446	RP11-137L	chr10	+	75255283	75279828	1141
ENSG00000(	254.8048	197.5032	343.0476	44.94453	54.30549	34.52253	2.5486	1.52E-21	1.64E-20	EBF2	chr8	-	25699246	25902913	5145
ENSG00000(	0	4.817151	0	0.749076	2.761296	4.109825	-0.45472	0.71772	0.80996	C16orf3	chr16	-	90095316	90096309	994
ENSG00000(	76.6486	85.50443	91.03955	53.18436	83.75931	63.2913	0.3367	0.25808	0.37673	C6orf226	chr6	-	42858005	42858554	550
ENSG00000(	1329.957	1257.276	1262.679	1439.723	1711.083	1749.963	-0.34683	0.004949	0.01227	PPP3R1	chr2	-	68358370	68488362	3023
ENSG00000(	0	0	0	1.498151	0	4.93179	-1.7113	0.20719	0.3164	PSG3	chr19	-	43225790	43244721	1961
ENSG00000(	270.3417	316.7277	262.5633	771.5478	885.4556	867.995	-1.5661	1.22E-25	1.55E-24	FANCG	chr9	-	35073832	35080013	2631
ENSG00000(	489.9296	449.1993	405.06	241.9514	195.1316	272.8924	0.91659	2.54E-07	1.12E-06	AP4M1	chr7	+	99699172	99707968	3408
ENSG00000(	38.3243	25.29004	52.77655	11.23613	12.88605	18.08323	1.4125	0.003809	0.009664	C2orf16	chr2	+	27799389	27805588	6200
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	RP11-404E	chr9	-	76089294	76090989	1696
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	KRTAP1-5	chr17	-	39182278	39183454	1177
ENSG00000(	132.5814	124.0416	157.0102	14.98151	23.0108	12.32947	3.003	1.88E-19	1.85E-18	PLXNA4	chr7	-	1.32E+08	1.32E+08	13786
ENSG00000(	6936.698	6528.444	5500.636	421.7295	418.7966	470.1639	3.8468	1.19E-205	3.67E-203	CEBPD	chr8	-	48649471	48651648	2178
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	TMEM257	chrX	+	1.45E+08	1.45E+08	2441
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	PSG7	chr19	-	43428286	43441330	2496
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	OR3A2	chr17	-	3181193	3182268	1076
ENSG00000(	10.35792	26.49433	11.87472	12.73428	5.522592	4.93179	0.98328	0.15671	0.25273	ARIH2OS	chr3	-	48955221	48956818	1598
ENSG00000(	94.25706	95.13873	97.63662	89.88907	70.87326	67.40112	0.32501	0.23272	0.34641	C5orf54	chr5	-	1.6E+08	1.6E+08	2851
ENSG00000(	1.035792	3.612863	2.638828	18.72689	17.48821	25.48091	-2.8212	0.000272	0.000832	HMSD	chr18	+	61616535	61649008	682
ENSG00000(	3251.351	2961.344	3145.482	50.93714	57.98722	62.46933	5.7557	1.35E-307	1.02E-304	NPTXR	chr22	-	39214457	39239987	5784
ENSG00000(	143.9751	102.3645	138.5384	205.9958	115.9744	133.1583	-0.24182	0.36168	0.49136	FAM200A	chr7	-	99143931	99156159	2480
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	OR2F2	chr7	+	1.44E+08	1.44E+08	1114
ENSG00000(	929.1053	993.5374	1037.059	1922.877	1726.73	1650.506	-0.8398	5.19E-12	3.38E-11	PPP2R2A	chr8	+	26149007	26230196	3940
ENSG00000(	5.17896	6.021439	6.597069	16.47966	20.2495	13.9734	-1.4116	0.038063	0.076674	C19orf73	chr19	-	49621655	49622397	743

ENSG00000(	33.14534	43.35436	40.90183	38.20285	22.09037	23.01502	0.47387	0.2646	0.38444	ZNF880	chr19	+	52873170	52889048	2230
ENSG00000(	459.8916	440.7693	424.8512	246.4459	219.9832	304.949	0.77752	6.59E-06	2.50E-05	TRIM16	chr17	-	15531274	15587625	3206
ENSG00000(	4.143168	2.408575	1.319414	3.745378	2.761296	6.575719	-0.58703	0.57153	0.69037	FAM45B	chrX	+	1.3E+08	1.3E+08	1624
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	TAS2R40	chr7	+	1.43E+08	1.43E+08	1033
ENSG00000(	129.474	148.1274	154.3714	105.6197	73.63456	66.57916	0.80039	0.00217	0.005745	TIGD1	chr2	-	2.33E+08	2.33E+08	2448
ENSG00000(	0	0	0	1.498151	2.761296	5.753754	-2.4738	0.061229	0.11559	FXYD7	chr19	+	35634154	35645204	1111
ENSG00000(	1.035792	4.817151	2.638828	2.996302	1.840864	0	0.58038	0.62987	0.73999	XKR9	chr8	+	71581600	71702606	3174
ENSG00000(	23.82321	34.92434	17.15238	20.97412	21.16994	18.90519	0.30594	0.53675	0.66069	C12orf61	chr12	-	62995531	62997214	1684
ENSG00000(	13.46529	10.83859	11.87472	11.98521	19.32907	15.61733	-0.34875	0.56444	0.68398	C1orf229	chr1	-	2.47E+08	2.47E+08	2258
ENSG00000(	76.6486	52.98866	65.97069	134.0845	109.5314	105.2115	-0.82364	0.003071	0.007918	SLC12A8	chr3	-	1.25E+08	1.25E+08	3484
ENSG00000(	3.107376	2.408575	5.277655	5.243529	2.761296	6.575719	-0.38169	0.69368	0.79116	TMEM14E	chr3	-	1.52E+08	1.52E+08	1296
ENSG00000(	6.214751	7.225726	2.638828	1.498151	0	0	2.4376	0.03981	0.079702	APOL6	chr22	+	36044442	36057404	3069
ENSG00000(	595.5803	557.5852	515.8908	258.4311	183.166	185.7641	1.4036	2.96E-15	2.38E-14	FADS3	chr11	-	61640991	61659523	5314
ENSG00000(	2.071584	2.408575	0	1.498151	1.840864	0.821965	0.086517	0.94621	0.9675	OR2A1	chr7	+	1.44E+08	1.44E+08	933
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	TTC4P1	chr7	-	46039220	46040377	1158
ENSG00000(	0	0	0	2.996302	0	0.821965	-1.0802	0.41594	NA	C3orf36	chr3	-	1.34E+08	1.34E+08	1665
ENSG00000(	3000.689	2993.859	2950.209	1791.04	1699.117	2053.268	0.68892	1.83E-09	9.79E-09	CCNL2	chr1	-	1321091	1334708	4452
ENSG00000(	11554.26	11124.01	8222.587	10163.46	6960.307	8394.728	0.27523	0.072719	0.13397	UBA52	chr19	+	18682540	18688360	2845
ENSG00000(	6.214751	0	6.597069	2.247227	0.920432	1.64393	1.0776	0.34559	0.47508	MYBPHL	chr1	-	1.1E+08	1.1E+08	1372
ENSG00000(	160.5477	174.6217	139.8579	268.9181	225.5058	250.6993	-0.64558	0.001085	0.003026	PPT2	chr6	+	32121218	32131455	2202
ENSG00000(	73.54123	93.93444	51.45714	65.91865	58.90765	64.93523	0.2054	0.516	0.64259	C5orf55	chr5	-	441645	443258	1614
ENSG00000(	48.68222	37.33292	48.81831	14.98151	28.53339	13.15144	1.2254	0.00641	0.015541	ZNF630	chrX	-	47842756	47931025	2791
ENSG00000(	11.39371	46.96722	18.47179	23.97042	18.40864	37.81039	-0.06562	0.90423	0.94075	TIAF1	chr17	-	27400537	27418537	5337
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	OR52B4	chr11	-	4388493	4389616	1124
ENSG00000(	3.107376	2.408575	2.638828	2.247227	0	0.821965	0.97362	0.43019	0.56016	AC092675.	chr2	-	98947852	98972468	588
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AC106876.	chr2	+	2.34E+08	2.34E+08	643
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	C7orf71	chr7	+	26677490	26686889	1956
ENSG00000(	3.107376	8.430014	2.638828	0	0	0	3.3279	0.009717	0.02266	AC016722.	chr2	+	47043807	47049796	1588
ENSG00000(	3.107376	4.817151	2.638828	0	0.920432	2.465895	1.2164	0.30716	0.43293	AC064874.	chr2	-	2.37E+08	2.37E+08	441
ENSG00000(	777.8797	930.9144	580.5421	30.7121	60.74851	46.03004	4.0404	6.73E-68	2.83E-66	BTBD19	chr1	+	45274154	45281257	2659
ENSG00000(	82.86335	86.70872	73.88717	77.90386	92.96363	58.35951	0.089072	0.76132	0.84216	FAM185A	chr7	+	1.02E+08	1.02E+08	2217
ENSG00000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	AC005481.	chr7	+	1.57E+08	1.57E+08	3456
ENSG00000(	5.17896	2.408575	14.51355	6.74168	3.681728	4.109825	0.51235	0.56302	0.6828	RAB6C	chr2	+	1.31E+08	1.31E+08	3077
ENSG00000(	10.35792	12.04288	11.87472	3.745378	4.60216	7.397684	1.0278	0.17185	0.27283	AP000322.	chr21	-	35772615	35773370	756
ENSG00000(	0	1.204288	0	4.494453	0	1.64393	-1.2526	0.35322	0.48286	AC133919.	chr16	-	90106169	90114181	1381
ENSG00000(	6.214751	12.04288	1.319414	5.243529	1.840864	0	1.1825	0.26351	0.38329	AC062017.	chr2	+	2.4E+08	2.4E+08	455
ENSG00000(	18.64425	21.67718	34.30476	0	0	0	5.8848	6.04E-08	2.83E-07	AC112721.	chr2	-	2.38E+08	2.38E+08	588
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC004945.	chr7	+	78982726	78983708	983
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	AC023469.	chr2	-	1.52E+08	1.52E+08	469
ENSG00000(	23.82321	20.47289	59.37362	0	0	0	6.3013	4.21E-09	2.19E-08	AC112721.	chr2	-	2.38E+08	2.38E+08	541
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AC007405.	chr2	-	1.72E+08	1.72E+08	2117
ENSG00000(	2.071584	0	0	0.749076	0	1.64393	-0.07972	0.95303	NA	AC079354.	chr2	-	2.03E+08	2.03E+08	3093
ENSG00000(	0	0	1.319414	5.243529	15.64734	9.041614	-3.4181	0.002288	0.006035	ADRA2B	chr2	-	96778707	96781984	3278
ENSG00000(	402.9231	370.9206	366.797	247.1949	175.8025	222.7525	0.81525	6.85E-06	2.59E-05	LINC00152	chr2	+	87754887	87906324	1096

ENSG00000(	2.071584	3.612863	6.597069	0.749076	8.283888	10.68554	-0.58835	0.54365	0.66609	AC079305.	chr2	+	1.78E+08	1.78E+08	499
ENSG00000(	30.03797	37.33292	39.58241	3.745378	14.72691	20.54912	1.3991	0.01089	0.025111	DCDC2B	chr1	+	32674695	32681797	1863
ENSG00000(	0	1.204288	0	2.247227	5.522592	0	-1.4994	0.26185	0.38122	C10orf55	chr10	-	75669727	75682535	2513
ENSG00000(	2.071584	0	0	0.749076	1.840864	2.465895	-0.71633	0.59099	0.70751	RP13-131K	chr3	-	49022482	49027421	782
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	HIST2H2BA	chr1	+	1.21E+08	1.21E+08	752
ENSG00000(	10.35792	19.2686	13.19414	7.490755	3.681728	7.397684	1.1056	0.11698	0.19974	RP11-66D1	chr1	-	1.57E+08	1.57E+08	433
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	PROX1-IT1	chr1	+	2.14E+08	2.14E+08	229
ENSG00000(	18.64425	18.06432	7.916483	5.243529	4.60216	15.61733	0.75537	0.28522	0.40831	AC005104.	chr2	-	2.42E+08	2.42E+08	442
ENSG00000(	1656.231	1582.434	1695.447	847.2044	821.9458	687.9846	1.0633	5.64E-17	4.93E-16	SEC22B	chr1	+	1.45E+08	1.45E+08	2008
ENSG00000(	2.071584	0	0	5.243529	3.681728	3.28786	-1.7444	0.15272	0.24773	RP1-65J11.	chr1	+	31297075	31307131	1108
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	RP11-408H	chr3	-	1.72E+08	1.72E+08	3212
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	SDCBP2P1	chr6	+	74032560	74033173	614
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-91A1	chr1	+	52499063	52509951	762
ENSG00000(	0	0	0	2.996302	0	1.64393	-1.3112	0.33001	NA	CLDN10-AS	chr13	-	96131698	96186164	895
ENSG00000(	7.250543	4.817151	7.916483	14.98151	10.12475	13.9734	-0.89972	0.20471	0.31322	RP5-858B6	chr1	+	2.31E+08	2.31E+08	794
ENSG00000(	0	0	0	4.494453	3.681728	4.109825	-2.8125	0.029585	0.061403	RPS10P7	chr1	+	2.01E+08	2.01E+08	2329
ENSG00000(	77.68439	104.773	126.6637	3.745378	6.443024	11.50751	3.7356	9.26E-18	8.43E-17	RP11-211G	chr3	+	1.87E+08	1.87E+08	536
ENSG00000(	3.107376	4.817151	1.319414	0	0	0	2.6591	0.046093	0.090462	MEG9	chr14	+	1.02E+08	1.02E+08	2638
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	RPL17P17	chr3	+	65829565	65830121	557
ENSG00000(	3.107376	6.021439	5.277655	0	0	0	3.3751	0.008359	0.019766	LINC00473	chr6	-	1.66E+08	1.66E+08	2212
ENSG00000(	3.107376	0	1.319414	0.749076	0.920432	0.821965	0.52089	0.69371	0.79116	RP11-393I2	chr1	-	58521805	58522152	348
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-399K	chr10	-	77048091	77048440	350
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP4-800M2	chr1	-	52627858	52628698	841
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC011243.	chr2	+	1.34E+08	1.34E+08	415
ENSG00000(	2.071584	4.817151	5.277655	0	0	0	3.0935	0.017579	0.038668	MTND6P21	chr21	+	45892778	45893622	482
ENSG00000(	0	0	1.319414	4.494453	0.920432	0	-1.077	0.42632	0.55664	TMSB4XP3	chr7	+	29665486	29665599	114
ENSG00000(	3.107376	4.817151	5.277655	0.749076	0.920432	2.465895	1.3157	0.23302	0.34673	AC004041.	chr5	-	1.32E+08	1.32E+08	472
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-274J	chr9	-	95857221	95857811	238
ENSG00000(	0	0	1.319414	1.498151	0	0.821965	-0.38347	0.77483	NA	RP11-52I18	chr1	-	1.8E+08	1.8E+08	371
ENSG00000(	1.035792	0	6.597069	0	0	0	2.1847	0.10719	0.18573	RP11-332E	chr13	+	76452849	76455263	243
ENSG00000(	56.96855	49.3758	56.73479	11.23613	23.0108	13.9734	1.7251	5.63E-05	0.00019	FAM115B	chr7	+	1.43E+08	1.43E+08	2232
ENSG00000(	5.17896	2.408575	3.958241	18.72689	13.80648	9.041614	-1.6702	0.03263	0.066877	AC004471.	chr22	+	19109042	19112016	582
ENSG00000(	0	0	2.638828	0	0	1.64393	0.26729	0.84149	NA	RP11-285G	chr10	+	45432956	45451173	425
ENSG00000(	5.17896	10.83859	15.83297	14.98151	25.7721	15.61733	-0.78981	0.20857	0.31805	GS1-124K5	chr7	-	65956083	65958553	699
ENSG00000(	1.035792	0	0	0	2.761296	0	-0.44657	0.73574	NA	AL020996.	chr1	-	26145212	26147288	2077
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	RP11-310H	chr7	+	55640864	55656029	552
ENSG00000(	4.143168	2.408575	0	8.239831	6.443024	4.93179	-1.282	0.20486	0.31338	VN1R42P	chr7	+	64393651	64393994	344
ENSG00000(	0	0	0	5.992604	12.88605	12.32947	-4.2162	0.000322	0.000976	LINC00842	chr10	-	47096454	47151848	2877
ENSG00000(	18.64425	16.86003	13.19414	17.97781	24.85166	16.4393	-0.26282	0.62785	0.73868	RP11-545E	chr9	+	1.31E+08	1.31E+08	544
ENSG00000(	456.7842	487.7365	438.0454	442.7036	506.2376	478.3836	-0.04481	0.75981	0.84128	NUTM2A-A	chr10	-	88963632	89102369	2394
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	TRPC6P	chrX	-	1.55E+08	1.55E+08	880
ENSG00000(	12.4295	20.47289	9.235896	0	0.920432	0	4.3243	4.64E-05	0.000158	RP11-417E	chr6	-	1.7E+08	1.7E+08	647
ENSG00000(	4.143168	0	1.319414	5.243529	14.72691	2.465895	-1.6179	0.12304	0.20813	AC092198.	chrX	+	39868529	39871435	2691
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP3-328E1	chr1	+	1.48E+08	1.48E+08	282

ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	RP11-15M:	chr20	-	51785182	51796089	1620
ENSG00000(	446.4263	432.3393	464.4337	907.1305	692.1649	938.6839	-0.91613	2.62E-09	1.39E-08	EXOSC6	chr16	-	70284134	70285833	1700
ENSG00000(	387.3862	428.7264	393.1853	400.0063	433.5235	401.1189	-0.02959	0.84403	0.90056	VPS52	chr6	-	33218049	33239824	3338
ENSG00000(	2.071584	2.408575	1.319414	2.247227	3.681728	4.93179	-0.70719	0.52089	0.64664	RP11-29H2	chr1	-	1.56E+08	1.56E+08	662
ENSG00000(	2.071584	2.408575	0	5.243529	3.681728	0.821965	-0.8113	0.49552	0.62424	RP11-397P	chr1	-	2.04E+08	2.04E+08	328
ENSG00000(	20.71584	20.47289	36.94359	44.19546	40.49901	22.19305	-0.44729	0.33455	0.4625	RPL23AP5:	chr8	-	163251	163707	457
ENSG00000(	136.7245	116.8159	101.5949	38.20285	35.89685	18.90519	1.9064	5.76E-09	2.96E-08	RP11-632K	chr15	-	32812049	32829127	1673
ENSG00000(	7.250543	9.634302	5.277655	5.992604	8.283888	9.863579	-0.10686	0.88966	0.93153	CDRT15	chr17	-	14138990	14140179	766
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP13-297E	chrX	+	1851477	1874878	445
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	ATP6V0E1P	chr3	-	41900842	41901086	245
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AFF2-IT1	chrX	+	1.48E+08	1.48E+08	443
ENSG00000(	1.035792	0	0	2.247227	9.20432	4.109825	-2.5391	0.039339	0.078846	CSNK1A1P:	chr15	-	37090797	37110660	2147
ENSG00000(	18.64425	20.47289	10.55531	6.74168	1.840864	3.28786	1.8799	0.011286	0.025933	RP11-439E	chr1	-	2.47E+08	2.47E+08	3050
ENSG00000(	31.07376	38.53721	17.15238	5.243529	0	4.109825	2.947	2.44E-05	8.63E-05	AC093690.	chr2	-	28530558	28533326	2110
ENSG00000(	3.107376	1.204288	2.638828	1.498151	0	0.821965	1.0366	0.41655	0.54713	AC079613.	chr2	-	1.89E+08	1.9E+08	797
ENSG00000(	0	1.204288	0	0.749076	0	0	0.1572	0.90001	NA	RABGAP1L-	chr1	+	1.75E+08	1.75E+08	737
ENSG00000(	1.035792	15.65574	1.319414	0.749076	0.920432	3.28786	1.4585	0.18853	0.2935	RP11-223P	chr10	-	1.29E+08	1.29E+08	837
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	RP5-919F1	chr6	+	1.1E+08	1.1E+08	497
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC011431.	chr5	-	1.35E+08	1.35E+08	230
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP1-283K1	chr6	-	1.34E+08	1.34E+08	631
ENSG00000(	31.07376	28.90291	32.98534	23.97042	22.09037	31.23467	0.25736	0.55726	0.67774	LINC00630	chrX	+	1.02E+08	1.02E+08	2101
ENSG00000(	52.82539	31.31148	67.2901	121.3502	126.0992	80.55256	-1.1011	0.000817	0.002324	ZNF844	chr19	+	12175514	12192380	6620
ENSG00000(	0	1.204288	15.83297	0	2.761296	2.465895	1.2667	0.28225	0.4049	MTND5P28	chr2	+	1.21E+08	1.21E+08	1594
ENSG00000(	2.071584	8.430014	6.597069	4.494453	3.681728	5.753754	0.24345	0.78924	0.86218	TMSB4XP4	chr9	+	1.31E+08	1.31E+08	618
ENSG00000(	0	0	0	2.996302	2.761296	1.64393	-2.0518	0.12695	0.21323	RP11-24F1	chr3	-	46406446	46448550	656
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	SMPD4P1	chr22	-	20956882	21011201	2163
ENSG00000(	0	0	0	0	0.920432	3.28786	-1.1769	0.37857	NA	AC078851.	chr2	-	1.41E+08	1.41E+08	298
ENSG00000(	3.107376	3.612863	1.319414	11.23613	2.761296	2.465895	-0.85604	0.40249	0.53363	RP11-700P	chr7	+	56355923	56359118	2884
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	AC003090.	chr7	-	25632971	25790614	1870
ENSG00000(	3.107376	8.430014	5.277655	2.996302	8.283888	4.93179	0.0485	0.95671	0.97446	DHRSX-IT1	chrX	-	2252336	2254451	651
ENSG00000(	0	0	1.319414	21.72319	16.56778	15.61733	-4.2992	2.92E-05	0.000102	CKMT1A	chr15	+	43985084	43991420	1911
ENSG00000(	6.214751	1.204288	2.638828	137.8299	165.6778	148.7757	-5.2175	2.57E-24	3.10E-23	TINCR	chr19	-	5558178	5568045	3733
ENSG00000(	5.17896	8.430014	7.916483	7.490755	2.761296	9.041614	0.12833	0.87632	0.92254	RP11-61K9	chr13	+	20415967	20417812	444
ENSG00000(	7.250543	1.204288	3.958241	5.992604	5.522592	9.041614	-0.61957	0.49505	0.62381	RP3-476K8	chr1	-	26781144	26781678	535
ENSG00000(	1.035792	1.204288	6.597069	0	0	0	2.5314	0.059212	0.1124	TVP23CP1	chr7	+	90261220	90261882	639
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP5-884C9	chr1	-	38546244	38546583	340
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CENPVP1	chrX	+	51453887	51455227	1303
ENSG00000(	2.071584	3.612863	0	0	1.840864	2.465895	0.27955	0.82803	0.88936	RP1-292B1	chr6	-	1.51E+08	1.52E+08	853
ENSG00000(	0	6.021439	2.638828	2.247227	4.60216	0.821965	0.12762	0.91274	0.94661	RP11-216N	chr1	-	1.54E+08	1.54E+08	1309
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC007394.	chr2	+	1.5E+08	1.5E+08	531
ENSG00000(	12.4295	7.225726	6.597069	3.745378	6.443024	2.465895	0.95617	0.25562	0.37382	RP11-289I:	chr1	+	1.48E+08	1.48E+08	704
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-54H7	chr13	+	1.1E+08	1.1E+08	698
ENSG00000(	2.071584	0	0	0	2.761296	0	-0.15346	0.90925	NA	RBM48P1	chr4	+	1.27E+08	1.27E+08	1102
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	AK4P4	chr9	-	5855781	5856426	646

ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RP1-125I3.	chr1	+	26215461	26215600	140
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC073869.	chr2	+	1.32E+08	1.32E+08	1861
ENSG00000(	0	0	0	2.247227	0.920432	1.64393	-1.4644	0.28023	NA	RP4-613A2	chr1	+	2.3E+08	2.3E+08	591
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RFPL4A	chr19	+	56270380	56274541	1035
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	AC008277.	chr2	+	1.6E+08	1.6E+08	1149
ENSG00000(	0	1.204288	5.277655	0	0	0.821965	1.5257	0.25873	0.37743	UHRF2P1	chrX	+	73325407	73327793	2387
ENSG00000(	5.17896	6.021439	3.958241	0	0	0	3.4677	0.006396	0.015517	AC106786.	chr5	-	1.22E+08	1.22E+08	792
ENSG00000(	8.286335	9.634302	6.597069	2.996302	10.12475	8.219649	0.19335	0.80695	0.87472	RP11-131L	chr1	+	85742398	85913807	1950
ENSG00000(	0	0	0	2.247227	1.840864	0	-1.1573	0.3864	NA	AC020581.	chr7	-	1.37E+08	1.37E+08	274
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	AC011242.	chr2	-	43902292	43903461	1170
ENSG00000(	0	0	0	0	0	4.93179	-1.2404	0.35057	NA	AC012314.	chr19	-	54703321	54703838	410
ENSG00000(	4.143168	3.612863	2.638828	0	0	5.753754	0.62424	0.6042	0.71921	RP5-890O3	chr1	+	1314046	1314412	367
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CTB-111F1(	chr7	-	91268162	91272827	536
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RPL34P3	chr21	-	36844393	36844730	338
ENSG00000(	4.143168	1.204288	6.597069	8.988907	19.32907	11.50751	-1.5711	0.050801	0.098451	LINC00571	chr13	-	38624954	38717369	525
ENSG00000(	3.107376	0	0	0	0	0.821965	0.7418	0.57612	NA	RPS24P14	chr11	+	3580887	3581252	366
ENSG00000(	0	3.612863	1.319414	4.494453	0.920432	1.64393	-0.38789	0.75319	0.83675	DIP2A-IT1	chr21	+	47882384	47889219	428
ENSG00000(	2.071584	2.408575	0	0	0	0	1.5041	0.26224	NA	ADH5P3	chr1	+	2.4E+08	2.4E+08	1137
ENSG00000(	3.107376	2.408575	5.277655	2.247227	4.60216	8.219649	-0.41283	0.67219	0.77445	RP4-633O1	chr22	+	36784671	36792562	510
ENSG00000(	0	1.204288	2.638828	0	1.840864	0	0.54056	0.69028	NA	AF230666.	chr8	-	1.34E+08	1.34E+08	773
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	GOLGA6L1:	chrY	+	26314334	26320641	1298
ENSG00000(	1.035792	0	3.958241	0	0	0	1.6134	0.2311	NA	RP11-244K	chr6	+	1.5E+08	1.5E+08	492
ENSG00000(	0	0	0	0.749076	0	9.041614	-2.2409	0.096715	0.17064	RP1-90L6.2	chr22	+	27254597	27261749	6043
ENSG00000(	256.8764	283.0076	196.5927	435.2129	245.7553	433.1755	-0.59315	0.008671	0.020451	NSUN5P1	chr7	+	75039605	75046066	4792
ENSG00000(	0	0	0	2.996302	0	0.821965	-1.0802	0.41594	NA	AC091633.	chr3	+	1.95E+08	1.95E+08	810
ENSG00000(	0	0	0	0.749076	1.840864	3.28786	-1.711	0.20694	NA	RP5-1172N	chrX	+	41134992	41136031	835
ENSG00000(	1.035792	3.612863	1.319414	4.494453	0	0	0.24694	0.84851	0.90347	RP11-71G7	chr3	-	1.76E+08	1.76E+08	827
ENSG00000(	0	4.817151	0	2.996302	0	4.109825	-0.37435	0.77221	0.85025	AC093107.	chr7	+	1.35E+08	1.35E+08	615
ENSG00000(	2.071584	1.204288	9.235896	5.992604	11.96562	10.68554	-1.0757	0.22002	0.33169	AC024162.	chr3	+	6734006	6734775	432
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-467L	chr12	+	31907651	31908055	405
ENSG00000(	4.143168	2.408575	3.958241	0.749076	3.681728	1.64393	0.6411	0.5624	0.68226	BX842568.	chrX	-	36980269	36981498	1230
ENSG00000(	3.107376	0	2.638828	2.247227	2.761296	5.753754	-0.68955	0.54518	0.66736	RAD17P2	chr13	-	49618215	49620930	1977
ENSG00000(	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	AC007879.	chr2	-	2.08E+08	2.08E+08	741
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	AC026188.	chr3	-	3292371	3668980	728
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP1-127B2	chr22	+	45297427	45298351	925
ENSG00000(	1.035792	0	1.319414	0	1.840864	1.64393	-0.30298	0.82242	NA	RP11-644K	chr2	+	20251895	20254257	573
ENSG00000(	129.474	108.3859	75.20659	85.39461	77.31629	93.704	0.28967	0.29993	0.42482	RP4-717I23	chr1	-	93727743	93811582	2973
ENSG00000(	309.7018	342.0177	270.4798	108.616	68.11197	108.4994	1.6772	5.84E-14	4.33E-13	AC004383.	chrX	-	1.34E+08	1.34E+08	760
ENSG00000(	2.071584	1.204288	6.597069	0	0.920432	3.28786	0.88793	0.46183	0.59108	AC116609.	chr2	+	742488	747767	535
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	GHc-602D8	chrX	+	1.01E+08	1.01E+08	670
ENSG00000(	2.071584	0	2.638828	0.749076	0	0	1.2345	0.36288	NA	AC008073.	chr2	-	24422708	24424567	543
ENSG00000(	2.071584	2.408575	1.319414	482.4047	489.6698	405.2287	-7.4683	1.30E-39	2.67E-38	TSSC2	chr11	+	3402191	3430208	2337
ENSG00000(	0	4.817151	3.958241	2.247227	0.920432	0.821965	0.79311	0.51572	0.64238	RP11-353N	chr1	+	1.5E+08	1.5E+08	1988
ENSG00000(	1.035792	0	0	0	0	1.64393	-0.12526	0.92174	NA	CCDC74B-A	chr2	+	1.31E+08	1.31E+08	1841

ENSG00000(	38.3243	52.98866	27.70769	60.67512	65.35067	110.9653	-0.97191	0.008517	0.020115	RP11-54O7	chr1	-	852250	855072	1389
ENSG00000(	169.8699	205.9332	195.2732	118.3539	117.8153	114.2531	0.69856	0.001009	0.002827	LINC00205	chr21	+	46713200	46717269	1391
ENSG00000(	5.17896	8.430014	2.638828	0	2.761296	0	1.9579	0.092737	0.16476	MIR1255B:	chr7	+	81638493	81659271	2651
ENSG00000(	119.1161	110.7945	96.31721	222.4754	216.3015	207.9571	-0.97786	3.93E-06	1.53E-05	CD99P1	chrX	+	2527389	2575270	3071
ENSG00000(	3.107376	8.430014	5.277655	0	1.840864	3.28786	1.3824	0.19873	0.30615	RP11-403I:	chr1	+	1.49E+08	1.49E+08	5057
ENSG00000(	3.107376	1.204288	3.958241	0.749076	0.920432	1.64393	0.95748	0.4276	0.55782	RP11-554I8	chr10	+	6779344	6780988	917
ENSG00000(	0	0	0	0	5.522592	0.821965	-1.658	0.22147	0.33315	RP4-593M8	chr1	-	93046033	93046378	346
ENSG00000(	3.107376	12.04288	3.958241	0	5.522592	2.465895	1.0515	0.31093	0.43715	UBE2E1-AS:	chr3	-	23845515	23848396	778
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	COX5BP8	chr1	+	1.79E+08	1.79E+08	349
ENSG00000(	22.78742	3.612863	19.79121	20.22504	23.93123	19.72716	-0.4374	0.46778	0.59707	ENTPD3-AS	chr3	-	40355293	40494820	2036
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AP000295.	chr21	-	34636178	34638565	2228
ENSG00000(	30.03797	28.90291	26.38828	33.7084	33.13555	66.57916	-0.62695	0.14443	0.23657	CERS1	chr19	-	18979361	19007536	2558
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RPS20P14	chr3	+	1.87E+08	1.87E+08	360
ENSG00000(	27.96638	33.72006	26.38828	23.22134	39.57858	29.59074	-0.06183	0.88782	0.93022	RP6-206I17	chr1	-	1.44E+08	1.44E+08	2210
ENSG00000(	1.035792	7.225726	0	0	0	0	2.3119	0.087872	0.15763	RP11-437J:	chr6	-	1.14E+08	1.14E+08	507
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-197K	chr3	+	1.91E+08	1.91E+08	901
ENSG00000(	7.250543	0	5.277655	14.23244	19.32907	28.76877	-2.1023	0.004992	0.012364	AC007255.	chr7	-	29554385	29603286	889
ENSG00000(	0	1.204288	2.638828	1.498151	6.443024	5.753754	-1.4178	0.21925	0.33085	RP11-543D	chr1	-	48226804	48231219	407
ENSG00000(	2.071584	0	2.638828	0	0	0.821965	1.2046	0.37464	NA	DIAPH3-AS:	chr13	+	60718832	60727639	367
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC128677.	chr2	-	92222172	92223026	355
ENSG00000(	5.17896	0	0	0	0	0	1.5469	0.24589	NA	CDH23-AS1	chr10	-	73267910	73271630	378
ENSG00000(	3.107376	6.021439	3.958241	1.498151	7.363456	11.50751	-0.55074	0.55205	0.673	CFL1P1	chr10	+	89577685	89605369	2120
ENSG00000(	1.035792	0	0	0	3.681728	0	-0.68494	0.60991	NA	RP11-505P	chr6	-	74201748	74202465	370
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	DAZAP2P1	chr2	-	2.03E+08	2.03E+08	503
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC092570.	chr2	+	1.02E+08	1.02E+08	390
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	BANF1P4	chr1	-	1.75E+08	1.75E+08	270
ENSG00000(	4.143168	6.021439	2.638828	0	0	0	3.1879	0.013883	0.031284	RP1-56J10.	chr22	+	30994296	31002674	249
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-472N	chr10	+	31893528	31895146	421
ENSG00000(	9.322127	6.021439	2.638828	0.749076	0.920432	0.821965	2.2517	0.040247	0.08048	AC007091.	chr7	+	19393157	19618229	566
ENSG00000(	2.071584	0	1.319414	6.74168	10.12475	9.041614	-2.3747	0.020438	0.044211	FAM95B1	chr9	+	42466317	42474239	4692
ENSG00000(	1.035792	1.204288	0	2.996302	1.840864	2.465895	-1.1169	0.37978	0.5105	RP11-135J:	chr1	-	2.19E+08	2.19E+08	1126
ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	RP11-80I15	chr9	+	97885803	97886150	348
ENSG00000(	2.071584	3.612863	2.638828	2.247227	4.60216	1.64393	-0.01898	0.98613	0.99155	AC147651.	chr7	+	560028	564869	3506
ENSG00000(	0	3.612863	1.319414	2.247227	4.60216	1.64393	-0.58179	0.6281	0.73884	RP11-74C1	chr1	+	1.52E+08	1.52E+08	495
ENSG00000(	0	0	2.638828	0	2.761296	0.821965	-0.2421	0.85821	0.90984	NPM1P19	chr20	-	37606354	37607065	712
ENSG00000(	6.214751	7.225726	6.597069	136.3317	152.7917	175.9005	-4.4244	1.03E-25	1.31E-24	HLA-DPB1	chr6	+	33043703	33054978	1560
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC098592.	chr7	+	16977849	16978181	333
ENSG00000(	24.85901	46.96722	14.51355	5.243529	5.522592	5.753754	2.2531	0.000318	0.000965	AC005517.	chr17	+	15410180	15410668	489
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	ABCC5-AS1	chr3	+	1.84E+08	1.84E+08	469
ENSG00000(	0	0	5.277655	0	0.920432	0.821965	0.84842	0.53029	0.65508	RP11-424D	chr1	+	69521581	69650686	627
ENSG00000(	12.4295	12.04288	15.83297	0	2.761296	5.753754	2	0.019425	0.042277	AC019048.	chr2	-	7202858	7218011	555
ENSG00000(	1.035792	7.225726	3.958241	2.996302	6.443024	3.28786	-0.05402	0.95676	0.97447	RP11-251G	chr7	+	1.05E+08	1.05E+08	463
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC008171.	chr2	-	2.06E+08	2.06E+08	200
ENSG00000(	43.50326	44.55865	44.86007	53.18436	30.37426	68.22309	-0.19174	0.61587	0.72887	RP5-995J1:	chr20	+	42839600	42854667	1563

ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	CCNJP2	chr1	+	93221351	93222513	1163
ENSG00000(	4.143168	0	0	0	4.60216	4.93179	-0.76728	0.54684	0.66874	SEC13P1	chr3	+	33075355	33076302	948
ENSG00000(	8.286335	8.430014	3.958241	0.749076	1.840864	3.28786	1.541	0.11775	0.20071	AP001469.	chr21	+	47640183	47641992	525
ENSG00000(	0	0	1.319414	0	0.920432	1.64393	-0.44377	0.74139	NA	AC068657.	chr5	-	1.59E+08	1.59E+08	306
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	DPPA2P1	chrY	+	15342765	15343320	556
ENSG00000(	2.071584	1.204288	0	0	6.443024	0	-0.55373	0.67708	0.77848	RP11-353H	chr3	-	43526464	43527372	515
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-430G	chr1	+	62119866	62120580	715
ENSG00000(	2.071584	13.24716	1.319414	1.498151	2.761296	2.465895	1.0689	0.31001	0.43619	ASS1P2	chr2	-	39037574	39038796	1223
ENSG00000(	2.071584	6.021439	1.319414	0	0	0	2.6699	0.045268	0.089035	AC010136.	chr2	+	2.19E+08	2.19E+08	568
ENSG00000(	3.107376	2.408575	0	0	0	0	1.7825	0.18787	NA	RP11-183E	chr10	+	24446764	24447710	947
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	RP11-33A1	chr3	-	1.78E+08	1.78E+08	2100
ENSG00000(	0	0	0	0	0	13.15144	-2.5028	0.063389	0.11917	AC008074.	chr2	-	64622354	64680932	723
ENSG00000(	2.071584	8.430014	2.638828	0	3.681728	3.28786	0.73186	0.509	0.63644	RP11-458I	chr1	+	1.5E+08	1.5E+08	870
ENSG00000(	1.035792	3.612863	1.319414	0	0	0	1.9913	0.14206	0.23358	RP11-533C	chr6	+	41997791	41999120	161
ENSG00000(	14.50109	14.45145	13.19414	0	1.840864	0.821965	3.4451	0.000239	0.000737	AC016738.	chr2	-	1.02E+08	1.02E+08	3485
ENSG00000(	17.60846	8.430014	18.47179	15.73059	15.64734	14.79537	-0.04974	0.93286	0.95983	RP11-24J2	chr1	-	64560125	64636980	2189
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AL133244.	chr2	-	33281400	33288180	258
ENSG00000(	5.17896	2.408575	0	0	2.761296	2.465895	0.40423	0.74521	0.8304	RP4-710M	chr1	+	56880635	56881638	545
ENSG00000(	164.6909	192.686	159.6491	353.5637	362.6502	354.2669	-1.0452	3.93E-09	2.05E-08	AFG3L1P	chr16	+	90038994	90068569	3327
ENSG00000(	264.1269	215.5675	266.5216	283.1506	323.9921	301.6611	-0.2821	0.11198	0.1924	AC009948.	chr2	+	1.79E+08	1.79E+08	2007
ENSG00000(	0	0	0	2.247227	1.840864	1.64393	-1.6991	0.21004	NA	PRKRIRP8	chr1	-	2.41E+08	2.41E+08	2115
ENSG00000(	1.035792	0	0	1.498151	1.840864	0.821965	-0.93518	0.49005	NA	ZNF587P1	chr3	+	31835962	31837667	1386
ENSG00000(	3.107376	2.408575	1.319414	0.749076	2.761296	0	0.68347	0.58692	0.70411	AC002456.	chr7	-	90219933	90226667	450
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-598C	chr7	+	53070113	53071122	1010
ENSG00000(	0	0	1.319414	0	0.920432	2.465895	-0.65854	0.62673	NA	DDX11L1	chr1	+	11869	14412	1657
ENSG00000(	0	0	2.638828	2.996302	0	3.28786	-0.77759	0.55851	0.67901	AC068491.	chr2	+	1.12E+08	1.12E+08	1241
ENSG00000(	1.035792	0	0	0	1.840864	1.64393	-0.70101	0.60446	NA	RP11-561N	chr7	+	64011876	64012444	569
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	SMCR2	chr17	-	17577340	17581002	564
ENSG00000(	0	1.204288	1.319414	0	0	4.93179	-0.54285	0.68753	0.78648	HNRNPRP1	chr10	-	21913521	21915215	1695
ENSG00000(	7.250543	12.04288	14.51355	0	0	0	4.717	5.18E-05	0.000176	AC104809.	chr2	-	2.42E+08	2.42E+08	2345
ENSG00000(	7.250543	6.021439	1.319414	2.996302	1.840864	8.219649	0.14644	0.88101	0.92557	RP11-321N	chr6	-	86270033	86270928	596
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP3-471M	chr1	+	1.73E+08	1.73E+08	658
ENSG00000(	0	0	0	2.996302	0.920432	1.64393	-1.649	0.22411	NA	CTA-407F1	chr22	+	26043228	26045199	1628
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	ATP5C1P1	chr14	-	54457819	54458713	895
ENSG00000(	8.286335	1.204288	1.319414	6.74168	4.60216	2.465895	-0.26908	0.79217	0.8642	AC022400.	chr10	-	75473354	75473609	252
ENSG00000(	2.071584	0	1.319414	0	0.920432	0	0.84841	0.52989	NA	AC019070.	chr2	-	1.49E+08	1.49E+08	1024
ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	AC111155.	chr17	-	58804526	58804843	318
ENSG00000(	0	2.408575	15.83297	2.247227	0	0	2.0762	0.090089	0.16093	RP11-488L	chr1	+	2.47E+08	2.47E+08	270
ENSG00000(	0	0	0	0.749076	4.60216	0	-1.4494	0.28352	NA	RP11-728K	chr7	-	1.5E+08	1.5E+08	291
ENSG00000(	13.46529	6.021439	17.15238	0	0	0	4.8261	3.21E-05	0.000112	AC005022.	chr7	+	41141202	41173105	1220
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	AC097500.	chr2	-	1.87E+08	1.87E+08	477
ENSG00000(	4.143168	15.65574	13.19414	0.749076	3.681728	7.397684	1.3072	0.13216	0.22029	MIR181A2I	chr9	+	1.27E+08	1.27E+08	662
ENSG00000(	2.071584	0	1.319414	2.247227	1.840864	2.465895	-0.64114	0.60978	0.7236	RP11-383C	chr10	-	1.27E+08	1.27E+08	2600
ENSG00000(	1.035792	0	0	4.494453	0	3.28786	-1.5724	0.23956	0.35462	RP11-136K	chr6	+	1.51E+08	1.51E+08	639

ENSG00000(	5.17896	0	1.319414	0	1.840864	0	1.0756	0.42176	0.55231	TCEAL3-AS1	chrX	-	1.03E+08	1.03E+08	361
ENSG00000(	712.6248	874.3129	556.7926	263.6746	208.0176	277.0022	1.5097	4.84E-16	4.07E-15	EPB41L4A-/	chr5	+	1.11E+08	1.11E+08	2969
ENSG00000(	0	1.204288	1.319414	1.498151	0	0	0.30687	0.81977	NA	RP11-445P	chr10	-	5307996	5313199	692
ENSG00000(	0	0	0	1.498151	0.920432	2.465895	-1.4807	0.27499	NA	HMGN1P4	chr1	-	1.83E+08	1.83E+08	290
ENSG00000(	9.322127	2.408575	10.55531	5.992604	4.60216	1.64393	0.75136	0.40621	0.53707	AC016725.	chr2	-	1.35E+08	1.36E+08	976
ENSG00000(	0	1.204288	3.958241	11.23613	18.40864	13.15144	-2.7061	0.002786	0.007239	AC005076.	chr7	-	86780739	86781736	769
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP1-90G24	chr22	+	32669407	32673173	590
ENSG00000(	741.627	662.3582	635.9574	740.8357	663.6315	586.883	0.035309	0.80745	0.87498	GLTPD1	chr1	+	1260136	1264277	2190
ENSG00000(	0	2.408575	7.916483	0	2.761296	3.28786	0.55272	0.64692	0.75358	GAPDHP55	chr15	+	44355709	44356511	803
ENSG00000(	3.107376	8.430014	15.83297	0	2.761296	1.64393	2.209	0.028192	0.058855	EGFR-AS1	chr7	-	55247443	55256627	2806
ENSG00000(	0	0	0	0	0.920432	4.93179	-1.5674	0.24723	NA	HSPA8P16	chr7	+	84657144	84659008	1865
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	ARSEP1	chrY	+	14460540	14468218	635
ENSG00000(	4.143168	1.204288	6.597069	0	4.60216	7.397684	-0.00328	0.99757	0.99851	AC007319.	chr2	+	1.88E+08	1.88E+08	829
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-344H	chr1	+	27310119	27310515	397
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP4-622L5	chr1	-	32670370	32672415	786
ENSG00000(	3.107376	6.021439	2.638828	0	0	0	3.0489	0.019605	0.04262	RP11-430K	chr9	+	1.15E+08	1.15E+08	413
ENSG00000(	18.64425	13.24716	1.319414	8.239831	4.60216	1.64393	1.0629	0.22282	0.33496	RP11-75A9	chrX	-	46313532	46316634	2299
ENSG00000(	0	7.225726	0	0	0	0	1.9679	0.14595	0.2386	RP1-56L9.7	chr6	-	1.6E+08	1.6E+08	741
ENSG00000(	0	1.204288	0	0	0	3.28786	-0.57455	0.66797	NA	AP000936.	chr11	+	1.17E+08	1.17E+08	483
ENSG00000(	1317.527	1470.435	1609.685	2932.631	2729.081	2367.259	-0.86739	1.27E-11	8.04E-11	SNHG14	chr15	+	25224704	25664609	8842
ENSG00000(	4.143168	6.021439	9.235896	0	11.96562	9.863579	-0.14491	0.87703	0.92304	AC091729.	chr7	+	1114086	1117672	869
ENSG00000(	3.107376	1.204288	9.235896	14.23244	15.64734	14.79537	-1.5917	0.039432	0.078998	UBE2FP1	chr3	-	37185003	37185449	447
ENSG00000(	13.46529	6.021439	11.87472	20.97412	12.88605	21.37109	-0.77081	0.2121	0.32212	RP11-86H7	chr1	-	95104017	95285837	1331
ENSG00000(	0	0	0	4.494453	3.681728	0	-2.0439	0.13074	0.21825	RP11-39K2	chr9	+	5096666	5098193	1528
ENSG00000(	41.43168	48.17151	40.90183	6.74168	28.53339	23.83698	1.1151	0.022957	0.049031	LL22NC03-	chr22	+	22292609	22297799	3647
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	AC018804.	chr2	+	1.31E+08	1.31E+08	578
ENSG00000(	7.250543	14.45145	14.51355	0.749076	19.32907	3.28786	0.5763	0.49449	0.62324	RP5-1033H	chr1	+	94057756	94071130	722
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	RP11-578F	chr3	-	45201266	45201667	402
ENSG00000(	13.46529	18.06432	3.958241	7.490755	5.522592	4.109825	0.96116	0.21419	0.32459	RP11-472B	chr4	+	39481875	39483525	1532
ENSG00000(	3.107376	0	0	0.749076	0	0	0.76338	0.56438	NA	AC064834.	chr2	+	1.96E+08	1.96E+08	989
ENSG00000(	1.035792	0	1.319414	6.74168	5.522592	13.15144	-2.7076	0.011774	0.026921	AP001630.	chr21	-	44384749	44385473	437
ENSG00000(	0	0	0	0	6.443024	0.821965	-1.831	0.17712	0.27929	ELMO1-AS1	chr7	+	37037401	37053235	528
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CYP4F25P	chr9	+	69477881	69478916	520
ENSG00000(	0	0	0	5.243529	19.32907	28.76877	-4.9402	1.30E-05	4.75E-05	CENPVP3	chrX	-	51360961	51361446	486
ENSG00000(	14.50109	9.634302	29.0271	10.48706	20.2495	10.68554	0.33858	0.58277	0.70039	RP5-837J1.	chr17	+	33332107	33336762	4656
ENSG00000(	1.035792	1.204288	11.87472	0	0	2.465895	1.7478	0.15553	0.25135	RP11-343H	chr1	-	2.07E+08	2.07E+08	433
ENSG00000(	1.035792	1.204288	0	4.494453	0.920432	2.465895	-1.1958	0.34648	0.47603	INHBA-AS1	chr7	+	41733514	41818986	3005
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	PTPN2P2	chr13	+	31127807	31128830	1024
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	AP001271.	chr11	-	70412492	70417428	421
ENSG00000(	1.035792	0	3.958241	1.498151	0	0	0.88795	0.51175	0.63886	ATG12P2	chr2	-	2.24E+08	2.24E+08	416
ENSG00000(	1.035792	3.612863	0	0	0.920432	0	1.1485	0.39729	NA	POM121L1	chr22	-	25041133	25055114	9547
ENSG00000(	8.286335	1.204288	2.638828	28.46487	6.443024	10.68554	-1.6861	0.042248	0.083932	UBE2SP2	chr17	+	18580574	18581070	497
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	RP11-510C	chr1	-	75593515	75598743	670
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC107057.	chr2	-	5742637	5831620	468

ENSG00000(	11.39371	12.04288	5.277655	0	0	0	4.4675	0.00017	0.000536	AC112715.	chr2	+	2.38E+08	2.38E+08	350
ENSG00000(	21.75163	30.10719	18.47179	19.47596	21.16994	13.9734	0.35365	0.48971	0.6187	AC000123.	chr7	+	1.27E+08	1.27E+08	516
ENSG00000(	0	3.612863	1.319414	1.498151	0.920432	0	0.59539	0.65513	0.76039	AMMECR1-	chrX	-	1.1E+08	1.1E+08	561
ENSG00000(	3.107376	0	0	0	3.681728	3.28786	-0.68362	0.60324	0.7183	RP11-510C	chr1	-	75595659	75598261	2203
ENSG00000(	6.214751	3.612863	23.74945	5.992604	11.04518	3.28786	0.64486	0.42905	0.55921	AC009506.	chr2	+	1.6E+08	1.6E+08	1494
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	HCG14	chr6	+	28864307	28865099	413
ENSG00000(	0	1.204288	0	0.749076	0	0	0.1572	0.90001	NA	RP11-309L	chr7	-	1.29E+08	1.29E+08	560
ENSG00000(	6.214751	14.45145	10.55531	3.745378	3.681728	4.93179	1.2001	0.13563	0.22488	DNAJC27-A	chr2	+	25194259	25262563	4660
ENSG00000(	0	0	0	3.745378	1.840864	1.64393	-2.0159	0.13434	0.22333	RP3-522D1	chr1	+	1.13E+08	1.13E+08	587
ENSG00000(	2.071584	0	0	0	0	1.64393	0.14412	0.91322	NA	LINC00570	chr2	+	11534107	11543203	1330
ENSG00000(	3.107376	0	9.235896	0.749076	0.920432	0.821965	1.6491	0.17323	0.27454	SDHDP6	chr1	-	25620655	25621134	480
ENSG00000(	6.214751	3.612863	6.597069	0	0	0	3.5898	0.004444	0.011122	AC096559.	chr2	+	11988748	12718474	2183
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	SNX18P9	chr9	+	69451764	69452598	835
ENSG00000(	8.286335	6.021439	21.11062	11.98521	12.88605	8.219649	0.079204	0.9089	0.94397	CTC-203F4.	chr5	+	1.34E+08	1.35E+08	2479
ENSG00000(	24.85901	30.10719	15.83297	3.745378	1.840864	7.397684	2.2772	0.000725	0.002081	HOXD-AS1	chr2	-	1.77E+08	1.77E+08	4235
ENSG00000(	4.143168	3.612863	3.958241	1.498151	8.283888	4.109825	-0.19452	0.84279	0.89968	RP11-574K	chr10	+	75573276	75574495	445
ENSG00000(	4.143168	0	0	0.749076	0.920432	0	0.68566	0.61321	NA	RP4-604K5	chr1	-	87409368	87410425	233
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	PHEX-AS1	chrX	-	22180850	22191100	1906
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	RP11-10L1	chr4	+	1.04E+08	1.04E+08	258
ENSG00000(	0	1.204288	1.319414	2.996302	0	1.64393	-0.54115	0.68524	0.7846	AL590762.	chrX	-	70534762	70535729	640
ENSG00000(	1.035792	3.612863	2.638828	0	0.920432	0	1.7583	0.18467	0.28909	RP11-371A	chr10	+	23632886	23634110	892
ENSG00000(	14.50109	4.817151	9.235896	7.490755	5.522592	6.575719	0.50058	0.51633	0.6429	RP13-228J	chrX	-	1.55E+08	1.55E+08	1329
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-359D	chr4	-	77679707	77723117	110
ENSG00000(	0	6.021439	1.319414	0	0.920432	0	1.6434	0.22123	0.33301	AC104699.	chr2	+	25643986	25650512	414
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RPS6P8	chr6	-	74100761	74101490	730
ENSG00000(	5.17896	0	0	0	0	0	1.5469	0.24589	NA	RP11-262I	chr10	-	71754382	71767592	524
ENSG00000(	0	7.225726	0	0	0.920432	0	1.5108	0.26454	0.38438	RP1-15D23	chr1	+	1.73E+08	1.73E+08	799
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC069394.	chr2	+	1.39E+08	1.39E+08	553
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	AC110299.	chr2	+	2.42E+08	2.42E+08	678
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP5-1027C	chr1	-	88365592	88371397	787
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	MINOS1P3	chr3	-	27256307	27256509	203
ENSG00000(	8.286335	0	10.55531	0	2.761296	1.64393	1.6374	0.14799	0.24112	WARS2-IT1	chr1	+	1.2E+08	1.2E+08	2060
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AC090044.	chr3	+	898807	899774	497
ENSG00000(	0	0	0	2.996302	2.761296	3.28786	-2.35	0.076628	0.14015	CYCSP49	chrY	+	28695572	28695890	319
ENSG00000(	2.071584	1.204288	0	3.745378	0.920432	7.397684	-1.3526	0.25552	0.37375	RP11-533K	chr9	+	97258557	97275161	501
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RP11-499C	chr10	+	5037680	5039572	425
ENSG00000(	0	4.817151	0	0	1.840864	0	0.69806	0.6069	0.72127	PDCL3P6	chr1	+	52645520	52646225	706
ENSG00000(	0	2.408575	1.319414	0.749076	0	0.821965	0.63477	0.63934	NA	CTA-292E1(	chr22	-	29231881	29232125	245
ENSG00000(	24.85901	36.12863	22.43003	0	0	0	6.0523	1.87E-08	9.21E-08	RP11-48O2	chr1	+	1.6E+08	1.6E+08	1113
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP1-272L1	chr1	-	2.1E+08	2.1E+08	863
ENSG00000(	4.143168	1.204288	2.638828	2.247227	4.60216	0.821965	0.062239	0.9561	0.97397	RP11-179G	chr1	-	1.6E+08	1.6E+08	886
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	AP000697.	chr21	-	38071073	38073864	339
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	AC114730.	chr2	-	2.43E+08	2.43E+08	1228
ENSG00000(	0	0	0	1.498151	3.681728	0	-1.4292	0.2903	NA	AC005077.	chr7	-	75747043	75761505	631

ENSG00000(	0	6.021439	0	0.749076	0	0	1.3768	0.31019	0.43627	AC005014.	chr7	-	16623407	16626382	2976
ENSG00000(	8.286335	14.45145	11.87472	5.243529	28.53339	22.19305	-0.64632	0.33074	0.45858	SLC25A5-A	chrX	-	1.19E+08	1.19E+08	3062
ENSG00000(	5.17896	1.204288	7.916483	0.749076	0	0	2.7257	0.029221	0.060754	RP11-297H	chr1	-	1.7E+08	1.7E+08	1457
ENSG00000(	23.82321	54.19295	46.17948	62.17327	63.50981	47.67397	-0.47975	0.20661	0.31567	MSL3P1	chr2	-	2.35E+08	2.35E+08	2032
ENSG00000(	6.214751	0	0	3.745378	1.840864	4.93179	-0.53052	0.65481	0.76009	AF196972.	chrX	-	48364911	48367226	653
ENSG00000(	27.96638	14.45145	14.51355	112.3613	78.23672	75.62077	-2.1612	3.35E-08	1.61E-07	RP3-326I13	chrX	+	43036243	43085847	2228
ENSG00000(	5.17896	1.204288	7.916483	0	0	2.465895	1.8272	0.1284	0.21508	AC087380.	chr11	-	5539671	5546185	1478
ENSG00000(	0	1.204288	0	1.498151	0	0	-0.08768	0.94524	NA	RP11-302K	chr10	-	1.04E+08	1.04E+08	255
ENSG00000(	8.286335	0	1.319414	0	1.840864	0	1.5138	0.2475	0.3643	MCCD1P2	chr6	-	29962214	29963091	335
ENSG00000(	0	1.204288	7.916483	0.749076	1.840864	1.64393	0.77525	0.52665	0.65143	RP4-633I8.	chr1	-	8846270	8846972	703
ENSG00000(	3.107376	3.612863	6.597069	2.996302	3.681728	0.821965	0.67496	0.51647	0.64297	RP11-479C	chr7	+	65238607	65267054	731
ENSG00000(	2.071584	2.408575	0	7.490755	0.920432	2.465895	-0.94243	0.425	0.55545	RP11-169K	chr1	+	16119291	16119780	490
ENSG00000(	0	0	1.319414	0.749076	0.920432	8.219649	-1.8114	0.1646	0.26297	THAP5P1	chr7	-	1.58E+08	1.58E+08	262
ENSG00000(	2.071584	0	0	0	2.761296	0	-0.15346	0.90925	NA	AC019181.	chr2	-	1.66E+08	1.66E+08	310
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	AL121578.	chrX	+	37805137	37806028	892
ENSG00000(	1.035792	0	1.319414	0	0	0.821965	0.54471	0.68089	NA	RP11-496H	chr1	-	10114503	10114839	337
ENSG00000(	24.85901	25.29004	25.06886	18.72689	17.48821	7.397684	0.7535	0.16255	0.26048	RP3-486L4	chr6	+	88410228	88411243	413
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	SCEL-AS1	chr13	-	78173890	78180686	493
ENSG00000(	0	0	1.319414	1.498151	0	1.64393	-0.61204	0.65104	NA	MTND2P5	chr7	-	1.42E+08	1.42E+08	1006
ENSG00000(	6.214751	0	5.277655	0.749076	2.761296	0.821965	1.0682	0.36464	0.49441	RP11-151A	chr13	-	1.01E+08	1.01E+08	2372
ENSG00000(	4.143168	6.021439	0	5.992604	2.761296	2.465895	-0.10849	0.91918	0.95092	RP11-466F	chr1	+	1.66E+08	1.66E+08	2150
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP11-467I2	chr1	+	2.41E+08	2.41E+08	354
ENSG00000(	2.071584	0	2.638828	0	0	0	1.5584	0.24658	NA	AC011239.	chr2	-	23729913	23747214	584
ENSG00000(	0	2.408575	0	0	1.840864	0	0.16879	0.89944	NA	RP11-289H	chr1	-	1.44E+08	1.44E+08	2175
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP1-32B1.4	chr6	+	1.36E+08	1.36E+08	216
ENSG00000(	5.17896	19.2686	7.916483	2.996302	3.681728	0.821965	1.8474	0.038515	0.077438	AC017104.	chr2	+	2.32E+08	2.32E+08	1313
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	LINC00703	chr10	+	4426438	4452804	2390
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	C17orf72	chr17	+	62075711	62081664	3127
ENSG00000(	6.214751	16.86003	9.235896	30.7121	16.56778	23.01502	-1.0761	0.070738	0.13097	RP3-417O2	chr6	+	97233013	97243697	481
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	RP3-395M2	chr1	-	2423739	2424697	455
ENSG00000(	2.071584	1.204288	1.319414	0	6.443024	0.821965	-0.43415	0.72901	0.81844	C4B	chr6	+	31982539	32003195	5460
ENSG00000(	2.071584	3.612863	0	0	0	4.93179	0.13339	0.91907	0.95089	GPC6-AS2	chr13	-	94470677	94488397	587
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-290F	chr20	+	48884023	48896332	2010
ENSG00000(	1.035792	1.204288	2.638828	1.498151	1.840864	2.465895	-0.19239	0.87432	0.92106	RPL7P57	chrX	-	47700362	47701101	740
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	OR6D1P	chr10	+	45753633	45754571	939
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-48F1.	chr3	-	1.86E+08	1.86E+08	2285
ENSG00000(	3.107376	0	0	0	0	0.821965	0.7418	0.57612	NA	RP11-114B	chr1	-	33183335	33190838	395
ENSG00000(	2.071584	2.408575	1.319414	5.992604	1.840864	3.28786	-0.74366	0.50075	0.62891	RP11-1033	chr11	-	27910385	27912580	2196
ENSG00000(	0	3.612863	1.319414	2.996302	0.920432	1.64393	-0.139	0.91182	0.94588	RP11-351C	chr10	+	65249221	65249398	178
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	AP001476.	chr21	+	47456966	47459721	2198
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC010886.	chr2	+	2.19E+08	2.19E+08	2869
ENSG00000(	6.214751	1.204288	3.958241	1.498151	0	2.465895	1.1346	0.33257	0.4606	RPL19P12	chr7	-	1.03E+08	1.03E+08	591
ENSG00000(	4.143168	4.817151	2.638828	0	9.20432	4.93179	-0.21661	0.83642	0.89542	STK24-AS1	chr13	+	99229498	99231084	1278
ENSG00000(	0	0	1.319414	0.749076	0.920432	0	-0.15244	0.90808	NA	KRT18P27	chr13	+	90882638	90883936	1299

ENSG00000(	5.17896	10.83859	3.958241	34.45748	15.64734	39.45432	-2.0442	0.001092	0.003043	ADM5	chr19	+	50191921	50193832	1718
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	ATP5J2LP	chr21	-	37761176	37761410	235
ENSG00000(	4.143168	4.817151	5.277655	2.996302	2.761296	3.28786	0.54986	0.57384	0.69256	PRKAR2A-A	chr3	+	48885005	48889414	3447
ENSG00000(	16.57267	9.634302	11.87472	5.243529	1.840864	10.68554	1.0009	0.18948	0.29462	LINC00422	chr13	-	21877651	21922860	1178
ENSG00000(	1.035792	3.612863	5.277655	0	0	0	2.7452	0.038793	0.077916	MKRN5P	chrX	-	73380897	73382363	1467
ENSG00000(	7.250543	13.24716	18.47179	0	3.681728	6.575719	1.7077	0.048724	0.09488	AC063976.	chr5	+	1.32E+08	1.32E+08	3556
ENSG00000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	RP4-816N1	chr12	+	2891070	2891537	468
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	AC017035.	chr2	-	1.98E+08	1.98E+08	1115
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC006509.	chr2	+	47932607	47933118	395
ENSG00000(	0	0	3.958241	0.749076	3.681728	0.821965	-0.27419	0.83426	0.89385	GS1-259H1	chr7	-	99235865	99236390	526
ENSG00000(	1.035792	3.612863	0	0	0	0	1.5346	0.25314	NA	ATP5F1P1	chr13	+	52172552	52173596	569
ENSG00000(	5.17896	8.430014	1.319414	0.749076	0.920432	5.753754	0.81852	0.44418	0.57383	RSL24D1P6	chr20	-	30758193	30758593	401
ENSG00000(	6.214751	10.83859	13.19414	0	1.840864	4.109825	2.0156	0.032873	0.067287	RP11-439L	chr6	-	1.43E+08	1.43E+08	402
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	C4BPAP1	chr1	+	2.07E+08	2.07E+08	1893
ENSG00000(	0	0	2.638828	2.247227	2.761296	1.64393	-0.88701	0.49432	0.62306	PGAM1P6	chr2	-	24095138	24095884	747
ENSG00000(	12.4295	4.817151	7.916483	17.22874	19.32907	7.397684	-0.73558	0.29096	0.41504	RP11-181K	chr1	+	1.83E+08	1.83E+08	524
ENSG00000(	643.2268	615.391	829.9113	606.7512	891.8986	765.2493	-0.116	0.49583	0.62449	ATXN1L	chr16	+	71879894	71891231	7881
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-449I	chr10	-	30692126	30692705	580
ENSG00000(	24.85901	31.31148	10.55531	8.239831	10.12475	9.041614	1.2244	0.043821	0.086655	AL355490.	chr10	-	99179228	99185831	236
ENSG00000(	0	0	0	0.749076	1.840864	0.821965	-1.0455	0.43461	NA	RPL36P16	chr19	+	41675766	41676071	306
ENSG00000(	0	3.612863	1.319414	3.745378	5.522592	0.821965	-0.77364	0.51517	0.64184	AC136289.	chr3	-	63727969	63813121	1843
ENSG00000(	2.071584	0	0	2.247227	0	2.465895	-0.62438	0.6436	0.75092	RP11-495P	chr1	+	1.48E+08	1.48E+08	1331
ENSG00000(	5.17896	0	2.638828	0	2.761296	0	0.96628	0.46118	0.59058	RP11-492A	chr9	-	17447143	17448541	1399
ENSG00000(	1.035792	4.817151	6.597069	2.996302	1.840864	2.465895	0.60356	0.56924	0.68842	AC010127.	chr2	+	1.67E+08	1.67E+08	2260
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-159J	chr1	+	81892141	81893290	1150
ENSG00000(	4.143168	3.612863	1.319414	0	2.761296	0	1.1986	0.3429	0.472	RP11-328K	chr10	+	79073699	79075452	418
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	AC104438.	chr3	+	65573177	65573725	545
ENSG00000(	2.071584	10.83859	15.83297	0.749076	0.920432	0.821965	2.86	0.005676	0.013912	AC002117.	chr17	-	43227767	43238877	570
ENSG00000(	0	0	0	3.745378	4.60216	5.753754	-3.0194	0.017917	0.039318	AC010884.	chr2	-	1.06E+08	1.06E+08	472
ENSG00000(	0	0	3.958241	1.498151	0	0.821965	0.3778	0.78033	0.85524	LINC00365	chr13	-	30677315	30683012	2618
ENSG00000(	0	0	0	2.996302	4.60216	0.821965	-2.206	0.099375	0.17452	KRT8P45	chr1	+	1.57E+08	1.57E+08	1447
ENSG00000(	0	0	0	4.494453	1.840864	0.821965	-1.9797	0.14229	0.23373	RP11-438F	chr1	+	2.49E+08	2.49E+08	967
ENSG00000(	1.035792	1.204288	0	0.749076	0	0	0.55357	0.6746	NA	RP13-52K8	chrX	+	80664437	80682775	747
ENSG00000(	0	0	0	0	4.60216	1.64393	-1.6592	0.22125	0.33301	RP11-561I	chr1	+	2.42E+08	2.42E+08	532
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	PPIAP10	chr20	+	52037738	52038195	458
ENSG00000(	428.8178	391.3935	478.9472	353.5637	347.9233	356.7328	0.29399	0.058415	0.11117	SMIM13	chr6	+	11094266	11138964	4686
ENSG00000(	0	2.408575	1.319414	0.749076	2.761296	1.64393	-0.31542	0.80612	0.87429	TMLHE-AS1	chrX	+	1.55E+08	1.55E+08	1702
ENSG00000(	0	0	2.638828	0	2.761296	0.821965	-0.2421	0.85821	0.90984	RP11-134G	chr1	+	2.01E+08	2.02E+08	340
ENSG00000(	0	1.204288	2.638828	0	0	1.64393	0.59614	0.66038	NA	AP001439.	chr21	+	27530409	27548142	392
ENSG00000(	50.7538	57.80581	67.2901	96.63075	75.47542	60.00344	-0.4008	0.20641	0.31542	AC012318.	chr19	+	14599758	14600691	934
ENSG00000(	0	0	0	2.247227	3.681728	0	-1.606	0.23624	0.35065	AC008264.	chr7	+	1.31E+08	1.31E+08	367
ENSG00000(	45.57484	56.60152	98.95603	14.98151	13.80648	13.15144	2.1952	3.60E-07	1.57E-06	EIF4BP3	chr9	+	98908289	98910138	1850
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	AC023669.	chr7	+	46184535	46185286	752
ENSG00000(	3.107376	0	0	0.749076	0	0	0.76338	0.56438	NA	HMGB3P21	chr7	-	96764327	96764873	547

ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC008065.	chr2	-	1.72E+08	1.72E+08	348
ENSG00000(	0	0	0	1.498151	0.920432	3.28786	-1.678	0.21598	NA	HLA-DPB2	chr6	+	33080228	33102442	1617
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	LPP-AS1	chr3	-	1.88E+08	1.88E+08	494
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP1-148H1	chr20	-	46020673	46041071	750
ENSG00000(	0	0	2.638828	2.996302	1.840864	1.64393	-0.86118	0.50809	0.63561	FAM96AP2	chr1	-	2.28E+08	2.28E+08	477
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	AC096669.	chr2	+	1.08E+08	1.08E+08	1539
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-341G	chr4	+	13978790	13979652	863
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	RP11-430H	chr1	-	66041812	66044063	1797
ENSG00000(	26.93059	28.90291	32.98534	1.498151	9.20432	2.465895	2.6168	6.09E-05	0.000204	COL18A1-A	chr21	-	46827301	46829980	552
ENSG00000(	3.107376	2.408575	0	0	0	0	1.7825	0.18787	NA	AC017048.	chr2	+	1.78E+08	1.78E+08	699
ENSG00000(	118.0803	107.1816	96.31721	109.365	134.3831	215.3548	-0.50557	0.066731	0.12454	CTD-2119F	chr16	+	51679667	51681043	1377
ENSG00000(	6.214751	2.408575	6.597069	0.749076	5.522592	0	1.0342	0.34869	0.47836	AC012314.	chr19	-	54712960	54713286	327
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-365D	chr1	-	2.15E+08	2.15E+08	439
ENSG00000(	20.71584	8.430014	11.87472	2.247227	6.443024	3.28786	1.6378	0.035431	0.07191	RP5-884C9	chr1	+	38512986	38584697	593
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-30B1	chr7	+	3377521	3378233	601
ENSG00000(	79.75598	90.32158	59.37362	11.98521	11.04518	9.863579	2.737	2.26E-11	1.40E-10	RPL29P19	chr8	+	49297150	49297609	460
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	AC073626.	chr7	-	1.14E+08	1.14E+08	582
ENSG00000(	14.50109	2.408575	7.916483	1.498151	1.840864	1.64393	1.9655	0.044694	0.088091	ZMIZ1-AS1	chr10	-	80703085	80827652	2878
ENSG00000(	29.00217	36.12863	43.54065	175.2837	136.2239	129.0485	-2.0056	1.56E-11	9.78E-11	PTCHD3P1	chr10	+	29698331	29776674	2025
ENSG00000(	8.286335	0	0	0	0.920432	0	1.6906	0.21004	0.31976	RPS5P2	chr21	-	35507732	35508371	640
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-15J1(	chr9	-	70083601	70087216	706
ENSG00000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	AC008069.	chr2	-	17035087	17036551	950
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	TGFA-IT1	chr2	-	70694517	70695627	436
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RP11-470E	chr1	-	59597608	59664293	1111
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	AC007919.	chr3	+	1.72E+08	1.72E+08	217
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-153F	chr1	-	1.04E+08	1.04E+08	527
ENSG00000(	9.322127	1.204288	1.319414	17.22874	18.40864	15.61733	-1.871	0.016431	0.036363	AC124944.	chr3	+	1.96E+08	1.96E+08	2096
ENSG00000(	9.322127	7.225726	11.87472	4.494453	8.283888	4.93179	0.62648	0.41834	0.54898	RP11-305E	chr1	-	1.01E+08	1.01E+08	423
ENSG00000(	1.035792	3.612863	0	0	0.920432	0.821965	0.80481	0.54981	0.67125	AC096921.	chr3	-	30667915	30668289	375
ENSG00000(	0	1.204288	1.319414	3.745378	9.20432	3.28786	-2.0436	0.076306	0.1397	RP11-276H	chr1	+	16485761	16488378	544
ENSG00000(	4.143168	18.06432	10.55531	11.98521	12.88605	4.109825	0.15509	0.83546	0.89476	RP5-1142J:	chr7	-	1.57E+08	1.57E+08	208
ENSG00000(	37.28851	40.94578	34.30476	39.701	23.93123	52.60575	-0.04856	0.90621	0.94215	RP11-51O6	chr16	-	61089303	61089868	566
ENSG00000(	14.50109	10.83859	2.638828	22.47227	13.80648	36.16646	-1.2718	0.047431	0.092707	RP4-564F2	chr20	-	37034658	37045444	2004
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC019129.	chr2	+	44393405	44394082	678
ENSG00000(	0	1.204288	0	1.498151	1.840864	0	-0.64701	0.63267	NA	AC106900.	chr2	-	1.75E+08	1.75E+08	456
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-16L2	chr9	+	1.14E+08	1.14E+08	302
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	AC026954.	chr17	+	7233771	7238732	1293
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	AC139666.	chr3	+	1.96E+08	1.96E+08	1828
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	AC018737.	chr2	+	1.23E+08	1.23E+08	794
ENSG00000(	7.250543	1.204288	5.277655	0	0	0	3.2604	0.011823	0.027029	RP11-631F	chr6	-	1.49E+08	1.49E+08	311
ENSG00000(	117.0445	101.1602	145.1355	60.67512	66.2711	46.03004	1.0584	0.000188	0.00059	SH3BP5-AS	chr3	+	15295691	15306000	5570
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	AC013470.	chr7	+	12545633	12547104	462
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	IPO8P1	chr1	-	2.11E+08	2.11E+08	3109
ENSG00000(	0	0	0	7.490755	0.920432	0.821965	-2.2987	0.085916	0.15474	AC009227.	chr2	-	1.55E+08	1.55E+08	2362

ENSG00000(	1.035792	3.612863	0	0	5.522592	1.64393	-0.40388	0.75088	0.8347	AC011330.	chr15	+	43941321	43941478	158
ENSG00000(	4.143168	7.225726	3.958241	20.97412	7.363456	20.54912	-1.5443	0.036404	0.073661	PLA2G12AI	chr1	+	52834349	52834916	568
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	SOCS5P2	chr9	+	1.38E+08	1.38E+08	1359
ENSG00000(	1.035792	4.817151	0	2.247227	5.522592	1.64393	-0.5037	0.66817	0.77133	AC073629.	chr7	+	16248570	16248890	321
ENSG00000(	10.35792	3.612863	7.916483	42.69731	25.7721	27.12484	-2.0129	0.000609	0.001766	RASAL2-AS:	chr1	-	1.78E+08	1.78E+08	2329
ENSG00000(	0	1.204288	0	0.749076	0	0	0.1572	0.90001	NA	KB-1592A4	chr22	-	21495913	21496660	748
ENSG00000(	0	0	0	2.996302	0	0.821965	-1.0802	0.41594	NA	ZNF812	chr19	-	9800600	9811452	2098
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	UBE2D3P3	chr1	+	1.51E+08	1.51E+08	425
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	GS1-174L6	chr1	-	1.86E+08	1.86E+08	353
ENSG00000(	1.035792	1.204288	2.638828	11.98521	7.363456	8.219649	-2.1423	0.026137	0.055118	LAMTOR5-/	chr1	+	1.11E+08	1.11E+08	881
ENSG00000(	0	0	0	1.498151	1.840864	0	-0.93652	0.47589	NA	RP11-697E	chr11	-	1.32E+08	1.32E+08	577
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RPS17P13	chr7	+	37156384	37156790	407
ENSG00000(	3.107376	12.04288	1.319414	0.749076	0	0.821965	2.437	0.039583	0.079287	E2F3-IT1	chr6	+	20438052	20440409	400
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	OR11M1P	chr12	+	49021671	49022565	895
ENSG00000(	6.214751	10.83859	0	4.494453	0.920432	4.109825	0.68749	0.50918	0.63652	RP11-719K	chr16	+	14802801	14820195	1155
ENSG00000(	11.39371	13.24716	13.19414	0	0	0	4.9063	1.92E-05	6.87E-05	AC025165.	chr12	-	58005901	58013421	2355
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CITF22-49I	chr22	+	47741319	47769291	4364
ENSG00000(	0	0	0	6.74168	17.48821	13.15144	-4.4766	0.000103	0.000337	RP11-576D	chr1	+	2.05E+08	2.05E+08	2885
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC007182.	chr14	-	76041231	76045931	2159
ENSG00000(	0	1.204288	0	2.996302	7.363456	1.64393	-2.145	0.090125	0.16098	RP11-255B	chr8	-	1.28E+08	1.28E+08	1248
ENSG00000(	5.17896	3.612863	3.958241	0	1.840864	1.64393	1.4508	0.20612	0.315	FCF1P7	chr1	-	2.43E+08	2.43E+08	558
ENSG00000(	9.322127	6.021439	6.597069	10.48706	16.56778	10.68554	-0.71369	0.31138	0.43763	AC090945.	chr3	+	15919554	15921078	1525
ENSG00000(	10.35792	7.225726	14.51355	1.498151	2.761296	8.219649	1.2168	0.14551	0.23807	PCOLCE-AS:	chr7	-	1E+08	1E+08	2537
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC016716.	chr2	-	80255138	80257677	486
ENSG00000(	0	0	0	0.749076	2.761296	0.821965	-1.3133	0.33155	NA	RP1-86D1.!	chr6	+	1.29E+08	1.29E+08	549
ENSG00000(	9.322127	1.204288	0	27.7158	31.29469	34.52253	-2.8375	6.06E-05	0.000203	AC099850.	chr17	+	57183959	57195628	1338
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	TEX26-AS1	chr13	-	31456070	31507983	2053
ENSG00000(	9.322127	9.634302	1.319414	3.745378	4.60216	3.28786	0.70906	0.44209	0.5718	RP11-380G	chr10	+	89638449	89640184	499
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	AC015987.	chr7	+	1.36E+08	1.36E+08	804
ENSG00000(	9.322127	14.45145	7.916483	2.247227	0	6.575719	1.5955	0.078346	0.14281	AP001065.	chr21	-	45889812	45892399	1113
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-94M:	chr10	+	92213927	92262725	2368
ENSG00000(	4.143168	10.83859	2.638828	0	0	0	3.6648	0.003659	0.009313	SHMT1P1	chr1	-	44315972	44317283	1312
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	HMGN1P3-	chrX	-	77775090	77775683	290
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	FDPSP8	chr1	-	2.12E+08	2.12E+08	1089
ENSG00000(	1.035792	0	3.958241	0	0	0.821965	1.2459	0.35843	NA	RP11-54O1	chr9	-	97690833	97697228	487
ENSG00000(	0	0	0	2.996302	1.840864	3.28786	-2.1887	0.10174	0.17796	RP1-137H1	chrX	-	1.37E+08	1.37E+08	586
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC069213.	chr3	+	1.95E+08	1.95E+08	1680
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	HSPA8P7	chrX	-	1.14E+08	1.14E+08	1948
ENSG00000(	1.035792	0	0	2.996302	3.681728	0	-1.3849	0.30373	0.42885	CETN4P	chr4	-	1.24E+08	1.24E+08	469
ENSG00000(	0	1.204288	3.958241	0.749076	8.283888	9.863579	-1.4999	0.17552	0.27728	AP000704.	chr21	+	38338812	38344128	438
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP3-333H2	chr22	+	39688993	39691568	1778
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-57C1	chr9	-	1.34E+08	1.34E+08	265
ENSG00000(	1.035792	0	5.277655	2.996302	0.920432	4.93179	-0.38834	0.74317	0.82884	RP11-445C	chrX	+	56999943	57001229	644
ENSG00000(	1.035792	2.408575	0	0	0.920432	0	0.86086	0.52404	NA	RP11-235D	chr1	-	1.51E+08	1.51E+08	448

ENSG00000(	0	1.204288	0	0	0	1.64393	-0.12916	0.91993	NA	AC004878.	chr7	+	74855312	74864233	773
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	LINC00853	chr1	+	47644922	47646011	661
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	DUX4L9	chr4	-	1.91E+08	1.91E+08	1259
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	SRGAP3-AS	chr3	+	9055807	9057663	428
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	BEND3P2	chr9	+	94933523	94935776	2254
ENSG00000(	0	0	0	2.996302	0	0.821965	-1.0802	0.41594	NA	TMEM72-A	chr10	-	45306472	45455137	3300
ENSG00000(	91.14969	119.2245	94.99779	130.3391	128.8605	133.1583	-0.35995	0.13484	0.22398	RP11-134G	chr1	-	2.01E+08	2.01E+08	598
ENSG00000(	3.107376	0	2.638828	0	0	0	1.8293	0.17689	NA	AC093843.	chr2	+	2.22E+08	2.22E+08	512
ENSG00000(	8.286335	4.817151	3.958241	2.996302	6.443024	4.93179	0.23488	0.79319	0.86487	COL4A2-AS	chr13	-	1.11E+08	1.11E+08	1522
ENSG00000(	0	0	0	13.48336	15.64734	7.397684	-4.4544	0.000112	0.000361	THRB-IT1	chr3	-	24496627	24500925	1754
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	AC019109.	chr2	+	2.25E+08	2.25E+08	1874
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	LINC00265	chrY	+	26422392	26423173	782
ENSG00000(	4.143168	7.225726	9.235896	43.44638	11.96562	25.48091	-1.8737	0.003995	0.0101	RP11-651P	chr3	-	1.5E+08	1.5E+08	1131
ENSG00000(	6.214751	7.225726	3.958241	7.490755	10.12475	13.9734	-0.77699	0.31143	0.43767	GCSHP5	chr1	-	1.68E+08	1.68E+08	522
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC093698.	chr2	-	2.09E+08	2.09E+08	498
ENSG00000(	0	0	0	2.247227	7.363456	7.397684	-3.2755	0.009193	0.021557	RP11-123K	chr9	-	1.29E+08	1.29E+08	506
ENSG00000(	3.107376	0	0	7.490755	0.920432	8.219649	-1.7463	0.13644	0.22597	LINC00240	chr6	+	26988232	26991703	507
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	AC107079.	chr2	-	2.38E+08	2.38E+08	669
ENSG00000(	4.143168	0	0	0	0.920432	0	0.95689	0.47805	NA	RP1-90J20.	chr6	-	2989960	2999368	413
ENSG00000(	1.035792	13.24716	1.319414	3.745378	10.12475	6.575719	-0.33306	0.72545	0.81586	RP11-535N	chr9	+	99449338	99483403	425
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	LINC00502	chr10	+	92806923	92821916	445
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	LINC00393	chr13	-	73987610	74222390	485
ENSG00000(	0	3.612863	1.319414	0.749076	0.920432	0	0.87418	0.5154	0.64203	OPA1-AS1	chr3	-	1.93E+08	1.93E+08	492
ENSG00000(	0	0	1.319414	0	2.761296	0.821965	-0.69816	0.6064	NA	RP4-796I17	chr22	+	44352907	44353228	322
ENSG00000(	0	0	2.638828	0	0	2.465895	0.027772	0.98358	NA	AL592494.	chr1	-	1.21E+08	1.21E+08	426
ENSG00000(	20.71584	25.29004	14.51355	8.988907	23.93123	23.01502	0.11861	0.83215	0.89252	RPL29P11	chr3	-	37058011	37058505	492
ENSG00000(	50.7538	57.80581	56.73479	50.18806	48.7829	78.08667	-0.09982	0.76785	0.84711	YBX1P1	chr14	-	66479548	66480507	960
ENSG00000(	0	0	0	6.74168	0.920432	10.68554	-3.3378	0.008227	0.019484	CTC-260E6.	chr19	+	20235248	20236293	483
ENSG00000(	2.071584	1.204288	3.958241	0	0	0	2.2785	0.091433	0.16293	AC009518.	chr7	+	1.32E+08	1.32E+08	1229
ENSG00000(	357.3482	297.4591	306.104	289.8922	324.9125	438.9293	-0.13072	0.49258	0.62156	RP4-758J18	chr1	+	1334902	1337426	2228
ENSG00000(	3.107376	1.204288	9.235896	1.498151	7.363456	0.821965	0.39576	0.71017	0.80405	AC083949.	chr2	-	42370378	42397441	657
ENSG00000(	1120.727	987.5159	967.1303	1131.104	988.544	1394.874	-0.19168	0.19316	0.29903	C17orf89	chr17	+	79213039	79215081	741
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	AC068279.	chr2	-	87607003	87607890	888
ENSG00000(	4.143168	3.612863	3.958241	8.239831	4.60216	5.753754	-0.58527	0.51778	0.64403	IKBKGP1	chrX	-	1.54E+08	1.54E+08	1075
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTA-250D1	chr22	-	42377308	42378221	515
ENSG00000(	2.071584	2.408575	3.958241	0	4.60216	1.64393	0.33555	0.77625	0.85302	TSSC1-IT1	chr2	-	3302112	3305236	718
ENSG00000(	16.57267	21.67718	13.19414	11.23613	5.522592	4.109825	1.2073	0.072427	0.13355	BEND3P3	chr10	-	81444248	81444739	492
ENSG00000(	0	0	0	0	5.522592	0	-1.3606	0.30939	NA	RP11-276H	chr9	-	89699076	89700066	991
ENSG00000(	12.4295	18.06432	3.958241	3.745378	14.72691	23.83698	-0.26168	0.72079	0.81224	RP5-1142A	chr16	+	88797588	88807826	4521
ENSG00000(	0	7.225726	0	0	0	0	1.9679	0.14595	0.2386	AC007899.	chr2	+	37375673	37376447	775
ENSG00000(	7.250543	3.612863	18.47179	4.494453	3.681728	4.93179	1.0235	0.22355	0.3358	RPS4XP16	chr13	+	52028300	52035451	807
ENSG00000(	4.143168	2.408575	1.319414	0	2.761296	1.64393	0.62891	0.60613	0.72079	VPS26BP1	chr3	-	48001817	48002571	755
ENSG00000(	3.107376	4.817151	9.235896	8.239831	2.761296	6.575719	-0.05334	0.95188	0.97123	RP11-3B12	chr7	+	1.25E+08	1.25E+08	3252
ENSG00000(	1.035792	0	0	0	0	2.465895	-0.37334	0.77636	NA	RP11-448G	chr1	+	1.98E+08	1.98E+08	247

ENSG00000(	0	1.204288	0	1.498151	0.920432	0	-0.40353	0.76332	NA	AC005534.	chr7	-	1.56E+08	1.56E+08	742
ENSG00000(	14.50109	32.51577	27.70769	35.95563	55.22592	61.64737	-1.0134	0.019016	0.041471	AP001347.	chr21	+	15399742	15516789	1332
ENSG00000(	109.7939	108.3859	109.5113	140.8262	137.1444	149.5976	-0.38132	0.092368	0.16423	LINC00863	chr10	+	89102493	89117639	3287
ENSG00000(	1.035792	0	0	0	1.840864	0	-0.17777	0.89006	NA	APOC4	chr19	+	45445495	45452822	1829
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	KRT8P30	chr2	-	2.2E+08	2.2E+08	650
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	LINC00162	chr21	-	46419122	46424642	734
ENSG00000(	8.286335	8.430014	2.638828	7.490755	11.96562	16.4393	-0.79955	0.28876	0.4124	RP11-441C	chr10	+	1.01E+08	1.01E+08	666
ENSG00000(	2.071584	2.408575	0	0	0	0	1.5041	0.26224	NA	SUCLA2P1	chr6	+	30436659	30438028	1370
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-34H1	chr9	+	46334292	46334508	217
ENSG00000(	0	0	3.958241	2.996302	0	0.821965	-0.0016	0.99905	0.99932	LINC00184	chr1	+	2.35E+08	2.35E+08	2270
ENSG00000(	13.46529	0	1.319414	1891.416	1894.249	2101.764	-7.0596	2.17E-12	1.45E-11	PRRT4	chr7	-	1.28E+08	1.28E+08	3544
ENSG00000(	13.46529	12.04288	27.70769	34.45748	21.16994	15.61733	-0.41697	0.45114	0.58072	RP11-82L1	chr9	-	91703519	91724849	585
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	AC007312.	chr7	-	33316446	33316703	258
ENSG00000(	15.53688	14.45145	9.235896	9.737982	17.48821	11.50751	0.029898	0.96208	0.97811	RP5-1086K	chr1	-	1.17E+08	1.17E+08	2295
ENSG00000(	40.39588	32.51577	18.47179	66.66772	59.82808	87.12828	-1.1889	0.001664	0.004493	RP11-206L	chr1	-	661611	663527	1236
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	PGM5-AS1	chr9	-	70970105	70972768	572
ENSG00000(	3.107376	6.021439	0	2.996302	0	4.109825	0.26528	0.82383	0.88627	AC017002.	chr2	-	1.12E+08	1.12E+08	881
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP1-278O2	chr20	+	10733738	10734614	438
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	U82695.9	chrX	+	1.53E+08	1.53E+08	700
ENSG00000(	1.035792	0	0	0.749076	0	3.28786	-0.84629	0.53252	NA	KCNC4-AS1	chr1	-	1.11E+08	1.11E+08	748
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC009303.	chr2	-	1.19E+08	1.19E+08	352
ENSG00000(	0	2.408575	0	7.490755	11.04518	13.15144	-2.9922	0.004177	0.010514	RP11-54O7	chr1	-	947377	948573	471
ENSG00000(	2.071584	2.408575	7.916483	0	0.920432	0	2.4664	0.050853	0.098528	RP11-403H	chr9	+	6902670	6978859	553
ENSG00000(	0	2.408575	2.638828	0	11.04518	1.64393	-0.96522	0.42638	0.55666	CTA-282F2.	chr22	+	34121000	34146830	2618
ENSG00000(	54.89697	54.19295	47.4989	11.23613	23.93123	22.19305	1.4229	0.00081	0.002305	INE1	chrX	+	47064320	47065264	945
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP11-160H	chr1	+	1.74E+08	1.74E+08	335
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP13-228J	chrX	-	1.54E+08	1.54E+08	335
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	TMEM233	chr12	+	1.2E+08	1.2E+08	1573
ENSG00000(	0	0	0	1.498151	2.761296	3.28786	-2.0751	0.1224	0.20728	RP11-524H	chr6	-	54704916	54705653	586
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-297K	chr1	-	1.61E+08	1.61E+08	379
ENSG00000(	6.214751	2.408575	3.958241	0	0	0.821965	2.5581	0.041914	0.083387	PPP1R8P1	chr1	-	48790752	48791795	1044
ENSG00000(	0	0	0	0	3.681728	2.465895	-1.6477	0.22446	0.33686	RP11-409K	chr9	-	1.33E+08	1.33E+08	341
ENSG00000(	3.107376	2.408575	3.958241	1.498151	0	0	1.7186	0.17654	0.27852	RP11-295G	chr9	-	1.36E+08	1.36E+08	531
ENSG00000(	0	7.225726	0	0	0.920432	0	1.5108	0.26454	0.38438	CTD-2210P	chr5	-	43666867	43667334	468
ENSG00000(	11.39371	10.83859	9.235896	16.47966	12.88605	20.54912	-0.62801	0.30651	0.43213	AL049840.	chr14	+	1.04E+08	1.04E+08	1543
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	AC010082.	chr7	-	18468685	18470361	546
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	RP11-6F6.1	chr9	-	1.09E+08	1.09E+08	456
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP13-228J	chrX	-	1.55E+08	1.55E+08	994
ENSG00000(	0	0	0	2.247227	7.363456	2.465895	-2.7483	0.034727	0.07065	AC006509.	chr2	+	47922955	47984932	725
ENSG00000(	0	2.408575	0	0	2.761296	0	-0.08034	0.95255	NA	SNX18P15	chr1	-	1.43E+08	1.43E+08	733
ENSG00000(	2.071584	0	3.958241	0	0	0.821965	1.4726	0.27605	0.39753	AP004289.	chr8	-	1E+08	1E+08	2205
ENSG00000(	2.071584	0	2.638828	0	0.920432	1.64393	0.52711	0.69222	0.79004	UBE2D3P1	chr20	-	5273034	5273477	444
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	AC091492.	chr3	+	12369502	12369773	272
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-330N	chr1	+	48283738	48285909	1807

ENSG00000(	0	0	0	5.243529	1.840864	0.821965	-2.1141	0.11577	0.198	RP4-784A1	chr1	-	53757463	53757810	237
ENSG00000(	14.50109	12.04288	14.51355	2.996302	8.283888	6.575719	1.1228	0.11706	0.19984	EIF4BP7	chrX	-	1.11E+08	1.11E+08	1813
ENSG00000(	22.78742	22.88147	21.11062	11.98521	2.761296	2.465895	1.8017	0.008058	0.019129	RP11-228B	chr9	+	1.31E+08	1.31E+08	2055
ENSG00000(	1.035792	0	0	0	1.840864	2.465895	-0.90898	0.50286	NA	EIF1AX-AS1	chrX	+	20158086	20158562	378
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	RP11-223E	chr13	-	30993656	30996374	448
ENSG00000(	0	3.612863	3.958241	1.498151	0	2.465895	0.61283	0.62758	0.73857	RPL18AP2	chr21	-	47840467	47840948	482
ENSG00000(	0	0	1.319414	0.749076	0.920432	0	-0.15244	0.90808	NA	HMGB3P22	chr5	+	1.79E+08	1.79E+08	597
ENSG00000(	1.035792	0	1.319414	1.498151	0	0	0.26794	0.842	NA	AC096574.	chr2	+	2.39E+08	2.39E+08	2509
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-383G	chr1	-	2.05E+08	2.05E+08	686
ENSG00000(	0	1.204288	3.958241	2.247227	0	7.397684	-0.6649	0.5901	0.70687	GS1-184P1	chrX	-	24447690	24448037	348
ENSG00000(	1.035792	6.021439	1.319414	0	5.522592	1.64393	0.1791	0.88066	0.92529	RP11-426L	chr1	-	1.13E+08	1.13E+08	449
ENSG00000(	0	1.204288	0	0	0.920432	3.28786	-0.84421	0.53376	NA	WWC3-AS1	chrX	-	9992882	10006694	578
ENSG00000(	2.071584	4.817151	2.638828	30.7121	23.93123	27.94681	-2.905	2.52E-05	8.91E-05	LINC00337	chr1	+	6296300	6299504	1302
ENSG00000(	1.035792	1.204288	0	2.247227	0	1.64393	-0.44193	0.74269	0.82838	RP11-123N	chr9	-	1.26E+08	1.26E+08	858
ENSG00000(	1.035792	0	2.638828	2.247227	1.840864	0	-0.10473	0.93698	0.96179	PFN1P4	chr1	+	1.48E+08	1.48E+08	402
ENSG00000(	1.035792	2.408575	2.638828	0.749076	1.840864	2.465895	0.18895	0.87584	0.9222	DAP3P1	chr1	+	1.56E+08	1.56E+08	278
ENSG00000(	0	0	1.319414	0.749076	2.761296	0	-0.68322	0.61404	NA	GRTP1-AS1	chr13	+	1.14E+08	1.14E+08	867
ENSG00000(	0	0	5.277655	0	0.920432	1.64393	0.57528	0.66878	0.77175	AL450226.	chr17	+	2135974	2136904	710
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RP4-660H1	chr1	-	73214604	73364823	499
ENSG00000(	2.071584	3.612863	10.55531	5.243529	13.80648	7.397684	-0.64176	0.45086	0.58052	SNORA71A	chr20	-	37055949	37056086	138
ENSG00000(	7.250543	2.408575	2.638828	2.247227	3.681728	6.575719	-0.00168	0.99864	0.99905	RP11-405C	chr6	+	7183316	7185520	1676
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RPL3P7	chr6	-	1.08E+08	1.08E+08	1212
ENSG00000(	9.322127	0	0	4.494453	1.840864	5.753754	-0.26173	0.81888	0.88301	SETP20	chr4	-	1.1E+08	1.1E+08	852
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	XXbac-BPG	chr6	+	58291908	58298496	301
ENSG00000(	1.035792	2.408575	3.958241	8.239831	13.80648	6.575719	-1.7153	0.060242	0.11408	OR52K3P	chr11	+	4496043	4497123	943
ENSG00000(	0	0	2.638828	0	0	0.821965	0.55859	0.66971	NA	RP11-429E	chr20	-	60313275	60330112	937
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC013268.	chr2	-	1.11E+08	1.11E+08	1456
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	AC083900.	chr2	-	2.09E+08	2.09E+08	469
ENSG00000(	0	0	2.638828	0	5.522592	1.64393	-0.88487	0.50402	0.6317	RP11-295P	chr10	+	13752415	13754054	373
ENSG00000(	12.4295	7.225726	3.958241	6.74168	7.363456	11.50751	-0.0909	0.90608	0.94205	RP5-1160K	chr1	+	1.1E+08	1.1E+08	596
ENSG00000(	0	0	2.638828	2.996302	2.761296	8.219649	-1.785	0.1367	0.22635	ARSDP1	chrY	+	14474827	14499123	1215
ENSG00000(	0	1.204288	6.597069	4.494453	3.681728	0.821965	-0.18313	0.87548	0.92198	AL133216.	chr10	+	38717074	38736820	992
ENSG00000(	0	0	0	0	4.60216	0.821965	-1.4643	0.27877	NA	RP11-255A	chr9	-	33574359	33574586	228
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC023271.	chr2	-	2.04E+08	2.04E+08	458
ENSG00000(	9.322127	2.408575	1.319414	2.247227	0	1.64393	1.3173	0.25604	0.37441	RANP4	chrX	-	1.36E+08	1.36E+08	655
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	LINC00237	chr20	-	21068245	21086999	1220
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AC074112.	chr7	+	85050438	85118609	788
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	PSME2P2	chr13	+	49345264	49345965	700
ENSG00000(	1.035792	1.204288	0	0	0	1.64393	0.19975	0.8819	NA	MORF4L1P	chr13	-	41773968	41774943	976
ENSG00000(	121.1877	101.1602	94.99779	62.92235	29.45382	31.23467	1.3323	8.37E-05	0.000276	RP11-361F	chr6	+	1.48E+08	1.48E+08	1477
ENSG00000(	2.071584	3.612863	6.597069	3.745378	8.283888	7.397684	-0.58802	0.51886	0.64516	DYNC1I2P1	chr10	+	52024738	52026575	1838
ENSG00000(	692.9448	832.1628	591.0974	122.0993	89.2819	159.4612	2.4956	4.13E-34	7.21E-33	CTD-2228K	chr5	+	478238	480999	2762
ENSG00000(	10.35792	7.225726	10.55531	2.247227	6.443024	6.575719	0.80576	0.3175	0.44434	RP11-809C	chr10	+	674578	677195	1657
ENSG00000(	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	AC018643.	chr7	+	1.32E+08	1.32E+08	414

ENSG00000(	0	1.204288	1.319414	0	0	4.109825	-0.38581	0.7757	0.85283	AC073957.	chr7	+	1068661	1083527	535
ENSG00000(	308.666	307.0934	257.2857	244.1986	355.2868	399.475	-0.19072	0.34366	0.4729	AC103965.	chr15	-	84867600	84898888	4253
ENSG00000(	0	6.021439	7.916483	0	0	0	3.1275	0.017638	0.038775	AC005779.	chr19	-	45687584	45688190	303
ENSG00000(	5.17896	4.817151	10.55531	9.737982	7.363456	4.93179	-0.10395	0.89752	0.93635	NPM1P39	chr1	+	27533421	27534287	867
ENSG00000(	0	0	0	4.494453	0.920432	0	-1.4809	0.27346	NA	LINC00618	chr14	+	97409916	97411731	448
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	AC012462.	chr2	+	2.16E+08	2.16E+08	825
ENSG00000(	2.071584	1.204288	2.638828	0.749076	0.920432	2.465895	0.36305	0.76873	0.8478	BRI3P1	chr1	+	1.01E+08	1.01E+08	378
ENSG00000(	1.035792	0	0	0	1.840864	0	-0.17777	0.89006	NA	RP5-828K2	chr20	-	22252690	22254092	1403
ENSG00000(	1.035792	1.204288	3.958241	0	1.840864	2.465895	0.3572	0.77642	0.85305	DUTP6	chr1	+	1.67E+08	1.67E+08	462
ENSG00000(	0	0	0	2.247227	4.60216	8.219649	-3.0927	0.01515	0.033781	XXbac-BPG	chr6	-	28805646	28806783	709
ENSG00000(	330.4176	295.0505	286.3128	103.3724	95.72493	85.48435	1.671	5.98E-17	5.22E-16	RP11-390P	chr6	+	1.39E+08	1.39E+08	917
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	LINC00457	chr13	-	35009587	35214822	413
ENSG00000(	2.071584	0	0	1.498151	0	0	0.18632	0.88758	NA	AATK-AS1	chr17	+	79139307	79156964	1577
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP4-758J2	chr1	+	54555529	54555766	238
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-481K	chr12	-	98984501	98984992	492
ENSG00000(	5.17896	1.204288	0	1.498151	0.920432	0	0.88429	0.50075	0.62891	AC073283.	chr2	+	47294961	47298343	860
ENSG00000(	618.3678	578.0581	625.4021	276.4089	344.2416	332.8958	0.93256	1.11E-09	6.05E-09	PLEKHM1	chr17	-	43513266	43568115	5263
ENSG00000(	5.17896	0	0	0	0	0	1.5469	0.24589	NA	ZNF33BP1	chr10	-	38083204	38085037	1834
ENSG00000(	5.17896	2.408575	2.638828	0	0	0	2.833	0.03208	0.065917	RPS12P26	chr15	+	90749804	90750199	396
ENSG00000(	2.071584	0	2.638828	0	3.681728	0	0.22281	0.86768	0.91691	LINC00092	chr9	-	98782014	98790247	1726
ENSG00000(	0	0	0	2.996302	0	4.93179	-2.0073	0.13803	0.22814	RP11-338E	chr12	+	65022124	65023756	281
ENSG00000(	2.071584	3.612863	1.319414	2.247227	0.920432	1.64393	0.39465	0.74054	0.82645	AB019441.	chr14	-	1.06E+08	1.06E+08	627
ENSG00000(	1.035792	0	0	0	2.761296	0	-0.44657	0.73574	NA	TBC1D4-AS	chr13	-	75949647	75951430	425
ENSG00000(	16.57267	18.06432	15.83297	6.74168	6.443024	13.15144	0.88272	0.16525	0.26384	AC093818.	chr2	-	1.73E+08	1.73E+08	1397
ENSG00000(	40.39588	20.47289	36.94359	31.46117	53.38506	31.23467	-0.23349	0.59036	0.70701	MIR137HG	chr1	-	98453556	98515419	2639
ENSG00000(	22.78742	7.225726	11.87472	1.498151	1.840864	0.821965	2.92	0.001038	0.002905	AL589743.	chr14	+	19650018	19718563	4676
ENSG00000(	4.143168	2.408575	9.235896	8.239831	13.80648	1.64393	-0.5182	0.56415	0.68374	RP11-197N	chr10	-	16763351	16790376	697
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC079790.	chr2	+	1.53E+08	1.53E+08	507
ENSG00000(	3.107376	0	2.638828	0.749076	11.96562	0	-0.80889	0.50546	0.63317	AC007362.	chr2	-	2.07E+08	2.07E+08	555
ENSG00000(	0	0	0	7.490755	3.681728	4.93179	-3.2203	0.010551	0.024397	HSPA7	chr1	+	1.62E+08	1.62E+08	1927
ENSG00000(	1.035792	9.634302	2.638828	5.243529	5.522592	11.50751	-0.65397	0.4766	0.6059	AP001628.	chr21	-	44251150	44256587	285
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	PLA2G12AI	chr13	+	39476524	39476787	264
ENSG00000(	1.035792	1.204288	0	0	0.920432	0	0.54457	0.68095	NA	CHCHD4P5	chr1	+	2.46E+08	2.46E+08	427
ENSG00000(	3.107376	2.408575	1.319414	0	2.761296	0.821965	0.66827	0.59506	0.71097	RP4-814D1	chr7	+	1.57E+08	1.57E+08	465
ENSG00000(	6.214751	19.2686	17.15238	19.47596	8.283888	13.9734	0.011195	0.98615	0.99155	ARL2BPP1(	chr22	-	18585223	18586415	531
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC008937.	chr5	-	56195868	56206541	914
ENSG00000(	53.86118	50.58008	30.34652	8.988907	27.61296	22.19305	1.1735	0.013827	0.031169	TRAPPC12-	chr2	-	3485013	3486180	908
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	DDX26B-AS	chrX	-	1.35E+08	1.35E+08	398
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AP000936.	chr11	-	1.17E+08	1.17E+08	681
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	AC117490.	chr3	-	1.96E+08	1.96E+08	60
ENSG00000(	524.1107	568.4238	604.2915	116.8558	263.2436	129.0485	1.7273	7.99E-13	5.50E-12	RP11-640N	chr1	+	1.45E+08	1.45E+08	3056
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-730A	chr10	-	13099902	13100676	775
ENSG00000(	5.17896	9.634302	1.319414	1.498151	7.363456	5.753754	0.13811	0.885	0.92818	ST13P6	chr8	+	1.34E+08	1.34E+08	1102
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP5-937E2	chrX	-	1.49E+08	1.49E+08	1167

ENSG00000(	0	0	1.319414	2.996302	1.840864	1.64393	-1.374	0.30064	0.42567	AC007255.	chr7	-	29638411	29724871	663
ENSG00000(	14.50109	4.817151	10.55531	14.98151	20.2495	19.72716	-0.81834	0.19183	0.29751	RP11-378J	chr1	+	2.23E+08	2.23E+08	1313
ENSG00000(	9.322127	2.408575	2.638828	0	0	0	3.3444	0.009444	0.022085	LINC00705	chr10	+	4697619	4704611	1745
ENSG00000(	4.143168	1.204288	2.638828	0	1.840864	0	1.3883	0.28392	0.40688	RP11-466F	chr1	+	1.66E+08	1.66E+08	472
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	UBE2Q2P2	chr15	+	82647360	82712277	758
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	RP11-782C	chr1	-	1.43E+08	1.43E+08	766
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-536C	chr1	+	1.6E+08	1.6E+08	645
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-227D	chr20	+	21378456	21381029	520
ENSG00000(	0	0	1.319414	0	0	1.64393	-0.1317	0.91874	NA	AC018693.	chr2	+	39088862	39090275	550
ENSG00000(	4.143168	4.817151	0	0.749076	4.60216	6.575719	-0.30648	0.78053	0.85532	RP4-758J1	chr1	-	1365919	1369953	634
ENSG00000(	0	0	2.638828	0	0.920432	0	0.55591	0.6721	NA	RP11-57H1	chr10	+	1.15E+08	1.15E+08	315
ENSG00000(	1.035792	0	0	0	1.840864	0	-0.17777	0.89006	NA	RP4-612C1	chr1	-	93665312	93665496	185
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	LINC00113	chr21	+	29094698	29123552	572
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-344A	chr10	+	68812367	68814786	505
ENSG00000(	0	1.204288	0	0.749076	0	0.821965	-0.12128	0.92635	NA	RP11-439E	chr1	+	2.47E+08	2.47E+08	1960
ENSG00000(	0	2.408575	0	2.247227	5.522592	1.64393	-1.3219	0.29522	0.41958	RP11-539I1	chr10	-	1.19E+08	1.19E+08	657
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	DNAJC19P4	chr3	-	3026915	3027259	345
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	RP1-91J24.	chr6	-	1.45E+08	1.45E+08	501
ENSG00000(	33.14534	28.90291	25.06886	17.97781	14.72691	19.72716	0.70998	0.13905	0.2295	RP11-415J	chr1	+	33772967	33791644	801
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	AC019100.	chr2	-	1.09E+08	1.09E+08	611
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	RP11-325F	chr7	-	1.05E+08	1.05E+08	640
ENSG00000(	8.286335	9.634302	1.319414	5.992604	2.761296	9.041614	0.10553	0.90565	0.94172	AP001055.	chr21	-	45578623	45579959	863
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	AC093865.	chr2	-	2.13E+08	2.14E+08	433
ENSG00000(	0	0	0	0	4.60216	1.64393	-1.6592	0.22125	0.33301	RP11-449J	chr1	+	2.25E+08	2.25E+08	423
ENSG00000(	0	0	0	3.745378	0	1.64393	-1.4934	0.26982	NA	XXbac-B47(	chr22	-	18559293	18560563	805
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	HMGB3P1	chr20	-	33421378	33422265	573
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-384C	chr1	-	2.12E+08	2.12E+08	468
ENSG00000(	1246.058	1300.631	1422.328	579.7845	545.8162	543.3188	1.2462	3.04E-23	3.50E-22	RP11-513I1	chr6	+	34247456	34254545	7090
ENSG00000(	0	0	0	2.247227	5.522592	5.753754	-2.9379	0.022186	0.047593	SNX18P3	chr9	-	38566257	38568208	1750
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	SLC25A5P8	chr9	-	32333455	32334352	898
ENSG00000(	0	1.204288	2.638828	0	6.443024	0	-0.45493	0.73139	0.82033	RP11-820K	chr12	-	31687649	31688181	533
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	FREM2-AS1	chr13	-	39395935	39401707	465
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-292F	chr9	-	46270841	46274928	876
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RP11-433C	chr4	+	1.82E+08	1.82E+08	342
ENSG00000(	18.64425	14.45145	7.916483	90.63814	88.36147	115.8971	-2.7612	2.54E-12	1.69E-11	RP11-426A	chr9	-	1.38E+08	1.38E+08	2919
ENSG00000(	4.143168	0	1.319414	0	4.60216	0	0.17828	0.89281	0.93378	CT62	chr15	-	71402583	71407833	2822
ENSG00000(	12.4295	2.408575	3.958241	0	5.522592	3.28786	0.92787	0.37123	0.50181	ATP6V0E1P	chr5	+	1.32E+08	1.32E+08	226
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	TDGF1P3	chrX	+	1.1E+08	1.1E+08	2710
ENSG00000(	18.64425	18.06432	14.51355	20.97412	18.40864	24.65895	-0.30731	0.55589	0.67653	AC008993.	chr19	-	60105	70966	622
ENSG00000(	106.6866	132.4716	92.35896	44.19546	29.45382	60.8254	1.2798	6.85E-05	0.000228	RP5-1103G	chr20	-	300957	328868	762
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	AC129778.	chr9	+	42751727	42752381	321
ENSG00000(	26.93059	21.67718	21.11062	65.91865	23.93123	61.64737	-1.0877	0.016946	0.037409	SFTA1P	chr10	-	10826400	10836943	693
ENSG00000(	0	0	0	3.745378	6.443024	3.28786	-2.9412	0.021875	0.046998	AC099754.	chr3	-	26660821	26664181	454
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-395L	chr2	+	1.14E+08	1.14E+08	496

ENSG00000(	1.035792	0	0	0	0	1.64393	-0.12526	0.92174	NA	RP11-3B7.1	chr3	+	49297518	49298744	1227
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP11-1114	chrX	+	1.36E+08	1.36E+08	651
ENSG00000(	0	0	3.958241	0.749076	0	3.28786	-0.04032	0.97604	0.9862	TGIF2P1	chr1	-	2.45E+08	2.45E+08	685
ENSG00000(	0	2.408575	1.319414	3.745378	2.761296	2.465895	-0.93776	0.43789	0.56749	AC080125.	chr2	-	1.86E+08	1.86E+08	684
ENSG00000(	0	1.204288	0	1.498151	0	0	-0.08768	0.94524	NA	CTD-2384B	chr5	-	75987264	76012040	600
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-207C	chr9	-	5719021	5720244	543
ENSG00000(	3.107376	6.021439	2.638828	19.47596	15.64734	14.79537	-1.9147	0.009802	0.022838	RP11-764K	chr9	-	68397878	68409893	2878
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AP000345.	chr22	-	23854681	23855789	477
ENSG00000(	1.035792	0	0	0	0.920432	1.64393	-0.43567	0.74499	NA	RP3-509I15	chr6	+	1.39E+08	1.39E+08	1053
ENSG00000(	0	3.612863	3.958241	2.247227	3.681728	4.109825	-0.3374	0.76329	0.84366	RPL21P3	chr20	+	18465909	18466696	478
ENSG00000(	0	0	0	2.996302	3.681728	3.28786	-2.4933	0.058396	0.11114	AC104134.	chr2	+	88838238	88875128	1747
ENSG00000(	0	0	2.638828	0.749076	0.920432	3.28786	-0.56913	0.66892	0.77186	RBMS1P1	chr12	-	66627859	66629014	1156
ENSG00000(	0	2.408575	1.319414	0	0.920432	0	0.92035	0.49653	NA	TNPO1P1	chr10	+	86150664	86151801	1138
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	RP11-63P1	chr9	+	74920346	74958126	2078
ENSG00000(	123.2592	108.3859	114.789	104.1215	67.19154	88.77221	0.40668	0.12419	0.20954	BOLA3-AS1	chr2	+	74375136	74377188	1804
ENSG00000(	2.071584	3.612863	3.958241	0	2.761296	4.93179	0.25305	0.82378	0.88627	MPRIP-AS1	chr17	-	16979352	16981066	1058
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP4-665J23	chr1	+	91317316	91319843	580
ENSG00000(	2.071584	1.204288	2.638828	0.749076	5.522592	3.28786	-0.52464	0.64585	0.75297	RPS15AP10	chr1	-	46111488	46111869	382
ENSG00000(	2.071584	7.225726	1.319414	10.48706	4.60216	0	-0.41299	0.70185	0.79743	AC079776.	chr2	-	1.31E+08	1.31E+08	2454
ENSG00000(	2.071584	7.225726	0	0	0	0.821965	2.0038	0.13029	0.21764	RP3-508I15	chr22	+	39135008	39145046	500
ENSG00000(	0	2.408575	0	2.247227	0	1.64393	-0.37942	0.77921	0.85467	RP11-736E	chr7	+	1.13E+08	1.13E+08	651
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP13-93L1	chr9	+	92087152	92087607	456
ENSG00000(	3.107376	7.225726	6.597069	3.745378	8.283888	0.821965	0.3423	0.72096	0.81235	RFPL1S	chr22	-	29832818	29874115	5559
ENSG00000(	284.8428	313.1148	254.6469	400.0063	299.1404	302.4831	-0.23201	0.20772	0.31699	JPX	chrX	+	73164159	73290243	2194
ENSG00000(	27.96638	19.2686	31.66593	5.243529	8.283888	9.041614	1.7238	0.003033	0.007828	RP11-262D	chrX	+	71364034	71381600	2269
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP1-8B22.1	chr1	+	18921908	18922130	223
ENSG00000(	0	2.408575	1.319414	0	0.920432	0.821965	0.58326	0.66656	NA	PLCB1-IT1	chr20	+	8229351	8237564	373
ENSG00000(	3.107376	0	0	0.749076	0	0	0.76338	0.56438	NA	AC006548.	chr22	+	17378335	17378436	102
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-38J22	chr1	+	2.06E+08	2.06E+08	390
ENSG00000(	92.18548	91.52587	81.80365	86.89276	121.497	95.34793	-0.18776	0.4809	0.61004	RP11-773D	chr10	-	81563813	81586350	829
ENSG00000(	3417.077	3341.898	3208.814	1044.96	1104.518	992.1117	1.6635	3.52E-52	1.03E-50	ARHGAP23	chr17	+	36584662	36668628	6276
ENSG00000(	0	0	0	1.498151	0.920432	1.64393	-1.2565	0.35231	NA	RP11-390F	chr9	+	6716548	6727438	1501
ENSG00000(	6.214751	3.612863	2.638828	0.749076	0	0	2.5755	0.04106	0.081899	RP4-610C1	chr20	-	29521637	29522987	553
ENSG00000(	2.071584	0	0	1.498151	0	1.64393	-0.28088	0.83599	NA	GBP1P1	chr1	+	89873238	89891802	1740
ENSG00000(	6.214751	0	2.638828	1.498151	0.920432	0	1.247	0.32844	0.45614	AC092619.	chr2	-	2.39E+08	2.39E+08	1975
ENSG00000(	3.107376	0	0	0	3.681728	4.109825	-0.79881	0.54068	0.66379	RP11-180I2	chr10	+	78907410	78909858	427
ENSG00000(	0	0	1.319414	0	0.920432	0.821965	-0.17431	0.89516	NA	RPL15P4	chr6	+	31495891	31496470	580
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	GAPDHP16	chr21	+	16146622	16147583	962
ENSG00000(	0	0	5.277655	1.498151	2.761296	0	0.17283	0.89623	0.93574	RP11-330C	chr1	+	93197557	93198814	797
ENSG00000(	0	0	1.319414	1.498151	0.920432	5.753754	-1.6168	0.21834	0.32975	CYP4A22-A	chr1	-	47562325	47644943	921
ENSG00000(	29.00217	22.88147	17.15238	35.95563	50.62376	21.37109	-0.6135	0.19582	0.30249	AC069282.	chr7	+	47996390	47996915	526
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	PCDH8P1	chr13	+	53774116	53776547	2432
ENSG00000(	62.14751	61.41867	62.01245	31.46117	24.85166	50.13986	0.78413	0.033782	0.068962	LINC00475	chr9	+	94903580	94922396	2506
ENSG00000(	0	0	0	0	2.761296	1.64393	-1.2339	0.35779	NA	RP11-165N	chr9	-	1.15E+08	1.15E+08	450

ENSG00000(	4.143168	13.24716	7.916483	0.749076	5.522592	3.28786	1.2316	0.17962	0.28242	RP11-396C	chr1	+	2.26E+08	2.26E+08	595
ENSG00000(	0	0	0	0.749076	1.840864	0	-0.68825	0.58858	NA	TTTY16	chrY	-	7567398	7569288	192
ENSG00000(	5.17896	3.612863	17.15238	0	0	0	4.2452	0.000475	0.001402	AC005237.	chr2	-	2.42E+08	2.42E+08	559
ENSG00000(	1.035792	3.612863	5.277655	2.247227	10.12475	2.465895	-0.48706	0.6338	0.74338	C3orf83	chr3	-	12556433	12602558	901
ENSG00000(	5.17896	1.204288	0	3.745378	3.681728	0	-0.13004	0.91625	0.94889	RP11-383B	chr10	-	18820778	18822265	413
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP3-370M2	chr22	+	40356401	40360687	1287
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	XX-C2158C	chr6	-	1.71E+08	1.71E+08	439
ENSG00000(	2.071584	2.408575	0	0.749076	0.920432	1.64393	0.29222	0.82239	0.88537	AC068610.	chr7	+	1.15E+08	1.15E+08	1187
ENSG00000(	0	0	0	0	0	4.93179	-1.2404	0.35057	NA	AC002480.	chr7	-	22611226	22701411	1282
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	ZNF385D-A	chr3	+	21584308	21621451	705
ENSG00000(	0	3.612863	0	1.498151	0	0	0.55191	0.68269	NA	KB-1027C1	chr22	-	22239621	22240012	392
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-328J2	chr7	-	1.19E+08	1.2E+08	1577
ENSG00000(	6.214751	2.408575	1.319414	29.21395	29.45382	53.42772	-3.2158	1.19E-06	4.89E-06	AC098973.	chr3	+	27844253	27932792	543
ENSG00000(	0	0	5.277655	1.498151	1.840864	3.28786	-0.25293	0.84099	0.89827	RP11-210H	chr6	+	1.19E+08	1.19E+08	1179
ENSG00000(	0	2.408575	2.638828	0	0	2.465895	0.5704	0.67147	0.77389	RP11-19J3.	chr9	-	95301335	95301466	132
ENSG00000(	2.071584	0	2.638828	0	0.920432	0	1.1678	0.38936	NA	RP11-527D	chr1	+	2.42E+08	2.42E+08	504
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	AP000320.	chr21	-	35743101	35747647	471
ENSG00000(	4.143168	2.408575	2.638828	1.498151	11.04518	7.397684	-0.92861	0.33988	0.46858	C2CD4D	chr1	-	1.52E+08	1.52E+08	1757
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	UBE2D3P2	chr3	+	37176149	37176593	445
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-412H	chr1	-	2.19E+08	2.19E+08	390
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-384B	chr1	+	87511558	87512383	826
ENSG00000(	1.035792	1.204288	19.79121	0	1.840864	0	2.6115	0.028252	0.058958	AC003077.	chr7	+	1.11E+08	1.11E+08	2494
ENSG00000(	1.035792	2.408575	2.638828	7.490755	0.920432	1.64393	-0.58105	0.61152	0.72525	RPL35P5	chr7	-	66071725	66072094	370
ENSG00000(	7.250543	10.83859	9.235896	8.239831	15.64734	9.863579	-0.28122	0.68572	0.78496	NCBP2-AS1	chr3	+	1.97E+08	1.97E+08	562
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	RP1-159M2	chr6	-	1.13E+08	1.13E+08	1178
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	TRIM53AP	chr11	-	89726704	89732909	1544
ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	RP4-630C2	chr7	+	1.24E+08	1.24E+08	328
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-360D	chr1	+	1.74E+08	1.74E+08	255
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC098826.	chr2	+	1.33E+08	1.33E+08	471
ENSG00000(	1.035792	1.204288	1.319414	0	1.840864	0	0.52252	0.69958	NA	MTOR-AS1	chr1	+	11203955	11209594	705
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	AC007679.	chr2	+	2.07E+08	2.07E+08	781
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-771D	chr6	-	52011612	52015917	462
ENSG00000(	3318.677	2943.279	3215.411	2.247227	0	3.28786	10.296	1.07E-102	8.46E-101	ZNF469	chr16	+	88493879	88507165	13279
ENSG00000(	3.107376	3.612863	1.319414	0	0	0	2.4523	0.067889	0.12644	RP11-109D	chr9	-	72433899	72435655	1375
ENSG00000(	225.8026	252.9004	240.1333	370.7924	200.6542	502.2206	-0.57552	0.022517	0.048206	MTND2P28	chr1	+	565020	566063	1044
ENSG00000(	0	4.817151	3.958241	0	0	0	2.4241	0.072706	0.13396	RP5-997D2	chr1	+	54751078	54753044	1111
ENSG00000(	0	0	1.319414	0	0.920432	1.64393	-0.44377	0.74139	NA	AC017035.	chr2	+	1.98E+08	1.98E+08	1026
ENSG00000(	1.035792	3.612863	0	0	0.920432	0	1.1485	0.39729	NA	RP11-70P1	chr1	+	25907969	25916847	483
ENSG00000(	1.035792	1.204288	0	0.749076	0.920432	0	0.21038	0.87653	NA	RPL35AP4	chr6	-	33357151	33357252	102
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC005487.	chr7	+	1.08E+08	1.08E+08	665
ENSG00000(	367.7061	315.5234	335.1311	731.8468	484.1472	557.2922	-0.79713	6.92E-06	2.62E-05	SBDSP1	chr7	+	72300004	72307909	1714
ENSG00000(	11.39371	2.408575	2.638828	0	0.920432	9.863579	0.49894	0.64671	0.75341	AC064875.	chr2	-	13106910	13147138	1942
ENSG00000(	0	2.408575	1.319414	0	3.681728	0.821965	-0.164	0.9014	0.93881	EIF2S2P5	chr1	+	1.15E+08	1.15E+08	968
ENSG00000(	25.8948	15.65574	7.916483	5.243529	9.20432	6.575719	1.1681	0.089445	0.15998	RP11-619F	chr10	+	79114162	79136371	701

ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RNF19BPY	chrY	-	3646038	3647587	1550
ENSG0000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-143N	chr9	+	72701	88826	575
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP5-843L1	chr20	+	55152619	55173677	698
ENSG0000(	0	3.612863	1.319414	0	0	0	1.6005	0.2346	NA	TAF13P2	chr2	+	74578261	74578546	286
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RPL14P5	chrX	-	969238	970836	730
ENSG0000(	109.7939	62.62296	88.40072	71.91125	46.94203	69.86702	0.4599	0.14798	0.24112	FAM195B	chr17	-	79780287	79791178	2979
ENSG0000(	0	0	0	0	1.840864	4.109825	-1.6043	0.23668	0.35119	AC005534.	chr7	-	1.56E+08	1.56E+08	514
ENSG0000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	CTA-134P2	chr1	-	1.59E+08	1.59E+08	3384
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-641C	chr3	-	60715788	60716377	590
ENSG0000(	2.071584	0	2.638828	0	0	0.821965	1.2046	0.37464	NA	IPO7P2	chr13	-	24696204	24697953	1750
ENSG0000(	2.071584	0	5.277655	6.74168	0	0	0.062194	0.96121	0.97756	RP4-784A1	chr1	+	53793905	53802181	567
ENSG0000(	1.035792	0	0	2.247227	0	0	-0.31629	0.80869	NA	AP000619.	chr11	-	1.03E+08	1.03E+08	1000
ENSG0000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	FAM225B	chr9	-	1.16E+08	1.16E+08	7380
ENSG0000(	4.143168	0	0	0	0	0.821965	0.9919	0.46158	NA	RP1-30E17	chrX	-	1.27E+08	1.28E+08	481
ENSG0000(	3.107376	6.021439	9.235896	2.247227	3.681728	5.753754	0.55641	0.5465	0.66852	RP11-54K1	chr9	-	33019680	33020163	484
ENSG0000(	0	6.021439	5.277655	2.996302	1.840864	9.041614	-0.26215	0.80342	0.87246	AC007272.	chr2	+	2.02E+08	2.02E+08	963
ENSG0000(	404.9946	397.4149	386.5882	455.4379	405.9105	484.1373	-0.17805	0.24078	0.35606	SLC26A6	chr3	-	48663156	48672926	5682
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC005522.	chr7	-	76601996	76606278	453
ENSG0000(	35.21692	24.08575	47.4989	37.45378	23.93123	41.09825	0.050791	0.90588	0.94188	RP11-75C9	chr9	+	8858130	8862255	1959
ENSG0000(	0	1.204288	2.638828	0	0	0	1.2853	0.33195	NA	RP13-379L	chr20	-	56644110	56647126	1014
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-345I1	chr1	+	1.79E+08	1.79E+08	721
ENSG0000(	3.107376	4.817151	2.638828	0	0	0	2.885	0.028519	0.059468	RP11-325E	chrX	+	79965427	79966204	778
ENSG0000(	0	4.817151	0	2.996302	0.920432	12.32947	-1.317	0.26152	0.38081	RP11-269F	chr1	-	45224709	45241482	580
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	LL22NC03-	chr22	+	22693926	22695567	1642
ENSG0000(	0	0	6.597069	1.498151	3.681728	0	0.21091	0.87131	0.91912	AC007000.	chr7	-	76701068	76701554	487
ENSG0000(	1314.42	1342.781	1432.883	1325.864	1415.624	1258.428	0.03192	0.7853	0.85883	FGD5-AS1	chr3	-	14961854	14989931	3792
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	NPM1P18	chr7	+	36858564	36859295	732
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	TCEB1P6	chrY	-	19949081	19949408	328
ENSG0000(	0	0	0	21.72319	22.09037	22.19305	-5.3291	9.73E-07	4.04E-06	RP11-513G	chr3	-	1.94E+08	1.94E+08	910
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC017002.	chr2	+	1.12E+08	1.12E+08	792
ENSG0000(	1.035792	0	6.597069	0	0	0.821965	1.7189	0.20056	0.30811	AL773572.	chr21	-	42548249	42558715	1011
ENSG0000(	3.107376	0	1.319414	0.749076	0.920432	2.465895	0.079049	0.9512	0.97074	RP11-242C	chr1	-	29471006	29473506	279
ENSG0000(	1.035792	3.612863	1.319414	1.498151	7.363456	2.465895	-0.71568	0.52278	0.64815	AC087501.	chr17	+	9355514	9373331	715
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP1-45I4.2	chr6	-	1.43E+08	1.43E+08	455
ENSG0000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	RP11-267N	chr1	+	1.63E+08	1.63E+08	1133
ENSG0000(	0	1.204288	1.319414	1.498151	0	0	0.30687	0.81977	NA	DBH-AS1	chr9	-	1.37E+08	1.37E+08	2139
ENSG0000(	0	0	1.319414	6.74168	0.920432	0.821965	-1.6454	0.21092	0.32081	RP11-365P	chr13	+	1.12E+08	1.12E+08	684
ENSG0000(	5.17896	6.021439	3.958241	9.737982	3.681728	9.041614	-0.50844	0.54926	0.67079	RP11-417C	chr10	+	75764895	75787673	442
ENSG0000(	3.107376	2.408575	2.638828	7.490755	1.840864	9.041614	-0.99037	0.31505	0.44164	RP11-511I2	chr1	-	47846600	47874149	483
ENSG0000(	6.214751	12.04288	0	0.749076	0.920432	1.64393	1.911	0.089498	0.16001	LEPREL1-AS	chr3	+	1.9E+08	1.9E+08	730
ENSG0000(	0	0	2.638828	0	0.920432	1.64393	0.005124	0.99699	NA	RP11-468E	chr14	+	24505662	24520237	899
ENSG0000(	0	0	1.319414	7.490755	3.681728	7.397684	-2.757	0.020444	0.044221	RP5-850O1	chr1	+	50927141	50936822	503
ENSG0000(	0	0	0	8.239831	3.681728	4.93179	-3.287	0.008765	0.020644	PROSER2-A	chr10	-	11891612	11936699	3141
ENSG0000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP4-603I14	chr1	+	46836258	46836627	370

ENSG00000(	61.11172	43.35436	50.13772	5.243529	18.40864	10.68554	2.1204	1.21E-05	4.43E-05	MIAT	chr22	+	27042392	27072438	10216
ENSG00000(	6.214751	7.225726	21.11062	11.98521	12.88605	6.575719	0.11137	0.87564	0.92207	RP11-592B	chr10	-	51287081	51371070	2353
ENSG00000(	0	2.408575	1.319414	0	0	0	1.2548	0.34239	NA	RP11-2L8.1	chr3	+	1.78E+08	1.78E+08	560
ENSG00000(	77.68439	55.39724	59.37362	29.21395	38.65814	33.70056	0.91325	0.009694	0.022616	RP1-180E2	chr6	+	52442283	52444325	664
ENSG00000(	0	0	0	2.996302	12.88605	4.109825	-3.4985	0.004835	0.012013	AC004540.	chr7	-	26411764	26416321	611
ENSG00000(	4.143168	6.021439	9.235896	3.745378	13.80648	9.863579	-0.45361	0.5727	0.69137	RP1-234P1	chr6	+	75994730	76006283	445
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	AC025918.	chr15	+	59182166	59186281	383
ENSG00000(	0	2.408575	6.597069	4.494453	2.761296	0.821965	0.09277	0.93601	0.96146	CTD-2313N	chr11	+	71589499	71595607	216
ENSG00000(	5.17896	0	2.638828	8.988907	2.761296	6.575719	-1.0021	0.32877	0.45649	RP1-309F2	chr20	-	57438583	57463864	893
ENSG00000(	4.143168	0	0	0	0.920432	0	0.95689	0.47805	NA	RP11-44M(	chr7	+	1E+08	1E+08	570
ENSG00000(	5.17896	6.021439	10.55531	3.745378	0	4.93179	1.1031	0.25613	0.37445	DNAJC19P5	chr2	-	1.78E+08	1.78E+08	316
ENSG00000(	3.107376	7.225726	5.277655	1.498151	3.681728	1.64393	0.999	0.32502	0.45255	UBXN7-AS1	chr3	+	1.96E+08	1.96E+08	2008
ENSG00000(	0	0	0	2.996302	5.522592	0.821965	-2.349	0.07765	0.14168	LINC00626	chr1	+	1.69E+08	1.69E+08	955
ENSG00000(	21.75163	32.51577	32.98534	48.68991	23.0108	55.89361	-0.54347	0.22044	0.33216	FAM229A	chr1	-	32826871	32829879	2759
ENSG00000(	98.40023	109.5902	129.3026	224.7227	261.4027	219.4646	-1.0616	7.10E-07	2.99E-06	ERCC6	chr10	-	50663414	50747584	8008
ENSG00000(	0	2.408575	0	0	0	1.64393	0.21935	0.86915	NA	RPS18P1	chr20	+	5513524	5513981	458
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	RP3-348I23	chr6	-	20722559	20723886	332
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	GS1-594A7	chrX	+	15621004	15639607	574
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-80H5	chr10	-	91406046	91410579	368
ENSG00000(	0	1.204288	1.319414	0.749076	1.840864	3.28786	-0.79845	0.53874	0.66251	TRMT2B-AS	chrX	+	1E+08	1E+08	401
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	NIPA2P1	chr7	-	90949443	90950418	976
ENSG00000(	8.286335	3.612863	1.319414	8.988907	10.12475	9.041614	-0.94228	0.26444	0.38438	MKRN7P	chr20	-	45092541	45093763	1223
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	RP11-452K	chr10	+	99094321	99102770	615
ENSG00000(	0	0	0	3.745378	7.363456	2.465895	-2.9384	0.022216	0.047645	RP11-569G	chr1	+	26653179	26653524	346
ENSG00000(	96.32865	145.7188	91.03955	81.64923	104.9292	131.5144	0.066804	0.81276	0.87847	RUSC1-AS1	chr1	-	1.55E+08	1.55E+08	1836
ENSG00000(	2.071584	1.204288	0	0	0	2.465895	0.22121	0.87044	NA	RP11-46A1	chr1	+	1.81E+08	1.81E+08	543
ENSG00000(	2.071584	3.612863	2.638828	0.749076	0	0	2.0157	0.12474	0.21032	CTB-70D19	chr5	-	1.43E+08	1.43E+08	615
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	AC002398.	chr19	-	36279778	36288787	2167
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC004603.	chr19	+	43326015	43331030	1873
ENSG00000(	9.322127	6.021439	22.43003	9.737982	10.12475	22.19305	-0.15701	0.81641	0.88106	LINC00115	chr1	-	761586	762902	1317
ENSG00000(	0	1.204288	1.319414	2.996302	4.60216	6.575719	-1.8759	0.10885	0.18797	RP3-410B1	chrX	-	17988317	18122764	708
ENSG00000(	4.143168	19.2686	11.87472	0.749076	6.443024	1.64393	1.7689	0.047779	0.093287	RP11-574E	chr9	-	69718152	69721729	885
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC023590.	chr8	+	1.19E+08	1.19E+08	781
ENSG00000(	2.071584	2.408575	1.319414	0	0	0	1.9715	0.14607	NA	RP11-288L	chr1	+	27995979	27996787	489
ENSG00000(	0	0	2.638828	53.18436	35.89685	34.52253	-4.9507	6.21E-09	3.17E-08	AC074289.	chr2	+	64370373	64479993	1504
ENSG00000(	3.107376	1.204288	1.319414	1.498151	0.920432	2.465895	0.15606	0.89839	0.93708	RP3-476K8	chr1	-	26789247	26793773	529
ENSG00000(	74.57702	61.41867	36.94359	219.4791	113.2131	86.30632	-1.2496	0.000427	0.001268	RP11-384K	chr4	+	1.2E+08	1.2E+08	2486
ENSG00000(	0	6.021439	5.277655	0	2.761296	0.821965	1.1831	0.33585	0.46411	AC019171.	chr2	-	39325290	39325586	297
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	RP4-758J18	chr1	+	1355625	1358071	543
ENSG00000(	4.143168	6.021439	1.319414	1.498151	0.920432	2.465895	0.96622	0.38758	0.51842	RP13-258C	chrX	-	91931518	91931953	436
ENSG00000(	8.286335	0	2.638828	0	1.840864	7.397684	0.19757	0.86648	0.91587	RP11-57C1	chr10	+	89367742	89419036	495
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	XXbac-BPG	chr6	+	32223488	32233615	3458
ENSG00000(	2.071584	0	3.958241	0	0	0	1.8862	0.16413	0.26236	AC007879.	chr2	+	2.08E+08	2.08E+08	551
ENSG00000(	4.143168	6.021439	5.277655	0.749076	6.443024	3.28786	0.48518	0.62245	0.73432	RIMKLBP2	chr1	-	2.19E+08	2.19E+08	654

ENSG00000(	45.57484	51.78437	48.81831	88.39091	85.60018	69.04505	-0.72534	0.019052	0.041537	NOL7	chr6	+	13615559	13632971	1184
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-57G1	chr10	+	69553528	69554003	476
ENSG00000(	2.071584	1.204288	3.958241	3.745378	2.761296	1.64393	-0.14646	0.89615	0.9357	CACYBPP1	chr10	-	86214435	86215812	684
ENSG00000(	1.035792	0	6.597069	0	1.840864	6.575719	-0.11547	0.92497	0.95456	AC026150.	chr15	+	30488239	30506743	4260
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP4-566D2	chr1	-	2.28E+08	2.28E+08	671
ENSG00000(	25.8948	27.69862	22.43003	0	0	0.821965	5.2208	1.01E-07	4.65E-07	PCA3	chr9	+	79379352	79402485	3922
ENSG00000(	15.53688	3.612863	17.15238	0	0	0.821965	4.078	0.000211	0.000656	RP4-575N6	chr1	-	1.02E+08	1.02E+08	403
ENSG00000(	0	0	0	11.23613	2.761296	0	-2.7918	0.034572	0.070376	AC022431.	chr5	-	55807394	55902059	765
ENSG00000(	1.035792	2.408575	1.319414	2.996302	6.443024	5.753754	-1.3428	0.21117	0.3211	RP3-441A1	chr6	-	37783553	37786994	419
ENSG00000(	0	0	0	5.243529	0.920432	3.28786	-2.382	0.073154	0.13469	RP11-395B	chr7	-	1.01E+08	1.01E+08	2083
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-313E	chr9	+	75085290	75085992	392
ENSG00000(	5.17896	6.021439	3.958241	7.490755	3.681728	19.72716	-0.91833	0.27106	0.39176	NTF4	chr19	-	49559050	49568333	1748
ENSG00000(	1.035792	6.021439	0	2.996302	0	1.64393	0.39761	0.75398	0.83729	RP11-339B	chr9	-	1.31E+08	1.31E+08	407
ENSG00000(	18.64425	19.2686	3.958241	6.74168	4.60216	8.219649	1.0145	0.1707	0.27109	SATB2-AS1	chr2	+	2E+08	2E+08	3314
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP5-1077I2	chr20	-	13224711	13226016	446
ENSG00000(	3.107376	6.021439	11.87472	0	0	0	3.9414	0.001425	0.003888	AC009950.	chr2	+	2.31E+08	2.31E+08	773
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC017076.	chr2	-	6968645	6980595	799
ENSG00000(	704.3385	803.2599	602.9721	112.3613	127.94	125.7606	2.5195	2.69E-48	7.08E-47	ELFN1	chr7	+	1727755	1787590	3845
ENSG00000(	7.250543	12.04288	2.638828	2.996302	10.12475	8.219649	0.04986	0.9525	0.97169	LINC00035	chr7	+	73149368	73150384	558
ENSG00000(	0	0	0	1.498151	0.920432	0.821965	-0.99775	0.45448	NA	RP3-526F5	chrX	+	1.43E+08	1.43E+08	318
ENSG00000(	7.250543	0	5.277655	17.22874	13.80648	8.219649	-1.4608	0.079342	0.14433	MTND1P23	chr1	+	564442	564813	372
ENSG00000(	81.82756	81.89156	75.20659	106.3687	77.31629	86.30632	-0.17608	0.5238	0.64904	RP11-139H	chr15	-	55609382	55611359	866
ENSG00000(	0	2.408575	1.319414	0	0	0	1.2548	0.34239	NA	AC005550.	chr7	-	15728700	15730479	312
ENSG00000(	15.53688	9.634302	15.83297	10.48706	17.48821	8.219649	0.17622	0.7823	0.85666	AC074138.	chr19	-	37176342	37178351	815
ENSG00000(	0	3.612863	1.319414	0.749076	0	1.64393	0.60055	0.6524	0.75824	RP11-192N	chr10	+	29986832	29987157	326
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	OR7E19P	chr19	-	9376066	9377015	948
ENSG00000(	2.071584	1.204288	3.958241	0	0	4.93179	0.36817	0.7713	0.84963	AC102953.	chr7	+	1499573	1503644	498
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP3-340N1	chr1	-	20510735	20512979	510
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-436D	chr6	+	98723022	98727735	226
ENSG00000(	10.35792	6.021439	5.277655	19.47596	15.64734	4.93179	-0.80438	0.2776	0.39938	RP11-460N	chr7	+	64544481	64560610	586
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	RP11-464C	chr10	+	3976711	3978005	591
ENSG00000(	0	0	0	0.749076	5.522592	4.109825	-2.4974	0.058964	0.11206	RP11-211N	chr9	+	46843638	46846025	2245
ENSG00000(	3.107376	7.225726	2.638828	3.745378	1.840864	0.821965	0.81156	0.44818	0.57787	RP11-190J	chr10	+	1.04E+08	1.04E+08	850
ENSG00000(	4.143168	0	0	0.749076	0	0	1.0202	0.44849	NA	RP11-403E	chrX	-	63364752	63366932	1771
ENSG00000(	3.107376	3.612863	3.958241	0	0	0	2.9061	0.027122	0.056934	OFD1P1Y	chrY	+	19921687	19937209	1225
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-467I2	chr1	-	2.41E+08	2.41E+08	204
ENSG00000(	6.214751	20.47289	13.19414	3.745378	8.283888	1.64393	1.4043	0.07826	0.14267	CCT8P1	chr1	-	1.47E+08	1.47E+08	1657
ENSG00000(	15.53688	26.49433	22.43003	2.247227	5.522592	8.219649	1.8863	0.004683	0.011672	PRICKLE2-A	chr3	+	64173220	64186641	2496
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC026167.	chr3	+	6190171	6407572	299
ENSG00000(	1.035792	0	0	0	3.681728	1.64393	-1.1227	0.40737	0.53818	RP11-57H1	chr1	-	95628775	95699538	2447
ENSG00000(	43.50326	57.80581	22.43003	29.96302	8.283888	18.90519	1.0655	0.038099	0.076734	RP4-798A1	chr1	+	16787443	16794976	3245
ENSG00000(	0	0	0	1.498151	2.761296	4.93179	-2.3528	0.076622	0.14015	FGF13-AS1	chrX	+	1.38E+08	1.38E+08	849
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-114G	chr13	-	90129862	90152763	666
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC005740.	chr5	-	1.41E+08	1.41E+08	522

ENSG0000(	0	0	0	0.749076	0	3.28786	-1.135	0.39451	NA	RP11-463P	chr10	-	48324788	48332197	599
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC009274.	chr7	-	1.3E+08	1.3E+08	370
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	YBX1P8	chrX	-	46544200	46545142	943
ENSG0000(	2.071584	1.204288	5.277655	0.749076	0.920432	5.753754	0.1444	0.90007	0.93783	TLK2P1	chr17	-	32363700	32366891	3192
ENSG0000(	1.035792	1.204288	2.638828	11.23613	15.64734	8.219649	-2.4734	0.007381	0.017681	RP5-1070A	chr1	+	98676303	98738214	2229
ENSG0000(	7.250543	8.430014	9.235896	14.23244	9.20432	14.79537	-0.58366	0.3925	0.52329	MEMO1P1	chr21	+	37502669	37504208	1540
ENSG0000(	9.322127	4.817151	3.958241	1.498151	0.920432	2.465895	1.5631	0.12713	0.21348	PAICSP1	chr9	+	37878113	37879490	1217
ENSG0000(	2.071584	0	0	5.992604	0	0	-0.78758	0.56071	0.68112	MTND4P32	chrX	+	1.02E+08	1.02E+08	1237
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC092570.	chr2	+	1.02E+08	1.02E+08	469
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC108938.	chr2	+	1.11E+08	1.11E+08	1531
ENSG0000(	5.17896	4.817151	6.597069	14.23244	11.04518	8.219649	-0.93271	0.21941	0.33105	LINC00869	chr1	+	1.49E+08	1.49E+08	695
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-552E	chr6	-	40326483	40337213	824
ENSG0000(	0	0	0	4.494453	4.60216	0.821965	-2.4429	0.065334	0.12229	PRSS44	chr3	-	46850849	46854048	1146
ENSG0000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-24H1	chr3	+	62912046	62912557	512
ENSG0000(	55.93276	62.62296	39.58241	43.44638	30.37426	46.852	0.38263	0.30046	0.42551	RP4-706A1	chr1	+	77594768	77595384	617
ENSG0000(	83.89914	108.3859	77.84541	92.88537	112.2927	125.7606	-0.28856	0.27939	0.4016	UQCRFS1P:	chr22	+	40271293	40272119	825
ENSG0000(	19.68005	30.10719	44.86007	13.48336	3.681728	1.64393	2.1592	0.000957	0.00269	RP11-180C	chr1	-	70825245	70826120	575
ENSG0000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP1-300G1	chr6	-	82236819	82244632	784
ENSG0000(	5.17896	6.021439	3.958241	18.72689	17.48821	14.79537	-1.6204	0.020279	0.043922	RP11-90D4	chr12	-	8448582	8549399	3033
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-53M:	chr8	-	55435339	55435875	537
ENSG0000(	0	0	0	1.498151	1.840864	0.821965	-1.2806	0.34348	NA	AC007461.	chr17	+	70068474	70089622	2063
ENSG0000(	0	0	2.638828	0	4.60216	0.821965	-0.60079	0.65475	0.76009	SEPT7P3	chr7	+	35985904	36013282	621
ENSG0000(	0	2.408575	0	2.247227	3.681728	6.575719	-1.6875	0.16565	0.26434	AC011475.	chr19	+	10751715	10752093	81
ENSG0000(	2.071584	2.408575	0	0.749076	3.681728	2.465895	-0.41566	0.73622	0.82347	AC004383.	chrX	+	1.34E+08	1.34E+08	289
ENSG0000(	3.107376	1.204288	0	0	0	0	1.4526	0.27741	NA	AP001476.	chr21	+	47476430	47477481	355
ENSG0000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	MTND3P1	chr13	-	22687258	22687477	220
ENSG0000(	0	0	1.319414	1.498151	0	2.465895	-0.80883	0.55106	NA	AHCTF1P1	chr2	-	1.62E+08	1.62E+08	6821
ENSG0000(	0	1.204288	0	8.988907	15.64734	6.575719	-3.5061	0.001641	0.004438	AC073043.	chr2	-	2.01E+08	2.01E+08	1021
ENSG0000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	AC098823.	chr2	-	2.32E+08	2.32E+08	2609
ENSG0000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP11-157L	chr9	+	46117312	46117651	340
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP4-683M8	chr1	+	48519217	48532873	789
ENSG0000(	454.7126	498.5751	440.6842	164.7966	254.9597	267.9606	1.0165	1.65E-07	7.43E-07	BAIAP2-AS1	chr17	-	79002933	79008501	4462
ENSG0000(	0	0	1.319414	0	0	3.28786	-0.58083	0.66501	NA	RP1-228P1	chr12	+	48478833	48479204	372
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RPS27AP3	chr20	+	35677657	35678110	454
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC022596.	chr17	-	16721297	16725893	1873
ENSG0000(	2.071584	6.021439	13.19414	1.498151	16.56778	6.575719	-0.1905	0.83025	0.89105	SLC25A39P	chr1	+	2.03E+08	2.03E+08	1065
ENSG0000(	0	1.204288	6.597069	3.745378	0	1.64393	0.33618	0.7884	0.86153	RP1-69D17	chr6	-	1.3E+08	1.3E+08	728
ENSG0000(	1.035792	0	1.319414	0	1.840864	4.109825	-0.80554	0.54252	0.66511	AC073343.	chr7	-	6833765	6836573	602
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP3-389A2	chrX	-	17723459	17723811	353
ENSG0000(	2.071584	0	0	4.494453	3.681728	0	-1.1743	0.37167	0.50217	AC124944.	chr3	+	1.96E+08	1.96E+08	625
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CLCP2	chr13	+	1.15E+08	1.15E+08	421
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-167P	chr10	+	74261504	74262714	162
ENSG0000(	2.071584	0	5.277655	0	9.20432	0	-0.21691	0.86359	0.91377	AP4B1-AS1	chr1	+	1.14E+08	1.14E+08	1734
ENSG0000(	22.78742	22.88147	30.34652	3.745378	2.761296	23.01502	1.2693	0.060163	0.114	TEX22	chr14	+	1.06E+08	1.06E+08	2571

ENSG00000(	8.286335	13.24716	18.47179	20.97412	12.88605	13.9734	-0.26032	0.66842	0.77154	LINC00685	chrX	+	281725	282586	428
ENSG00000(	4.143168	1.204288	7.916483	44.19546	80.99802	69.04505	-3.7118	6.01E-11	3.61E-10	AC010536.	chr16	-	87727144	87729753	2610
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	TRIM64FP	chr2	+	96180575	96185855	1336
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	TCEB1P21	chr2	-	71183029	71183364	336
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	HNRNPA1P	chr20	-	44374376	44374926	551
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	RP11-438H	chr1	-	2.48E+08	2.48E+08	1453
ENSG00000(	0	2.408575	3.958241	0	2.761296	0.821965	0.53822	0.67786	0.77911	RP1-137D1	chr6	-	1.7E+08	1.7E+08	2282
ENSG00000(	1.035792	0	2.638828	0	3.681728	2.465895	-0.4811	0.71059	0.80433	RP11-50E1	chr10	+	52388910	52391396	2089
ENSG00000(	4.143168	1.204288	2.638828	2.247227	0.920432	0.821965	0.73261	0.54069	0.66379	AC007790.	chr7	-	1.33E+08	1.33E+08	782
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP5-1050E	chr9	+	92501142	92523200	916
ENSG00000(	482.679	541.9295	395.8241	503.3788	462.9773	572.0876	-0.11401	0.48603	0.61518	ABC7-4238	chr12	+	73725	91218	1817
ENSG00000(	0	0	0	2.247227	2.761296	5.753754	-2.5938	0.048031	0.093732	RPS12P5	chr3	+	29432339	29432709	371
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC004987.	chr7	-	39836192	39837510	1319
ENSG00000(	23.82321	30.10719	22.43003	17.22874	14.72691	18.90519	0.56403	0.25794	0.37662	AC022431.	chr5	-	55800462	55800899	438
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-753E	chrX	+	24650374	24650718	345
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-410C	chr1	+	2.21E+08	2.21E+08	540
ENSG00000(	4.143168	0	0	0	0	0.821965	0.9919	0.46158	NA	LEMD1-AS1	chr1	+	2.05E+08	2.05E+08	2781
ENSG00000(	26.93059	21.67718	25.06886	6.74168	6.443024	6.575719	1.804	0.002238	0.005912	RP11-276H	chr9	+	89563614	89616948	4387
ENSG00000(	0	4.817151	3.958241	0	0	0.821965	1.9248	0.14742	0.24047	ZNF32-AS1	chr10	+	44139320	44140495	434
ENSG00000(	0	2.408575	0	0	0	1.64393	0.21935	0.86915	NA	AC005034.	chr2	-	75878414	75878753	340
ENSG00000(	0	0	2.638828	1.498151	1.840864	1.64393	-0.58431	0.65913	0.76364	RP11-307P	chr6	-	1.48E+08	1.48E+08	603
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	MRPL35P3	chr10	+	76287342	76287705	364
ENSG00000(	0	0	6.597069	0	0	0	1.83	0.17508	0.27674	PTP4A1P3	chr7	+	90736689	90737108	420
ENSG00000(	2.071584	4.817151	5.277655	5.992604	9.20432	14.79537	-1.1754	0.16189	0.25956	GRM7-AS3	chr3	-	6673376	6847136	947
ENSG00000(	44.53905	55.39724	35.62417	75.65663	55.22592	68.22309	-0.54583	0.1077	0.18644	GTF2H2B	chr5	+	69711179	69743885	2106
ENSG00000(	0	0	2.638828	1.498151	0	0	0.308	0.81734	NA	ISM1-AS1	chr20	-	13218448	13220321	652
ENSG00000(	6.214751	6.021439	3.958241	0.749076	5.522592	4.93179	0.4692	0.62746	0.73849	AC009961.	chr2	-	1.61E+08	1.61E+08	401
ENSG00000(	0	1.204288	1.319414	1.498151	2.761296	3.28786	-1.0861	0.39058	0.52139	RP11-61N2	chr11	-	49455025	49455990	966
ENSG00000(	1.035792	2.408575	0	0.749076	0	0	0.91766	0.49624	NA	AC093382.	chr2	-	2.17E+08	2.17E+08	379
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	PSPHP1	chr7	+	55832490	55840981	261
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC005682.	chr7	+	22921512	22922009	498
ENSG00000(	2.071584	1.204288	1.319414	1.498151	3.681728	2.465895	-0.52967	0.65521	0.76041	ARPC3P1	chr20	+	47751017	47751549	533
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	AC091813.	chr7	-	79173227	79174169	943
ENSG00000(	16.57267	16.86003	19.79121	76.40571	87.44104	94.52597	-2.2395	1.75E-09	9.40E-09	TMEM191A	chr22	+	21055220	21058894	1961
ENSG00000(	2.071584	0	1.319414	0.749076	0	0	0.90441	0.50226	NA	AC091729.	chr7	+	1120499	1121814	302
ENSG00000(	0	0	0	2.247227	0.920432	4.109825	-2.0097	0.13586	0.22515	RP4-813D1	chr20	+	55841853	55858054	1166
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	SMARCE1P:	chr6	-	85139302	85140520	1219
ENSG00000(	2.071584	4.817151	3.958241	0	1.840864	3.28786	0.82726	0.47345	0.60257	RP3-323P2	chrX	+	57148095	57153676	665
ENSG00000(	8.286335	7.225726	11.87472	8.239831	13.80648	8.219649	-0.1335	0.85072	0.9049	CFLAR-AS1	chr2	-	2.02E+08	2.02E+08	1072
ENSG00000(	13.46529	19.2686	7.916483	11.98521	10.12475	8.219649	0.39857	0.54445	0.66668	ZNF192P1	chr6	+	28129559	28137372	1628
ENSG00000(	13.46529	12.04288	10.55531	3.745378	4.60216	3.28786	1.493	0.053072	0.10232	RP11-474D	chr10	-	69720459	69721221	763
ENSG00000(	29.00217	13.24716	25.06886	0	0	0	5.7365	1.68E-07	7.56E-07	AC104809.	chr2	+	2.42E+08	2.42E+08	3148
ENSG00000(	76.6486	113.203	76.526	158.804	128.8605	124.9387	-0.6275	0.016342	0.036184	CTA-217C2	chr22	-	45529710	45559662	1267
ENSG00000(	15.53688	14.45145	11.87472	2.247227	0	0.821965	3.1963	0.000487	0.001433	AC005682.	chr7	-	22903493	22920969	1467

ENSG00000	0	1.204288	0	0.749076	0	1.64393	-0.39763	0.76659	NA	RP11-739N	chr1	+	2.04E+08	2.04E+08	486
ENSG00000	8.286335	3.612863	2.638828	32.21025	19.32907	27.12484	-2.2515	0.000615	0.001784	RP11-157P	chr20	-	60880488	60881381	681
ENSG00000	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-217B	chr9	+	1.08E+08	1.08E+08	469
ENSG00000	5.17896	0	5.277655	0	0	1.64393	1.7017	0.18756	0.29227	RPS26P56	chrX	+	1.29E+08	1.29E+08	240
ENSG00000	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	AC083822.	chr3	+	1.96E+08	1.96E+08	201
ENSG00000	0	1.204288	0	2.996302	2.761296	0	-1.1798	0.38259	0.51332	VN2R10P	chr16	+	77254303	77255155	853
ENSG00000	3.107376	12.04288	6.597069	0	0	0	4.0003	0.001157	0.003214	RP11-145A	chr1	-	2.26E+08	2.26E+08	534
ENSG00000	7.250543	0	5.277655	2.996302	5.522592	2.465895	0.16848	0.87227	0.91976	RP11-523H	chr13	+	20248764	20250024	376
ENSG00000	0	1.204288	0	2.247227	4.60216	1.64393	-1.7149	0.18874	0.29376	AC055811.	chr17	+	17145324	17146200	877
ENSG00000	12.4295	10.83859	5.277655	2.996302	6.443024	4.93179	0.90953	0.26147	0.38076	RPL10AP6	chr3	-	61728129	61728780	652
ENSG00000	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	TERF1P5	chr13	+	19254634	19255846	1212
ENSG00000	9.322127	2.408575	7.916483	0	1.840864	1.64393	2.0175	0.061388	0.11582	AC009336.	chr2	+	1.77E+08	1.77E+08	1121
ENSG00000	2.071584	1.204288	0	0	1.840864	1.64393	-0.02642	0.98424	0.99091	ST7-AS2	chr7	-	1.17E+08	1.17E+08	1351
ENSG00000	0	0	0	2.996302	0	10.68554	-2.7683	0.036117	0.073162	AC084809.	chr17	+	31203777	31205655	591
ENSG00000	59.04014	65.03154	29.0271	14.23244	9.20432	18.90519	1.7952	0.000139	0.000445	AC058791.	chr7	-	1.31E+08	1.31E+08	2228
ENSG00000	15.53688	31.31148	14.51355	22.47227	28.53339	29.59074	-0.37871	0.45058	0.58023	RP11-119F	chr10	-	81422844	81526085	616
ENSG00000	0	0	2.638828	5.243529	14.72691	4.93179	-2.5775	0.019098	0.041626	AC093375.	chr2	-	1.57E+08	1.57E+08	1603
ENSG00000	1.035792	1.204288	1.319414	0.749076	0	0	1.0069	0.45773	NA	PARD3-AS1	chr10	+	35104695	35105314	302
ENSG00000	7.250543	0	2.638828	1.498151	0.920432	5.753754	0.22385	0.84546	0.90132	IFNA20P	chr9	+	21321299	21321826	528
ENSG00000	5.17896	2.408575	1.319414	8.239831	8.283888	6.575719	-1.1657	0.20417	0.31246	RPS14P3	chr1	+	19934608	19935062	455
ENSG00000	2.071584	0	0	0	0	0	0.74702	0.55047	NA	C12orf77	chr12	-	25146358	25150453	1516
ENSG00000	2.071584	0	0	0	2.761296	0	-0.15346	0.90925	NA	AC013480.	chr2	-	42242765	42252442	346
ENSG00000	0	0	0	11.23613	11.04518	9.041614	-4.2422	0.000276	0.000844	RP11-31F1	chr9	+	547317	549531	449
ENSG00000	4.143168	0	0	0	0	0	1.2752	0.32937	NA	RBMX2P1	chr21	-	16201475	16202310	836
ENSG00000	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC104058.	chr2	-	1.87E+08	1.87E+08	297
ENSG00000	32.10955	19.2686	25.06886	7.490755	6.443024	9.863579	1.6041	0.005552	0.01364	TPI1P1	chr1	+	77165474	77166223	750
ENSG00000	0	4.817151	0	0.749076	4.60216	8.219649	-1.1015	0.3549	0.48458	MRPL23-AS	chr11	-	2004467	2011150	1876
ENSG00000	50.7538	36.12863	31.66593	45.69361	55.22592	64.11326	-0.45938	0.20971	0.31939	RP11-31F1	chr1	+	1.13E+08	1.14E+08	2314
ENSG00000	0	0	0	7.490755	0.920432	0	-2.0459	0.1308	0.2183	SLC25A5P5	chr7	+	32511125	32512021	897
ENSG00000	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AC093642.	chr2	-	2.43E+08	2.43E+08	565
ENSG00000	0	0	1.319414	0.749076	6.443024	0.821965	-1.5568	0.23869	0.35363	CTD-2015B	chr5	+	24170479	24171355	877
ENSG00000	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	RP11-1L9.1	chrX	+	13395307	13421138	453
ENSG00000	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	ANKRD18D	chr3	-	1.98E+08	1.98E+08	2897
ENSG00000	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	RP11-420K	chr1	-	39715510	39723321	558
ENSG00000	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-506B	chr6	+	1.13E+08	1.13E+08	894
ENSG00000	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	GAPDHP32	chr1	-	1.2E+08	1.2E+08	998
ENSG00000	14.50109	4.817151	13.19414	2.247227	1.840864	2.465895	2.0302	0.020832	0.044988	XXyac-YX65	chr6	+	1.7E+08	1.7E+08	980
ENSG00000	7.250543	8.430014	6.597069	1.498151	7.363456	8.219649	0.3509	0.68059	0.78119	CYP2D8P1	chr22	-	42545877	42551007	1490
ENSG00000	0	2.408575	1.319414	0	0.920432	1.64393	0.29993	0.82362	0.8862	RP11-379B	chr6	-	82554902	82643197	822
ENSG00000	0	0	0	2.996302	0	0.821965	-1.0802	0.41594	NA	RP3-512E2	chr6	+	90659835	90662905	876
ENSG00000	3.107376	2.408575	9.235896	0	5.522592	0	1.0875	0.35088	0.48055	RP11-430L	chr1	-	16695645	16696025	381
ENSG00000	1.035792	0	0	2.996302	3.681728	3.28786	-1.9798	0.12366	0.20883	RP13-401N	chr20	+	25731854	25733397	320
ENSG00000	0	0	6.597069	2.996302	1.840864	4.93179	-0.44814	0.70848	0.80296	AC018641.	chr7	-	32496575	32497370	796
ENSG00000	1.035792	2.408575	5.277655	3.745378	0	0.821965	0.64032	0.59817	0.71374	ADAM1B	chr12	+	1.12E+08	1.12E+08	2000

ENSG00000(	26.93059	32.51577	15.83297	11.23613	11.04518	17.26126	0.89342	0.10141	0.1775	CTA-292E1(	chr22	+	29196671	29244547	516
ENSG00000(	1.035792	0	0	1.498151	0	0	-0.08447	0.94679	NA	RP11-551L	chr12	-	31149973	31158938	616
ENSG00000(	10.35792	3.612863	7.916483	0	2.761296	0	2.387	0.030621	0.063289	RP11-776H	chr1	-	61005921	61106163	1798
ENSG00000(	3.107376	0	0	2.996302	2.761296	3.28786	-1.0246	0.41035	0.5411	UPF3AP1	chr17	-	16648945	16650075	1126
ENSG00000(	271.3775	249.2876	257.2857	367.7961	350.6846	307.4149	-0.39704	0.019095	0.041623	TMEM185B	chr2	-	1.21E+08	1.21E+08	2131
ENSG00000(	6.214751	0	0	8.239831	4.60216	6.575719	-1.2724	0.23677	0.35129	FTOP1	chr2	-	43024365	43025852	861
ENSG00000(	1.035792	1.204288	1.319414	2.247227	0	3.28786	-0.43189	0.73644	0.82368	RP11-524C	chr10	+	70259289	70259725	437
ENSG00000(	0	3.612863	0	0	0	1.64393	0.50971	0.70603	NA	RP5-882O7	chr1	-	45309593	45309754	162
ENSG00000(	0	0	3.958241	0.749076	0.920432	1.64393	0.12779	0.92372	0.95381	AC016700.	chr2	-	70321026	70330352	793
ENSG00000(	0	0	2.638828	7.490755	6.443024	15.61733	-2.8448	0.007411	0.017748	AC104655.	chr2	+	1.06E+08	1.06E+08	797
ENSG00000(	1.035792	0	3.958241	0	0	0	1.6134	0.2311	NA	UPK1A-AS1	chr19	-	36158850	36164193	795
ENSG00000(	3.107376	7.225726	19.79121	3.745378	7.363456	6.575719	0.67888	0.40821	0.53902	KIRREL-IT1	chr1	+	1.58E+08	1.58E+08	587
ENSG00000(	0	3.612863	0	0	0.920432	0.821965	0.52233	0.70023	NA	AC074375.	chr2	-	42907228	42907419	192
ENSG00000(	9.322127	6.021439	7.916483	5.243529	7.363456	5.753754	0.31599	0.69125	0.7894	RP1-102H1	chr6	+	88081311	88102519	542
ENSG00000(	6.214751	2.408575	1.319414	5.992604	0.920432	4.93179	-0.19627	0.85196	0.90558	RPS7P10	chr13	-	22202552	22203154	603
ENSG00000(	1.035792	0	0	0	1.840864	7.397684	-1.7401	0.19037	0.29574	RP1-37C10	chr1	+	17305421	17331586	636
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	RP11-348F	chrX	+	51139363	51208513	586
ENSG00000(	1.035792	0	0	1.498151	4.60216	0.821965	-1.4881	0.2639	0.38373	BTBD9-AS1	chr6	+	38449468	38450307	560
ENSG00000(	0	0	0	14.23244	16.56778	4.93179	-4.3962	0.000157	0.000499	RP11-417L	chr9	-	1.1E+08	1.1E+08	1580
ENSG00000(	0	0	1.319414	0	2.761296	3.28786	-1.196	0.37513	0.50574	AC012512.	chr2	+	2.25E+08	2.25E+08	718
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RPL7P22	chr5	+	72021246	72021978	733
ENSG00000(	1.035792	1.204288	2.638828	0	2.761296	1.64393	0.10214	0.93634	0.96165	RP4-633I8.	chr1	+	8858534	8859565	415
ENSG00000(	6.214751	3.612863	5.277655	0	2.761296	1.64393	1.4306	0.19355	0.29944	AGKP1	chrY	+	16750976	16752238	1263
ENSG00000(	0	2.408575	2.638828	109.365	93.88406	87.95025	-5.5133	1.50E-16	1.28E-15	RP11-255A	chr9	+	33580693	33605289	852
ENSG00000(	3.107376	1.204288	3.958241	1.498151	2.761296	0.821965	0.53657	0.64553	0.75267	FTH1P20	chr2	-	1.82E+08	1.82E+08	548
ENSG00000(	1.035792	3.612863	0	0	0	0	1.5346	0.25314	NA	SPANXA2-C	chrX	+	1.41E+08	1.41E+08	1701
ENSG00000(	2.071584	1.204288	2.638828	0	0	0	1.9938	0.14152	NA	RP11-258F	chr10	-	38064299	38073059	712
ENSG00000(	0	0	0	0	1.840864	3.28786	-1.4188	0.29365	NA	RPL39P40	chr21	-	18872997	18873142	146
ENSG00000(	3.107376	1.204288	3.958241	8.239831	11.04518	4.109825	-1.2917	0.16726	0.2665	RP4-765C7	chr1	-	1.78E+08	1.78E+08	4755
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC004911.	chr7	+	1.45E+08	1.45E+08	871
ENSG00000(	7.250543	4.817151	2.638828	0	0	0	3.4077	0.007733	0.018453	AC017060.	chr7	-	17503069	17598533	442
ENSG00000(	3.107376	0	0	1.498151	0	0	0.45456	0.7352	NA	RP11-136K	chr6	-	1.51E+08	1.51E+08	614
ENSG00000(	3.107376	13.24716	15.83297	0	0	1.64393	3.3656	0.001648	0.004456	RP11-45A1	chr9	-	1.19E+08	1.19E+08	1854
ENSG00000(	6.214751	8.430014	7.916483	4.494453	3.681728	1.64393	1.0459	0.24135	0.3568	FTLP3	chr20	+	4004552	4005091	528
ENSG00000(	0	0	5.277655	0	1.840864	1.64393	0.34259	0.79734	0.86794	RP11-276E	chr9	-	1.16E+08	1.16E+08	420
ENSG00000(	5.17896	2.408575	5.277655	0	0	0	3.1932	0.013698	0.030905	OFD1P2Y	chrY	-	20242567	20258088	1149
ENSG00000(	2.071584	0	0	0	5.522592	2.465895	-1.1335	0.39016	0.52086	RPL21P11(	chr13	+	73277831	73278276	446
ENSG00000(	0	0	2.638828	0.749076	0	0.821965	0.31	0.81829	NA	AC092155.	chr2	-	62817390	62889789	932
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	CTA-351J1.	chr7	+	1.05E+08	1.05E+08	610
ENSG00000(	4.143168	0	1.319414	0.749076	0	0	1.3958	0.30321	0.42835	RP11-290L	chr9	+	39154072	39155476	1190
ENSG00000(	0	0	3.958241	1.498151	7.363456	6.575719	-1.5091	0.19591	0.30259	RP11-315I:	chr9	+	23681892	23682660	769
ENSG00000(	0	0	0	1.498151	2.761296	1.64393	-1.7322	0.2011	NA	SHANK2-AS	chr11	+	70477199	70481595	2252
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	AC019349.	chr17	-	39705858	39710747	2141
ENSG00000(	3.107376	2.408575	1.319414	0	0.920432	0	1.696	0.20217	0.30995	UBE2V1P1	chr20	-	3342527	3342971	445

ENSG00000	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-358H	chr1	-	2.23E+08	2.23E+08	316
ENSG00000	0	0	0	6.74168	7.363456	10.68554	-3.8836	0.001193	0.003303	RP11-128N	chr20	+	2187863	2193797	536
ENSG00000	3.107376	2.408575	9.235896	12.73428	7.363456	6.575719	-0.78466	0.35304	0.48275	AP006216.	chr11	+	1.17E+08	1.17E+08	419
ENSG00000	2.071584	2.408575	2.638828	0.749076	0.920432	0.821965	1.0515	0.3987	0.52974	RP11-336A	chr10	-	5754137	5786030	945
ENSG00000	2.071584	3.612863	1.319414	2.247227	7.363456	2.465895	-0.61858	0.5654	0.68477	RP1-1J6.2	chr20	-	39726969	39766643	1462
ENSG00000	0	0	1.319414	0	0	1.64393	-0.1317	0.91874	NA	AC019118.	chr2	+	3160527	3161568	435
ENSG00000	1.035792	1.204288	0	0.749076	0.920432	3.28786	-0.683	0.60497	0.71977	AC005037.	chr2	+	2.02E+08	2.02E+08	501
ENSG00000	5.17896	10.83859	17.15238	6.74168	5.522592	6.575719	0.73137	0.33328	0.46137	RP11-137H	chr10	-	82289353	82295698	598
ENSG00000	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-509J	chr9	-	3684076	3689626	679
ENSG00000	1.035792	2.408575	6.597069	0	0.920432	0	2.1562	0.095842	0.16933	RP11-359N	chr6	-	14280358	14285376	3152
ENSG00000	10.35792	13.24716	11.87472	2.247227	11.04518	0	1.265	0.15269	0.24771	AC074093.	chr2	+	1.45E+08	1.46E+08	4635
ENSG00000	1.035792	2.408575	0	0	0.920432	4.109825	-0.32753	0.80401	0.87283	RP11-666A	chr1	-	1.49E+08	1.49E+08	513
ENSG00000	2.071584	6.021439	5.277655	3.745378	0	0.821965	1.1621	0.30648	0.4321	IGBP1P1	chr14	+	35408530	35409693	1009
ENSG00000	2.071584	0	0	5.992604	7.363456	8.219649	-2.5099	0.024573	0.052167	AC012309.	chr19	+	37742814	37756437	1699
ENSG00000	3.107376	1.204288	6.597069	5.243529	14.72691	7.397684	-1.171	0.18825	0.29316	ENTPD1-AS	chr10	-	97512963	97849995	4241
ENSG00000	32.10955	24.08575	30.34652	0.749076	7.363456	0.821965	3.0786	1.56E-05	5.66E-05	AC005281.	chr7	+	12536055	12581536	1094
ENSG00000	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-412H	chr1	-	2.19E+08	2.19E+08	1051
ENSG00000	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	ANKRD20A	chr13	-	25324795	25326309	1515
ENSG00000	52.82539	57.80581	58.05421	22.47227	41.41944	79.7306	0.22756	0.58445	0.70191	LENG8-AS1	chr19	-	54955991	54960223	871
ENSG00000	91.14969	107.1816	93.67838	78.65293	57.98722	115.0751	0.2089	0.48376	0.61301	RP1-50O24	chr1	+	27202624	27204736	306
ENSG00000	4.143168	0	1.319414	0.749076	0	3.28786	0.28864	0.82471	0.88676	RP11-122K	chr10	-	1.35E+08	1.35E+08	184
ENSG00000	0	0	0	2.996302	1.840864	1.64393	-1.8657	0.16751	0.26679	RP11-570G	chr10	+	73949699	73950334	636
ENSG00000	0	1.204288	0	0	0	0	0.45211	0.71784	NA	SDCBPP1	chr10	-	6335063	6336647	890
ENSG00000	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	RP11-426A	chr9	-	1.38E+08	1.38E+08	1117
ENSG00000	0	1.204288	0	1.498151	0	2.465895	-0.80408	0.55336	NA	FGF12-AS3	chr3	+	1.92E+08	1.92E+08	291
ENSG00000	19.68005	27.69862	21.11062	5.992604	4.60216	4.93179	2.0117	0.001408	0.003849	FAM66C	chr12	+	8332805	8368747	2623
ENSG00000	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-142L	chr1	-	1.92E+08	1.92E+08	780
ENSG00000	0	0	1.319414	0	0.920432	0.821965	-0.17431	0.89516	NA	TMEM256P	chr2	+	2.22E+08	2.22E+08	341
ENSG00000	3.107376	0	1.319414	0	0.920432	0.821965	0.76619	0.56963	0.68872	SNRPGP12	chr10	-	1.12E+08	1.12E+08	213
ENSG00000	0	0	3.958241	0	0	0	1.1937	0.35828	NA	CTA-384D8	chr22	+	50984844	50986081	157
ENSG00000	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP11-31L2	chr10	-	1.03E+08	1.03E+08	816
ENSG00000	0	2.408575	0	0	0	0	0.74702	0.55047	NA	CTA-929C8	chr22	+	27706612	27713417	5052
ENSG00000	95.29286	97.54731	84.44248	128.841	105.8497	102.7456	-0.28078	0.26861	0.38892	HSBP1L1	chr18	+	77724561	77730822	1057
ENSG00000	1.035792	8.430014	0	0	0	0	2.506	0.063419	0.11921	AC079781.	chr7	+	97499479	97499601	123
ENSG00000	6.214751	2.408575	5.277655	0.749076	0.920432	3.28786	1.1894	0.27385	0.39495	SMCR5	chr17	-	17680000	17682843	2844
ENSG00000	7.250543	2.408575	9.235896	2.247227	5.522592	4.93179	0.50404	0.58096	0.69903	AC007966.	chr2	-	1.87E+08	1.87E+08	1179
ENSG00000	0	1.204288	0	0	1.840864	0	-0.18234	0.88799	NA	AF127936.	chr21	+	16134031	16135411	695
ENSG00000	379.0998	411.8664	401.1018	370.7924	357.1276	345.2253	0.15028	0.3234	0.4508	RP11-27I1.	chr9	+	1.24E+08	1.24E+08	3519
ENSG00000	3.107376	7.225726	5.277655	3.745378	3.681728	9.041614	-0.07551	0.93322	0.95995	RP5-1024G	chr1	+	53704282	53708455	1181
ENSG00000	4.143168	0	0	0	0.920432	4.93179	-0.27819	0.83345	0.89318	AC007365.	chr2	+	64871746	64873832	627
ENSG00000	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP4-737A2	chr1	+	58326204	58346577	1262
ENSG00000	0	2.408575	0	0.749076	3.681728	0	-0.46829	0.72905	0.81844	TAS2R46	chr12	-	11213964	11214893	930
ENSG00000	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	RP11-298E	chr10	-	3282563	3299402	390
ENSG00000	20.71584	4.817151	7.916483	14.23244	9.20432	0.821965	0.42227	0.61191	0.72553	SRRM5	chr19	+	44100769	44118649	2698

ENSG0000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-694D	chr3	+	1.68E+08	1.68E+08	865
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	FABP7P1	chr1	-	2.44E+08	2.44E+08	391
ENSG0000(	0	0	0	5.243529	10.12475	14.79537	-4.1563	0.000426	0.001265	RP11-654E	chrX	+	23369130	23369567	438
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	KRTAP3-4P	chr17	-	39160733	39161012	280
ENSG0000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	NAALADL2-	chr3	-	1.75E+08	1.75E+08	1038
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-706D	chr3	-	1.77E+08	1.77E+08	522
ENSG0000(	3.107376	6.021439	7.916483	0	0	0.821965	2.9884	0.013497	0.030478	PGAM4	chrX	-	77223458	77225135	1678
ENSG0000(	3.107376	3.612863	0	14.98151	3.681728	11.50751	-1.831	0.053637	0.10328	RP1-167F1	chr6	-	19535175	19839311	794
ENSG0000(	0	0	1.319414	0	5.522592	0	-0.99212	0.46461	0.59373	AC110926.	chr2	+	1.28E+08	1.28E+08	2825
ENSG0000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	AC015923.	chr17	-	61458592	61491673	524
ENSG0000(	0	0	0	0.749076	0.920432	0.821965	-0.73223	0.57364	NA	RP11-289F	chr9	-	83484673	83486210	791
ENSG0000(	10.35792	2.408575	2.638828	3.745378	4.60216	12.32947	-0.34826	0.70122	0.79696	CACTIN-AS1	chr19	+	3607245	3613928	1913
ENSG0000(	0	0	6.597069	3.745378	2.761296	2.465895	-0.35533	0.76808	0.84729	OSTCP8	chr9	-	33968069	33968516	448
ENSG0000(	21.75163	26.49433	23.74945	14.23244	11.04518	4.93179	1.188	0.040708	0.081318	RP11-203B	chr6	-	56979692	57039034	899
ENSG0000(	6.214751	1.204288	2.638828	2.996302	0	0	1.1905	0.34031	0.46908	AC011893.	chr2	+	1.37E+08	1.37E+08	1862
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP3-419C1	chr1	+	1.93E+08	1.93E+08	571
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC005082.	chr7	+	23245632	23247664	2033
ENSG0000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	MEIS1-AS3	chr2	-	66653867	66660602	707
ENSG0000(	14.50109	19.2686	6.597069	9.737982	12.88605	16.4393	0.05328	0.93363	0.96019	SUGT1P	chr9	-	33503653	33510709	476
ENSG0000(	96.32865	79.48299	63.33186	57.67882	55.22592	92.06007	0.22328	0.48398	0.61311	RP4-756H1	chr7	+	66119525	66134842	508
ENSG0000(	1.035792	2.408575	0	0.749076	0	0	0.91766	0.49624	NA	RP11-278H	chr1	+	2.44E+08	2.44E+08	1799
ENSG0000(	7.250543	6.021439	5.277655	8.988907	3.681728	2.465895	0.25232	0.77602	0.85296	AC097724.	chr2	-	28931819	28959071	726
ENSG0000(	1.035792	1.204288	3.958241	16.47966	11.04518	17.26126	-2.5629	0.00272	0.007079	RP11-148B	chr1	+	94798823	94800404	480
ENSG0000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RP11-166N	chr10	+	32570614	32571757	466
ENSG0000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	EEF1GP3	chr3	-	40637698	40638985	1288
ENSG0000(	0	0	0	2.996302	1.840864	0	-1.3549	0.31496	NA	LINC00348	chr13	+	71589273	71742549	948
ENSG0000(	1.035792	7.225726	0	6.74168	1.840864	11.50751	-1.0512	0.31482	0.44152	RP4-635E1	chr1	+	11128528	11133154	2682
ENSG0000(	4.143168	6.021439	3.958241	0	0	0	3.3516	0.008907	0.020944	AC004112.	chr7	-	1.12E+08	1.12E+08	561
ENSG0000(	0	0	0	12.73428	9.20432	27.12484	-4.8641	1.63E-05	5.91E-05	RP1-212P9	chr1	+	29194087	29197779	1747
ENSG0000(	7.250543	10.83859	9.235896	2.996302	6.443024	3.28786	0.9966	0.22684	0.33981	AC010894.	chr2	+	1.75E+08	1.75E+08	561
ENSG0000(	0	0	1.319414	4.494453	0	0	-0.82548	0.54208	NA	RP11-350G	chr1	-	1.54E+08	1.54E+08	883
ENSG0000(	2.071584	0	0	5.992604	2.761296	4.93179	-1.8901	0.11614	0.19851	AC093901.	chr2	-	1.19E+08	1.19E+08	778
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	DUTP3	chr7	+	1.47E+08	1.47E+08	415
ENSG0000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-48F1	chr3	+	1.86E+08	1.86E+08	690
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-569A	chr1	+	2.03E+08	2.03E+08	314
ENSG0000(	4.143168	13.24716	7.916483	1.498151	7.363456	4.109825	0.85902	0.32703	0.45474	RP11-500G	chr10	+	1.24E+08	1.24E+08	951
ENSG0000(	1.035792	1.204288	1.319414	0	1.840864	0.821965	0.26006	0.84549	0.90132	AC005154.	chr7	+	30583669	30584047	379
ENSG0000(	10.35792	1.204288	2.638828	0	0	0.821965	2.6766	0.033018	0.067553	RP11-36N2	chr1	+	2.46E+08	2.46E+08	581
ENSG0000(	4.143168	0	2.638828	1.498151	2.761296	4.93179	-0.32169	0.77985	0.85498	GSTM3P2	chr2	-	1.6E+08	1.6E+08	441
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	KB-1183D5	chr22	+	21622450	21623192	743
ENSG0000(	34.18113	30.10719	36.94359	152.0623	116.8949	95.34793	-1.8244	9.41E-09	4.72E-08	ERVMER34·	chr4	-	53588785	53617807	3830
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-474I	chr1	-	1.62E+08	1.62E+08	575
ENSG0000(	2.071584	1.204288	5.277655	0	1.840864	0.821965	1.1761	0.34644	0.47603	LA16c-395I	chr16	-	1675629	1676161	329
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-182I	chr1	-	65437908	65468159	2804

ENSG00000(	0	1.204288	3.958241	3.745378	0	0.821965	0.079913	0.95107	0.97069	RP11-298J:	chr10	-	1.27E+08	1.27E+08	830
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP11-432J:	chr10	-	1.34E+08	1.34E+08	634
ENSG00000(	0	0	0	0	2.761296	1.64393	-1.2339	0.35779	NA	RP11-561C	chr9	+	70843567	70844228	340
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	ISCA2P1	chr22	-	27040853	27041300	448
ENSG00000(	2.071584	0	1.319414	0	0	2.465895	0.24177	0.8585	NA	BSN-AS2	chr3	-	49586739	49591799	2603
ENSG00000(	0	0	0	1.498151	2.761296	0	-1.199	0.3707	NA	RP11-80B9	chr1	+	2.41E+08	2.41E+08	572
ENSG00000(	11.39371	8.430014	9.235896	12.73428	10.12475	18.08323	-0.46148	0.48178	0.61096	RP5-1068B	chr1	-	2.3E+08	2.3E+08	478
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC007271.	chr2	-	1.03E+08	1.03E+08	382
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC010423.	chr5	-	1.03E+08	1.03E+08	1783
ENSG00000(	0	0	3.958241	0	2.761296	0.821965	0.071752	0.95751	0.97494	AC068491.	chr2	-	1.12E+08	1.12E+08	418
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	LINC00161	chr21	+	29911640	29912677	870
ENSG00000(	2.071584	0	0	4.494453	0.920432	0	-0.74405	0.58064	0.69872	CEP164P1	chr10	-	45497670	45642669	2472
ENSG00000(	4.143168	10.83859	3.958241	0	0.920432	2.465895	1.9757	0.070027	0.12982	IL9RP3	chr16	-	79336	88321	1674
ENSG00000(	13.46529	25.29004	17.15238	4.494453	1.840864	1.64393	2.5443	0.000752	0.002155	RP1-120G2	chr1	-	6264900	6265840	378
ENSG00000(	1599.263	1498.134	1248.165	2853.229	1986.292	2330.271	-0.71992	1.33E-06	5.44E-06	DANCR	chr4	+	53578597	53586518	878
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP4-714D9	chr1	+	1.01E+08	1.01E+08	252
ENSG00000(	0	1.204288	7.916483	9.737982	11.04518	9.041614	-1.5144	0.10617	0.18422	AC010890.	chr2	+	1.34E+08	1.34E+08	535
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AP000432.	chr21	-	19031594	19032702	516
ENSG00000(	0	1.204288	1.319414	2.996302	0	0.821965	-0.36171	0.78818	0.86142	RP4-533D7	chr1	+	46512490	46514040	649
ENSG00000(	15059.38	19449.25	27406.86	1950.593	15653.79	7690.304	1.2061	0.073567	0.13537	RNA28S5	chrX	-	1.08E+08	1.08E+08	432
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC078883.	chr2	-	1.73E+08	1.73E+08	558
ENSG00000(	0	2.408575	2.638828	2.247227	6.443024	4.109825	-1.0613	0.34696	0.47652	RHEBP2	chr10	+	47396223	47396822	600
ENSG00000(	8.286335	3.612863	10.55531	17.97781	13.80648	14.79537	-0.98727	0.14619	0.2389	AC003088.	chr7	-	1.1E+08	1.1E+08	495
ENSG00000(	0	3.612863	2.638828	0	0	0	1.93	0.15472	0.25026	HAUS4P1	chr1	-	1.7E+08	1.7E+08	1145
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	LINC00423	chr13	-	33451569	33485788	903
ENSG00000(	0	0	0	4.494453	0.920432	0	-1.4809	0.27346	NA	RP11-547D	chr1	-	1980642	1981509	437
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	RP11-82H1	chr1	+	84710017	84710260	244
ENSG00000(	5.17896	4.817151	10.55531	8.988907	5.522592	7.397684	-0.09871	0.90222	0.93932	COX6A1P2	chr6	+	37012607	37013177	571
ENSG00000(	0	1.204288	2.638828	1.498151	0	0.821965	0.37902	0.77836	0.85409	HMGN1P24	chr13	-	96461564	96461861	298
ENSG00000(	3.107376	0	1.319414	0.749076	2.761296	1.64393	-0.12416	0.92213	0.95285	LTA	chr6	+	31539831	31542101	1507
ENSG00000(	1.035792	0	6.597069	0.749076	0.920432	1.64393	0.80457	0.52362	0.64892	ABHD17AP	chr17	+	20717933	20747570	1044
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	CENPC1P1	chr12	+	89893870	89896447	2578
ENSG00000(	1.035792	0	0	1.498151	0	0.821965	-0.37092	0.78098	NA	RP4-591B8	chr1	+	1.15E+08	1.15E+08	427
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	RP11-142G	chrX	+	13353360	13391753	580
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-544A	chr9	+	1.34E+08	1.34E+08	559
ENSG00000(	1.035792	0	1.319414	0.749076	0	0	0.56083	0.6714	NA	AL049758.	chr22	-	43249409	43249805	397
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC112229.	chr2	+	1.11E+08	1.11E+08	337
ENSG00000(	11.39371	3.612863	3.958241	2.247227	2.761296	4.93179	0.81574	0.38763	0.51843	NBPF2P	chr1	-	21751118	21754460	661
ENSG00000(	10.35792	14.45145	10.55531	3.745378	3.681728	0.821965	1.8739	0.025258	0.053457	RP5-956O1	chr1	-	2.3E+08	2.3E+08	861
ENSG00000(	16.57267	13.24716	19.79121	19.47596	7.363456	16.4393	0.17667	0.76793	0.84716	RP3-417G1	chrX	+	1.33E+08	1.33E+08	416
ENSG00000(	1.035792	1.204288	5.277655	14.23244	4.60216	4.109825	-1.391	0.158	0.25449	RP1-97J1.2	chr6	+	1.12E+08	1.12E+08	762
ENSG00000(	3.107376	9.634302	5.277655	11.23613	20.2495	4.109825	-0.88997	0.26577	0.38575	AC007285.	chr7	+	30028216	30065276	893
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC007036.	chr7	-	30216003	30218630	674
ENSG00000(	2.071584	1.204288	0	11.23613	14.72691	8.219649	-2.7746	0.004524	0.011306	SLC8A1-AS:	chr2	+	40013593	40482349	935

ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AC105461.	chr2	-	2.33E+08	2.33E+08	391
ENSG00000(	36.25272	67.44011	43.54065	174.5346	128.8605	112.6092	-1.4843	1.51E-06	6.12E-06	LINC00511	chr17	-	70319264	70636611	2265
ENSG00000(	0	0	0	0.749076	1.840864	0.821965	-1.0455	0.43461	NA	AC005077.	chr7	-	75719749	75738097	2399
ENSG00000(	0	7.225726	0	2.247227	4.60216	0.821965	-0.05953	0.96142	0.97769	ITGB2-AS1	chr21	+	46340966	46349593	2282
ENSG00000(	1609.621	1527.037	1451.355	187.2689	259.5618	175.9005	2.8756	2.81E-75	1.36E-73	C14orf132	chr14	+	96505661	96560417	7774
ENSG00000(	0	2.408575	0	0.749076	0.920432	0.821965	-0.02765	0.98373	NA	RP11-395B	chr7	-	1.01E+08	1.01E+08	407
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	FDX1P2	chr21	+	27064492	27064866	375
ENSG00000(	2.071584	2.408575	1.319414	0	3.681728	0.821965	0.27177	0.82956	0.89068	RP11-418J	chr1	-	1.2E+08	1.2E+08	783
ENSG00000(	1323.742	1246.438	1101.711	1457.701	1322.661	1730.236	-0.29555	0.031164	0.064282	WDR46	chr6	-	33246885	33257304	2358
ENSG00000(	9.322127	8.430014	9.235896	2.247227	0	1.64393	2.3206	0.017585	0.038674	LINC00629	chrX	+	1.34E+08	1.34E+08	844
ENSG00000(	3975.369	4696.722	3141.524	1855.46	2462.156	3434.991	0.60022	0.046055	0.090417	RPL41P1	chr20	+	21735866	21736171	306
ENSG00000(	0	2.408575	0	0.749076	0	0	0.55104	0.6711	NA	RP11-12A1	chr9	+	1.28E+08	1.28E+08	633
ENSG00000(	1.035792	0	5.277655	0	8.283888	1.64393	-0.47002	0.70185	0.79743	RP11-191G	chr1	+	51983981	52027301	362
ENSG00000(	12.4295	4.817151	3.958241	2.247227	5.522592	5.753754	0.59174	0.50547	0.63317	RP11-4E23	chr9	-	20683303	20684687	359
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP3-466I7.	chr6	+	1.09E+08	1.09E+08	494
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	SDHDP2	chr7	+	1.35E+08	1.35E+08	465
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	RP11-4C20	chr10	+	1.3E+08	1.3E+08	371
ENSG00000(	1.035792	2.408575	0	2.996302	1.840864	1.64393	-0.61823	0.62326	0.73498	AC107983.	chr17	+	18476045	18476415	371
ENSG00000(	6.214751	0	0	0	0	0	1.7844	0.18526	0.28968	AC004448.	chr17	+	19322348	19327670	520
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CTD-2021A	chr7	-	51456127	51456811	685
ENSG00000(	88.04231	104.773	101.5949	80.15108	46.94203	101.1017	0.35761	0.24476	0.36105	RP11-543P	chr12	-	3320775	3321096	322
ENSG00000(	11.39371	15.65574	15.83297	26.21764	29.45382	13.15144	-0.65631	0.23989	0.35506	AL592494.	chr1	+	1.21E+08	1.21E+08	3662
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	L29074.3	chrX	-	1.47E+08	1.47E+08	534
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	AC084149.	chr2	-	77879539	77881794	284
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-565P	chr1	-	1.62E+08	1.62E+08	517
ENSG00000(	811.0251	845.41	523.8073	532.5927	425.2396	886.9001	0.23663	0.52486	0.64983	RP11-742N	chr11	+	82400571	82400944	374
ENSG00000(	1.035792	2.408575	3.958241	4.494453	0.920432	3.28786	-0.20807	0.85308	0.90636	AC096574.	chr2	+	2.39E+08	2.39E+08	2057
ENSG00000(	3.107376	1.204288	0	5.992604	2.761296	2.465895	-1.0109	0.38485	0.51568	LMCD1-AS1	chr3	-	7994492	8653610	2683
ENSG00000(	0	3.612863	1.319414	5.243529	7.363456	8.219649	-1.7172	0.09877	0.17359	RP11-460N	chr7	+	64535401	64539158	232
ENSG00000(	1.035792	0	0	0.749076	0.920432	0	-0.14603	0.91115	NA	RP11-267C	chr18	+	48872619	49088939	3188
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP3-471C1	chr6	-	19730658	19734798	470
ENSG00000(	0	0	0	3.745378	2.761296	0	-1.7329	0.20153	0.30918	CTA-85E5.1	chr22	-	30404731	30476469	902
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	AC009238.	chr2	+	96101881	96102304	424
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-319F	chr10	-	54733248	54735575	415
ENSG00000(	4.143168	1.204288	3.958241	0.749076	0.920432	0	1.6816	0.18098	0.28401	RPL12P44	chr3	+	44979165	44979974	502
ENSG00000(	29.00217	33.72006	43.54065	47.19176	65.35067	36.98842	-0.48547	0.21418	0.32459	ZNF717	chr3	-	75758794	75834734	3875
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC011742.	chr2	+	26382892	26384005	434
ENSG00000(	0	9.634302	0	0	0	1.64393	1.464	0.27235	0.39312	LINC00595	chr10	+	80027085	80090352	804
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP11-545A	chr1	+	1.8E+08	1.8E+08	2471
ENSG00000(	0	1.204288	5.277655	0	0	0	1.9545	0.14956	0.2434	IL21-AS1	chr4	+	1.24E+08	1.24E+08	3748
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	MKRNP2	chr6	+	35410821	35417643	792
ENSG00000(	2.071584	0	0	0.749076	3.681728	5.753754	-1.4798	0.24194	0.35756	RP11-165F	chr9	-	454304	492112	1295
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC068535.	chr2	+	1.05E+08	1.05E+08	471
ENSG00000(	3.107376	0	0	0.749076	0	2.465895	-0.00771	0.99546	0.99707	DDX11L16	chrX	-	1.55E+08	1.55E+08	1643

ENSG00000(	3.107376	3.612863	6.597069	1.498151	0	4.109825	0.96486	0.3843	0.51506	AC092755.	chr15	-	59936497	59964501	97
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP5-1198C	chr1	-	44553630	44554149	520
ENSG00000(	1.035792	0	2.638828	0	5.522592	0	-0.34175	0.79785	0.8683	WDR11-AS	chr10	-	1.23E+08	1.23E+08	2242
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	AF178030.	chr8	+	1.17E+08	1.17E+08	402
ENSG00000(	0	0	0	1.498151	0	4.109825	-1.5377	0.25628	NA	AC011290.	chr7	-	39585245	39605838	414
ENSG00000(	8.286335	2.408575	5.277655	2.996302	1.840864	3.28786	0.82325	0.40573	0.53658	AC092641.	chr2	-	1.71E+08	1.71E+08	772
ENSG00000(	5.17896	0	3.958241	396.261	789.7307	608.254	-7.289	1.27E-47	3.26E-46	EPPK1	chr8	-	1.45E+08	1.45E+08	7997
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP11-77G2	chr10	-	76783233	76784009	380
ENSG00000(	0	3.612863	1.319414	0	1.840864	0.821965	0.53618	0.68701	0.78601	RP5-1104E	chr22	-	39871812	39872827	498
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC092535.	chr4	+	1145160	1147489	2165
ENSG00000(	0	0	2.638828	1.498151	3.681728	0.821965	-0.75971	0.56324	0.68292	RP1-45I4.3	chr6	-	1.43E+08	1.43E+08	552
ENSG00000(	0	1.204288	3.958241	0	0.920432	1.64393	0.59306	0.6555	0.7606	RP3-410C9	chr20	-	26167556	26232162	1213
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	AC009518.	chr7	+	1.33E+08	1.33E+08	799
ENSG00000(	7.250543	8.430014	10.55531	8.239831	6.443024	19.72716	-0.36882	0.61004	0.72378	ST7-AS1	chr7	-	1.17E+08	1.17E+08	1889
ENSG00000(	12.4295	26.49433	25.06886	0.749076	10.12475	1.64393	2.1775	0.004407	0.011036	RP11-121A	chr9	+	1.27E+08	1.27E+08	373
ENSG00000(	5.17896	2.408575	1.319414	0	0.920432	0.821965	1.6091	0.2028	0.31071	CNN2P1	chr22	-	30442265	30443182	918
ENSG00000(	0	6.021439	1.319414	0	0	0	2.1383	0.11496	0.19679	SUB1P1	chr8	+	11647514	11647897	384
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RBMY2JP	chrY	+	7995171	8012244	1059
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	LINC00552	chr13	-	1.14E+08	1.14E+08	2577
ENSG00000(	1.035792	0	2.638828	0	9.20432	0	-0.83702	0.52093	0.64664	AC079145.	chr2	+	20189978	20203971	541
ENSG00000(	1.035792	3.612863	5.277655	0	0	0	2.7452	0.038793	0.077916	RP5-1100E	chrX	-	1.02E+08	1.02E+08	348
ENSG00000(	0	0	2.638828	0	0	0.821965	0.55859	0.66971	NA	PFN1P7	chr1	-	1.49E+08	1.49E+08	399
ENSG00000(	0	1.204288	0	0	3.681728	0	-0.65196	0.62789	NA	SPATA13-A	chr13	-	24826887	24828577	433
ENSG00000(	0	1.204288	5.277655	23.22134	11.04518	18.90519	-2.7537	0.001279	0.003529	HCG15	chr6	+	28953980	28955261	1032
ENSG00000(	0	3.612863	0	2.996302	1.840864	0.821965	-0.42098	0.74646	0.83142	RP11-445L	chr6	+	83642320	83648396	480
ENSG00000(	4.143168	8.430014	7.916483	0.749076	4.60216	1.64393	1.327	0.17507	0.27674	RP11-203J	chr9	+	1.31E+08	1.31E+08	1105
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	RP11-69I8.	chr6	+	1.32E+08	1.32E+08	495
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	AC017101.	chr2	-	1.88E+08	1.88E+08	571
ENSG00000(	5.17896	2.408575	2.638828	0.749076	0	1.64393	1.4919	0.21997	0.33166	RP11-261C	chr1	+	2.43E+08	2.43E+08	694
ENSG00000(	320.0597	285.4162	200.5509	340.0803	299.1404	385.5015	-0.34141	0.08611	0.15498	WASH7P	chr1	-	14363	29806	1783
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-365D	chr1	+	2.36E+08	2.36E+08	1724
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-563D	chr1	+	1.94E+08	1.94E+08	832
ENSG00000(	5.17896	7.225726	11.87472	1.498151	0.920432	4.109825	1.6097	0.089101	0.15945	NBPF13P	chr1	-	1.46E+08	1.47E+08	3808
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	LINC00845	chr10	+	62776033	62786178	696
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-136C	chr3	+	43128971	43129560	509
ENSG00000(	1.035792	1.204288	1.319414	0	2.761296	2.465895	-0.35498	0.78327	0.85729	FAM155A-I	chr13	-	1.08E+08	1.08E+08	819
ENSG00000(	8.286335	18.06432	13.19414	23.97042	3.681728	4.109825	0.2719	0.71894	0.81066	AC105760.	chr2	-	2.38E+08	2.38E+08	2341
ENSG00000(	2.071584	0	0	1.498151	0	4.109825	-0.78262	0.56002	0.6806	RP11-166N	chr10	+	32555217	32558402	696
ENSG00000(	9.322127	10.83859	6.597069	7.490755	2.761296	4.109825	0.79803	0.3301	0.45788	MIS18A-AS	chr21	+	33650174	33653299	769
ENSG00000(	0	6.021439	0	1.498151	0.920432	1.64393	0.36256	0.77936	0.85472	SMIM2-AS1	chr13	+	44716682	44813010	499
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC116035.	chr3	+	30566237	30568677	436
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	HCG4B	chr6	-	29893760	29894750	991
ENSG00000(	0	10.83859	0	0	0	0	2.5435	0.060316	0.11416	RP11-305C	chr3	+	1.36E+08	1.36E+08	581
ENSG00000(	17.60846	13.24716	15.83297	26.96672	21.16994	8.219649	-0.25773	0.66287	0.76691	KLLN	chr10	-	89618918	89623194	4277

ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-96L7	chr9	+	1.02E+08	1.02E+08	439
ENSG00000(	1.035792	1.204288	5.277655	0	5.522592	1.64393	0.050266	0.96671	0.98044	AC015933.	chr18	+	25534483	25543651	440
ENSG00000(	8.286335	9.634302	1.319414	7.490755	6.443024	3.28786	0.1515	0.86416	0.91416	RP11-458D	chr1	-	1.45E+08	1.45E+08	784
ENSG00000(	29.00217	13.24716	21.11062	16.47966	14.72691	27.94681	0.099693	0.85346	0.90665	RP3-327A1	chrX	-	1.19E+08	1.19E+08	810
ENSG00000(	0	0	0	2.247227	1.840864	7.397684	-2.6705	0.041359	0.08241	RP5-837I24	chr1	+	81967479	81969153	1675
ENSG00000(	6.214751	7.225726	3.958241	4.494453	0	4.109825	0.83304	0.41023	0.54105	HSFY3P	chrY	-	2749724	2751693	1191
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP4-544H6	chr1	-	87819207	87837338	889
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC009229.	chr2	-	38430505	38466732	622
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	AC016994.	chr2	+	1.07E+08	1.07E+08	552
ENSG00000(	0	0	0	39.701	46.0216	60.00344	-6.4025	7.23E-10	4.01E-09	KRT16P2	chr17	-	16733157	16744006	1575
ENSG00000(	2.071584	0	0	2.247227	0	0	-0.04193	0.97501	NA	RP11-791G	chr4	-	83415939	83417431	1493
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	AC009502.	chr2	+	2.21E+08	2.21E+08	496
ENSG00000(	1.035792	0	0	0	0	1.64393	-0.12526	0.92174	NA	AC140076.	chr3	+	17506642	17507002	361
ENSG00000(	0	0	2.638828	1.498151	0	0	0.308	0.81734	NA	RP11-282E	chr9	+	66664325	66665950	1626
ENSG00000(	1.035792	4.817151	2.638828	0	4.60216	3.28786	0.085165	0.94161	0.9649	MTND4P15	chr9	+	94873147	94874179	1033
ENSG00000(	9.322127	10.83859	6.597069	2.996302	5.522592	3.28786	1.0673	0.20084	0.30837	RP11-258C	chrX	-	53193573	53193739	167
ENSG00000(	0	1.204288	0	2.247227	3.681728	3.28786	-1.8306	0.15661	0.25262	AC005042.	chr2	+	1.59E+08	1.59E+08	800
ENSG00000(	0	0	0	2.247227	1.840864	0	-1.1573	0.3864	NA	LINC00434	chr13	-	60788486	60789080	419
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	AC139452.	chr3	+	32827138	32827608	471
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	HAUS6P1	chr7	+	53255081	53256631	1551
ENSG00000(	239.2679	234.8361	254.6469	439.7073	405.9105	408.5166	-0.78164	1.23E-06	5.05E-06	PARG	chr10	-	51026325	51130715	2537
ENSG00000(	0	0	1.319414	1.498151	0	0	-0.08979	0.94423	NA	NANOGP6	chr10	-	1.02E+08	1.02E+08	846
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	ARHGEF7-A	chr13	-	1.12E+08	1.12E+08	321
ENSG00000(	13.46529	27.69862	2.638828	17.97781	20.2495	16.4393	-0.29267	0.65187	0.75778	RBM26-AS1	chr13	+	79980444	79997090	1756
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-162D	chr9	+	1.24E+08	1.24E+08	440
ENSG00000(	12.4295	12.04288	13.19414	8.988907	7.363456	2.465895	0.91844	0.21126	0.32116	AC017074.	chr2	-	1.14E+08	1.14E+08	561
ENSG00000(	7.250543	0	0	0	0	0	1.994	0.1408	0.23194	AC019172.	chr2	+	3891774	3895001	717
ENSG00000(	0	0	0	1.498151	0.920432	0.821965	-0.99775	0.45448	NA	AC008060.	chr7	+	1.55E+08	1.55E+08	468
ENSG00000(	0	0	2.638828	0	1.840864	0	0.2163	0.87177	NA	AC079753.	chr2	+	1.14E+08	1.14E+08	547
ENSG00000(	0	1.204288	7.916483	0.749076	2.761296	0.821965	0.75369	0.53984	0.6633	RP4-669P1	chr22	+	42528550	42529005	456
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	RP11-3L10	chr7	+	1.21E+08	1.21E+08	418
ENSG00000(	436.0684	415.4793	365.4776	591.0206	658.1089	632.091	-0.62427	1.95E-05	6.99E-05	TP73-AS1	chr1	-	3652548	3663900	6358
ENSG00000(	3.107376	0	0	2.996302	2.761296	0	-0.50409	0.70438	0.79947	RP11-160H	chr1	-	1.74E+08	1.74E+08	688
ENSG00000(	0	0	2.638828	14.98151	3.681728	4.93179	-2.4988	0.025148	0.053242	DLG1-AS1	chr3	+	1.97E+08	1.97E+08	1694
ENSG00000(	1.035792	6.021439	1.319414	2.996302	4.60216	2.465895	-0.21236	0.84513	0.90109	FTH1P16	chr11	-	77445520	77446071	552
ENSG00000(	0	0	3.958241	2.247227	0	1.64393	-0.01549	0.99079	0.99468	PPIAP2	chr20	-	25348911	25349402	492
ENSG00000(	3.107376	3.612863	2.638828	2.247227	0.920432	3.28786	0.41666	0.70725	0.80203	EIF4A2P2	chr10	+	74959584	74960983	1070
ENSG00000(	2.071584	3.612863	3.958241	0	0.920432	1.64393	1.3649	0.26426	0.38417	RP11-571F	chr9	+	34191553	34191879	327
ENSG00000(	7.250543	0	0	8.988907	9.20432	10.68554	-1.6211	0.10011	0.17564	RP11-112J	chr9	+	35772160	35790429	546
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	HPN-AS1	chr19	-	35549963	35597208	1124
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC007386.	chr2	-	65187187	65187768	582
ENSG00000(	22.78742	9.634302	15.83297	22.47227	2.761296	15.61733	0.21849	0.74904	0.83322	KIF9-AS1	chr3	+	47205987	47285546	2353
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-118F	chr9	+	94768344	94768826	483
ENSG00000(	0	0	0	8.239831	5.522592	4.93179	-3.4527	0.005273	0.013006	AC012501.	chr2	-	1.54E+08	1.54E+08	586

ENSG00000(	3.107376	2.408575	0	0	0	0	1.7825	0.18787	NA	RPL37P1	chr20	+	34176246	34176529	284
ENSG00000(	0	0	0	9.737982	16.56778	18.08323	-4.744	2.69E-05	9.45E-05	AC009299.	chr2	+	1.62E+08	1.62E+08	2333
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	AC008746.	chr19	-	54941832	54945878	529
ENSG00000(	5.17896	0	0	2.996302	0.920432	0	0.25499	0.84803	0.90304	ZMYM4-AS:	chr1	-	35824423	35831678	459
ENSG00000(	0	0	2.638828	3.745378	16.56778	18.08323	-3.1849	0.00211	0.005601	RP11-265B	chr9	+	71736209	71737148	822
ENSG00000(	0	8.430014	1.319414	0	0	7.397684	0.26643	0.83284	0.89306	RP5-1042K	chr22	+	40829140	40829645	355
ENSG00000(	0	3.612863	2.638828	0	2.761296	4.109825	-0.10273	0.93416	0.96038	RP11-397P	chr1	-	2.04E+08	2.04E+08	643
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC019185.	chr2	-	2.09E+08	2.09E+08	389
ENSG00000(	0	0	2.638828	5.992604	1.840864	3.28786	-1.4958	0.22562	0.33833	RP1-155G6	chr20	-	47657000	47662581	556
ENSG00000(	3.107376	9.634302	15.83297	0	0	0	4.4042	0.000243	0.000747	AC053503.	chr2	-	2.2E+08	2.2E+08	519
ENSG00000(	0	0	3.958241	0	0	0.821965	0.91937	0.49384	NA	AC069213.	chr3	+	1.95E+08	1.95E+08	367
ENSG00000(	0	1.204288	0	2.247227	8.283888	0.821965	-2.0347	0.11278	0.19359	FCF1P1	chr7	+	23658952	23662445	571
ENSG00000(	5.17896	7.225726	2.638828	0	3.681728	0	1.563	0.18026	0.28315	AP001471.	chr21	-	47513178	47517444	672
ENSG00000(	3.107376	0	2.638828	13.48336	5.522592	5.753754	-1.7588	0.076445	0.13989	ATP5G1P4	chr3	-	1.73E+08	1.73E+08	441
ENSG00000(	5.17896	2.408575	0	0	4.60216	3.28786	-0.01161	0.99234	0.99518	CTB-58E17.	chr17	+	36905613	36906969	1357
ENSG00000(	5.17896	3.612863	5.277655	0	7.363456	5.753754	0.096303	0.92488	0.95453	LINC00310	chr21	+	35552978	35562220	1198
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-397C	chr1	-	66508183	66516401	456
ENSG00000(	0	0	0	2.996302	0	1.64393	-1.3112	0.33001	NA	RP11-169D	chr11	+	72281704	72284273	2450
ENSG00000(	4.143168	1.204288	3.958241	13.48336	16.56778	7.397684	-1.7855	0.032626	0.066877	AC073415.	chr2	+	1.09E+08	1.09E+08	153
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	AKR1B15	chr7	+	1.34E+08	1.34E+08	1989
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	TSSK5P1	chr8	-	1.45E+08	1.45E+08	907
ENSG00000(	2.071584	1.204288	3.958241	2.247227	1.840864	1.64393	0.24359	0.83435	0.8939	STK4-AS1	chr20	-	43592435	43595043	2065
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC124861.	chr2	-	2.41E+08	2.41E+08	429
ENSG00000(	6.214751	3.612863	0	0	3.681728	6.575719	-0.02458	0.98303	0.99027	RP11-89N1	chr7	-	33769904	33771676	577
ENSG00000(	1.035792	0	1.319414	0	1.840864	0	0.17192	0.89859	NA	RP11-18B1	chr9	+	1.16E+08	1.16E+08	1223
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	XX-C283C7	chr22	+	50753060	50754437	531
ENSG00000(	0	0	1.319414	7.490755	18.40864	13.9734	-3.8411	0.000357	0.001074	RP13-188A	chrX	+	55934556	56041606	1007
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-839D	chr11	-	1.13E+08	1.13E+08	1081
ENSG00000(	3.107376	1.204288	1.319414	0	0	0	1.9243	0.1561	NA	AC006458.	chr7	+	15105832	15108276	653
ENSG00000(	8.286335	8.430014	2.638828	3.745378	0	4.109825	1.0749	0.28771	0.4114	RP11-316N	chr10	+	1.02E+08	1.02E+08	846
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-104D	chrX	-	50773422	50774357	936
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	USP9YP14	chrY	+	20642973	20649286	563
ENSG00000(	0	3.612863	6.597069	3.745378	0.920432	9.041614	-0.36747	0.73419	0.82224	AC109333.	chr17	-	4922509	4923388	583
ENSG00000(	38.3243	56.60152	36.94359	0	0	0	6.6817	1.58E-10	9.21E-10	RP11-145A	chr1	+	2.26E+08	2.26E+08	1530
ENSG00000(	1579.583	1464.414	1267.957	1752.837	1663.221	1714.619	-0.2495	0.041392	0.082468	SCAMP4	chr19	+	1905213	1926016	2954
ENSG00000(	0	2.408575	3.958241	0	0	0	1.9515	0.15023	0.24432	RP1-249H1	chr6	-	1.14E+08	1.14E+08	413
ENSG00000(	7.250543	3.612863	0	7.490755	10.12475	23.01502	-1.6487	0.05427	0.10439	LTB	chr6	-	31548302	31550299	1388
ENSG00000(	10.35792	3.612863	7.916483	1.498151	12.88605	14.79537	-0.35839	0.66702	0.7705	RP11-413N	chr9	+	1.39E+08	1.39E+08	864
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP5-973N2	chr6	+	41836360	41837469	403
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	AC003051.	chr17	+	67573392	67899141	3085
ENSG00000(	3.107376	6.021439	2.638828	1.498151	7.363456	0.821965	0.24485	0.81738	0.88167	MIR1302-2	chr9	+	27657	30891	2923
ENSG00000(	2.071584	6.021439	0	1.498151	0.920432	3.28786	0.37257	0.75561	0.83829	RPS20P15	chr3	+	27503997	27504307	311
ENSG00000(	0	3.612863	1.319414	2.247227	0	4.93179	-0.38601	0.7598	0.84128	RP11-223A	chr1	-	42801057	42804047	661
ENSG00000(	32.10955	30.10719	50.13772	41.94823	50.62376	47.67397	-0.31871	0.403	0.53403	SLC2A1-AS:	chr1	+	43424720	43449029	3075

ENSG00000(	2.071584	0	0	1.498151	1.840864	0	-0.31976	0.81368	NA	RP11-809N	chr6	+	1.05E+08	1.05E+08	278
ENSG00000(	6.214751	14.45145	10.55531	8.988907	12.88605	14.79537	-0.22202	0.74123	0.82706	SOCS5P4	chrX	-	70263064	70265320	1566
ENSG00000(	9.322127	8.430014	7.916483	14.98151	15.64734	8.219649	-0.55358	0.41665	0.5472	RP11-152N	chr10	+	75012549	75014107	762
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP3-525N1	chrX	-	1.19E+08	1.19E+08	688
ENSG00000(	10.35792	25.29004	17.15238	9.737982	15.64734	21.37109	0.1634	0.78274	0.85696	AC092614.	chr2	-	1.92E+08	1.92E+08	909
ENSG00000(	13.46529	12.04288	3.958241	29.96302	34.97642	36.98842	-1.693	0.001887	0.005052	SPAG5-AS1	chr17	+	26925808	26944393	2141
ENSG00000(	0	4.817151	0	1.498151	0	0	0.79721	0.55675	0.67732	AC018647.	chr7	+	35756055	35774497	1651
ENSG00000(	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	RP11-444D	chr1	-	1.84E+08	1.84E+08	364
ENSG00000(	24.85901	30.10719	38.263	2.247227	6.443024	3.28786	2.8123	6.94E-06	2.62E-05	PGM5P2	chr9	-	69080240	69147854	1968
ENSG00000(	4.143168	7.225726	9.235896	4.494453	2.761296	2.465895	0.92709	0.30965	0.43585	RP11-139K	chr10	+	1.15E+08	1.15E+08	390
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RNF11B	chr20	-	14527830	14528269	440
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP5-1166A	chr7	+	1.22E+08	1.22E+08	607
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP13-140E	chrX	-	89294212	89294833	622
ENSG00000(	7.250543	8.430014	5.277655	0	8.283888	1.64393	0.9282	0.35427	0.48409	RP11-262H	chr9	-	66516697	66520781	1135
ENSG00000(	0	0	2.638828	0.749076	1.840864	3.28786	-0.74259	0.57243	0.69122	RP11-119F	chr10	+	70434113	70434857	745
ENSG00000(	1.035792	0	3.958241	0	0	0	1.6134	0.2311	NA	RP11-162A	chr10	-	1.25E+08	1.25E+08	348
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CNTN4-AS2	chr3	-	2152093	2185925	426
ENSG00000(	0	1.204288	0	0	1.840864	0	-0.18234	0.88799	NA	RP1-28O10	chr1	-	2.1E+08	2.1E+08	449
ENSG00000(	5.17896	0	0	0	0	0	1.5469	0.24589	NA	AC019100.	chr2	+	1.09E+08	1.09E+08	1131
ENSG00000(	0	0	1.319414	9.737982	8.283888	5.753754	-3.1143	0.006683	0.016132	RP1-167A1	chr6	-	1.67E+08	1.67E+08	385
ENSG00000(	7.250543	6.021439	6.597069	5.243529	1.840864	7.397684	0.39582	0.65153	0.75752	RP11-165J	chr9	-	96197614	96199403	691
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	AC005392.	chr19	+	43657431	43665014	500
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	SUMO2P2	chr9	+	23632104	23632358	255
ENSG00000(	20.71584	14.45145	2.638828	25.46857	12.88605	23.83698	-0.6601	0.30306	0.42819	RP11-864N	chr11	-	74456761	74457159	399
ENSG00000(	4.143168	2.408575	2.638828	0	0	0	2.6697	0.044906	0.088441	RP11-492E	chr9	+	1.32E+08	1.32E+08	2449
ENSG00000(	1.035792	0	1.319414	3.745378	9.20432	4.93179	-2.215	0.050979	0.098763	ALG1L8P	chr11	+	67552744	67559806	760
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP1-101K1	chr6	+	1.53E+08	1.53E+08	663
ENSG00000(	2.071584	0	0	3.745378	3.681728	8.219649	-2.0603	0.08131	0.14742	RP4-781K5	chr1	+	2.35E+08	2.35E+08	3574
ENSG00000(	2.071584	2.408575	1.319414	0	0	0	1.9715	0.14607	NA	AC018804.	chr2	+	1.31E+08	1.31E+08	618
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-431K	chr1	+	8268732	8275270	497
ENSG00000(	5.17896	6.021439	6.597069	0	0.920432	4.109825	1.4699	0.16966	0.26969	RP11-242C	chr1	+	29479001	29479503	320
ENSG00000(	6.214751	7.225726	6.597069	8.239831	3.681728	6.575719	0.094882	0.9085	0.94369	HNRNPA1P	chr9	-	91025444	91026378	935
ENSG00000(	2.071584	4.817151	1.319414	2.996302	0	0	0.95011	0.45564	0.58533	SOX21-AS1	chr13	+	95364970	95366749	1536
ENSG00000(	0	0	0	0.749076	2.761296	0	-0.97685	0.45852	NA	AC005160.	chr7	+	40815157	40824816	381
ENSG00000(	3.107376	4.817151	2.638828	0	0.920432	0.821965	1.836	0.13577	0.22508	RP11-162J	chr6	-	1.49E+08	1.49E+08	714
ENSG00000(	2.071584	4.817151	0	0	0	0.821965	1.639	0.22316	0.33532	RP11-490F	chr9	+	96800312	96800627	316
ENSG00000(	210.2658	248.0833	253.3274	367.047	446.4095	379.7478	-0.74378	1.89E-05	6.79E-05	RP11-488L	chr1	-	2.47E+08	2.47E+08	1465
ENSG00000(	0	0	1.319414	5.243529	0.920432	2.465895	-1.6995	0.19286	0.29873	RP11-243J	chr1	-	1.56E+08	1.56E+08	157
ENSG00000(	2.071584	1.204288	2.638828	0	0	0	1.9938	0.14152	NA	LINC00355	chr13	-	64560504	64650144	1878
ENSG00000(	2.071584	0	0	2.247227	0	2.465895	-0.62438	0.6436	0.75092	RP11-25J2	chr13	+	80140881	80144983	348
ENSG00000(	0	1.204288	2.638828	0	0	0	1.2853	0.33195	NA	RP11-73O6	chr6	-	1.3E+08	1.3E+08	769
ENSG00000(	7.250543	0	2.638828	0	5.522592	2.465895	0.25473	0.83018	0.89105	RP11-307P	chr6	+	1.48E+08	1.48E+08	773
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	HNRNPA3P	chr20	+	35248806	35249826	662
ENSG00000(	0	0	1.319414	0.749076	4.60216	1.64393	-1.4273	0.28203	0.4047	MED28P3	chr2	+	1.87E+08	1.87E+08	531

ENSG00000(	0	0	2.638828	0	0	1.64393	0.26729	0.84149	NA	GSTM3P1	chr20	+	21482033	21482606	574
ENSG00000(	7.250543	3.612863	3.958241	0	2.761296	2.465895	1.2203	0.2638	0.38363	DNMBP-AS:	chr10	+	1.02E+08	1.02E+08	2034
ENSG00000(	0	8.430014	2.638828	1.498151	5.522592	1.64393	0.27645	0.80585	0.87413	AP001619.	chr21	-	43294865	43297722	447
ENSG00000(	0	0	0	0	3.681728	3.28786	-1.8162	0.1806	0.28356	RP11-301N	chr1	+	1.48E+08	1.48E+08	517
ENSG00000(	2.071584	2.408575	0	0	0	0	1.5041	0.26224	NA	RP11-15M:	chr20	-	51812768	51825244	485
ENSG00000(	0	0	0	25.46857	18.40864	16.4393	-5.1949	2.25E-06	8.98E-06	RP11-301G	chr6	-	68597538	68599231	1605
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-275C	chr1	-	2.28E+08	2.28E+08	619
ENSG00000(	0	0	0	4.494453	0	0	-1.1446	0.38559	NA	RP11-418J:	chr1	-	1.2E+08	1.2E+08	898
ENSG00000(	0	0	2.638828	1.498151	0.920432	0.821965	-0.19167	0.88706	NA	AC006042.	chr7	+	8153655	8156191	524
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP5-1059H	chr1	+	1.68E+08	1.68E+08	548
ENSG00000(	2.071584	4.817151	3.958241	0.749076	0	0	2.3693	0.064313	0.12061	GCOM2	chr4	+	68904262	68905368	1107
ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	AP001271.	chr11	-	70323382	70323697	206
ENSG00000(	0	1.204288	0	0	3.681728	0.821965	-0.89986	0.50718	NA	MTND6P5	chr9	+	5091093	5091604	512
ENSG00000(	0	0	0	5.243529	3.681728	0	-2.1664	0.10825	0.1871	RP4-565E6	chr1	-	1.46E+08	1.46E+08	2513
ENSG00000(	1.035792	7.225726	1.319414	1.498151	1.840864	4.93179	0.16273	0.88376	0.9273	RP11-318C	chr1	-	1.76E+08	1.76E+08	657
ENSG00000(	12.4295	21.67718	21.11062	2.996302	24.85166	20.54912	0.18259	0.78035	0.85524	RP11-536C	chr1	-	1.6E+08	1.6E+08	1578
ENSG00000(	0	0	0	0	5.522592	2.465895	-1.9938	0.14085	0.23199	CALR4P	chr1	-	52027538	52060569	946
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	AC114788.	chr2	-	2.4E+08	2.4E+08	3489
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC098826.	chr2	-	1.33E+08	1.33E+08	651
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AP000344.	chr22	+	23788785	23803020	641
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	VTI1BP4	chr9	+	1.31E+08	1.31E+08	527
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC072062.	chr2	+	2.16E+08	2.16E+08	1132
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC009229.	chr2	+	38458710	38459459	750
ENSG00000(	0	3.612863	3.958241	0	0	3.28786	0.74625	0.56831	0.68742	ASH1L-IT1	chr1	-	1.55E+08	1.55E+08	448
ENSG00000(	346.9903	438.3607	349.6447	133.3354	163.8369	179.1884	1.2476	8.64E-11	5.14E-10	RP1-283E3	chr1	+	1655951	1668690	1808
ENSG00000(	1.035792	0	0	2.247227	4.60216	0	-1.4074	0.29566	0.42005	RP4-738P1	chr1	+	1.69E+08	1.69E+08	618
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	XXyac-YX15	chr1	+	1.48E+08	1.48E+08	1537
ENSG00000(	19.68005	0	1.319414	2.247227	0	0	2.2615	0.063008	0.11858	GLUD1P2	chr10	+	48952491	48980269	932
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC002553.	chr17	+	15943505	15943994	81
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	AC012363.	chr2	+	1.21E+08	1.21E+08	771
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC007365.	chr2	+	64892741	64893198	458
ENSG00000(	22.78742	27.69862	14.51355	15.73059	9.20432	22.19305	0.44248	0.42846	0.5586	AC012358.	chr2	+	55451416	55453044	1434
ENSG00000(	15.53688	7.225726	7.916483	1.498151	0	0.821965	3.0281	0.002709	0.007057	RP4-773A1	chr1	+	1.12E+08	1.12E+08	2131
ENSG00000(	2.071584	0	0	0	3.681728	0	-0.35836	0.79134	NA	RP1-180M:	chr22	-	32286330	32287420	490
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	AL392086.	chr10	-	6867825	6868186	360
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC006370.	chrY	+	15863673	15970474	689
ENSG00000(	7.250543	9.634302	19.79121	17.22874	20.2495	17.26126	-0.5624	0.35249	0.48222	SLC9A7P1	chr12	-	98847613	98850923	3311
ENSG00000(	104.615	85.50443	91.03955	33.7084	48.7829	46.03004	1.1208	0.000277	0.000846	RP11-958N	chr16	+	16450081	16471364	9932
ENSG00000(	4.143168	2.408575	1.319414	0	0	0	2.42	0.071961	0.13287	CARM1P1	chr9	-	2907073	3053408	1185
ENSG00000(	0	0	0	1.498151	0	4.109825	-1.5377	0.25628	NA	AC008850.	chr5	+	96278003	96278888	362
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC093166.	chr2	+	1.12E+08	1.12E+08	330
ENSG00000(	1.035792	3.612863	7.916483	0	0	0	3.0926	0.018031	0.039524	RP13-143G	chr6	-	1.36E+08	1.36E+08	1570
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	RP11-184B	chr9	-	1.28E+08	1.28E+08	442
ENSG00000(	3.107376	0	0	2.996302	0.920432	3.28786	-0.76578	0.55048	0.67168	SUCLA2-AS:	chr13	+	48575525	48576688	552

ENSG00000(	13.46529	12.04288	3.958241	24.71949	37.73771	27.12484	-1.5078	0.008043	0.019096	AC007276.	chr7	+	29689843	29782210	2326
ENSG00000(	0	0	1.319414	0	0.920432	0.821965	-0.17431	0.89516	NA	RP4-533D7	chr1	+	46600203	46604753	339
ENSG00000(	1.035792	3.612863	0	2.247227	0	0	0.55949	0.67862	0.77969	RP4-805N2	chr1	-	23337327	23342343	510
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-59J5.	chr10	-	61496753	61513203	870
ENSG00000(	0	0	1.319414	0.749076	0	4.109825	-0.96956	0.47459	0.60383	PSPC1P1	chr13	-	19775777	19801572	665
ENSG00000(	6.214751	4.817151	2.638828	2.996302	11.04518	4.93179	-0.38985	0.66798	0.7712	RP11-79N2	chr6	-	53605547	53611820	850
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	FAM66A	chr8	+	12219527	12268510	921
ENSG00000(	0	0	0	5.243529	0	0	-1.3189	0.32312	NA	PSMA2P3	chr2	+	2.03E+08	2.03E+08	675
ENSG00000(	0	0	0	0	7.363456	0.821965	-1.9869	0.14257	0.2341	OR5P4P	chr11	+	7767537	7768453	917
ENSG00000(	7.250543	12.04288	6.597069	11.98521	13.80648	17.26126	-0.68594	0.3023	0.4274	RP11-77P6	chr10	+	88281702	88282443	643
ENSG00000(	2.071584	0	0	2.247227	0.920432	0.821965	-0.4987	0.71119	0.80478	SNAP25-AS	chr20	-	10002620	10349424	3207
ENSG00000(	3.107376	0	1.319414	1.498151	0.920432	0.821965	0.29567	0.82101	0.88423	CTD-2031P	chr5	+	55290995	55299477	2289
ENSG00000(	0	0	0	1.498151	1.840864	0	-0.93652	0.47589	NA	RP11-141N	chr13	-	33907983	33909403	466
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	KRT8P44	chr6	+	1.63E+08	1.63E+08	1350
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	RP11-130C	chr9	-	673478	685555	1120
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP1-153P1	chr6	+	37512921	37518636	998
ENSG00000(	2.071584	2.408575	2.638828	11.98521	0.920432	4.109825	-1.0416	0.31971	0.44689	AL353791.	chr9	+	40028620	40032417	3798
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-191N	chr1	-	2.22E+08	2.22E+08	423
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	MACROD2-	chr20	+	14535030	14617170	665
ENSG00000(	1.035792	0	0	1.498151	2.761296	1.64393	-1.3252	0.32231	0.44963	SRGAP3-AS	chr3	+	9258579	9259771	567
ENSG00000(	0	1.204288	5.277655	3.745378	1.840864	3.28786	-0.37508	0.74862	0.83297	RP11-423F	chr1	+	2.31E+08	2.31E+08	573
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC104695.	chr2	-	28671034	28673051	849
ENSG00000(	1.035792	2.408575	0	0	0	1.64393	0.52159	0.70059	NA	RPL3P2	chr6	+	31248094	31249296	1203
ENSG00000(	2.071584	0	1.319414	0	0.920432	1.64393	0.23689	0.86055	0.91133	RP11-103C	chr6	+	1.28E+08	1.28E+08	752
ENSG00000(	64.2191	26.49433	25.06886	9.737982	23.0108	30.4127	0.85443	0.10159	0.17777	AC007383.	chr2	+	2.07E+08	2.07E+08	752
ENSG00000(	0	0	2.638828	0	0.920432	2.465895	-0.20473	0.87997	0.92501	RP11-312B	chr1	-	6894393	6894678	286
ENSG00000(	14.50109	6.021439	2.638828	5.243529	4.60216	5.753754	0.52317	0.54185	0.6646	RP11-439E	chr1	+	2.47E+08	2.47E+08	2600
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-704J	chr6	-	1.34E+08	1.34E+08	753
ENSG00000(	10.35792	6.021439	11.87472	3.745378	12.88605	11.50751	0.012708	0.98639	0.99166	RP11-276H	chr1	+	16481706	16483824	904
ENSG00000(	0	1.204288	3.958241	0	5.522592	0	-0.06213	0.96245	0.97823	RP11-382D	chr1	+	2.36E+08	2.36E+08	282
ENSG00000(	0	7.225726	1.319414	2.996302	3.681728	4.109825	-0.27232	0.80702	0.87475	RP5-1074L	chr1	-	1.11E+08	1.11E+08	2611
ENSG00000(	0	0	0	2.247227	5.522592	0.821965	-2.2243	0.096516	0.17035	RP5-1112F	chr20	-	50448336	50479451	2326
ENSG00000(	2.071584	1.204288	0	1.498151	3.681728	5.753754	-1.2384	0.29919	0.42415	PIN4P1	chr15	-	44168047	44168442	396
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	AC012668.	chr2	-	2.16E+08	2.16E+08	228
ENSG00000(	0	0	0	7.490755	11.04518	10.68554	-4.1328	0.000442	0.00131	TRIM60P18	chr7	+	63815456	63816577	828
ENSG00000(	6.214751	3.612863	0	5.243529	13.80648	4.93179	-1.0628	0.26577	0.38575	AC108463.	chr2	-	1.12E+08	1.12E+08	347
ENSG00000(	9.322127	3.612863	11.87472	5.243529	0	0	1.7826	0.091632	0.1632	MTND5P1	chr21	-	45893606	45894980	1375
ENSG00000(	0	0	6.597069	3.745378	1.840864	3.28786	-0.34411	0.77587	0.85287	RPL7AP65	chr17	+	18215218	18215965	748
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	AC011933.	chr17	+	73334908	73335228	321
ENSG00000(	2.071584	2.408575	0	0	0	0	1.5041	0.26224	NA	CTD-2330K	chr3	+	49941278	49954370	600
ENSG00000(	6.214751	3.612863	10.55531	1.498151	0.920432	3.28786	1.5295	0.12365	0.20882	AC073343.	chr7	+	6703605	6748532	564
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	RAPGEF4-A	chr2	-	1.74E+08	1.74E+08	4625
ENSG00000(	4.143168	1.204288	2.638828	3.745378	8.283888	1.64393	-0.61547	0.55686	0.67739	RP11-166C	chr7	-	66772592	66773343	378
ENSG00000(	0	0	1.319414	1.498151	0	0.821965	-0.38347	0.77483	NA	RP11-383C	chr10	+	1.27E+08	1.27E+08	3530

ENSG00000(	7.250543	0	0	2.247227	0	0	0.94694	0.48123	0.61035	HCG20	chr6	+	30734602	30760027	1202
ENSG00000(	1.035792	0	0	0	4.60216	0.821965	-1.1271	0.40572	0.53658	AC069257.	chr3	+	1.96E+08	1.96E+08	422
ENSG00000(	6.214751	1.204288	0	0	0	0	2.1793	0.10812	0.18693	C14orf144	chr14	+	1.05E+08	1.05E+08	1624
ENSG00000(	0	1.204288	3.958241	0	0	0	1.651	0.221	NA	AC010967.	chr2	-	52949815	53137158	489
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP4-663N1	chr1	+	1.16E+08	1.16E+08	2610
ENSG00000(	0	0	1.319414	0	2.761296	1.64393	-0.88471	0.51431	NA	RP3-395M2	chr1	+	2512999	2515972	626
ENSG00000(	4.143168	0	1.319414	7.490755	7.363456	9.863579	-1.7852	0.071967	0.13287	VN1R51P	chr9	-	99855976	99856920	945
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP3-522D1	chr1	-	1.13E+08	1.13E+08	156
ENSG00000(	0	2.408575	0	8.988907	10.12475	5.753754	-2.6438	0.015146	0.033781	AC097721.	chr2	-	1.39E+08	1.39E+08	928
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	POLR2J2	chr7	-	1.02E+08	1.02E+08	1714
ENSG00000(	0	1.204288	0	1.498151	0	2.465895	-0.80408	0.55336	NA	TOP3BP1	chr22	-	22577580	22578959	1380
ENSG00000(	0	1.204288	2.638828	2.247227	0	1.64393	-0.04025	0.97577	0.98601	RP11-151F	chr9	-	1.13E+08	1.13E+08	478
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RANP5	chr1	+	1.1E+08	1.1E+08	655
ENSG00000(	12.4295	0	0	0	6.443024	6.575719	-0.02578	0.98478	0.99109	CFL1P3	chr1	-	64308862	64309356	490
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	SEC63P1	chr1	+	98011257	98012514	1258
ENSG00000(	3.107376	7.225726	5.277655	2.996302	12.88605	9.041614	-0.5987	0.48326	0.61254	RP11-69E1	chr1	+	40030832	40038875	551
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	Z83001.1	chr11	-	31658875	31789501	598
ENSG00000(	151.2256	142.106	171.5238	0	2.761296	0	6.9307	5.84E-24	6.95E-23	RP11-135J2	chr1	-	2.19E+08	2.19E+08	724
ENSG00000(	0	4.817151	1.319414	0	0	1.64393	1.0533	0.43331	0.56311	AC023469.	chr2	+	1.52E+08	1.52E+08	657
ENSG00000(	8.286335	10.83859	10.55531	71.16218	78.23672	82.19649	-2.8946	1.88E-11	1.18E-10	RP11-222A	chr10	+	67330208	67526299	1227
ENSG00000(	8.286335	2.408575	9.235896	0.749076	5.522592	4.109825	0.81803	0.39273	0.52346	RP11-100G	chr9	+	94871295	94872377	779
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-255A	chr9	-	33512957	33514771	395
ENSG00000(	4.143168	3.612863	5.277655	1.498151	0.920432	4.93179	0.66799	0.52491	0.64984	AC133106.	chr2	+	1.9E+08	1.9E+08	397
ENSG00000(	0	4.817151	2.638828	0.749076	0	0	1.7482	0.1929	0.29873	RP11-475E	chr1	-	1.09E+08	1.09E+08	744
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	HLA-U	chr6	+	29901878	29902063	186
ENSG00000(	0	0	1.319414	2.247227	5.522592	1.64393	-1.8102	0.16114	0.25864	AC012368.	chr2	-	64313484	64315380	563
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	IFNA14	chr9	-	21239201	21239978	778
ENSG00000(	1.035792	0	0	0	4.60216	0.821965	-1.1271	0.40572	0.53658	RP5-884G6	chr1	-	1E+08	1E+08	655
ENSG00000(	0	2.408575	1.319414	2.247227	0	0	0.35636	0.79265	0.86445	RP5-837M2	chr1	-	1.01E+08	1.01E+08	592
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP1-197O1	chrX	-	1.31E+08	1.31E+08	430
ENSG00000(	7.250543	1.204288	3.958241	0	0	0.821965	2.5103	0.047609	0.093016	RP11-417C	chr10	-	79193330	79193540	211
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-39K2	chr9	+	5099560	5100229	670
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	AC110620.	chr2	+	1.36E+08	1.36E+08	228
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AC016912.	chr2	-	46619436	46621306	570
ENSG00000(	15.53688	8.430014	6.597069	14.98151	12.88605	17.26126	-0.51448	0.42477	0.55527	RP11-452F	chr1	+	2.23E+08	2.23E+08	767
ENSG00000(	10.35792	4.817151	1.319414	5.243529	2.761296	0.821965	0.75704	0.45837	0.58781	AP000692.	chr21	+	37732928	37734338	596
ENSG00000(	3.107376	1.204288	1.319414	0	8.283888	0	-0.35652	0.77742	0.85338	AC092839.	chr2	-	54743185	54767834	536
ENSG00000(	5.17896	8.430014	3.958241	4.494453	11.04518	9.863579	-0.47095	0.56247	0.68231	MFI2-AS1	chr3	+	1.97E+08	1.97E+08	951
ENSG00000(	0	0	0	2.996302	0	2.465895	-1.5141	0.2635	NA	ST13P19	chr1	-	2.1E+08	2.1E+08	1124
ENSG00000(	1.035792	2.408575	1.319414	0.749076	0	0	1.3221	0.32896	NA	AC003991.	chr7	+	87848674	87921781	821
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	PHBP3	chr1	+	59465348	59466166	819
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	MTND1P17	chr22	-	17357108	17357311	204
ENSG00000(	1.035792	0	0	0	0	1.64393	-0.12526	0.92174	NA	RP1-122O8	chr6	+	90383188	90385502	472
ENSG00000(	0	0	0	0	1.840864	3.28786	-1.4188	0.29365	NA	RP11-516A	chrX	+	67352710	67353279	570

ENSG00000(	4.143168	2.408575	7.916483	0.749076	1.840864	6.575719	0.53725	0.60317	0.71825	LINC00568	chr1	+	1.5E+08	1.5E+08	566
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-12L8	chr1	+	1.16E+08	1.16E+08	1396
ENSG00000(	2.071584	0	1.319414	1.498151	0	0.821965	0.29567	0.82667	NA	AC099684.	chr17	+	1921010	1924000	1747
ENSG00000(	12.4295	19.2686	17.15238	5.992604	8.283888	3.28786	1.3762	0.045659	0.089719	AP001469.	chr21	+	47666804	47667596	390
ENSG00000(	3.107376	2.408575	0	0.749076	0	0	1.4206	0.29439	0.41879	RP3-467K1	chr1	-	15729475	15735929	5178
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC105339.	chr15	-	83379223	83382778	2569
ENSG00000(	17.60846	26.49433	21.11062	0	5.522592	3.28786	2.675	0.000397	0.001185	CASP16	chr16	+	3194220	3199964	2161
ENSG00000(	1.035792	0	1.319414	1.498151	0	3.28786	-0.60338	0.65141	0.75747	RPL3P1	chr21	-	37541268	37542478	1211
ENSG00000(	6.214751	3.612863	14.51355	8.239831	7.363456	4.93179	0.2085	0.79616	0.86694	RP11-84A1	chr1	+	10002981	10010032	440
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC004941.	chr7	+	1.49E+08	1.49E+08	3120
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	AL589685.	chr1	+	1.56E+08	1.56E+08	177
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-410N	chr20	+	31169765	31181702	370
ENSG00000(	1.035792	0	1.319414	2.247227	2.761296	0	-0.6401	0.63096	0.74097	AC007952.	chr17	+	18996287	19000150	1921
ENSG00000(	0	0	0	5.243529	0.920432	2.465895	-2.2485	0.09265	0.16463	TLE1P1	chrX	+	64627964	64628565	589
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	MTND1P11	chr9	+	5094139	5095014	876
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	PPIAP19	chr10	-	1.16E+08	1.16E+08	492
ENSG00000(	0	2.408575	2.638828	0	0	0	1.6365	0.22501	NA	AC121251.	chr3	-	23431152	23431400	249
ENSG00000(	0	2.408575	0	1.498151	0	6.575719	-1.073	0.41505	0.54557	RP1-317E2	chr1	-	26143240	26146263	517
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-244N	chr9	-	1E+08	1E+08	954
ENSG00000(	7.250543	0	0	23.22134	16.56778	26.30288	-2.7728	0.000707	0.002032	GEMIN8P4	chr1	-	90459152	90459880	729
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-342N	chr1	-	43307569	43312058	610
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	PTPN2P1	chr1	-	1.79E+08	1.79E+08	1072
ENSG00000(	0	0	2.638828	8.239831	6.443024	4.109825	-2.2073	0.052608	0.10151	AL022341.	chr16	-	698473	699200	389
ENSG00000(	227.8742	286.6205	197.9121	27.7158	34.05598	38.63235	2.804	1.65E-26	2.17E-25	RNF144A-A	chr2	-	7052408	7058813	2954
ENSG00000(	0	0	0	1.498151	2.761296	3.28786	-2.0751	0.1224	0.20728	RP4-724E1	chr7	+	50934444	51090687	762
ENSG00000(	5.17896	1.204288	1.319414	5.243529	3.681728	1.64393	-0.34412	0.75253	0.83619	RP11-778D	chr3	+	1.84E+08	1.84E+08	732
ENSG00000(	0	0	0	7.490755	6.443024	3.28786	-3.3169	0.008025	0.019061	C1orf143	chr1	+	2.19E+08	2.19E+08	813
ENSG00000(	2.071584	9.634302	5.277655	5.243529	3.681728	0	0.75142	0.47019	0.59927	OFD1P17	chr5	+	37209466	37212483	3018
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	NLGN1-AS1	chr3	-	1.74E+08	1.74E+08	815
ENSG00000(	2.071584	7.225726	1.319414	8.239831	4.60216	3.28786	-0.51443	0.60058	0.71593	LINC00693	chr3	+	28616282	28799296	1609
ENSG00000(	0	0	2.638828	2.247227	0	1.64393	-0.33245	0.80579	0.8741	AL390877.	chr1	-	1.18E+08	1.18E+08	420
ENSG00000(	0	2.408575	0	0	0.920432	0.821965	0.212	0.87508	NA	ATF4P3	chr17	-	74221832	74222887	1056
ENSG00000(	0	0	0	7.490755	1.840864	2.465895	-2.7168	0.037492	0.075651	NPM1P30	chr10	+	21399611	21402317	828
ENSG00000(	3.107376	1.204288	1.319414	0	0	0	1.9243	0.1561	NA	LINC00578	chr3	+	1.77E+08	1.77E+08	612
ENSG00000(	11.39371	3.612863	10.55531	2.247227	6.443024	7.397684	0.60674	0.46961	0.59883	AC074363.	chr2	+	1.68E+08	1.68E+08	462
ENSG00000(	353.205	438.3607	444.6424	167.0438	221.8241	187.408	1.0968	2.53E-09	1.34E-08	HCG11	chr6	+	26522076	26526807	4732
ENSG00000(	18.64425	14.45145	11.87472	5.992604	7.363456	10.68554	0.8536	0.19641	0.30314	GAPDHP1	chrX	-	39646386	39647390	1005
ENSG00000(	2.071584	0	2.638828	0	0	0	1.5584	0.24658	NA	AP001476.	chr21	+	47472510	47473019	415
ENSG00000(	0	0	0	1.498151	2.761296	1.64393	-1.7322	0.2011	NA	AC073271.	chr2	-	1.5E+08	1.5E+08	315
ENSG00000(	6.214751	0	3.958241	1.498151	1.840864	4.93179	0.24271	0.82876	0.89005	EFCAB14-A	chr1	+	47139708	47157770	500
ENSG00000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	GS1-304P7	chr1	+	1.87E+08	1.87E+08	1021
ENSG00000(	2.071584	2.408575	6.597069	0	7.363456	4.109825	-0.03984	0.97079	0.98297	AC093495.	chr3	+	14186320	14189784	575
ENSG00000(	2.071584	7.225726	2.638828	0	0	0.821965	2.4603	0.052607	0.10151	RP11-436G	chr9	+	45949232	45949823	592
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	UBBP2	chr1	-	2.18E+08	2.18E+08	231

ENSG00000(	3.107376	4.817151	2.638828	7.490755	4.60216	0	-0.16053	0.88114	0.92567	AC012442.	chr2	+	1.13E+08	1.13E+08	529
ENSG00000(	0	7.225726	1.319414	2.996302	0	2.465895	0.4368	0.72439	0.81505	COL6A4P2	chr3	+	1.3E+08	1.3E+08	2612
ENSG00000(	18.64425	10.83859	26.38828	8.239831	17.48821	31.23467	-0.02734	0.9636	0.97889	MT-ATP8	chrMT	+	8366	8572	207
ENSG00000(	0	0	0	0	0.920432	3.28786	-1.1769	0.37857	NA	AC136604.	chr5	+	1.79E+08	1.79E+08	777
ENSG00000(	3.107376	9.634302	7.916483	0	0	0	3.9292	0.001468	0.003997	RP11-127L	chr10	+	1.06E+08	1.06E+08	954
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-350G	chr1	-	1.54E+08	1.54E+08	769
ENSG00000(	7.250543	6.021439	10.55531	29.96302	12.88605	14.79537	-1.2079	0.06523	0.12212	RP5-1125A	chr20	-	32570858	32582163	660
ENSG00000(	63.18331	68.6444	47.4989	14.23244	13.80648	14.79537	2.0184	1.01E-06	4.19E-06	RP3-508I15	chr22	-	39063590	39077825	1325
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	ORM2	chr9	+	1.17E+08	1.17E+08	980
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP11-497D	chr6	-	1.47E+08	1.47E+08	1466
ENSG00000(	0	0	0	0.749076	0.920432	0.821965	-0.73223	0.57364	NA	LYPLA2P1	chr6	-	33333325	33334020	696
ENSG00000(	109.7939	131.2674	106.8725	50.93714	52.46462	68.22309	1.0088	0.000281	0.00086	KDM5B-AS1	chr1	+	2.03E+08	2.03E+08	748
ENSG00000(	6.214751	0	1.319414	0	0	0	2.1977	0.10512	0.18272	RP11-132N	chr6	+	85399143	85419252	762
ENSG00000(	2.071584	3.612863	0	0	0	2.465895	0.70466	0.59825	0.71377	RP11-220I1	chr9	-	37205109	37205365	257
ENSG00000(	1.035792	3.612863	1.319414	0	1.840864	0	1.0352	0.43559	0.56513	AL589743.	chr14	-	19670480	19686002	777
ENSG00000(	938.4275	823.7328	662.3457	944.5843	671.9154	802.2378	0.003963	0.98091	0.9889	C19orf24	chr19	+	1275026	1279248	1653
ENSG00000(	8.286335	18.06432	26.38828	28.46487	24.85166	27.94681	-0.61707	0.24056	0.35587	RP11-186N	chr10	-	12286750	12289844	1914
ENSG00000(	2.071584	1.204288	0	3.745378	2.761296	2.465895	-1.0161	0.40264	0.53379	AC016734.	chr2	-	63849309	63849965	657
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	RP11-113A	chr9	+	36013181	36014130	950
ENSG00000(	0	0	3.958241	1.498151	0	4.93179	-0.46236	0.72522	0.81571	CTD-2555K	chr14	-	23064715	23067855	2673
ENSG00000(	270.3417	223.9975	261.2439	113.1104	165.6778	152.8855	0.80626	0.00014	0.000446	GUSBP11	chr22	-	23980674	24059543	5004
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-522L	chrX	+	1.02E+08	1.02E+08	659
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-235C	chr9	-	1.08E+08	1.08E+08	631
ENSG00000(	11.39371	4.817151	2.638828	0	0.920432	0.821965	2.6258	0.021501	0.046281	AC008753.	chr19	-	54357835	54372361	439
ENSG00000(	35.21692	48.17151	39.58241	15.73059	33.13555	64.11326	0.11953	0.7981	0.86849	RP11-206L	chr1	-	700237	714006	1317
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-516A	chrX	-	67290362	67291609	1248
ENSG00000(	0	1.204288	1.319414	0	0.920432	1.64393	-0.02084	0.98774	NA	RP11-730A	chr10	-	13184185	13184977	793
ENSG00000(	3.107376	0	0	4.494453	0	2.465895	-0.69851	0.59509	0.71097	AC073063.	chr7	-	99040513	99041119	607
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-804H	chr3	-	50722982	50723222	241
ENSG00000(	3.107376	0	5.277655	0	1.840864	1.64393	0.87319	0.48848	0.61758	RP5-1043L	chr20	+	58662895	59102516	2043
ENSG00000(	0	1.204288	0	0	0	1.64393	-0.12916	0.91993	NA	CTB-20D2.1	chr7	+	1.07E+08	1.07E+08	280
ENSG00000(	211.3015	220.3847	171.5238	200.7522	191.4499	215.3548	-0.00864	0.96493	0.97974	RP11-1148	chrX	-	48438162	48439545	450
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RPS26P4	chr21	-	40863470	40863824	355
ENSG00000(	1.035792	4.817151	0	1.498151	4.60216	4.93179	-0.69056	0.54823	0.66988	RP11-148G	chr3	+	48701209	48706607	196
ENSG00000(	1.035792	0	1.319414	1.498151	0	0	0.26794	0.842	NA	RP11-537H	chr9	+	34084330	34096223	635
ENSG00000(	1.035792	4.817151	6.597069	0	3.681728	3.28786	0.65438	0.55941	0.67993	AC015971.	chr2	+	86789193	86845889	1948
ENSG00000(	1.035792	0	0	2.247227	1.840864	0	-0.86384	0.52422	NA	AC106873.	chr7	-	1.17E+08	1.17E+08	459
ENSG00000(	1.035792	1.204288	0	0.749076	1.840864	7.397684	-1.4462	0.2479	0.36482	RP11-91A1	chr1	+	52516590	52518355	391
ENSG00000(	0	0	0	5.243529	2.761296	0.821965	-2.2748	0.08857	0.15864	RP11-520B	chr9	-	99837953	99844227	2262
ENSG00000(	0	0	3.958241	0	0	1.64393	0.57053	0.67342	NA	ITPKB-IT1	chr1	-	2.27E+08	2.27E+08	746
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	FAM197Y7	chrY	-	9205412	9235047	2325
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC007040.	chr2	+	71221573	71229884	1211
ENSG00000(	2.071584	0	5.277655	0	9.20432	1.64393	-0.40933	0.73299	0.8214	RP5-1125A	chr20	-	32602775	32605555	603
ENSG00000(	30.03797	33.72006	29.0271	23.97042	22.09037	10.68554	0.68537	0.15945	0.25649	AC068039.	chr2	+	1.73E+08	1.73E+08	2102

ENSG00000(	42.46747	46.96722	48.81831	44.19546	42.33987	65.75719	-0.13979	0.69592	0.79281	RP11-325F	chr7	-	1.05E+08	1.05E+08	686
ENSG00000(	15.53688	13.24716	11.87472	14.98151	22.09037	15.61733	-0.34776	0.54585	0.66798	RP11-216B	chr9	-	1.31E+08	1.31E+08	970
ENSG00000(	3.107376	0	0	0.749076	0	0	0.76338	0.56438	NA	RP1-224A6	chr1	-	22350487	22351461	615
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC079154.	chr2	-	1.25E+08	1.25E+08	542
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AP001468.	chr21	+	47604993	47608855	557
ENSG00000(	4.143168	3.612863	0	1.498151	0.920432	0	1.1036	0.39127	0.52202	RP4-800M:	chr1	-	52625933	52626272	340
ENSG00000(	99.43602	143.3102	76.526	123.5975	94.8045	104.3895	-0.0159	0.95455	0.97296	CCT6P1	chr7	+	65216129	65228341	1315
ENSG00000(	2.071584	7.225726	3.958241	1.498151	7.363456	0	0.47281	0.66645	0.76995	CDY4P	chrY	-	14913906	14915763	1513
ENSG00000(	4.143168	10.83859	1.319414	13.48336	11.96562	4.93179	-0.79786	0.34111	0.46996	RP4-625H1	chr6	-	19803602	19804973	1016
ENSG00000(	1.035792	6.021439	0	0	0.920432	2.465895	0.69386	0.59157	0.70795	AC024937.	chr3	+	1.96E+08	1.96E+08	344
ENSG00000(	9.322127	9.634302	3.958241	0	2.761296	4.109825	1.4795	0.13546	0.22472	PTMAP1	chr6	+	30601409	30601675	267
ENSG00000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	RP11-549L	chr10	-	1.12E+08	1.12E+08	470
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTSL1P3	chr10	-	48980162	48981273	393
ENSG00000(	0	0	0	0	5.522592	0	-1.3606	0.30939	NA	AC005013.	chr7	+	28997283	28998961	588
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	LINC00687	chr20	-	11781111	11851363	696
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	RP4-633I8.	chr1	+	8865919	8867110	353
ENSG00000(	18.64425	3.612863	2.638828	0	0	0	4.1595	0.000726	0.002084	RP11-15B2	chr9	+	84887671	85179347	805
ENSG00000(	3.107376	0	3.958241	0	0	1.64393	1.2286	0.35606	0.48557	ARL5AP3	chr1	-	68515043	68515428	386
ENSG00000(	21.75163	19.2686	36.94359	8.988907	18.40864	19.72716	0.69644	0.19685	0.30372	AC004951.	chr7	-	44043645	44047465	1866
ENSG00000(	11.39371	16.86003	21.11062	7.490755	18.40864	5.753754	0.60589	0.35425	0.48409	RP5-864K1	chr1	+	39325672	39385068	630
ENSG00000(	0	0	0	0	1.840864	2.465895	-1.2108	0.36631	NA	RP11-400N	chr1	+	2.22E+08	2.22E+08	1148
ENSG00000(	18.64425	9.634302	19.79121	26.96672	17.48821	23.83698	-0.48884	0.36544	0.49529	TSTD3	chr6	+	99968569	99979794	962
ENSG00000(	7.250543	9.634302	10.55531	11.23613	13.80648	7.397684	-0.22772	0.74401	0.8295	RP11-173B	chr13	-	76203370	76206271	2044
ENSG00000(	2.071584	3.612863	7.916483	0	6.443024	3.28786	0.39258	0.7147	0.80747	AC073052.	chr2	-	2.25E+08	2.25E+08	714
ENSG00000(	13.46529	13.24716	7.916483	2.996302	3.681728	2.465895	1.7367	0.032777	0.06712	SDAD1P1	chr8	-	26236775	26240469	3174
ENSG00000(	11.39371	20.47289	29.0271	14.98151	27.61296	13.9734	0.096559	0.86297	0.91328	RP5-994D1	chr1	-	43241484	43242461	484
ENSG00000(	16.57267	3.612863	19.79121	0	1.840864	0	3.6494	0.000403	0.001203	CXorf28	chrX	+	3189861	3202694	674
ENSG00000(	16.57267	31.31148	7.916483	4.494453	7.363456	4.93179	1.618	0.021095	0.045528	AP006222.	chr1	-	227615	267253	2257
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	TUBB4AP1	chrX	+	1.23E+08	1.23E+08	1325
ENSG00000(	5.17896	1.204288	5.277655	8.988907	10.12475	13.9734	-1.3444	0.10358	0.18058	RP11-176D	chr1	-	2.15E+08	2.15E+08	518
ENSG00000(	2140.982	2344.748	1833.985	862.186	1134.893	1033.21	1.0586	5.08E-14	3.79E-13	OST4	chr2	-	27293340	27294641	561
ENSG00000(	2.071584	0	2.638828	0	0.920432	0.821965	0.81976	0.54181	0.66459	RP3-342P2	chr1	+	40428352	40429076	725
ENSG00000(	0	0	0	0	2.761296	2.465895	-1.4428	0.28594	NA	RP1-290I1(	chr6	-	10423373	10426409	539
ENSG00000(	0	3.612863	5.277655	0	0.920432	0	1.9012	0.15157	0.24616	U51244.2	chr2	-	45901840	45902615	374
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-106N	chr10	+	1.17E+08	1.17E+08	2378
ENSG00000(	0	1.204288	5.277655	4.494453	0	3.28786	-0.21929	0.85892	0.91034	RP11-567J:	chr10	+	1.21E+08	1.21E+08	400
ENSG00000(	20.71584	18.06432	7.916483	56.92974	42.33987	49.3179	-1.6055	0.000456	0.001347	AC017099.	chr2	+	98280680	98319527	1356
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP13-225C	chr9	-	1.3E+08	1.3E+08	397
ENSG00000(	53.86118	25.29004	27.70769	8.988907	13.80648	9.041614	1.6924	0.001371	0.003761	RAB11FIP1	chrX	+	73422669	73424430	1762
ENSG00000(	4.143168	3.612863	1.319414	5.243529	0	0.821965	0.42101	0.72255	0.81352	RP3-523C2	chr6	+	1.32E+08	1.32E+08	1831
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC106875.	chr2	+	11821586	11823454	1170
ENSG00000(	3.107376	2.408575	0	0.749076	0	0	1.4206	0.29439	0.41879	TMSB10P1	chr2	-	2.37E+08	2.37E+08	132
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RPL15P18	chr13	-	1.01E+08	1.01E+08	612
ENSG00000(	11.39371	13.24716	11.87472	1.498151	6.443024	5.753754	1.3001	0.095344	0.16859	EEF1A1P11	chr1	+	96912486	96913874	1389

ENSG00000(	24.85901	26.49433	31.66593	31.46117	51.54419	24.65895	-0.36339	0.4145	0.545	RP11-98I9.	chr6	+	99872798	99879249	1638
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	DAP3P2	chr2	+	1.72E+08	1.72E+08	510
ENSG00000(	0	0	0	0	1.840864	2.465895	-1.2108	0.36631	NA	AC006460.	chr2	-	1.92E+08	1.92E+08	808
ENSG00000(	6.214751	3.612863	2.638828	0.749076	0	1.64393	1.7497	0.13873	0.22911	RP11-339B	chr9	+	1.31E+08	1.31E+08	1734
ENSG00000(	0	0	2.638828	2.247227	0	5.753754	-1.024	0.43511	0.56488	AC023271.	chr2	-	2.04E+08	2.04E+08	1090
ENSG00000(	4.143168	0	0	9.737982	5.522592	5.753754	-1.806	0.094701	0.1676	RP11-298C	chrX	-	25663839	25664444	606
ENSG00000(	4.143168	4.817151	3.958241	11.23613	5.522592	6.575719	-0.76212	0.37416	0.5046	RP11-236F	chr9	+	67285298	67298632	786
ENSG00000(	4.143168	14.45145	23.74945	1.498151	11.96562	0	1.4503	0.11241	0.19304	RP3-510D1	chr1	-	9228327	9262678	548
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-179B	chr10	+	60064313	60065381	328
ENSG00000(	19.68005	4.817151	18.47179	13.48336	12.88605	13.15144	0.116	0.85693	0.90909	AC068057.	chr2	+	1.05E+08	1.05E+08	709
ENSG00000(	534.4686	556.3809	434.0871	1.498151	0.920432	0	8.5864	3.17E-40	6.58E-39	RP11-392C	chr1	-	2.2E+08	2.2E+08	811
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC009411.	chr2	-	21861303	21872435	548
ENSG00000(	0	0	0	2.247227	4.60216	0	-1.7927	0.18635	0.29091	RP11-526K	chr20	-	24472108	24482981	823
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	IMMP2L-IT:	chr7	-	1.1E+08	1.1E+08	557
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AC093159.	chr2	+	62690262	62691205	424
ENSG00000(	14.50109	9.634302	11.87472	7.490755	10.12475	5.753754	0.58736	0.39934	0.53041	KIAA1984-/	chr9	-	1.4E+08	1.4E+08	2386
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	ITPKB-AS1	chr1	+	2.27E+08	2.27E+08	538
ENSG00000(	0	0	0	4.494453	7.363456	2.465895	-3.0227	0.018004	0.039473	RP11-108N	chr1	+	17197440	17200587	2520
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	RP11-483N	chrX	-	7031046	7031445	400
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	SNRPGP9	chr2	+	1.1E+08	1.1E+08	225
ENSG00000(	5.17896	1.204288	0	1.498151	0	0.821965	0.90838	0.48947	0.61851	AC004837.	chr7	-	39739940	39742895	731
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP3-340B1	chr6	+	35512409	35513446	595
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-550P	chr1	-	1.59E+08	1.59E+08	1063
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-114N	chr3	+	1.77E+08	1.77E+08	587
ENSG00000(	1.035792	2.408575	0	0.749076	0	1.64393	0.28892	0.83045	NA	AC006461.	chr2	+	72515914	72516239	326
ENSG00000(	5.17896	3.612863	13.19414	0	0	0	4.0119	0.001112	0.003095	AC010731.	chr2	-	2.07E+08	2.07E+08	440
ENSG00000(	9.322127	20.47289	15.83297	7.490755	12.88605	17.26126	0.25899	0.68112	0.78164	SPCS2P4	chr1	-	28421582	28422933	1252
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	AP000459.	chr21	-	24733426	24757182	1725
ENSG00000(	339.7397	364.8992	261.2439	186.5198	173.0412	150.4196	0.91767	3.04E-06	1.19E-05	C1orf233	chr1	-	1533392	1535476	2085
ENSG00000(	0	0	1.319414	1.498151	0	0	-0.08979	0.94423	NA	PAICSP2	chr9	+	94373625	94374774	1150
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	MACC1-AS1	chr7	+	20181539	20193154	639
ENSG00000(	14.50109	6.021439	6.597069	3.745378	0	0	2.2903	0.027867	0.05827	RPL39P	chr20	-	55034484	55034639	156
ENSG00000(	3.107376	2.408575	1.319414	0	1.840864	0	1.2077	0.35718	0.48669	RP5-872K7	chr20	-	21129382	21143531	795
ENSG00000(	2.071584	0	2.638828	0	0.920432	2.465895	0.29604	0.82257	0.88543	RP11-574F	chr1	+	1.6E+08	1.6E+08	557
ENSG00000(	18.64425	15.65574	9.235896	48.68991	31.29469	39.45432	-1.3977	0.003836	0.009726	RP3-341D1	chrX	-	1E+08	1E+08	3216
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	HK2P1	chrX	-	79827370	79830106	2737
ENSG00000(	1.035792	0	0	1.498151	5.522592	3.28786	-1.9997	0.12031	0.20424	AC144450.	chr2	-	1550437	1623885	786
ENSG00000(	2.071584	0	1.319414	0.749076	4.60216	2.465895	-0.81383	0.5139	0.64083	RP13-476E	chr6	-	53655673	53659072	483
ENSG00000(	3.107376	2.408575	0	0	0	0	1.7825	0.18787	NA	AC093166.	chr2	+	1.13E+08	1.13E+08	1017
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC012462.	chr2	+	2.16E+08	2.16E+08	391
ENSG00000(	44.53905	45.76293	60.69303	57.67882	34.05598	37.81039	0.20813	0.57551	0.69389	ZNF883	chr9	-	1.16E+08	1.16E+08	2319
ENSG00000(	15.53688	9.634302	10.55531	122.0993	127.94	107.6774	-3.2399	1.33E-17	1.21E-16	RP3-399L1	chr6	+	1.14E+08	1.15E+08	2016
ENSG00000(	2.071584	2.408575	3.958241	0	0	0	2.5267	0.059095	0.11225	RP11-1B20	chr1	+	2.27E+08	2.27E+08	814
ENSG00000(	4.143168	3.612863	1.319414	8.239831	7.363456	9.863579	-1.2855	0.14979	0.24375	RP11-495P	chr1	-	1.48E+08	1.48E+08	285

ENSG00000(	0	3.612863	1.319414	2.996302	0	0	0.38924	0.77184	0.85002	AC092295.	chr19	+	37019220	37026137	434
ENSG00000(	121.1877	175.826	143.8161	0	0	0	8.2653	2.78E-17	2.47E-16	HOTAIR	chr12	-	54356092	54368740	2421
ENSG00000(	12.4295	8.430014	3.958241	5.992604	0.920432	4.93179	0.93121	0.2967	0.42117	RP4-534N1	chr1	+	32398621	32399576	517
ENSG00000(	53.86118	50.58008	64.65128	62.17327	66.2711	78.08667	-0.28694	0.35848	0.48812	FCF1P2	chr3	-	48332283	48332865	583
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC005152.	chr17	-	70017992	70030233	346
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	AC079779.	chr2	+	286419	301515	694
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-554K	chr1	-	2.14E+08	2.14E+08	370
ENSG00000(	30.03797	27.69862	31.66593	20.22504	16.56778	23.83698	0.54049	0.24346	0.35945	AC005682.	chr7	+	22893875	22901021	1021
ENSG00000(	3.107376	1.204288	11.87472	4.494453	2.761296	6.575719	0.1725	0.85769	0.90953	RP11-321E	chr7	+	63961203	63962107	905
ENSG00000(	9.322127	4.817151	0	0	0	0	3.1809	0.015569	0.03462	RP11-170J	chr10	-	1.04E+08	1.04E+08	469
ENSG00000(	0	0	0	0	5.522592	0	-1.3606	0.30939	NA	AC090587.	chr11	-	3875548	3876739	494
ENSG00000(	13.46529	6.021439	3.958241	3.745378	1.840864	4.93179	1.0172	0.25804	0.37673	PSMD10P1	chr20	+	49530268	49530948	681
ENSG00000(	7.250543	0	3.958241	0	0	0	2.8135	0.035169	0.071451	RP11-20O2	chr1	+	1.1E+08	1.1E+08	253
ENSG00000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	RP11-129C	chr10	+	25156574	25157119	268
ENSG00000(	75.61281	73.46155	52.77655	18.72689	21.16994	18.08323	1.7688	3.59E-06	1.40E-05	PROB1	chr5	-	1.39E+08	1.39E+08	3251
ENSG00000(	2.071584	3.612863	5.277655	0	0	0.821965	2.3523	0.065568	0.12268	TTC3-AS1	chr21	-	38559967	38566227	1097
ENSG00000(	0	3.612863	1.319414	0	0	0	1.6005	0.2346	NA	RP4-676J1	chr6	+	84693447	84717042	835
ENSG00000(	0	2.408575	0	2.996302	5.522592	4.109825	-1.7082	0.15822	0.2548	RP11-492I2	chr1	+	1.76E+08	1.76E+08	629
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP3-335N1	chr6	+	51464600	51487682	913
ENSG00000(	0	6.021439	0	1.498151	0.920432	4.109825	-0.08604	0.94554	0.96725	RP5-826L7	chr6	+	1.64E+08	1.64E+08	600
ENSG00000(	7.250543	14.45145	6.597069	5.992604	6.443024	9.863579	0.31438	0.6766	0.77823	ARL17B	chr17	-	44352150	44439130	2197
ENSG00000(	8.286335	8.430014	11.87472	2.247227	3.681728	9.041614	0.83689	0.30679	0.4325	TNKS2-AS1	chr10	-	93542596	93558048	609
ENSG00000(	1.035792	0	5.277655	0.749076	0	1.64393	0.84179	0.52257	0.64796	RP11-671E	chr10	-	46221142	46221486	345
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-787B	chr9	+	1.19E+08	1.19E+08	509
ENSG00000(	8.286335	9.634302	9.235896	17.97781	15.64734	18.08323	-0.88107	0.1559	0.25187	AP001065.	chr21	+	45905460	45910171	912
ENSG00000(	595.5803	534.7037	540.9597	2465.957	2556.04	2325.339	-2.1309	3.18E-71	1.41E-69	DHFR	chr5	-	79922047	79950802	3917
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-145H	chr6	+	2637170	2640235	834
ENSG00000(	2.071584	2.408575	2.638828	0	0.920432	0	1.7487	0.1868	0.29146	SRGAP3-AS	chr3	+	9234177	9236137	1189
ENSG00000(	0	3.612863	0	0.749076	7.363456	3.28786	-1.1672	0.34234	0.4713	SAPCD1	chr6	+	31730576	31732628	916
ENSG00000(	5.17896	1.204288	1.319414	0	9.20432	0	-0.15441	0.90024	0.93793	RP11-316K	chrX	+	1.5E+08	1.5E+08	494
ENSG00000(	0	0	2.638828	0	0	1.64393	0.26729	0.84149	NA	RP11-211A	chr1	+	2.27E+08	2.27E+08	821
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	AC015815.	chr17	-	75108843	75108930	87
ENSG00000(	0	1.204288	0	2.996302	0.920432	8.219649	-2.1416	0.092176	0.16395	AC008781.	chr5	+	1.41E+08	1.41E+08	622
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	AC136896.	chr15	-	27402762	27406466	970
ENSG00000(	1.035792	3.612863	6.597069	0.749076	2.761296	1.64393	0.8716	0.43972	0.56948	RP11-309I	chr13	+	24553949	24609166	1721
ENSG00000(	0	7.225726	0	2.996302	0	0	0.71353	0.59449	0.71047	RP5-884M(	chr7	+	1.06E+08	1.06E+08	3049
ENSG00000(	4.143168	7.225726	5.277655	8.988907	5.522592	5.753754	-0.2621	0.75529	0.83813	RP13-39P1	chr10	+	79542624	79552934	2028
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	EIF4BP2	chr10	+	21317928	21319721	1794
ENSG00000(	0	7.225726	2.638828	0	4.60216	4.109825	0.13394	0.9096	0.9445	AC010095.	chr2	-	1.09E+08	1.09E+08	477
ENSG00000(	5.17896	7.225726	5.277655	1.498151	0	0.821965	2.2435	0.043416	0.085969	AC003101.	chr17	+	29898161	29902678	459
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP1-309H1	chr6	-	22589366	22594062	743
ENSG00000(	15.53688	26.49433	15.83297	23.97042	9.20432	21.37109	0.072777	0.89753	0.93635	RP5-894A1	chr7	-	1.41E+08	1.41E+08	2262
ENSG00000(	2.071584	12.04288	3.958241	0	0.920432	3.28786	1.6547	0.13448	0.2235	Z69666.2	chr16	+	175736	177218	801
ENSG00000(	109.7939	134.8802	85.7619	85.39461	76.39586	63.2913	0.54886	0.049873	0.096871	MRPL45P2	chr17	-	45527934	45569858	1763

ENSG00000(	4.143168	4.817151	3.958241	0	3.681728	1.64393	1.0239	0.35909	0.48869	AC013400.	chr2	+	20068635	20084808	2995
ENSG00000(	10.35792	1.204288	1.319414	6.74168	2.761296	3.28786	0.027385	0.97857	0.98755	NLGN4Y-AS	chrY	-	16905522	16915913	532
ENSG00000(	0	0	0	9.737982	6.443024	5.753754	-3.6973	0.002354	0.006198	THRB-AS1	chr3	+	24535578	24541833	1216
ENSG00000(	211.3015	193.8903	186.0373	291.3904	388.4223	349.3351	-0.79277	1.93E-05	6.93E-05	RP11-206L	chr1	+	762988	794826	6606
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	FAM207BP	chr13	+	19271143	19271647	505
ENSG00000(	7.250543	6.021439	2.638828	0	0	0	3.5319	0.00539	0.01326	AP000473.	chr21	+	18003146	18013002	550
ENSG00000(	76.6486	33.72006	39.58241	34.45748	35.89685	26.30288	0.62732	0.13077	0.21828	RP11-110G	chr8	+	52811885	52859733	936
ENSG00000(	2.071584	1.204288	0	1.498151	0.920432	0	0.25153	0.85224	NA	AC073641.	chr2	-	2.25E+08	2.25E+08	429
ENSG00000(	7.250543	4.817151	0	0	0	0.821965	2.3781	0.065946	0.1233	RP11-211G	chr3	+	1.87E+08	1.87E+08	672
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	MRPS18CP	chr22	-	44879375	44879597	223
ENSG00000(	5.17896	7.225726	9.235896	4.494453	2.761296	0	1.3139	0.18383	0.28788	HMGB3P4	chr13	+	1E+08	1E+08	514
ENSG00000(	0	0	1.319414	1.498151	0	0.821965	-0.38347	0.77483	NA	RP4-705D1	chr20	-	16695489	16711593	1101
ENSG00000(	0	1.204288	0	1.498151	23.0108	2.465895	-3.1398	0.008126	0.019276	PABPC1P1:	chr9	-	17589159	17591316	2007
ENSG00000(	1.035792	0	0	0	1.840864	4.93179	-1.39	0.30221	0.42732	RP11-157P	chr20	+	60928066	60931536	690
ENSG00000(	0	0	6.597069	0	0	0	1.83	0.17508	0.27674	RP11-119H	chr4	-	1.14E+08	1.14E+08	415
ENSG00000(	10.35792	12.04288	10.55531	4.494453	8.283888	5.753754	0.77118	0.29568	0.42005	AK3P5	chr10	+	33233409	33233927	519
ENSG00000(	4.143168	7.225726	5.277655	2.247227	0	2.465895	1.4462	0.17518	0.27689	BACH1-IT2	chr21	+	30743268	30746029	806
ENSG00000(	1.035792	0	7.916483	2.247227	5.522592	0.821965	0.031877	0.97821	0.98729	RP11-567G	chr1	-	2.4E+08	2.4E+08	2720
ENSG00000(	14.50109	19.2686	9.235896	0	0	0	5.0865	7.83E-06	2.94E-05	MIR4500H(	chr13	-	88096247	88323514	1670
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AL592494.	chr1	-	1.21E+08	1.21E+08	369
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-234P	chrX	-	51646434	51646946	154
ENSG00000(	0	4.817151	2.638828	1.498151	1.840864	0	0.76487	0.54957	0.67103	RP11-162G	chr10	-	38107534	38109910	2240
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-249L	chr6	-	1.09E+08	1.09E+08	259
ENSG00000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	AC012123.	chr18	+	30349758	30354376	1661
ENSG00000(	0	1.204288	3.958241	0	6.443024	1.64393	-0.45455	0.71782	0.80997	RP4-784A1	chr1	+	53753696	53755378	675
ENSG00000(	1.035792	3.612863	0	2.996302	0	0.821965	0.16555	0.89997	0.9378	RP3-400N2	chr22	+	31688485	31734007	554
ENSG00000(	0	0	1.319414	2.996302	0	0	-0.52076	0.6968	NA	PCDH9-AS2	chr13	+	67399301	67489163	538
ENSG00000(	2.071584	3.612863	18.47179	2.996302	8.283888	3.28786	0.62518	0.49474	0.62352	RP11-57H1	chr1	-	95708781	95729610	371
ENSG00000(	3.107376	1.204288	1.319414	5.243529	0	3.28786	-0.43946	0.71343	0.80638	AC104653.	chr2	-	1.15E+08	1.15E+08	578
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-91I2(	chr8	-	61544068	61548830	3564
ENSG00000(	0	0	0	0	0	4.93179	-1.2404	0.35057	NA	RP11-463P	chr10	+	48357926	48358600	227
ENSG00000(	0	0	0	0	5.522592	2.465895	-1.9938	0.14085	0.23199	AC096664.	chr2	+	63944256	63945033	778
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-473E	chr9	+	1.37E+08	1.37E+08	428
ENSG00000(	11.39371	13.24716	14.51355	5.243529	4.60216	7.397684	1.0894	0.12712	0.21347	AC007551.	chr7	-	35794574	35840226	702
ENSG00000(	0	6.021439	0	0	0.920432	0	1.3099	0.33429	0.46228	RP11-439E	chr1	-	2.47E+08	2.47E+08	322
ENSG00000(	2.071584	3.612863	1.319414	0	1.840864	2.465895	0.50763	0.68125	0.78174	LL0XNC01-	chrX	+	1.03E+08	1.03E+08	418
ENSG00000(	24.85901	6.021439	18.47179	0.749076	0	4.109825	2.9092	0.001106	0.003081	RP11-290D	chr13	+	45924458	45925485	310
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	EEF1DP1	chr19	+	14181154	14182052	896
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP4-764O2	chr20	-	7127114	7234849	874
ENSG00000(	25.8948	14.45145	14.51355	7.490755	26.69253	35.34449	-0.3119	0.59848	0.7139	UBAC2-AS1	chr13	-	99848696	99852964	1706
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC012365.	chr2	+	1.18E+08	1.18E+08	488
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	ST6GALNA(	chr2	-	84267009	84267844	836
ENSG00000(	11.39371	10.83859	7.916483	14.23244	8.283888	12.32947	-0.19485	0.77184	0.85002	RASA4CP	chr7	-	44066550	44081491	3193
ENSG00000(	15.53688	10.83859	6.597069	13.48336	6.443024	14.79537	-0.06371	0.92575	0.95511	RP13-216E	chrX	+	73168808	73169393	451

ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	AC008281.	chr2	-	2.21E+08	2.21E+08	613
ENSG00000(	6.214751	8.430014	7.916483	4.494453	0.920432	6.575719	0.78542	0.37904	0.50979	RP11-757C	chr11	+	71604456	71605479	1024
ENSG00000(	0	0	0	0	2.761296	4.93179	-1.9489	0.15029	0.24438	RP11-544N	chr1	+	1.61E+08	1.61E+08	1109
ENSG00000(	6.214751	6.021439	2.638828	2.247227	2.761296	4.109825	0.60652	0.53656	0.66053	AC097381.	chr4	+	7940728	7942022	1295
ENSG00000(	10.35792	2.408575	14.51355	9.737982	4.60216	4.109825	0.49488	0.54946	0.67096	AC016722.	chr2	+	47126414	47135817	1835
ENSG00000(	2.071584	6.021439	0	2.996302	0	0	0.893	0.49359	0.6225	RP11-159C	chr1	-	53237866	53238320	455
ENSG00000(	4.143168	0	3.958241	2.247227	2.761296	0	0.495	0.68895	0.78754	RP11-88G1	chr9	+	1.33E+08	1.33E+08	648
ENSG00000(	7.250543	2.408575	3.958241	0	0	0	3.2793	0.011033	0.025407	RP11-268G	chrX	-	27193037	27417114	1879
ENSG00000(	0	7.225726	2.638828	0	2.761296	0	1.2071	0.34982	0.4796	AKT3-IT1	chr1	-	2.44E+08	2.44E+08	517
ENSG00000(	0	0	1.319414	1.498151	0	0	-0.08979	0.94423	NA	SLC25A6P5	chr9	+	1.09E+08	1.09E+08	1038
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	UGT1A12P	chr2	+	2.34E+08	2.34E+08	853
ENSG00000(	0	2.408575	0	5.243529	1.840864	4.109825	-1.5524	0.20854	0.31805	RP11-567G	chr3	+	1.87E+08	1.87E+08	246
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-452J	chr1	-	2.47E+08	2.47E+08	222
ENSG00000(	2.071584	0	1.319414	17.22874	34.05598	23.01502	-3.8653	6.56E-06	2.49E-05	AC144521.	chr3	+	18486516	18959184	1119
ENSG00000(	9.322127	7.225726	2.638828	4.494453	9.20432	1.64393	0.30219	0.7393	0.82538	OR2A9P	chr7	+	1.44E+08	1.44E+08	2913
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	HCG23	chr6	+	32358287	32361463	610
ENSG00000(	1.035792	1.204288	0	0	0	4.109825	-0.44697	0.74153	0.82736	RP1-86D1.	chr6	-	1.29E+08	1.29E+08	1828
ENSG00000(	0	0	0	2.247227	3.681728	0.821965	-1.8992	0.15988	0.2571	AC009955.	chr2	-	2.2E+08	2.2E+08	271
ENSG00000(	1.035792	3.612863	0	7.490755	0.920432	4.109825	-1.0814	0.35208	0.48182	AC006483.	chr7	+	5600374	5600686	313
ENSG00000(	0	0	1.319414	0	0	2.465895	-0.38078	0.77353	NA	SUMO2P8	chr6	-	1.09E+08	1.09E+08	286
ENSG00000(	1.035792	1.204288	1.319414	4.494453	2.761296	2.465895	-1.086	0.35618	0.48568	RP11-364L	chr4	-	1.44E+08	1.44E+08	843
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP13-228J	chrX	+	1.55E+08	1.55E+08	973
ENSG00000(	0	3.612863	3.958241	0	0.920432	1.64393	1.0081	0.43522	0.56493	RP4-677H1	chr1	-	70684272	70686706	457
ENSG00000(	48.68222	61.41867	44.86007	119.103	74.55499	90.41614	-0.86503	0.005793	0.014167	AC133528.	chr2	+	2.43E+08	2.43E+08	415
ENSG00000(	0	1.204288	0	3.745378	0	3.28786	-1.4086	0.29351	0.41779	RP11-318K	chr9	-	66693277	66721073	1452
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RPL5P32	chr15	+	28140850	28141728	879
ENSG00000(	0	2.408575	5.277655	4.494453	0	4.109825	-0.14897	0.90111	0.93859	MTND1P9	chr20	-	55932482	55933425	944
ENSG00000(	1.035792	0	0	0	0.920432	4.93179	-1.2175	0.36851	0.49877	RP1-186E2	chr10	-	10818186	10818624	439
ENSG00000(	242.3753	293.8462	259.9245	471.1685	287.1748	397.831	-0.53793	0.006918	0.016678	RP11-697E	chr15	+	90818266	90820841	2576
ENSG00000(	0	2.408575	0	4.494453	0	0	-0.46297	0.73291	0.8214	ACTBP14	chr10	+	70782534	70783622	1089
ENSG00000(	8.286335	2.408575	1.319414	0	0	0	3.0453	0.020333	0.04402	EXOSC3P1	chr21	+	33869122	33869621	500
ENSG00000(	1.035792	0	0	0	0.920432	3.28786	-0.88129	0.51584	NA	RP5-979D1	chr1	+	23466818	23467635	818
ENSG00000(	2.071584	0	0	0	1.840864	0	0.093542	0.94384	NA	RPL30P13	chr12	-	40462045	40462392	348
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-265D	chrX	+	1.35E+08	1.35E+08	405
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-224C	chr1	-	2.18E+08	2.18E+08	711
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	RP11-439L	chr6	-	1.43E+08	1.43E+08	2398
ENSG00000(	4.143168	6.021439	2.638828	0.749076	4.60216	2.465895	0.60003	0.56739	0.68658	RP11-313P	chr7	+	72476064	72555749	1333
ENSG00000(	12.4295	1.204288	1.319414	12.73428	16.56778	7.397684	-1.1136	0.1897	0.29489	AKR7A2P1	chr1	+	1.13E+08	1.13E+08	915
ENSG00000(	1.035792	0	3.958241	0.749076	0	0	1.2761	0.34694	NA	AL591893.	chr1	+	1.52E+08	1.52E+08	4109
ENSG00000(	0	0	5.277655	0	1.840864	0	0.76764	0.57145	0.69031	AC067945.	chr2	-	1.92E+08	1.92E+08	618
ENSG00000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	RP11-408A	chr9	+	14593575	14594198	624
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-91A1	chr1	+	52446145	52446486	342
ENSG00000(	4.143168	1.204288	0	0.749076	3.681728	2.465895	-0.22656	0.85324	0.90645	RP5-931E1	chrX	+	1.23E+08	1.23E+08	853
ENSG00000(	23.82321	31.31148	23.74945	7.490755	13.80648	16.4393	1.0253	0.057772	0.11014	RP1-20N2.(	chr6	+	1.44E+08	1.44E+08	2079

ENSG00000(	14.50109	9.634302	7.916483	50.18806	30.37426	57.53754	-2.0189	5.83E-05	0.000196	AC091729.	chr7	+	1200010	1204903	1401
ENSG00000(	7.250543	1.204288	1.319414	0	0	0.821965	2.1635	0.09696	0.17096	RP11-266K	chr1	-	31805914	31819646	439
ENSG00000(	0	0	1.319414	0	4.60216	4.109825	-1.6068	0.2253	0.33798	HMGN1P2	chr21	+	33078868	33079177	310
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	DUTP1	chr3	+	1.25E+08	1.25E+08	470
ENSG00000(	0	3.612863	0	0.749076	0	2.465895	0.084701	0.95002	0.96996	RP11-386I	chr1	+	93396253	93399655	3403
ENSG00000(	1.035792	0	0	2.247227	0	0.821965	-0.59967	0.65659	NA	AC074338.	chr7	-	33075824	33075994	171
ENSG00000(	4.143168	1.204288	1.319414	6.74168	6.443024	4.93179	-1.1786	0.23933	0.35436	AC020571.	chr2	+	1.97E+08	1.97E+08	1413
ENSG00000(	1.035792	0	0	0	4.60216	2.465895	-1.4386	0.28462	0.40765	RP11-106A	chr9	+	6662424	6663792	734
ENSG00000(	0	6.021439	0	0	1.840864	1.64393	0.48288	0.71578	0.8084	RP11-80I15	chr9	+	97875990	97876743	529
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-91I1:	chr1	+	92065728	92065878	151
ENSG00000(	1.035792	2.408575	0	1.498151	1.840864	0	0.034606	0.97936	0.98794	RP11-432J:	chr10	-	1.34E+08	1.34E+08	1623
ENSG00000(	0	0	1.319414	0	2.761296	0	-0.44505	0.73801	NA	OR5AW1P	chrX	-	1.3E+08	1.3E+08	1006
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	RP11-32P2	chr2	-	15537559	15537906	348
ENSG00000(	19.68005	26.49433	39.58241	8.239831	27.61296	15.61733	0.70967	0.19296	0.29879	CALM2P2	chr10	+	71923441	71923880	440
ENSG00000(	3.107376	1.204288	1.319414	0	0.920432	0	1.4539	0.27974	0.40201	RP11-264C	chr9	+	1.19E+08	1.19E+08	1756
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	ABHD17AP	chr22	-	21022124	21025272	909
ENSG00000(	2.071584	2.408575	0	0	0	0	1.5041	0.26224	NA	AC005550.	chr7	+	15728003	15735116	697
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-439K	chr9	+	85834246	85849157	444
ENSG00000(	2.071584	0	0	0	1.840864	0	0.093542	0.94384	NA	AC006355.	chr7	+	78754055	78755066	1012
ENSG00000(	2.071584	1.204288	5.277655	5.992604	0	0	0.33594	0.78623	0.85964	MED4-AS1	chr13	+	48651273	48654127	542
ENSG00000(	0	1.204288	0	2.247227	0	0.821965	-0.5853	0.66478	NA	RP11-417B	chr9	+	1.27E+08	1.27E+08	246
ENSG00000(	0	0	0	2.996302	0	1.64393	-1.3112	0.33001	NA	RP11-20J1!	chr10	-	44787706	44789157	915
ENSG00000(	13700.42	13559.08	11019.74	9248.836	7907.431	11770.54	0.40302	0.00544	0.013374	RPL41	chr12	+	56510370	56511727	699
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC068491.	chr2	+	1.12E+08	1.12E+08	617
ENSG00000(	21.75163	31.31148	30.34652	43.44638	23.0108	26.30288	-0.15911	0.72724	0.81727	CTB-63M22	chr5	+	1.66E+08	1.66E+08	295
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	RP11-396D	chr1	-	2.02E+08	2.02E+08	331
ENSG00000(	3.107376	39.74149	30.34652	3.745378	23.0108	18.08323	0.65435	0.35656	0.48612	AGBL5-IT1	chr2	+	27283906	27284683	339
ENSG00000(	35.21692	24.08575	36.94359	32.21025	32.21512	46.03004	-0.19416	0.64035	0.74818	VIM-AS1	chr10	-	17256238	17271984	1351
ENSG00000(	16.57267	28.90291	3.958241	12.73428	19.32907	13.15144	0.13118	0.83911	0.8972	AC007038.	chr2	+	2.11E+08	2.11E+08	2199
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC016710.	chr2	+	1.4E+08	1.4E+08	466
ENSG00000(	8.286335	9.634302	9.235896	14.98151	17.48821	14.79537	-0.75395	0.23425	0.34829	EIF4A1P10	chrX	-	91368245	91369460	1216
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-101P	chr13	+	21861545	21868998	678
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	CCDC26	chr8	-	1.3E+08	1.31E+08	1721
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-348F	chrX	-	51099796	51139314	451
ENSG00000(	83.89914	103.5687	159.6491	62.17327	110.4518	64.11326	0.54388	0.08647	0.15552	ANKRD10-I	chr13	-	1.12E+08	1.12E+08	380
ENSG00000(	1.035792	3.612863	1.319414	1.498151	10.12475	9.041614	-1.472	0.15318	0.24837	EPHA1-AS1	chr7	+	1.43E+08	1.43E+08	5018
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	KCNQ5-AS1	chr6	-	73844526	73853237	1101
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	AC009229.	chr2	-	38359779	38366088	351
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	TCP1P1	chr7	+	42834505	42842093	1610
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	RP11-84D1	chr1	+	25287836	25289588	820
ENSG00000(	3.107376	0	2.638828	0.749076	2.761296	0	0.47078	0.71788	0.80997	NAP1L1P2	chrY	-	2797042	2799161	1089
ENSG00000(	12.4295	7.225726	7.916483	23.97042	21.16994	18.90519	-1.1433	0.055614	0.10656	TRAC	chr14	+	23016447	23021097	974
ENSG00000(	0	0	0	2.996302	3.681728	6.575719	-2.9151	0.023384	0.049893	RP11-73M:	chr1	-	32037186	32041174	591
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RPL19P20	chrX	+	44508375	44508965	591

ENSG00000(	1.035792	0	0	0	0.920432	1.64393	-0.43567	0.74499	NA	AC108059.	chr2	-	1.29E+08	1.29E+08	725
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC008154.	chr7	-	1.34E+08	1.34E+08	327
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC069513.	chr3	-	1.95E+08	1.95E+08	1684
ENSG00000(	100.4718	118.0202	101.5949	124.3465	99.40666	166.0369	-0.2835	0.27676	0.39833	GS1-124K5	chr7	-	65992918	66007536	5249
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP11-255J	chr9	-	2900320	2900804	485
ENSG00000(	112.9013	93.93444	77.84541	104.1215	137.1444	89.59418	-0.20779	0.44806	0.57777	ADAM1A	chr12	+	1.12E+08	1.12E+08	2608
ENSG00000(	2.071584	0	1.319414	0	5.522592	1.64393	-0.68124	0.59749	0.71311	RP11-390B	chr10	-	17737708	17742231	557
ENSG00000(	6.214751	0	0	15.73059	2.761296	17.26126	-2.0554	0.038892	0.078076	RP11-168C	chr1	+	2.01E+08	2.01E+08	3496
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	AC009495.	chr2	-	1.67E+08	1.67E+08	372
ENSG00000(	6.214751	1.204288	1.319414	0.749076	0	1.64393	1.2816	0.30722	0.43297	RP11-775D	chr7	+	1.3E+08	1.3E+08	427
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-12A2	chr9	-	67789326	67789530	205
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	PTGES3P3	chr4	-	1.71E+08	1.71E+08	483
ENSG00000(	2.071584	1.204288	2.638828	0.749076	3.681728	2.465895	-0.15793	0.89342	0.93409	RP11-397C	chr10	+	11072297	11072831	433
ENSG00000(	3.107376	2.408575	1.319414	2.247227	0	1.64393	0.562	0.65083	0.75708	SERPINH1P	chr9	+	34318405	34319653	1249
ENSG00000(	100.4718	95.13873	97.63662	49.43899	120.5766	125.7606	-0.00821	0.97981	0.98818	RP11-561C	chr15	-	85747141	85778026	2525
ENSG00000(	13.46529	18.06432	6.597069	7.490755	0	2.465895	1.6822	0.054776	0.10524	LINC00242	chr6	-	1.7E+08	1.7E+08	2418
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC034193.	chr3	-	10099657	10099971	315
ENSG00000(	0	0	1.319414	3.745378	0.920432	0.821965	-1.171	0.38355	0.5142	AC096664.	chr2	-	63978831	63979764	934
ENSG00000(	4.143168	1.204288	1.319414	5.243529	4.60216	2.465895	-0.69072	0.52016	0.64606	KRT18P4	chr20	+	48573282	48574569	1288
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-38L1	chr10	-	46937463	46951699	889
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	LINC00582	chr1	-	2.32E+08	2.32E+08	597
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC022201.	chr2	+	70630066	70649810	577
ENSG00000(	0	0	0	3.745378	5.522592	4.109825	-2.9378	0.021961	0.047171	AC011891.	chr7	+	12693804	12694610	432
ENSG00000(	1.035792	2.408575	2.638828	0	0	3.28786	0.55808	0.66845	0.77154	RP11-8L18	chr10	-	34952787	34953029	243
ENSG00000(	11.39371	12.04288	15.83297	0	0.920432	5.753754	2.2306	0.013167	0.029774	TTTY10	chrY	-	22627554	22681114	1628
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	HMGN1P37	chrX	-	1.54E+08	1.54E+08	303
ENSG00000(	0	0	0	0.749076	2.761296	0	-0.97685	0.45852	NA	PPP1R12BI	chrY	-	28424070	28500565	1671
ENSG00000(	0	6.021439	3.958241	0	0.920432	0	2.0542	0.11822	0.20139	LINC00710	chr10	-	10969021	10994143	1460
ENSG00000(	0	0	0	5.992604	6.443024	1.64393	-2.9843	0.020054	0.043477	AC098973.	chr3	-	27872379	27875627	2833
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	WBP2P1	chr18	-	22596398	22597168	771
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	HNRNPA1P	chr7	+	84612863	84613825	963
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-407H	chr1	-	2.49E+08	2.49E+08	967
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	ST13P13	chr10	+	1.05E+08	1.05E+08	1092
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-227H	chr10	-	70975089	70992246	1933
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP4-726N1	chr20	+	18040137	18051652	400
ENSG00000(	1.035792	3.612863	5.277655	0	0	0	2.7452	0.038793	0.077916	AC004691.	chr7	-	30836307	30843026	547
ENSG00000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	AC072062.	chr2	+	2.16E+08	2.16E+08	452
ENSG00000(	0	0	0	0	0	6.575719	-1.5834	0.24075	0.35606	RP11-498J	chr10	-	1.21E+08	1.21E+08	229
ENSG00000(	41.43168	36.12863	44.86007	62.92235	67.19154	76.44274	-0.74393	0.024874	0.052732	RP11-104G	chr9	+	41954580	41955037	458
ENSG00000(	0	0	9.235896	0	0	0	2.298	0.090303	0.1612	REV3L-IT1	chr6	-	1.12E+08	1.12E+08	382
ENSG00000(	1.035792	0	5.277655	2.247227	0	2.465895	0.25687	0.84056	0.89793	RP11-483F	chr10	-	1.01E+08	1.01E+08	303
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	FABP5P4	chr13	-	92832968	92833138	171
ENSG00000(	7.250543	4.817151	7.916483	0	0	0	3.906	0.001547	0.004201	RP4-580N2	chr1	-	2.36E+08	2.36E+08	190
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP5-1044H	chr1	-	65745139	65772204	512

ENSG00000(	2.071584	3.612863	2.638828	0.749076	4.60216	2.465895	0.080681	0.94239	0.96523	TUBB8P1	chr9	-	21811620	21812346	727
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP11-470P	chr9	+	72087382	72109429	442
ENSG00000(	1.035792	1.204288	0	0	0	0.821965	0.53698	0.68444	NA	ORM1	chr9	+	1.17E+08	1.17E+08	996
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-14I4.	chr6	+	1E+08	1.01E+08	821
ENSG00000(	72.50543	87.913	72.56776	90.63814	94.8045	102.7456	-0.30389	0.2583	0.37699	KRT8P12	chr3	+	1.6E+08	1.6E+08	1397
ENSG00000(	1.035792	1.204288	0	2.247227	1.840864	0.821965	-0.68104	0.60508	0.71987	AC008269.	chr2	+	2.08E+08	2.08E+08	646
ENSG00000(	0	6.021439	10.55531	1.498151	0	0	2.3321	0.058891	0.11195	RP11-175B	chr13	-	51095069	51101585	731
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP5-1091N	chrX	-	70236381	70236755	375
ENSG00000(	8.286335	7.225726	7.916483	11.98521	2.761296	7.397684	0.062992	0.93721	0.96186	ACAP2-IT1	chr3	-	1.95E+08	1.95E+08	690
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC069154.	chr2	+	1.2E+08	1.2E+08	542
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-135A	chr10	+	32636325	32663416	265
ENSG00000(	1.035792	2.408575	2.638828	0	0.920432	4.109825	0.18442	0.8828	0.92678	AC006947.	chr17	+	64672490	64673522	484
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	GK-IT1	chrX	+	30689752	30690283	397
ENSG00000(	7.250543	12.04288	14.51355	5.243529	2.761296	5.753754	1.1633	0.13579	0.22509	AC046143.	chr3	+	1.94E+08	1.94E+08	972
ENSG00000(	0	0	2.638828	7.490755	10.12475	2.465895	-2.2731	0.046026	0.090367	RP1-241P1	chrX	+	1.15E+08	1.15E+08	444
ENSG00000(	1.035792	6.021439	0	0	0	0	2.0906	0.12335	0.20852	RP11-193I2	chr3	-	42092673	42093186	514
ENSG00000(	29.00217	10.83859	22.43003	35.95563	14.72691	22.19305	-0.21834	0.6874	0.78639	RP5-857K2	chr1	+	568137	568818	682
ENSG00000(	7.250543	2.408575	0	0	0.920432	0	2.0311	0.12331	0.20852	HYI-AS1	chr1	+	43919598	43922666	545
ENSG00000(	1.035792	1.204288	0	0	0	2.465895	-0.0579	0.9659	NA	LRRC3-AS1	chr21	-	45870869	45875167	784
ENSG00000(	16.57267	20.47289	15.83297	23.97042	23.93123	27.12484	-0.4871	0.32811	0.45586	AC018633.	chr7	-	32660019	32801399	1724
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	AC090587.	chr11	+	3875842	3876629	527
ENSG00000(	1.035792	0	0	0.749076	3.681728	0	-0.92481	0.49544	NA	RP13-225C	chr9	-	1.3E+08	1.3E+08	589
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC092635.	chr2	+	13677798	13749293	455
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	LINC00452	chr13	+	1.15E+08	1.15E+08	1607
ENSG00000(	6.214751	1.204288	6.597069	3.745378	0.920432	9.863579	-0.04795	0.96155	0.97779	CICP3	chr1	+	657472	660283	2455
ENSG00000(	0	0	2.638828	0	4.60216	0	-0.41561	0.7593	0.84091	AC147651.	chr7	+	601595	605256	572
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC010975.	chr2	-	79720842	79727970	669
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	OR8B9P	chr11	-	1.24E+08	1.24E+08	925
ENSG00000(	4.143168	0	14.51355	1.498151	4.60216	1.64393	1.0269	0.33416	0.46224	RP11-442N	chr1	+	28969740	28975093	688
ENSG00000(	1.035792	0	1.319414	0	2.761296	0	-0.09868	0.94199	NA	MICD	chr6	-	29938578	29940241	813
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	HLA-DRB6	chr6	-	32520490	32527799	1235
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP3-395M2	chr1	-	2424876	2425918	514
ENSG00000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	RP11-378J2	chr1	-	2.23E+08	2.23E+08	445
ENSG00000(	0	0	0	3.745378	3.681728	1.64393	-2.3426	0.077905	0.14208	RP1-290I1(	chr6	+	10434549	10457014	656
ENSG00000(	7.250543	6.021439	7.916483	8.239831	7.363456	8.219649	-0.1563	0.83895	0.89715	LINC00858	chr10	+	86039736	86054415	2685
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	OFD1P4Y	chrY	-	20615036	20634023	1179
ENSG00000(	0	0	0	4.494453	0	0	-1.1446	0.38559	NA	RP11-12M5	chr1	-	1.8E+08	1.8E+08	544
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-494C	chr22	+	50239577	50239738	162
ENSG00000(	1.035792	3.612863	3.958241	1.498151	0	2.465895	0.78601	0.51706	0.64348	AC018638.	chr7	-	1.28E+08	1.28E+08	246
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	NPM1P25	chr10	-	97949122	97949975	854
ENSG00000(	9.322127	8.430014	25.06886	14.23244	5.522592	4.109825	0.75598	0.30249	0.42761	RALGAPA1I	chr9	+	1.08E+08	1.08E+08	6232
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	AC133141.	chr3	-	25482655	25482993	339
ENSG00000(	3.107376	3.612863	3.958241	0	0	0	2.9061	0.027122	0.056934	RP11-262H	chr9	-	66493572	66494196	625
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC007349.	chr7	+	36790292	36802686	587

ENSG00000(	0	0	0	2.996302	6.443024	0.821965	-2.4792	0.061122	0.11541	AJ006998.2	chr21	-	16742841	16774624	1000
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	ANKRD26P	chr13	+	31885426	31887058	950
ENSG00000(	13.46529	18.06432	13.19414	3.745378	4.60216	12.32947	1.0318	0.14369	0.23558	RP1-92O14	chr1	+	43850784	43854826	731
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-329B	chr3	-	1.84E+08	1.84E+08	2591
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	PIP5K1P2	chr7	+	1.59E+08	1.59E+08	1120
ENSG00000(	0	0	2.638828	0	0	0.821965	0.55859	0.66971	NA	AC073850.	chr7	-	80291647	80291901	255
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-301N	chr1	+	1.48E+08	1.48E+08	536
ENSG00000(	1.035792	7.225726	0	0	0	1.64393	1.3844	0.29592	0.42033	RP11-184I2	chr1	-	44175063	44193014	469
ENSG00000(	5.17896	2.408575	2.638828	6.74168	5.522592	23.83698	-1.5937	0.065293	0.12222	RP11-490K	chr1	-	31736092	31736528	437
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	SPINK8	chr3	-	48348336	48369831	440
ENSG00000(	2.071584	2.408575	3.958241	0.749076	8.283888	0.821965	-0.16525	0.883	0.92688	RPS10P18	chr10	-	1.26E+08	1.26E+08	495
ENSG00000(	0	0	0	2.996302	1.840864	3.28786	-2.1887	0.10174	0.17796	RLIMP1	chr13	+	41192875	41195485	1680
ENSG00000(	2.071584	4.817151	3.958241	0	0	0.821965	2.3415	0.067023	0.12503	LYST-AS1	chr1	+	2.36E+08	2.36E+08	521
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	AC097635.	chr3	+	20053944	20054098	155
ENSG00000(	3.107376	2.408575	9.235896	2.996302	7.363456	8.219649	-0.30102	0.74058	0.82645	RP1-64K7.4	chr20	+	32668955	32669754	230
ENSG00000(	2.071584	1.204288	1.319414	1.498151	2.761296	2.465895	-0.38957	0.74576	0.83076	RGS17P1	chr13	-	41566915	41567467	553
ENSG00000(	2.071584	0	0	1.498151	0.920432	0	-0.08493	0.94997	NA	PATL2	chr15	-	44957930	45003514	2100
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	CTD-2554C	chr19	+	38320191	38322797	2607
ENSG00000(	10.35792	6.021439	5.277655	2.247227	2.761296	3.28786	1.2117	0.18686	0.29148	ALG13-AS1	chrX	-	1.11E+08	1.11E+08	195
ENSG00000(	3.107376	0	0	0	0.920432	0	0.70943	0.5938	NA	ATP5A1P5	chr9	+	43399987	43401315	1329
ENSG00000(	1.035792	1.204288	0	1.498151	0	1.64393	-0.25796	0.84879	NA	RP11-342D	chrX	+	45042496	45193162	736
ENSG00000(	0	0	0	2.996302	0	1.64393	-1.3112	0.33001	NA	AC004019.	chr22	+	17897744	17898875	1132
ENSG00000(	0	2.408575	0	0.749076	0	0	0.55104	0.6711	NA	AC005189.	chr7	+	43806889	43807198	310
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	AC105053.	chr2	+	86042253	86052514	1711
ENSG00000(	0	0	7.916483	0	0.920432	0	1.6015	0.23603	0.35043	RP11-52J3.	chr6	-	1.58E+08	1.58E+08	743
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC092155.	chr2	-	62759718	62760194	477
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP4-682E1	chr1	+	86495537	86496272	736
ENSG00000(	0	4.817151	0	0	3.681728	0.821965	0.066928	0.95989	0.97656	RP11-421E	chr1	-	2.07E+08	2.07E+08	112
ENSG00000(	5.17896	7.225726	5.277655	1.498151	2.761296	10.68554	0.20997	0.82103	0.88423	AC068580.	chr11	-	1784239	1784979	252
ENSG00000(	2.071584	0	3.958241	0	2.761296	0	0.68253	0.60836	0.72249	UBE2V1P3	chrY	-	3734347	3734763	417
ENSG00000(	15.53688	4.817151	2.638828	9.737982	11.96562	6.575719	-0.2447	0.75784	0.83978	RP11-58A1	chr1	+	6607965	6608679	401
ENSG00000(	2.071584	2.408575	0	0	0.920432	0.821965	0.78234	0.561	0.68128	MYCBP2-AS	chr13	-	77654646	77655325	428
ENSG00000(	3.107376	0	1.319414	2.247227	0	3.28786	-0.20483	0.87375	0.92068	RP11-7G23	chr9	+	45729709	45730417	194
ENSG00000(	6.214751	6.021439	3.958241	0	0.920432	0	2.9058	0.016428	0.036361	AC053503.	chr2	+	2.2E+08	2.2E+08	1598
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP1-102G2	chr1	-	1.75E+08	1.75E+08	670
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC003986.	chr7	+	19183916	19185876	1526
ENSG00000(	1.035792	1.204288	5.277655	0	0	0	2.3025	0.088097	0.15791	AC015691.	chr11	-	5592477	5593422	946
ENSG00000(	1.035792	1.204288	0	0.749076	1.840864	0	-0.0892	0.94757	NA	AC079776.	chr2	-	1.31E+08	1.31E+08	563
ENSG00000(	5.17896	2.408575	3.958241	1.498151	4.60216	8.219649	-0.25212	0.79772	0.86824	RP11-119B	chr20	-	3868886	3869515	441
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	SSU72P7	chr11	-	4359893	4360475	583
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP11-90J7.	chr10	+	80053599	80060760	520
ENSG00000(	0	0	0	2.247227	1.840864	5.753754	-2.453	0.063695	0.11961	NKX1-2	chr10	-	1.26E+08	1.26E+08	1580
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	RP11-366C	chr13	-	43416550	43417023	227
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-363G	chr13	+	23425912	23428277	2042

ENSG00000(	0	0	0	9.737982	3.681728	21.37109	-4.3256	0.000237	0.000732	LINC00379	chr13	-	91779867	91783661	464
ENSG00000(	0	8.430014	6.597069	0	0.920432	3.28786	1.3575	0.2506	0.36802	SACS-AS1	chr13	+	23993110	24002818	2044
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC105761.	chr2	-	82495551	82497051	1501
ENSG00000(	8.286335	0	3.958241	0	1.840864	1.64393	1.3298	0.27275	0.39355	RP11-245N	chrX	+	45364633	45489447	2214
ENSG00000(	1.035792	0	1.319414	7.490755	0	0	-0.98832	0.458	0.58759	RP4-717I23	chr1	-	93744518	93744686	169
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-481G	chr10	-	80760241	80763560	2018
ENSG00000(	4.143168	3.612863	11.87472	0	0	2.465895	2.2749	0.044898	0.088441	RPL21P44	chr4	-	54852754	54853225	472
ENSG00000(	0	7.225726	5.277655	2.996302	3.681728	7.397684	-0.15827	0.87685	0.9229	RP11-197P	chr9	-	77624744	77630952	670
ENSG00000(	4.143168	2.408575	6.597069	8.988907	3.681728	13.15144	-0.87398	0.31277	0.43921	ACVR2B-AS	chr3	-	38492518	38496311	2517
ENSG00000(	0	0	0	1.498151	2.761296	0	-1.199	0.3707	NA	MSX2P1	chr17	+	56234389	56235161	773
ENSG00000(	1.035792	8.430014	9.235896	3.745378	7.363456	4.109825	0.24817	0.78638	0.85976	RP5-981O7	chr7	-	1.52E+08	1.52E+08	673
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	SUCLA2P3	chr2	-	25302770	25304558	1357
ENSG00000(	3.107376	13.24716	2.638828	0	2.761296	1.64393	1.7009	0.11746	0.20038	PRDX3P1	chr22	-	39118748	39119510	763
ENSG00000(	0	0	5.277655	0	0.920432	1.64393	0.57528	0.66878	0.77175	AL590762.	chrX	-	70633684	70633936	253
ENSG00000(	0	2.408575	0	0.749076	0	2.465895	-0.218	0.87233	NA	RP11-492N	chr10	-	29187925	29188422	492
ENSG00000(	3.107376	0	1.319414	0.749076	0	0.821965	0.81847	0.54398	0.66628	GOLGA2P4	chr22	+	43180468	43183106	777
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	RP11-390F	chr9	+	6704471	6707780	422
ENSG00000(	0	0	1.319414	0	2.761296	0	-0.44505	0.73801	NA	AC011288.	chr7	+	13141016	13743774	575
ENSG00000(	2.071584	3.612863	1.319414	0.749076	0	0	1.786	0.17995	0.28279	MTND5P2	chr13	+	96344792	96346226	1142
ENSG00000(	1.035792	6.021439	1.319414	0	2.761296	0	1.0745	0.40299	0.53403	METTL21AP	chr21	-	40607312	40607946	635
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-44N1	chr8	+	99973656	99980512	464
ENSG00000(	0	3.612863	3.958241	0	0	0	2.2049	0.10381	0.18087	AC073115.	chr7	+	46030504	46040497	532
ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	RP11-302K	chr10	+	1.04E+08	1.04E+08	95
ENSG00000(	1.035792	0	1.319414	2.247227	3.681728	0	-0.80527	0.54219	0.66484	RP4-713B5	chr1	-	93850044	93850555	512
ENSG00000(	75.61281	72.25726	63.33186	8.239831	4.60216	9.041614	3.1662	1.53E-12	1.04E-11	HOXB-AS5	chr17	+	46800530	46802819	1276
ENSG00000(	44.53905	46.96722	18.47179	35.20655	27.61296	25.48091	0.3132	0.4855	0.61462	RPL4P4	chr3	-	1.85E+08	1.85E+08	1284
ENSG00000(	9.322127	6.021439	7.916483	3.745378	8.283888	3.28786	0.55204	0.50923	0.63656	NAMPTL	chr10	-	36810649	36813162	2514
ENSG00000(	361.4914	345.6306	249.3692	53.18436	24.85166	27.94681	3.129	8.10E-30	1.23E-28	LINC00341	chr14	-	95873606	95876427	2822
ENSG00000(	1.035792	0	7.916483	0	0	0	2.4101	0.074732	0.13721	AC007879.	chr2	+	2.08E+08	2.08E+08	974
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC016753.	chr2	-	85718053	85718903	851
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RP1-60O19	chr6	+	1.07E+08	1.07E+08	419
ENSG00000(	15.53688	22.88147	27.70769	5.243529	4.60216	2.465895	2.2563	0.000795	0.002267	RP11-462L	chr10	+	33247773	33371030	1048
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	RP11-494K	chr1	+	2.05E+08	2.05E+08	562
ENSG00000(	14.50109	6.021439	9.235896	7.490755	2.761296	0.821965	1.248	0.15473	0.25026	RP11-345K	chr10	-	75182017	75182454	438
ENSG00000(	1.035792	0	1.319414	1.498151	4.60216	4.109825	-1.4787	0.22873	0.34215	MAST4-AS1	chr5	-	66297211	66299781	777
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	UBE2V1P9	chrX	-	89544535	89544902	368
ENSG00000(	0	0	0	0	3.681728	1.64393	-1.4596	0.2805	NA	PKP4P1	chr2	+	2.1E+08	2.1E+08	2158
ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	RP11-184A	chr10	+	3793259	3805418	759
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	AL121578.	chrX	+	37853597	37854043	447
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	RP11-383F	chr7	-	1.39E+08	1.39E+08	551
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC114755.	chr2	-	1.07E+08	1.07E+08	361
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	ASNSP5	chr1	+	1.43E+08	1.43E+08	153
ENSG00000(	2.071584	8.430014	3.958241	4.494453	0.920432	0	1.0819	0.33476	0.46277	AC004741.	chr7	+	16250113	16310229	2252
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	FLJ14082	chr2	+	96194603	96198143	3541

ENSG00000(	0	0	0	0.749076	0.920432	5.753754	-1.9975	0.13896	0.22941	RP11-21N7	chr1	-	1.55E+08	1.55E+08	301
ENSG00000(	21.75163	24.08575	25.06886	32.95932	28.53339	24.65895	-0.27656	0.54269	0.66525	SOS1-IT1	chr2	-	39219420	39220998	1191
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-305L	chr9	+	93881344	93945044	561
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	AC011242.	chr2	-	43907604	43908761	1158
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	KARSP1	chr13	+	42499734	42501485	1752
ENSG00000(	0	0	0	0.749076	0	4.93179	-1.5344	0.25706	NA	RP1-130G2	chr6	-	20042686	20043171	486
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP1-274L7	chrX	-	1.3E+08	1.3E+08	1646
ENSG00000(	2.071584	3.612863	0	0	0	0	1.8175	0.17961	NA	EEF1DP3	chr13	+	32420978	32527609	3283
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-556N	chr4	+	76751904	76753858	1955
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AP001187.	chr11	-	64658898	64660921	1781
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP3-495K2	chr6	-	1.69E+08	1.69E+08	934
ENSG00000(	0	0	0	0	0	4.93179	-1.2404	0.35057	NA	AL845154.	chr13	-	1.15E+08	1.15E+08	514
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC007322.	chrY	+	24017478	24019697	605
ENSG00000(	3.107376	0	2.638828	0	0	0	1.8293	0.17689	NA	AC013460.	chr2	+	7561392	7590385	2253
ENSG00000(	13.46529	3.612863	6.597069	18.72689	8.283888	12.32947	-0.66571	0.3591	0.48869	RP11-314N	chr20	+	1342266	1343229	480
ENSG00000(	49.71801	81.89156	114.789	16.47966	61.66894	38.63235	1.0535	0.013569	0.030627	RP11-159G	chr3	+	88108424	88188123	1377
ENSG00000(	5.17896	2.408575	1.319414	2.996302	1.840864	0	0.65586	0.58318	0.70073	RP11-295K	chr1	+	1.86E+08	1.86E+08	314
ENSG00000(	2.071584	1.204288	3.958241	5.243529	2.761296	0	-0.1223	0.91731	0.94981	RP11-365C	chr1	+	2.24E+08	2.24E+08	474
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	AC018730.	chr2	-	1.05E+08	1.05E+08	3103
ENSG00000(	6.214751	2.408575	1.319414	0	2.761296	1.64393	0.89883	0.45048	0.58016	AC096649.	chr2	+	1.76E+08	1.76E+08	497
ENSG00000(	1.035792	0	3.958241	0	0.920432	3.28786	0.1455	0.91153	0.94567	RP11-142N	chr10	+	14033815	14049525	570
ENSG00000(	0	0	0	1.498151	0.920432	4.109825	-1.8535	0.1707	0.27109	RPL31P20	chr3	+	24472239	24472598	360
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP4-738P1	chr1	-	1.69E+08	1.69E+08	787
ENSG00000(	0	0	0	5.243529	1.840864	0	-1.8401	0.17492	0.27673	DYNLT3P2	chr2	+	1.29E+08	1.29E+08	295
ENSG00000(	0	1.204288	1.319414	0.749076	0	0	0.61214	0.64459	NA	MRPS18AP	chr3	-	48297840	48298428	589
ENSG00000(	1.035792	0	1.319414	0.749076	0	0.821965	0.26466	0.84506	NA	RP5-971N1	chr20	+	8000549	8008603	1929
ENSG00000(	1.035792	6.021439	1.319414	0	0	0	2.4683	0.066378	0.12397	RP4-644L1	chr20	-	39326535	39327256	273
ENSG00000(	1.035792	16.86003	3.958241	0	0	0	3.9017	0.001888	0.005053	AC018866.	chr2	-	1.21E+08	1.21E+08	470
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC016751.	chr2	-	1.77E+08	1.77E+08	306
ENSG00000(	5.17896	3.612863	6.597069	0	0	4.109825	1.4457	0.20907	0.31868	UBE2Q1-AS	chr1	+	1.55E+08	1.55E+08	432
ENSG00000(	0	0	0	2.247227	0	1.64393	-1.1086	0.40518	NA	AC118754.	chr17	-	4400689	4402969	370
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	SNRPFP2	chr1	+	26213851	26214101	251
ENSG00000(	24.85901	19.2686	23.74945	21.72319	34.05598	4.109825	0.17678	0.77054	0.84912	RP11-391N	chr9	+	68726629	68745997	425
ENSG00000(	0	3.612863	0	0	0	0.821965	0.85103	0.52479	NA	RP11-522L	chrX	+	1.02E+08	1.02E+08	1084
ENSG00000(	0	0	2.638828	0	0	1.64393	0.26729	0.84149	NA	RP11-293G	chr1	+	2.36E+08	2.36E+08	247
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	AC006030.	chr2	-	74533855	74535135	1281
ENSG00000(	3.107376	1.204288	1.319414	0	0	0.821965	1.4908	0.26826	0.38858	ATP8A2P2	chr13	+	33051411	33052978	1568
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RPS15P5	chr3	+	54660242	54660673	432
ENSG00000(	0	0	6.597069	0	0	2.465895	0.76628	0.56986	0.68881	XIST	chrX	-	73040486	73072588	19275
ENSG00000(	2.071584	3.612863	0	2.996302	10.12475	0.821965	-0.97705	0.38925	0.51982	RP11-456P	chr1	+	1.62E+08	1.62E+08	1364
ENSG00000(	160.5477	172.2131	127.9831	94.38352	94.8045	110.9653	0.61544	0.00939	0.021973	ZNF688	chr16	-	30580667	30584055	2506
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CCNB1IP1P	chr1	+	45424229	45425067	839
ENSG00000(	16.57267	6.021439	5.277655	4.494453	3.681728	5.753754	0.90803	0.27384	0.39495	DDX50P1	chr2	+	32426669	32429068	2400
ENSG00000(	0	0	2.638828	0	2.761296	1.64393	-0.42198	0.75446	0.83765	RP11-510H	chr6	-	1.25E+08	1.25E+08	484

ENSG00000(	4.143168	3.612863	1.319414	1.498151	1.840864	1.64393	0.67684	0.55434	0.67513	RP1-308E4	chr1	+	28780052	28780445	394
ENSG00000(	0	0	0	0.749076	0.920432	2.465895	-1.2662	0.34855	NA	RP5-1174J:	chrX	+	41607475	41607861	387
ENSG00000(	0	0	2.638828	1.498151	0	0	0.308	0.81734	NA	RP11-384C	chr1	+	2.13E+08	2.13E+08	496
ENSG00000(	9.322127	22.88147	15.83297	14.23244	8.283888	23.01502	0.062711	0.91912	0.95089	PET100	chr19	+	7694623	7696842	1815
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-48L1	chr9	+	29636484	29636851	368
ENSG00000(	5.17896	8.430014	11.87472	3.745378	7.363456	7.397684	0.41317	0.60408	0.71912	AC018462.	chr2	-	62296582	62374016	1684
ENSG00000(	10.35792	16.86003	11.87472	3.745378	3.681728	2.465895	1.7983	0.021327	0.045956	RP11-361K	chr1	+	2.18E+08	2.18E+08	1963
ENSG00000(	0	0	0	5.243529	18.40864	8.219649	-4.2179	0.000343	0.001034	EMX2OS	chr10	-	1.19E+08	1.19E+08	1924
ENSG00000(	14.50109	28.90291	27.70769	10.48706	14.72691	18.08323	0.68107	0.21322	0.32351	RP13-766D	chr17	+	79481073	79494802	783
ENSG00000(	59.04014	27.69862	34.30476	42.69731	45.10117	34.52253	-0.00541	0.98932	0.99376	RP11-398K	chr6	+	73972938	74011124	3362
ENSG00000(	4.143168	2.408575	3.958241	0.749076	0	0	2.3363	0.068751	0.12777	RP5-1049G	chr20	-	46259010	46260182	860
ENSG00000(	1.035792	6.021439	0	0	0	0	2.0906	0.12335	0.20852	RP11-524G	chr9	-	1.24E+08	1.24E+08	662
ENSG00000(	1.035792	1.204288	5.277655	0	0	0	2.3025	0.088097	0.15791	CTC-546K2	chr5	+	1.21E+08	1.21E+08	821
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	AC016831.	chr7	-	1.31E+08	1.31E+08	352
ENSG00000(	0	1.204288	1.319414	2.247227	0	0	0.055815	0.96714	NA	RP11-505P	chr6	+	74233341	74280319	586
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	RP11-157F	chr3	+	57168170	57168751	582
ENSG00000(	24.85901	1.204288	6.597069	2.996302	20.2495	9.041614	0.039351	0.9627	0.9784	STEAP3-AS1	chr2	-	1.2E+08	1.2E+08	3218
ENSG00000(	0	0	0	5.243529	1.840864	2.465895	-2.417	0.068122	0.12676	RP11-363N	chr10	+	978966	988683	407
ENSG00000(	0	1.204288	1.319414	0	0.920432	0.821965	0.25429	0.85125	NA	RP11-507K	chr10	+	51023142	51023608	467
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP4-710M:	chr1	-	56673239	56674128	890
ENSG00000(	5.17896	8.430014	6.597069	0	3.681728	7.397684	0.73863	0.45094	0.58059	OGFR-AS1	chr20	-	61431979	61436939	668
ENSG00000(	42.46747	55.39724	55.41538	14.98151	61.66894	45.20807	0.32705	0.46142	0.59073	RP11-312C	chr1	-	2.06E+08	2.06E+08	758
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-130C	chr9	+	659986	660326	341
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-479G	chr10	-	33324397	33324592	196
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	HNRNPA1P	chr1	-	58513847	58514963	963
ENSG00000(	15.53688	33.72006	14.51355	6.74168	13.80648	18.08323	0.68974	0.25234	0.37009	Z83851.1	chr22	-	42760406	42765242	1142
ENSG00000(	0	3.612863	0	0	2.761296	0.821965	0.014495	0.99143	0.9949	AC004549.	chr7	-	27773014	27780014	859
ENSG00000(	0	3.612863	2.638828	0	0.920432	0.821965	1.1047	0.40473	0.53556	GK3P	chr4	-	1.66E+08	1.66E+08	2232
ENSG00000(	0	0	0	1.498151	2.761296	0	-1.199	0.3707	NA	RP11-399E	chr1	-	41840676	41841341	394
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	RP11-206L	chr1	+	696291	697369	456
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC128709.	chr3	-	1.97E+08	1.97E+08	600
ENSG00000(	4.143168	9.634302	5.277655	2.247227	0.920432	0	2.0362	0.060312	0.11416	AC016999.	chr2	-	2.39E+08	2.39E+08	452
ENSG00000(	3.107376	6.021439	1.319414	0	0	0	2.8409	0.031771	0.065344	AC007014.	chr16	+	11120881	11121620	740
ENSG00000(	2.071584	0	2.638828	0.749076	0	1.64393	0.56854	0.66981	0.77266	AC016734.	chr2	-	63869589	63871172	1334
ENSG00000(	0	0	0	7.490755	4.60216	3.28786	-3.1454	0.013005	0.029456	KIF25-AS1	chr6	-	1.68E+08	1.68E+08	2795
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-240N	chr6	+	1.38E+08	1.38E+08	535
ENSG00000(	0	0	0	1.498151	0.920432	4.109825	-1.8535	0.1707	0.27109	RHEBP1	chr10	+	46914088	46914795	708
ENSG00000(	1.035792	8.430014	9.235896	0	2.761296	0	2.1017	0.070074	0.12986	RP11-504P	chr1	-	2.24E+08	2.24E+08	246
ENSG00000(	27.96638	14.45145	18.47179	11.98521	18.40864	21.37109	0.23473	0.66808	0.77127	RP1-151F1	chr6	+	16761369	16762883	635
ENSG00000(	3.107376	0	3.958241	3.745378	2.761296	2.465895	-0.26998	0.81262	0.87847	YWHAZP3	chr10	+	23425852	23426590	738
ENSG00000(	3.107376	0	1.319414	1.498151	0	0.821965	0.53764	0.68804	0.78681	RP11-111F	chrX	+	1.11E+08	1.11E+08	287
ENSG00000(	9.322127	9.634302	2.638828	14.23244	8.283888	20.54912	-0.90783	0.20885	0.3184	AC004797.	chr17	-	47500970	47502298	1329
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	RP13-766D	chr17	+	79480089	79480210	122
ENSG00000(	1.035792	0	1.319414	0	0.920432	0.821965	0.21466	0.87415	NA	AC092431.	chr2	+	69824485	69826083	975

ENSG00000(	0	0	1.319414	24.71949	33.13555	23.83698	-4.887	6.15E-07	2.61E-06	RP1-290I1(	chr6	+	10409573	10416679	1575
ENSG00000(	30.03797	18.06432	46.17948	3.745378	4.60216	9.863579	2.2425	0.000234	0.000723	AC104695.	chr2	-	28607276	28617539	3001
ENSG00000(	0	1.204288	0	0.749076	0	0.821965	-0.12128	0.92635	NA	RP11-284F	chr1	-	1.57E+08	1.57E+08	758
ENSG00000(	0	0	1.319414	0	1.840864	0.821965	-0.46629	0.72905	NA	MTND2P2	chrX	+	1.02E+08	1.02E+08	945
ENSG00000(	3.107376	1.204288	3.958241	0	3.681728	0	0.81591	0.51898	0.64523	RP1-5O6.4	chr22	-	38783923	38784862	541
ENSG00000(	6.214751	3.612863	9.235896	5.243529	5.522592	10.68554	-0.15855	0.84787	0.90301	ZRANB2-AS	chr1	+	71547007	71955652	888
ENSG00000(	0	0	0	4.494453	0.920432	0.821965	-1.7795	0.18915	0.29421	AP000221.	chr21	-	26887785	26890650	1046
ENSG00000(	6.214751	2.408575	2.638828	10.48706	11.96562	8.219649	-1.2689	0.12835	0.21502	AC007128.	chr7	+	8301894	8384146	1853
ENSG00000(	3.107376	6.021439	6.597069	1.498151	0	3.28786	1.3495	0.21382	0.32412	TOB1-AS1	chr17	+	48944040	48987098	1351
ENSG00000(	0	0	0	0.749076	0.920432	2.465895	-1.2662	0.34855	NA	RP11-15I1:	chr1	+	2.12E+08	2.12E+08	510
ENSG00000(	11.39371	6.021439	15.83297	0	8.283888	6.575719	1.0371	0.23681	0.35131	RP11-31E2	chr1	-	1.99E+08	1.99E+08	2308
ENSG00000(	3.107376	0	2.638828	0	0.920432	0.821965	1.0313	0.43843	0.56806	RP11-574K	chr10	+	75601591	75606324	317
ENSG00000(	4.143168	3.612863	5.277655	1.498151	2.761296	0	1.2614	0.26341	0.38316	HMGB3P9	chr1	-	93112605	93113187	583
ENSG00000(	7.250543	4.817151	17.15238	14.23244	11.04518	11.50751	-0.32446	0.64131	0.74899	RP4-765A1	chr1	+	35816323	35817208	886
ENSG00000(	12.4295	14.45145	10.55531	0	0	1.64393	3.6572	0.000316	0.000957	AC093585.	chr2	-	2.42E+08	2.42E+08	428
ENSG00000(	1.035792	18.06432	0	0	0	0	1.4319	NA	NA	RP5-1042K	chr22	-	40768668	40784294	432
ENSG00000(	11.39371	13.24716	22.43003	0	0	0	5.2135	3.84E-06	1.49E-05	RP11-70J1:	chr9	-	4070906	4071884	635
ENSG00000(	1.035792	0	5.277655	6.74168	14.72691	9.041614	-1.9673	0.040119	0.080245	ALMS1-IT1	chr2	+	73683891	73686611	2107
ENSG00000(	0	1.204288	0	0	1.840864	6.575719	-1.584	0.23458	0.34872	SNAP47-AS	chr1	-	2.28E+08	2.28E+08	1708
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	ANKRD36B	chr2	+	89065324	89106126	5395
ENSG00000(	3.107376	1.204288	1.319414	0	0	0	1.9243	0.1561	NA	RP4-568F9	chr20	-	18303196	18339944	2490
ENSG00000(	1.035792	1.204288	0	0.749076	0	0	0.55357	0.6746	NA	RP5-857K2	chr1	-	536816	741274	750
ENSG00000(	0	2.408575	6.597069	0	0	0	2.4461	0.070095	0.12986	FNTAP2	chr13	+	22104829	22105462	634
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-10N1	chr1	+	24526730	24538183	1849
ENSG00000(	198.872	213.1589	195.2732	0	3.681728	0	7.0283	3.28E-29	4.84E-28	RP11-95P1	chr1	-	2.2E+08	2.2E+08	451
ENSG00000(	1.035792	0	0	0	0.920432	0.821965	-0.16752	0.89839	NA	RP11-382D	chr1	+	2.36E+08	2.36E+08	1388
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	POTEB	chr15	-	21040701	21071662	1706
ENSG00000(	0	0	2.638828	0	0.920432	1.64393	0.005124	0.99699	NA	AL596137.	chr10	-	52365750	52365953	195
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	LINC00364	chr13	+	67946519	67954108	611
ENSG00000(	1.035792	6.021439	6.597069	5.243529	8.283888	4.109825	-0.33393	0.71882	0.81058	AK3P3	chr7	+	23168797	23169460	664
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	BIRC6-AS1	chr2	-	32602699	32604667	697
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC017104.	chr2	-	2.32E+08	2.32E+08	321
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-76N2	chr1	-	88963992	88964359	368
ENSG00000(	197.8363	193.8903	166.2461	262.1764	209.8585	341.9374	-0.54077	0.011781	0.026936	CISD3	chr17	+	36886488	36891297	2326
ENSG00000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	RP11-172E	chr13	-	40918094	40924440	444
ENSG00000(	0	1.204288	0	0	0.920432	0.821965	-0.17164	0.89643	NA	RP11-384C	chr1	+	2.12E+08	2.12E+08	650
ENSG00000(	4.143168	3.612863	0	0	0.920432	0	1.7606	0.18718	0.29187	AC010974.	chr2	+	1.33E+08	1.33E+08	374
ENSG00000(	0	0	0	1.498151	5.522592	4.109825	-2.6308	0.044617	0.08796	HSPD1P6	chr3	-	36808608	36810290	1683
ENSG00000(	0	3.612863	5.277655	6.74168	11.04518	1.64393	-0.95302	0.35409	0.48393	CDC42-IT1	chr1	+	22385690	22390692	692
ENSG00000(	3.107376	1.204288	2.638828	8.239831	7.363456	11.50751	-1.6943	0.064491	0.12085	LRRC37A15	chr4	-	1.04E+08	1.04E+08	1355
ENSG00000(	8.286335	10.83859	9.235896	5.243529	6.443024	10.68554	0.31348	0.67351	0.77563	RPL4P6	chr22	-	40982704	40984007	1304
ENSG00000(	55.93276	50.58008	30.34652	41.19916	34.97642	32.05663	0.33662	0.38852	0.5193	RP11-195F	chr9	+	34665662	34681295	665
ENSG00000(	0	2.408575	1.319414	0.749076	0	2.465895	0.10861	0.9353	0.96103	AC016708.	chr2	+	2.16E+08	2.16E+08	318
ENSG00000(	1.035792	6.021439	5.277655	0.749076	3.681728	0	1.1223	0.33697	0.46548	MTAPP2	chr3	-	1.9E+08	1.9E+08	832

ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-165N	chr9	-	1.15E+08	1.15E+08	211
ENSG00000(	19.68005	9.634302	19.79121	5.243529	0.920432	2.465895	2.2477	0.004198	0.010563	PRRT3-AS1	chr3	+	9989088	9996471	614
ENSG00000(	7.250543	7.225726	13.19414	0	1.840864	2.465895	2.2751	0.020185	0.043733	RP4-613B2	chr3	-	42643455	42695880	722
ENSG00000(	7.250543	1.204288	1.319414	11.23613	0	0	-0.14554	0.90333	0.94026	AC108025.	chr2	-	5758459	5831250	1058
ENSG00000(	5.17896	4.817151	7.916483	18.72689	13.80648	20.54912	-1.4736	0.02958	0.061397	TMEM254-/	chr10	-	81806616	81838668	3121
ENSG00000(	3.107376	2.408575	0	1.498151	2.761296	0	0.26572	0.83671	0.89561	RP11-206L	chr1	-	736259	745541	523
ENSG00000(	0	0	0	0.749076	2.761296	5.753754	-2.3326	0.08012	0.14563	RP11-462G	chr10	+	1.33E+08	1.33E+08	472
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	TRBV5-4	chr7	-	1.42E+08	1.42E+08	544
ENSG00000(	0	0	0	1.498151	3.681728	1.64393	-1.9249	0.15383	0.24921	RP11-407B	chr3	-	1.94E+08	1.94E+08	2666
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC018712.	chr2	-	1.74E+08	1.74E+08	687
ENSG00000(	0	0	2.638828	0	0	0.821965	0.55859	0.66971	NA	RP11-431N	chrX	+	56644824	56650891	713
ENSG00000(	0	0	0	0	0.920432	4.109825	-1.3831	0.30514	NA	CTA-126B4	chr22	+	42834029	42842201	572
ENSG00000(	2.071584	15.65574	5.277655	1.498151	0.920432	0.821965	2.2754	0.030358	0.062817	RP11-275N	chr10	-	21629162	21661879	439
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	AC005086.	chr7	-	1.02E+08	1.02E+08	213
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC115283.	chr3	+	31310499	31310898	400
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-163G	chr1	+	42957410	42958164	755
ENSG00000(	1.035792	2.408575	7.916483	0.749076	0	0	2.3782	0.064443	0.12081	ECEL1P3	chr2	-	2.33E+08	2.33E+08	737
ENSG00000(	94.25706	85.50443	73.88717	113.1104	83.75931	143.0219	-0.41652	0.13729	0.22721	RP5-1180C	chr1	-	1.8E+08	1.8E+08	2667
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	EEF1A1P39	chr10	-	30590752	30591001	250
ENSG00000(	0	0	0	0	5.522592	0	-1.3606	0.30939	NA	FGF12-AS2	chr3	+	1.92E+08	1.92E+08	580
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-282I1	chr10	+	1.25E+08	1.25E+08	831
ENSG00000(	6.214751	2.408575	1.319414	0	0	0	2.7659	0.037352	0.075417	AC016738.	chr2	-	1.02E+08	1.02E+08	493
ENSG00000(	17.60846	13.24716	15.83297	2.996302	6.443024	3.28786	1.7448	0.016191	0.035887	HOXB-AS1	chr17	+	46620913	46628610	804
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP3-508I15	chr22	+	39130735	39134995	527
ENSG00000(	2.071584	3.612863	2.638828	4.494453	1.840864	0.821965	0.15691	0.88927	0.93125	AC018463.	chr2	+	11448151	11449067	917
ENSG00000(	0	2.408575	3.958241	0	0.920432	0.821965	1.1203	0.3977	0.5287	RP3-477O4	chr20	-	34064028	34078808	600
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	MTND1P28	chr2	+	1.18E+08	1.18E+08	950
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	AC004854.	chr7	+	44959268	44959928	349
ENSG00000(	2.071584	2.408575	0	0.749076	2.761296	0	0.23832	0.85688	0.90909	RP11-97N5	chrX	-	1.35E+08	1.35E+08	1134
ENSG00000(	18.64425	13.24716	18.47179	23.97042	27.61296	59.18147	-1.0945	0.031324	0.064555	SMIM12-AS	chr1	+	35316295	35317156	720
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-526K	chr10	+	51117659	51117988	330
ENSG00000(	2.071584	0	1.319414	0.749076	0	0.821965	0.56841	0.67506	NA	RP11-466F	chr1	+	1.66E+08	1.66E+08	470
ENSG00000(	2.071584	0	3.958241	1.498151	0.920432	0	0.80653	0.53966	0.66319	RP4-779E1	chr20	+	4173712	4176590	697
ENSG00000(	36.25272	26.49433	21.11062	76.40571	69.95283	85.48435	-1.43	6.44E-05	0.000215	RP5-1112D	chr6	+	1.12E+08	1.12E+08	557
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTD-2542C	chrX	+	16821356	16821476	121
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CNOT6LP1	chr15	-	56297911	56299374	1462
ENSG00000(	0	8.430014	5.277655	0	7.363456	0.821965	0.56817	0.6272	0.73826	SMYD3-IT1	chr1	-	2.46E+08	2.46E+08	361
ENSG00000(	0	0	0	0.749076	9.20432	0	-2.2485	0.095523	0.16885	C9orf147	chr9	-	1.15E+08	1.15E+08	863
ENSG00000(	7.250543	2.408575	3.958241	2.996302	2.761296	12.32947	-0.34212	0.7164	0.80893	RP11-405L	chr9	-	37490418	37490890	473
ENSG00000(	15.53688	18.06432	10.55531	9.737982	5.522592	11.50751	0.67454	0.30496	0.43028	GS1-124K5	chr7	-	65874130	65955046	1016
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	AC005518.	chr7	+	1.47E+08	1.47E+08	1116
ENSG00000(	5.17896	2.408575	7.916483	6.74168	0.920432	4.93179	0.23754	0.80632	0.87431	AC118138.	chr7	+	74765876	74789332	950
ENSG00000(	2.071584	6.021439	3.958241	0	0.920432	3.28786	1.148	0.32291	0.45025	ATP6V0CP1	chr17	-	4760052	4760669	618
ENSG00000(	241.3395	257.7176	204.5091	132.5864	117.8153	151.2415	0.80408	0.000108	0.00035	RP11-632C	chr6	+	1.18E+08	1.18E+08	474

ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	FTH1P5	chr6	-	50880425	50880969	545
ENSG0000(	5.17896	1.204288	2.638828	3.745378	1.840864	1.64393	0.25646	0.81745	0.88171	RPL4P5	chr9	-	7477045	7478320	1276
ENSG0000(	1.035792	0	0	2.247227	0	0	-0.31629	0.80869	NA	AP000688.	chr21	-	37441940	37498938	1221
ENSG0000(	3.107376	3.612863	1.319414	3.745378	1.840864	0	0.38562	0.74696	0.83172	HSPB1P2	chrX	-	49090415	49090960	546
ENSG0000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-173G	chr9	+	98054620	98057092	2473
ENSG0000(	8.286335	8.430014	14.51355	9.737982	8.283888	11.50751	0.065088	0.92489	0.95453	PHBP9	chr10	+	1.02E+08	1.02E+08	825
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP4-697K1	chr20	+	62133640	62136464	376
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-4M23	chr1	-	24275506	24275873	368
ENSG0000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-90J7.	chr10	+	80112354	80115857	381
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC010975.	chr2	-	79800890	79802719	588
ENSG0000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP11-241I2	chr10	+	32272813	32273482	342
ENSG0000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	SPATA31C1	chr9	+	90529408	90538572	3895
ENSG0000(	0	0	0	2.247227	0	1.64393	-1.1086	0.40518	NA	PHBP4	chr2	+	1.55E+08	1.55E+08	837
ENSG0000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	RP11-423C	chr1	+	1.43E+08	1.43E+08	1069
ENSG0000(	3.107376	3.612863	2.638828	0	0	0	2.6995	0.042216	0.083876	RP11-645N	chr7	+	1.03E+08	1.03E+08	1072
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	MIRLET7DH	chr9	-	96938884	96966850	1294
ENSG0000(	5.17896	2.408575	3.958241	0.749076	3.681728	4.109825	0.36881	0.72633	0.81645	XXYLT1-AS2	chr3	+	1.95E+08	1.95E+08	784
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	SSU72P8	chr7	+	1.24E+08	1.24E+08	585
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP1-40E16	chr6	-	3182978	3195990	1506
ENSG0000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	PGAM1P3	chr3	-	40364206	40364770	565
ENSG0000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	RP11-373A	chr9	-	29254073	29254424	352
ENSG0000(	3.107376	7.225726	19.79121	0.749076	8.283888	4.93179	0.97284	0.27684	0.3984	RP11-38O1	chr1	+	2.03E+08	2.03E+08	918
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC013472.	chr2	-	27173176	27232675	306
ENSG0000(	2.071584	0	0	2.996302	6.443024	1.64393	-1.598	0.19911	0.3067	RP11-334J(	chr9	-	1.34E+08	1.34E+08	473
ENSG0000(	12.4295	20.47289	15.83297	9.737982	6.443024	6.575719	1.0221	0.11713	0.19992	RP11-244J:	chr12	-	80496676	80497113	438
ENSG0000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	NAALADL2-	chr3	-	1.75E+08	1.75E+08	413
ENSG0000(	12.4295	22.88147	9.235896	8.239831	12.88605	27.12484	-0.10573	0.86819	0.91719	RP11-458F	chr7	+	66345695	66347968	351
ENSG0000(	0	1.204288	1.319414	2.247227	2.761296	2.465895	-1.0805	0.39251	0.52329	AC093162.	chr2	-	85489267	85489390	124
ENSG0000(	15.53688	10.83859	6.597069	1.498151	0	0	3.4913	0.000864	0.002447	STARD13-IT	chr13	-	33732724	33738546	452
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CICP6	chr3	-	1.98E+08	1.98E+08	2729
ENSG0000(	4.143168	1.204288	0	0	2.761296	0.821965	0.39695	0.76215	0.84288	BANF1P2	chr10	-	1.35E+08	1.35E+08	264
ENSG0000(	0	7.225726	1.319414	0.749076	0	0	1.894	0.15651	0.25256	CTD-2192J:	chr19	+	12663411	12664458	543
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC004074.	chrX	+	72442960	72443394	435
ENSG0000(	2.071584	3.612863	2.638828	1.498151	0.920432	0	1.2246	0.32593	0.4536	LL0XNC01-	chrX	+	1.03E+08	1.03E+08	919
ENSG0000(	0	0	0	0.749076	1.840864	5.753754	-2.1777	0.10453	0.18184	ELOVL2-AS:	chr6	+	11043993	11078459	903
ENSG0000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	FEZF1-AS1	chr7	+	1.22E+08	1.22E+08	2653
ENSG0000(	4.143168	4.817151	9.235896	3.745378	3.681728	1.64393	0.85136	0.37006	0.50052	AL022476.	chr22	+	43434591	43448372	2083
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP4-769N1	chrX	+	1.02E+08	1.02E+08	457
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CTD-3105H	chr19	+	12615719	12616790	428
ENSG0000(	0	0	0	0	9.20432	0	-2.0051	0.13944	0.23001	RP3-323N1	chr10	-	11210885	11213339	430
ENSG0000(	2.071584	2.408575	0	0	0	0	1.5041	0.26224	NA	LINC00159	chr21	-	33452629	33570125	438
ENSG0000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-385F	chr1	-	2.37E+08	2.37E+08	494
ENSG0000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	HMGN1P3	chrX	-	9833133	9833583	451
ENSG0000(	3.107376	2.408575	6.597069	10.48706	13.80648	13.9734	-1.5197	0.053524	0.1031	HMGN2P3	chr16	-	26043860	26044132	273

ENSG00000(	0	6.021439	0	0	0	0.821965	1.3469	0.32084	0.44795	AC004538.	chr7	+	11221359	11559802	2078
ENSG00000(	0	0	2.638828	6.74168	9.20432	2.465895	-2.156	0.061384	0.11582	RP4-635E1	chr1	+	11159732	11162157	487
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	MTND4P19	chr10	-	96533913	96534390	478
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	FANCD2P2	chr3	+	11901148	11932646	1400
ENSG00000(	21.75163	20.47289	10.55531	6.74168	14.72691	11.50751	0.65632	0.28997	0.4138	RP11-166C	chr7	+	66744765	66751606	1017
ENSG00000(	1.035792	3.612863	5.277655	5.992604	8.283888	13.15144	-1.3094	0.14141	0.23271	TPI1P2	chr7	+	1.29E+08	1.29E+08	752
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RPL4P3	chr1	-	1.72E+08	1.72E+08	1311
ENSG00000(	9.322127	3.612863	7.916483	0.749076	6.443024	4.93179	0.69429	0.45363	0.58332	DSCR9	chr21	+	38580804	38594037	1644
ENSG00000(	0	1.204288	0	0.749076	0	0	0.1572	0.90001	NA	AC005007.	chr7	-	11046026	11046503	478
ENSG00000(	97.36444	96.34302	91.03955	13.48336	25.7721	14.79537	2.368	5.94E-11	3.58E-10	GOLGA6L5	chr15	-	85051116	85060045	2337
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	MEMO1P4	chrX	+	1.23E+08	1.23E+08	386
ENSG00000(	15.53688	25.29004	19.79121	16.47966	11.04518	16.4393	0.43551	0.42971	0.55979	AC009245.	chr7	+	1.37E+08	1.37E+08	862
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-14O2	chr13	-	38055604	38058906	511
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	RP5-1139I:	chrX	+	1.18E+08	1.18E+08	2907
ENSG00000(	2.071584	3.612863	1.319414	0	0	0	2.2408	0.097211	0.17127	AC092667.	chr2	+	1.01E+08	1.01E+08	2586
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-692P	chrX	+	7975419	7986201	177
ENSG00000(	11.39371	19.2686	14.51355	0	1.840864	0	3.8964	7.33E-05	0.000243	SPTLC1P1	chr10	+	31649884	31650144	261
ENSG00000(	0	0	3.958241	0	0.920432	0	0.88424	0.51108	NA	RBBP8P1	chrX	-	1.18E+08	1.18E+08	1844
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-84O1	chr1	-	1.01E+08	1.01E+08	497
ENSG00000(	7.250543	13.24716	15.83297	10.48706	8.283888	11.50751	0.23295	0.72812	0.81787	TCEA1P2	chr3	+	37317087	37318089	940
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	OR3D1P	chr1	+	2.48E+08	2.48E+08	955
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	TCEB1P12	chrY	+	20230369	20230696	328
ENSG00000(	1.035792	4.817151	5.277655	0.749076	0	1.64393	1.5664	0.1964	0.30314	RP5-902P8	chr1	+	1210603	1215800	389
ENSG00000(	0	1.204288	5.277655	0	0	1.64393	1.1002	0.41222	0.54272	LINC00856	chr10	+	80008505	80434724	2692
ENSG00000(	0	2.408575	7.916483	0.749076	0	4.109825	0.74892	0.54323	0.6657	RP1-43E13	chr1	+	19536995	19567198	507
ENSG00000(	1.035792	0	0	4.494453	12.88605	9.041614	-3.2925	0.004046	0.010212	ERVMER61·	chr1	+	1.88E+08	1.88E+08	2393
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP11-313A	chr1	+	95527152	95533101	1096
ENSG00000(	2.071584	6.021439	0	0	3.681728	0	0.75234	0.5626	0.68243	RP1-196A1	chr16	+	501404	503461	278
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC114803.	chr2	+	2.2E+08	2.2E+08	311
ENSG00000(	1.035792	0	0	2.247227	0	3.28786	-1.1855	0.38111	0.51183	RP1-20B11	chr6	+	524171	525581	851
ENSG00000(	4.143168	6.021439	2.638828	0	1.840864	3.28786	1.0407	0.35454	0.48427	RP11-420G	chr6	-	2854891	2876744	1254
ENSG00000(	0	4.817151	0	6.74168	0.920432	0	-0.44135	0.73425	0.82224	RP11-488P	chr1	-	94218480	94241000	1671
ENSG00000(	3.107376	0	0	0.749076	0	0	0.76338	0.56438	NA	TFAMP1	chr7	+	1654226	1654961	736
ENSG00000(	2.071584	0	5.277655	0	5.522592	1.64393	0.029825	0.98068	0.98877	LRRC37A6P	chr10	-	27535279	27548384	5444
ENSG00000(	1.035792	1.204288	0	1.498151	0	0	0.24225	0.85676	NA	CTF2P	chr16	-	30915669	30921529	604
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	RPL7P4	chr6	-	30664583	30665312	730
ENSG00000(	3.107376	1.204288	0	312.3645	202.495	216.9987	-6.8151	4.13E-27	5.55E-26	ANKRD18B	chr9	+	33524392	33573007	3773
ENSG00000(	7.250543	34.92434	17.15238	3.745378	11.96562	10.68554	1.0913	0.11262	0.19335	U73166.2	chr3	+	50297735	50300790	2625
ENSG00000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	AC129778.	chr9	+	42808660	42812274	762
ENSG00000(	2.071584	0	0	5.992604	1.840864	0.821965	-1.2932	0.31505	0.44164	PA2G4P4	chr3	-	1.57E+08	1.57E+08	1182
ENSG00000(	5.17896	0	1.319414	0	2.761296	0	0.7678	0.56366	0.68319	RP11-741G	chr15	+	77570807	77571116	310
ENSG00000(	2.071584	0	0	2.247227	1.840864	0.821965	-0.69259	0.60374	0.71879	PROX1-AS1	chr1	-	2.14E+08	2.14E+08	5185
ENSG00000(	1.035792	1.204288	3.958241	0.749076	0.920432	1.64393	0.61102	0.62571	0.73703	GS1-115G2	chr1	+	1.84E+08	1.84E+08	423
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	ATP5G2P3	chr2	+	1.98E+08	1.98E+08	425

ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	OR51A10P	chr11	-	5489716	5490652	937
ENSG00000(	127.4024	83.09585	134.5802	27.7158	39.57858	40.27628	1.6625	1.78E-07	7.99E-07	PSMG3-AS1	chr7	+	1609709	1629262	5701
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP13-228J:	chrX	+	1.55E+08	1.55E+08	244
ENSG00000(	2.071584	0	3.958241	0	0	0.821965	1.4726	0.27605	0.39753	RP11-462D	chr20	-	17579900	17580452	553
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-432A	chr3	-	1.75E+08	1.75E+08	671
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	RP4-564M:	chr1	+	77533605	77544167	497
ENSG00000(	0	2.408575	2.638828	0	0	0.821965	1.2658	0.35072	NA	AC108463.	chr2	+	1.12E+08	1.12E+08	412
ENSG00000(	12.4295	15.65574	7.916483	0	0	0	4.821	3.12E-05	0.000109	RP11-360I:	chr10	+	28033715	28056723	745
ENSG00000(	12.4295	18.06432	22.43003	9.737982	0	9.041614	1.3445	0.076716	0.14022	PPP5D1	chr19	-	46984053	47104457	2777
ENSG00000(	32.10955	30.10719	34.30476	11.98521	22.09037	44.38611	0.29016	0.56093	0.68128	THAP7-AS1	chr22	+	21356175	21364631	2298
ENSG00000(	2.071584	7.225726	0	6.74168	11.04518	2.465895	-0.92604	0.35897	0.48864	RP11-1060	chr12	+	27855271	27855839	569
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP3-437I1(	chr1	-	29656132	29676626	2148
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	COL6A4P1	chr3	-	15193340	15247466	4317
ENSG00000(	0	0	0	0.749076	1.840864	0.821965	-1.0455	0.43461	NA	NOS2P3	chr17	+	20339650	20350557	3323
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	LIMD1-AS1	chr3	-	45720535	45730626	1536
ENSG00000(	0	0	0	2.996302	1.840864	11.50751	-3.1787	0.012516	0.028462	RP11-95M:	chr6	+	1.38E+08	1.38E+08	523
ENSG00000(	0	0	0	0.749076	0.920432	0.821965	-0.73223	0.57364	NA	RP11-297A	chr10	-	35386934	35415948	651
ENSG00000(	0	0	0	1.498151	7.363456	7.397684	-3.186	0.012012	0.027421	BASP1P1	chr13	-	23471480	23472144	665
ENSG00000(	1.035792	4.817151	6.597069	0	0.920432	0.821965	2.0139	0.098198	0.17272	RP11-379C	chr9	-	1.31E+08	1.31E+08	765
ENSG00000(	2.071584	8.430014	1.319414	0	0	0	3.0022	0.022439	0.048066	RP11-305L	chr9	-	93867239	93869586	815
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AOAH-IT1	chr7	-	36637440	36639726	573
ENSG00000(	3.107376	1.204288	5.277655	0.749076	0.920432	6.575719	0.16292	0.88482	0.92812	LINC00102	chrX	-	2531029	2533388	1340
ENSG00000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	LINC00453	chr13	+	1.15E+08	1.15E+08	525
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-74C1	chr1	+	2.04E+08	2.04E+08	1126
ENSG00000(	361.4914	513.0266	472.3501	253.1875	364.4911	298.3733	0.55367	0.003442	0.008806	CTB-89H12	chr5	-	1.49E+08	1.49E+08	8636
ENSG00000(	25.8948	38.53721	15.83297	2.247227	8.283888	13.9734	1.6209	0.011317	0.025993	RP11-517P	chr10	+	43916186	43917548	760
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	CEACAMP2	chr19	-	43064585	43065902	440
ENSG00000(	2.071584	14.45145	6.597069	3.745378	7.363456	3.28786	0.5993	0.49985	0.62814	CTC-228N2	chr5	+	1.27E+08	1.27E+08	1044
ENSG00000(	4.143168	3.612863	6.597069	3.745378	0.920432	3.28786	0.69074	0.49604	0.62469	FAM133DP	chr2	-	1.58E+08	1.58E+08	691
ENSG00000(	11.39371	13.24716	10.55531	3.745378	3.681728	4.93179	1.3763	0.073515	0.13529	ZNF32-AS2	chr10	+	44141390	44143467	905
ENSG00000(	0	2.408575	9.235896	4.494453	4.60216	0	0.25254	0.82765	0.88899	SF3A3P1	chr20	-	3470176	3471652	1477
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC114763.	chr2	+	1.39E+08	1.39E+08	826
ENSG00000(	0	0	0	0.749076	2.761296	0	-0.97685	0.45852	NA	RP11-69L1	chr6	-	7341087	7342289	1203
ENSG00000(	3.107376	0	2.638828	0.749076	2.761296	0	0.47078	0.71788	0.80997	RP13-228J:	chrX	+	1.55E+08	1.55E+08	426
ENSG00000(	5.17896	1.204288	3.958241	0.749076	7.363456	0	0.28857	0.80336	0.87244	RP11-390F	chr9	+	6834456	6835577	1122
ENSG00000(	0	3.612863	0	4.494453	1.840864	3.28786	-1.0036	0.4161	0.54674	GTF2IRD1P	chr7	-	66274980	66309813	2426
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	PHBP12	chr1	+	51246012	51246822	811
ENSG00000(	112.9013	128.8588	110.8308	49.43899	99.40666	70.68898	0.68143	0.020115	0.043597	FTX	chrX	-	73183790	73513409	2597
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	RPSAP8	chrX	-	99410883	99411771	889
ENSG00000(	0	1.204288	0	2.247227	0	0.821965	-0.5853	0.66478	NA	AC090804.	chr11	-	3913623	3914120	498
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP3-331H2	chr6	+	72038645	72039509	352
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	RP11-402G	chr9	-	1.17E+08	1.17E+08	550
ENSG00000(	0	0	1.319414	0	2.761296	0	-0.44505	0.73801	NA	TSEN15P2	chr1	+	52325450	52325807	358
ENSG00000(	22.78742	22.88147	17.15238	6.74168	1.840864	4.93179	2.0507	0.002429	0.006375	AC159540.	chr2	-	98081083	98095220	3563

ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AL929472.	chr1	-	38292232	38293886	45
ENSG00000(	2.071584	0	0	1.498151	0	0	0.18632	0.88758	NA	HMGB1P27	chr2	+	1.92E+08	1.92E+08	603
ENSG00000(	1.035792	0	2.638828	0	1.840864	0.821965	0.26638	0.84304	0.89989	AC004237.	chr5	+	1.32E+08	1.32E+08	502
ENSG00000(	3.107376	9.634302	2.638828	2.247227	0.920432	1.64393	1.3395	0.21004	0.31976	HM13-AS1	chr20	-	30155510	30161066	489
ENSG00000(	6.214751	1.204288	11.87472	4.494453	0	0	1.585	0.16269	0.26064	RP5-1198C	chr1	+	44509600	44570647	2644
ENSG00000(	2.071584	0	0	2.996302	0	0	-0.22919	0.86516	NA	UQCRHP1	chr6	-	31578860	31579133	274
ENSG00000(	3.107376	1.204288	2.638828	13.48336	19.32907	15.61733	-2.5007	0.002098	0.00557	RP11-469A	chr1	+	2E+08	2E+08	507
ENSG00000(	2.071584	0	0	0.749076	0	0.821965	0.18163	0.8922	NA	RP11-286H	chr7	+	1.29E+08	1.29E+08	1200
ENSG00000(	15.53688	19.2686	9.235896	19.47596	18.40864	18.90519	-0.34487	0.53962	0.66319	RPS23P8	chrX	+	70182814	70183143	330
ENSG00000(	185.4068	195.0946	234.8557	14.98151	23.0108	23.01502	3.3034	5.05E-30	7.66E-29	DNM3OS	chr1	-	1.72E+08	1.72E+08	568
ENSG00000(	0	0	11.87472	2.247227	0.920432	1.64393	0.90522	0.45954	0.58904	CTA-246H3	chr22	+	25723219	25735942	663
ENSG00000(	2.071584	0	0	5.243529	1.840864	5.753754	-1.7989	0.13986	0.23059	RP11-486B	chr1	+	42007740	42010258	2242
ENSG00000(	6.214751	0	0	0.749076	0	5.753754	-0.02267	0.98605	0.99155	USP12-AS2	chr13	+	27746396	27757135	279
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC010984.	chr2	+	1.31E+08	1.31E+08	1039
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	AC022816.	chr17	+	14277456	14324343	804
ENSG00000(	7.250543	0	1.319414	4.494453	0	0	0.60568	0.63901	0.7471	RP3-406P2	chr6	-	4019077	4021449	209
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	AC024084.	chr7	+	1.36E+08	1.36E+08	455
ENSG00000(	0	6.021439	2.638828	2.996302	0	0.821965	0.7821	0.53462	0.65901	AC112229.	chr2	-	1.11E+08	1.11E+08	3130
ENSG00000(	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	PRB4	chr12	-	11460017	11463369	913
ENSG00000(	0	0	0	10.48706	8.283888	28.76877	-4.8003	2.43E-05	8.61E-05	KLHL7-AS1	chr7	-	23140847	23145322	2564
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	YY1P1	chr10	-	72245092	72246081	668
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	TNPO1P2	chr17	+	18363705	18366369	2665
ENSG00000(	3.107376	0	3.958241	3.745378	1.840864	5.753754	-0.54207	0.62585	0.73715	FAM224B	chrY	-	19664680	19691634	2032
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CEACAM22	chr19	-	45041045	45124119	3016
ENSG00000(	3.107376	9.634302	0	1.498151	0.920432	0.821965	1.4572	0.2188	0.33029	PABPC1P3	chrX	-	73802923	73803381	459
ENSG00000(	5.17896	0	0	0	0	0	1.5469	0.24589	NA	ENO1-AS1	chr1	+	8938894	8939953	456
ENSG00000(	1.035792	4.817151	6.597069	1.498151	0	0.821965	1.7251	0.14949	0.24334	DDTP1	chr3	-	38556939	38557321	383
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RP11-409K	chr9	+	1.33E+08	1.33E+08	266
ENSG00000(	6.214751	10.83859	5.277655	0	0	0	4.0742	0.000844	0.002393	RP11-62F2	chr9	+	16625674	16626388	455
ENSG00000(	1.035792	2.408575	1.319414	0	0	0	1.6865	0.21314	NA	AC012462.	chr2	+	2.16E+08	2.16E+08	131
ENSG00000(	0	3.612863	0	0	0.920432	0	0.81649	0.54246	NA	AC011753.	chr2	-	1.1E+08	1.1E+08	610
ENSG00000(	2.071584	2.408575	3.958241	0	0	0	2.5267	0.059095	0.11225	AC097635.	chr3	-	20049344	20049739	396
ENSG00000(	36.25272	69.84869	38.263	0	5.522592	2.465895	3.9725	8.36E-10	4.61E-09	RP11-54O7	chr1	+	846815	850328	3043
ENSG00000(	3.107376	0	6.597069	4.494453	7.363456	7.397684	-0.84417	0.39115	0.52198	FBXW4P1	chr22	+	23605323	23606541	1219
ENSG00000(	5.17896	0	0	2.247227	0	0.821965	0.44703	0.73845	0.82485	RP11-681L	chr2	+	62083830	62084190	361
ENSG00000(	0	0	1.319414	3.745378	0.920432	4.109825	-1.7244	0.18529	0.28968	RP11-364B	chrX	+	1.39E+08	1.39E+08	819
ENSG00000(	4.143168	10.83859	9.235896	0	0	0	4.1876	0.000549	0.001602	AP000354.	chr22	-	24644042	24645434	664
ENSG00000(	212.3373	190.2775	138.5384	143.0734	160.1552	144.6658	0.27595	0.21672	0.32777	RP11-274B	chr7	+	1.28E+08	1.28E+08	507
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-272L	chr1	+	98240225	98240582	358
ENSG00000(	67.32647	69.84869	46.17948	74.15848	91.12277	86.30632	-0.44437	0.14091	0.23206	RP11-304N	chr11	-	127115	139117	2661
ENSG00000(	1.035792	0	1.319414	1.498151	2.761296	0	-0.48322	0.71879	0.81058	AC074011.	chr2	-	28856148	28887406	581
ENSG00000(	17.60846	12.04288	11.87472	6.74168	13.80648	14.79537	0.23068	0.71801	0.81008	AC127904.	chr3	+	1.97E+08	1.97E+08	958
ENSG00000(	377.0283	354.0606	357.5611	685.4041	647.0637	704.4239	-0.90095	1.61E-10	9.39E-10	AC092171.	chr7	+	5515435	5519442	3251
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	RP11-413E	chr1	+	90095284	90141945	437

ENSG00000(	0	8.430014	1.319414	9.737982	3.681728	2.465895	-0.58402	0.58446	0.70191	RP1-149A1	chr22	+	32772651	32780330	1558
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC106870.	chr2	+	30113237	30115220	691
ENSG00000(	0	2.408575	1.319414	0	0	0	1.2548	0.34239	NA	SC22CB-1D	chr22	+	33716851	33718799	484
ENSG00000(	2.071584	1.204288	2.638828	1.498151	1.840864	0	0.55627	0.66212	0.76643	AC021188.	chr2	-	96973001	96987469	740
ENSG00000(	1.035792	1.204288	1.319414	0	0.920432	0	0.95183	0.48289	NA	MEIS1-AS2	chr2	-	66666220	66668968	690
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP4-553F4	chr20	-	32375179	32398903	642
ENSG00000(	1.035792	0	1.319414	0	0.920432	0	0.55201	0.67753	NA	RHOQP3	chr2	-	1.31E+08	1.31E+08	621
ENSG00000(	1.035792	0	0	0.749076	0.920432	1.64393	-0.70513	0.60322	NA	SNAP23P	chr20	-	47654894	47655139	246
ENSG00000(	0	3.612863	7.916483	0.749076	6.443024	2.465895	0.19313	0.86244	0.91288	RP3-408N2	chr22	-	41184781	41185271	491
ENSG00000(	0	2.408575	0	5.243529	12.88605	6.575719	-2.6192	0.016863	0.037241	VN1R108P	chr20	+	25714900	25715729	830
ENSG00000(	2.071584	1.204288	0	0	0.920432	3.28786	-0.1956	0.88319	0.92688	RP11-318C	chr1	+	1.76E+08	1.76E+08	171
ENSG00000(	64.2191	46.96722	56.73479	23.22134	42.33987	42.74218	0.6272	0.097919	0.1723	ANKRD63	chr15	-	40573645	40574787	1143
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP1-215K1	chrX	+	84228223	84232835	1499
ENSG00000(	2.071584	0	2.638828	0	0	0.821965	1.2046	0.37464	NA	RP11-508N	chr9	-	1.1E+08	1.1E+08	2277
ENSG00000(	0	0	1.319414	0	0	1.64393	-0.1317	0.91874	NA	AC009961.	chr2	-	1.61E+08	1.61E+08	765
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	PSAT1P3	chr1	-	79520630	79521740	1111
ENSG00000(	3.107376	3.612863	0	2.996302	0	0	0.70821	0.59109	0.70756	SMARCE1P!	chr13	+	45168994	45170218	1225
ENSG00000(	4.143168	0	0	2.247227	1.840864	0	0.033901	0.97976	0.98817	HLA-K	chr6	+	29894236	29897009	1037
ENSG00000(	34.18113	44.55865	29.0271	29.21395	15.64734	27.94681	0.54484	0.22461	0.33701	YY2	chrX	+	21874105	21876845	2741
ENSG00000(	0	0	0	5.243529	3.681728	3.28786	-2.8004	0.030496	0.063065	RP4-792G4	chr1	-	63786555	63790112	941
ENSG00000(	2.071584	9.634302	11.87472	0.749076	7.363456	0.821965	1.1903	0.22982	0.34311	AC007279.	chr2	+	2.03E+08	2.03E+08	837
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-243J:	chr20	-	30396306	30396552	247
ENSG00000(	2.071584	0	1.319414	0	0	0.821965	0.88094	0.51378	NA	RP11-216N	chr9	+	42266980	42267558	579
ENSG00000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	AL132709.	chr14	-	1.02E+08	1.02E+08	588
ENSG00000(	3.107376	0	6.597069	1.498151	7.363456	4.93179	-0.4135	0.69743	0.79403	RP11-343N	chr1	-	1.21E+08	1.21E+08	2504
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	AC099535.	chr3	+	27527738	27528108	371
ENSG00000(	30.03797	21.67718	21.11062	0	0	0	5.867	6.43E-08	3.01E-07	RP4-794H1	chr1	+	59486059	59510286	530
ENSG00000(	0	4.817151	0	0	1.840864	0.821965	0.48581	0.71839	0.81024	RP11-49O1	chr9	+	97586554	97587055	424
ENSG00000(	0	2.408575	1.319414	3.745378	1.840864	1.64393	-0.68892	0.57942	0.69772	AC005532.	chr7	+	7294785	7317410	675
ENSG00000(	3.107376	2.408575	0	5.243529	2.761296	1.64393	-0.59327	0.60942	0.72335	RP11-417B	chr9	+	1.26E+08	1.27E+08	788
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTD-2186N	chr5	+	32222038	32222453	416
ENSG00000(	0	2.408575	2.638828	0	0	0	1.6365	0.22501	NA	RPEP3	chr1	+	28066465	28067140	676
ENSG00000(	3.107376	2.408575	0	4.494453	2.761296	5.753754	-0.95226	0.38868	0.5193	AC104135.	chr2	+	75167385	75169797	1266
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RPL31P2	chr20	-	32339973	32340349	377
ENSG00000(	10.35792	3.612863	23.74945	0	0	0	4.8076	4.18E-05	0.000144	AC093850.	chr2	+	2.17E+08	2.17E+08	648
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP5-968J1.	chr20	-	1784662	1798252	346
ENSG00000(	65.25489	84.30014	47.4989	90.63814	93.88406	108.4994	-0.56232	0.057463	0.10964	ZNF674-AS:	chrX	+	46404928	46407671	1906
ENSG00000(	0	0	0	2.996302	0.920432	0	-1.1048	0.40628	NA	RP11-195E	chr5	-	70370052	70389020	679
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-379C	chr9	-	1.31E+08	1.31E+08	380
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	GOT2P2	chr1	-	1.73E+08	1.73E+08	1251
ENSG00000(	4.143168	3.612863	0	5.243529	5.522592	8.219649	-1.0555	0.29014	0.41402	RP11-782C	chr1	+	1.43E+08	1.43E+08	1786
ENSG00000(	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	RP11-318K	chr9	+	66720898	66759372	507
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP4-595K1	chr1	-	76107031	76107772	742
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	RP5-936J1:	chr1	-	1.03E+08	1.03E+08	931

ENSG00000(	4.143168	0	3.958241	1.498151	0.920432	0.821965	0.92249	0.45735	0.58707	CTGLF10P	chr10	+	46174140	46195980	2418
ENSG00000(	8.286335	1.204288	6.597069	5.992604	0	0	1.067	0.3543	0.4841	FBXW11P1	chr21	-	32999440	33000913	1474
ENSG00000(	1.035792	1.204288	1.319414	2.247227	7.363456	6.575719	-1.7129	0.1201	0.20392	AC092338.	chr16	+	22393757	22418749	1290
ENSG00000(	0	0	0	14.23244	11.96562	4.109825	-4.1529	0.000447	0.001323	STMND1	chr6	+	17102489	17131603	2085
ENSG00000(	0	1.204288	0	0	0	1.64393	-0.12916	0.91993	NA	LINC00486	chr2	+	33050510	33151760	1794
ENSG00000(	11.39371	10.83859	3.958241	7.490755	7.363456	5.753754	0.32537	0.6754	0.77716	RP11-417J	chr1	+	1.43E+08	1.43E+08	738
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-486B	chr1	+	42001114	42001539	265
ENSG00000(	3.107376	1.204288	0	11.23613	5.522592	8.219649	-2.0489	0.042935	0.085146	AC005077.	chr7	-	75700787	75704281	3495
ENSG00000(	2.071584	0	7.916483	0.749076	1.840864	3.28786	0.5621	0.63279	0.7426	RP11-67K1	chr9	+	1.19E+08	1.19E+08	4996
ENSG00000(	39.36009	46.96722	31.66593	31.46117	21.16994	20.54912	0.66875	0.11944	0.20294	RP11-767N	chr1	-	46160356	46162747	598
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RPS18P12	chr17	-	14608393	14608851	459
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	MAGEA8-AS	chrX	-	1.49E+08	1.49E+08	476
ENSG00000(	1.035792	0	0	0.749076	0.920432	0	-0.14603	0.91115	NA	FAM204CP	chr13	-	76262692	76263333	642
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RPL9P8	chr15	-	83041000	83125316	673
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AC023115.	chr2	+	67314145	67485098	863
ENSG00000(	0	6.021439	0	3.745378	0.920432	0.821965	0.077288	0.95183	0.97123	RP3-525N1	chr6	-	69339854	69344919	2365
ENSG00000(	4.143168	2.408575	6.597069	0	3.681728	0	1.3798	0.24668	0.36344	PPIHP1	chr11	-	1.12E+08	1.12E+08	510
ENSG00000(	14.50109	13.24716	27.70769	3.745378	2.761296	4.93179	2.0929	0.003425	0.008766	RP3-508I15	chr22	-	39062513	39064755	410
ENSG00000(	1.035792	1.204288	1.319414	0	3.681728	0	-0.01311	0.99218	0.99518	AC004840.	chr7	+	2423756	2428232	608
ENSG00000(	0	0	0	2.247227	6.443024	1.64393	-2.5109	0.057035	0.10894	AC008063.	chr2	+	1.63E+08	1.63E+08	640
ENSG00000(	0	7.225726	0	4.494453	8.283888	12.32947	-1.4812	0.15161	0.24621	RP4-753M9	chr22	-	45396446	45399500	1633
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	LINC00309	chr2	-	64412212	64432619	3307
ENSG00000(	7.250543	3.612863	2.638828	3.745378	3.681728	0	0.70198	0.51686	0.64334	RP11-176F	chr9	-	33909607	33911120	791
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC007566.	chr7	-	92042290	92068876	1287
ENSG00000(	0	8.430014	1.319414	0	0	0.821965	2.0255	0.12653	0.21263	RP11-34A1	chr10	+	1E+08	1E+08	1168
ENSG00000(	6.214751	1.204288	9.235896	13.48336	1.840864	2.465895	-0.09791	0.91882	0.95073	RP11-395C	chr5	-	1.26E+08	1.26E+08	303
ENSG00000(	0	0	0	438.9583	492.4311	523.5917	-9.3573	6.73E-24	7.99E-23	MIR205HG	chr1	+	2.1E+08	2.1E+08	3348
ENSG00000(	4.143168	0	1.319414	1.498151	1.840864	1.64393	0.11269	0.92813	0.95681	RP11-314C	chr6	+	8784411	8785678	489
ENSG00000(	1.035792	0	1.319414	0	0.920432	0	0.55201	0.67753	NA	RP11-367G	chr6	-	1.14E+08	1.14E+08	465
ENSG00000(	0	2.408575	3.958241	1.498151	7.363456	2.465895	-0.65498	0.5662	0.68548	RP4-549L2	chr1	-	1.01E+08	1.01E+08	979
ENSG00000(	1.035792	2.408575	1.319414	0	0	0	1.6865	0.21314	NA	AP000356.	chr22	+	24994021	24995365	364
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AP001331.	chr8	-	1.09E+08	1.09E+08	1015
ENSG00000(	0	0	0	0	3.681728	14.79537	-1.4095	0.27137	0.39211	RP4-631H1	chr1	+	53386094	53386268	175
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC093166.	chr2	+	1.13E+08	1.13E+08	303
ENSG00000(	5.17896	0	0	3.745378	0	0	0.2654	0.84396	0.90054	AC005703.	chr17	-	15170778	15175607	1773
ENSG00000(	4.143168	3.612863	2.638828	3.745378	2.761296	7.397684	-0.35048	0.72107	0.81241	AC079250.	chr2	-	47917855	47918385	531
ENSG00000(	0	2.408575	5.277655	2.996302	1.840864	5.753754	-0.38982	0.72866	0.81825	AC006035.	chr7	-	16128696	16129261	561
ENSG00000(	31.07376	21.67718	56.73479	8.988907	33.13555	13.9734	0.93124	0.086002	0.15486	DSTNP1	chr21	-	48073470	48073934	465
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	DDX3YP2	chrX	-	73352839	73352949	111
ENSG00000(	0	2.408575	0	0	1.840864	0	0.16879	0.89944	NA	RP11-661D	chr14	-	1.03E+08	1.03E+08	469
ENSG00000(	2395.787	2297.781	2246.962	2422.51	2185.106	2797.147	-0.09322	0.44433	0.57397	HSBP1	chr16	+	83841448	83853342	5371
ENSG00000(	2.071584	1.204288	2.638828	2.996302	2.761296	4.93179	-0.67914	0.53754	0.66147	FAM201B	chr2	+	1.33E+08	1.33E+08	2173
ENSG00000(	0	0	0	0.749076	1.840864	2.465895	-1.5178	0.26323	NA	AC018737.	chr2	-	1.22E+08	1.22E+08	499
ENSG00000(	2.071584	3.612863	2.638828	1.498151	0	0.821965	1.2484	0.31708	0.44399	CTB-54D4.1	chr7	+	1.08E+08	1.08E+08	744

ENSG00000(	9.322127	3.612863	5.277655	10.48706	7.363456	7.397684	-0.41661	0.6027	0.71777	CDC20P1	chr9	+	89626567	89628066	1500
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CUBNP1	chr10	-	43189819	43210023	1790
ENSG00000(	3.107376	8.430014	0	0	0	0	2.8511	0.032566	0.066774	RP6-109B7	chr22	-	46451620	46454040	1181
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	LINC00326	chr6	+	1.33E+08	1.33E+08	2515
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	AC092431.	chr2	-	69927324	69940979	420
ENSG00000(	192.6573	204.7289	131.9414	311.6154	313.8673	290.1536	-0.7824	9.89E-05	0.000323	RP11-175C	chr10	+	98752207	98755716	3510
ENSG00000(	16.57267	3.612863	6.597069	2.247227	2.761296	5.753754	1.1676	0.18862	0.29361	LINC00271	chr6	+	1.36E+08	1.36E+08	1580
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RPL7L1P9	chr2	-	2.19E+08	2.19E+08	745
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-445P	chr10	+	5276321	5305371	680
ENSG00000(	0	0	0	0.749076	3.681728	0.821965	-1.5443	0.25498	NA	AC007238.	chr2	-	58687427	58689167	1741
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	RP11-428F	chr6	-	1.12E+08	1.12E+08	433
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	OR52B5P	chr11	+	5582197	5583147	951
ENSG00000(	8.286335	3.612863	5.277655	5.243529	7.363456	7.397684	-0.18403	0.82667	0.88834	RP1-140A9	chr1	+	1822910	1824097	906
ENSG00000(	1.035792	0	0	0	3.681728	0	-0.68494	0.60991	NA	RP13-26D1	chrX	-	69581336	69582224	349
ENSG00000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	AC009236.	chr2	+	45395722	45396553	553
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RP1-290I1(	chr6	-	10474733	10478735	256
ENSG00000(	1.035792	0	1.319414	2.996302	2.761296	4.109825	-1.4525	0.2367	0.35119	RP11-122N	chr1	+	2.12E+08	2.12E+08	1846
ENSG00000(	4.143168	0	0	0	4.60216	4.109825	-0.67094	0.60094	0.71625	AC006994.	chr2	+	2.11E+08	2.11E+08	839
ENSG00000(	5.17896	2.408575	0	2.247227	4.60216	1.64393	-0.09404	0.93473	0.9607	RP11-263K	chr1	+	1.55E+08	1.55E+08	912
ENSG00000(	0	2.408575	2.638828	10.48706	9.20432	13.15144	-2.3517	0.012718	0.028861	NPM1P9	chrX	-	14852598	14853441	844
ENSG00000(	2.071584	7.225726	5.277655	3.745378	0	0	1.4314	0.2217	0.33337	BX842568.	chrX	-	37003596	37004166	571
ENSG00000(	5.17896	1.204288	9.235896	0.749076	6.443024	4.109825	0.39606	0.69424	0.79159	RP11-316N	chr1	+	1.51E+08	1.51E+08	368
ENSG00000(	382.2072	451.6079	473.6695	328.8442	399.4675	305.7709	0.33676	0.047218	0.092352	HCG18	chr6	-	30255174	30294927	4862
ENSG00000(	0	0	0	1.498151	4.60216	1.64393	-2.0961	0.1186	0.2019	AC105402.	chr2	-	1.5E+08	1.5E+08	2045
ENSG00000(	7.250543	9.634302	9.235896	2.247227	17.48821	6.575719	0.0015	0.9985	0.99905	RP4-760C5	chr20	-	25989427	25991167	542
ENSG00000(	5.17896	4.817151	7.916483	11.98521	17.48821	18.90519	-1.3389	0.053491	0.10304	CTA-253N1	chr1	-	1.85E+08	1.85E+08	376
ENSG00000(	0	0	3.958241	2.247227	0.920432	5.753754	-0.84258	0.50151	0.62964	TSSK1A	chr22	+	19112392	19113159	768
ENSG00000(	0	0	0	0	2.761296	4.109825	-1.797	0.1853	0.28968	AC012513.	chr2	+	2.17E+08	2.17E+08	784
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-740C	chr1	+	1.6E+08	1.6E+08	666
ENSG00000(	0	0	3.958241	0.749076	0.920432	0	0.60606	0.65509	NA	RP11-354N	chr10	+	1.2E+08	1.2E+08	895
ENSG00000(	2.071584	0	2.638828	5.243529	5.522592	2.465895	-1.1599	0.3012	0.42632	RP5-1071N	chr1	+	21619783	21626267	2479
ENSG00000(	60.07593	52.98866	75.20659	0	6.443024	5.753754	3.8113	8.40E-12	5.38E-11	RP11-389K	chr9	-	93063184	93195787	1013
ENSG00000(	52.82539	85.50443	29.0271	143.0734	97.56579	123.2947	-1.1006	0.001135	0.003154	RP3-475N1	chr6	+	42908102	42911708	679
ENSG00000(	0	2.408575	2.638828	0	1.840864	0.821965	0.55733	0.67451	0.77646	AC078842.	chr7	+	1.37E+08	1.37E+08	1835
ENSG00000(	4.143168	18.06432	19.79121	1.498151	5.522592	1.64393	2.0376	0.016197	0.035893	RP4-569M2	chr20	+	45981305	45983377	1809
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	BTF3P10	chr6	+	1.5E+08	1.5E+08	498
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP1-34H18	chr12	+	77718421	77966055	991
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	SPATA20P1	chr21	-	39610149	39610586	438
ENSG00000(	2.071584	7.225726	6.597069	11.98521	18.40864	14.79537	-1.4038	0.055971	0.10714	AF129075.	chr21	-	30430394	30432416	794
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP5-1073C	chr1	+	1.14E+08	1.14E+08	773
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	HLA-T	chr6	+	29864431	29865563	450
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-346D	chr10	-	54210634	54230293	975
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-40C1	chr10	-	53004654	53005566	446
ENSG00000(	0	1.204288	0	0.749076	0	0	0.1572	0.90001	NA	HAR1B	chr20	-	61727150	61733631	551

ENSG00000(	6.214751	8.430014	2.638828	1.498151	3.681728	0	1.4193	0.18587	0.2904	TCF7L1-IT1	chr2	+	85413532	85414376	458
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	AC013468.	chr2	-	1.91E+08	1.91E+08	48
ENSG00000(	0	0	0	0	1.840864	3.28786	-1.4188	0.29365	NA	HMGB1P7	chr10	+	32202071	32202682	612
ENSG00000(	5.17896	0	0	0.749076	0	1.64393	0.63911	0.63479	0.74395	RP11-10J1	chr9	-	1.27E+08	1.27E+08	266
ENSG00000(	13.46529	15.65574	22.43003	9.737982	18.40864	9.863579	0.41794	0.48648	0.61559	MORF4L2-/	chrX	+	1.03E+08	1.03E+08	2086
ENSG00000(	4.143168	2.408575	1.319414	0	0	0	2.42	0.071961	0.13287	AC093702.	chr2	-	45240353	45240807	367
ENSG00000(	18.64425	48.17151	19.79121	3.745378	3.681728	7.397684	2.3903	0.000201	0.000627	RP11-617D	chr4	-	38614322	38666504	2368
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	RP5-1007G	chr1	+	34334554	34351059	1367
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RPL7P56	chrX	+	1.36E+08	1.36E+08	717
ENSG00000(	7.250543	6.021439	9.235896	1.498151	6.443024	4.93179	0.72127	0.40991	0.54065	YBX1P2	chr7	-	1.05E+08	1.05E+08	999
ENSG00000(	0	0	1.319414	2.996302	0.920432	0	-0.79043	0.56007	NA	EEF1B2P1	chr15	+	52797386	52798060	675
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC002451.	chr7	+	95225994	95243031	771
ENSG00000(	0	0	0	0	0	6.575719	-1.5834	0.24075	0.35606	RP11-389E	chr4	+	1.79E+08	1.79E+08	1034
ENSG00000(	6.214751	9.634302	14.51355	2.247227	1.840864	0.821965	2.2583	0.014314	0.032139	AC007099.	chr2	+	75767865	75769832	1101
ENSG00000(	13.46529	24.08575	15.83297	15.73059	22.09037	18.08323	-0.06365	0.90677	0.94251	LINC00852	chr3	+	10326103	10327430	1328
ENSG00000(	2.071584	2.408575	1.319414	9.737982	6.443024	11.50751	-1.931	0.038821	0.07795	RP13-15M:	chr1	+	9636485	9637043	559
ENSG00000(	19.68005	6.021439	10.55531	2.996302	11.04518	9.041614	0.61642	0.41204	0.54268	AC005592.	chr5	+	1.42E+08	1.42E+08	591
ENSG00000(	3.107376	4.817151	6.597069	14.23244	13.80648	9.863579	-1.2799	0.092302	0.16413	RP11-38L1	chr10	+	46951472	46966835	669
ENSG00000(	0	3.612863	1.319414	0	0	0	1.6005	0.2346	NA	RP11-34D1	chr10	-	1.02E+08	1.02E+08	471
ENSG00000(	0	6.021439	0	0	0	0.821965	1.3469	0.32084	0.44795	FARP1-AS1	chr13	-	99087659	99088094	323
ENSG00000(	0	0	0	4.494453	8.283888	13.15144	-3.9278	0.001055	0.002948	IFNA11P	chr9	-	21398613	21399138	526
ENSG00000(	7.250543	7.225726	9.235896	5.992604	11.04518	4.93179	0.10415	0.89358	0.93415	RP11-495P	chr1	-	1.48E+08	1.48E+08	678
ENSG00000(	1.035792	4.817151	5.277655	2.247227	7.363456	11.50751	-0.80692	0.39436	0.52522	AF127577.	chr21	+	16343791	16365175	824
ENSG00000(	0	0	0	3.745378	2.761296	7.397684	-2.9832	0.019899	0.04318	KRT8P10	chr2	-	1.84E+08	1.84E+08	1447
ENSG00000(	30.03797	43.35436	17.15238	254.6857	163.8369	154.5294	-2.617	1.02E-15	8.38E-15	ZNF826P	chr19	-	20451078	20607775	3330
ENSG00000(	5.17896	0	1.319414	0	0	0	1.9904	0.14228	0.23373	HNRNPA1P	chrX	-	73692852	73693788	937
ENSG00000(	2.071584	1.204288	0	0	2.761296	0	0.15603	0.90836	0.94364	RP4-583P1	chr20	+	62439429	62447874	533
ENSG00000(	0	2.408575	0	0	0	1.64393	0.21935	0.86915	NA	AC006159.	chr7	-	1.16E+08	1.16E+08	626
ENSG00000(	0	0	0	92.13629	115.9744	82.19649	-7.3039	3.91E-13	2.76E-12	PLSCR5	chr3	-	1.46E+08	1.46E+08	1969
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-1M1	chrX	-	6585906	6639585	517
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-85O2	chr9	+	1.27E+08	1.27E+08	460
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AP001422.	chr21	-	39695557	39705343	608
ENSG00000(	0	0	3.958241	0	0	1.64393	0.57053	0.67342	NA	CCDC147-A	chr10	-	1.06E+08	1.06E+08	795
ENSG00000(	2.071584	2.408575	3.958241	8.239831	7.363456	2.465895	-0.94056	0.33621	0.46455	SKP1P1	chr7	-	65888392	65888880	489
ENSG00000(	1.035792	0	6.597069	0.749076	0	4.109825	0.42096	0.74022	0.82613	AC018865.	chr2	+	1.31E+08	1.31E+08	1042
ENSG00000(	0	0	1.319414	0	0	4.93179	-0.89929	0.50711	0.63465	RPS3AP3	chr20	-	35650146	35650387	242
ENSG00000(	14.50109	10.83859	10.55531	0	1.840864	4.109825	2.2756	0.011599	0.026558	RP11-87H9	chr9	-	69082536	69108793	2033
ENSG00000(	0	1.204288	0	3.745378	0.920432	0	-0.95403	0.48189	NA	PSMC1P3	chr7	+	1.36E+08	1.36E+08	1318
ENSG00000(	4.143168	2.408575	3.958241	0	0	0	2.8785	0.028925	0.060214	RP5-965F6	chr1	-	1.13E+08	1.13E+08	547
ENSG00000(	2.071584	1.204288	0	3.745378	5.522592	4.109825	-1.5033	0.19017	0.29552	ITPR1-AS1	chr3	-	4532575	4534847	858
ENSG00000(	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	RP11-436K	chr1	-	61125303	61291256	2344
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AC005009.	chr7	-	86404397	86405338	269
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	C17orf105	chr17	+	41857803	41864980	3753
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	ZSWIM5P2	chr17	-	20487071	20494493	2038

ENSG00000(	49.71801	78.2787	47.4989	25.46857	52.46462	44.38611	0.51552	0.18065	0.2836	AC125232.	chr2	-	87257800	87303536	2199
ENSG00000(	0	0	0	3.745378	0.920432	1.64393	-1.8144	0.1802	0.28308	APCDD1L-A	chr20	+	57090435	57194944	2630
ENSG00000(	1.035792	0	0	0	0	1.64393	-0.12526	0.92174	NA	AC006994.	chr2	+	2.11E+08	2.11E+08	506
ENSG00000(	0	0	2.638828	0	0	2.465895	0.027772	0.98358	NA	RP1-39G22	chr1	-	40728344	40728656	313
ENSG00000(	41.43168	42.15007	34.30476	0	0.920432	1.64393	4.9812	2.76E-10	1.58E-09	LINC00704	chr10	-	4693009	4720346	846
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RPL36P2	chr20	+	49237300	49237614	315
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC107622.	chr3	+	20383960	20392420	2041
ENSG00000(	18.64425	3.612863	11.87472	11.98521	10.12475	9.863579	0.095438	0.89245	0.93347	RP11-723C	chr3	-	1.29E+08	1.29E+08	1298
ENSG00000(	4.143168	4.817151	1.319414	0	0	0	2.8253	0.032791	0.067136	RPS3P2	chr20	+	37166401	37167101	701
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	TBL1XR1-A	chr3	+	1.77E+08	1.77E+08	414
ENSG00000(	21.75163	51.78437	27.70769	64.4205	75.47542	101.1017	-1.2305	0.001196	0.00331	AC007246.	chr2	+	39663778	39892483	2517
ENSG00000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	RPL13AP17	chr7	+	77976459	77988775	1895
ENSG00000(	13.46529	8.430014	5.277655	17.97781	17.48821	16.4393	-0.86214	0.17537	0.27711	AC016700.	chr2	-	70351168	70352449	662
ENSG00000(	8.286335	0	3.958241	0	3.681728	2.465895	0.76765	0.51386	0.64083	RP1-225E1	chr6	-	1.39E+08	1.4E+08	829
ENSG00000(	1.035792	2.408575	0	0	3.681728	4.109825	-0.76929	0.54665	0.66859	RPL34P6	chr1	+	2.01E+08	2.01E+08	345
ENSG00000(	0	0	2.638828	5.243529	2.761296	1.64393	-1.3169	0.29413	0.41854	AC107072.	chr4	+	77558776	77565521	239
ENSG00000(	0	1.204288	1.319414	0.749076	0	0.821965	0.30451	0.82223	NA	AC017006.	chr2	-	46393928	46395117	364
ENSG00000(	12.4295	13.24716	18.47179	2.247227	8.283888	2.465895	1.63	0.031998	0.06577	ACTG1P10	chrX	-	53172014	53173095	1082
ENSG00000(	0	1.204288	0	0	0	2.465895	-0.37534	0.77612	NA	VDAC1P6	chrY	-	5075256	5076110	855
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	ATF4P2	chrX	+	1.54E+08	1.54E+08	1073
ENSG00000(	1.035792	6.021439	3.958241	1.498151	1.840864	3.28786	0.57312	0.60056	0.71593	RP3-426I6.	chr1	+	28065602	28065950	349
ENSG00000(	0	0	1.319414	0.749076	0.920432	0	-0.15244	0.90808	NA	RP11-564C	chr10	+	52415727	52420232	2762
ENSG00000(	6.214751	3.612863	0	17.97781	10.12475	3.28786	-1.4193	0.12525	0.21095	RP5-836N1	chr1	-	1.12E+08	1.12E+08	894
ENSG00000(	1.035792	0	1.319414	0	0	0.821965	0.54471	0.68089	NA	AC111200.	chr2	-	87157373	87157877	505
ENSG00000(	0	6.021439	0	2.247227	0.920432	2.465895	0.056759	0.96431	0.9794	AP000302.	chr21	-	34854806	34856565	666
ENSG00000(	1.035792	0	0	0.749076	0.920432	1.64393	-0.70513	0.60322	NA	AC006028.	chr7	+	2875255	2875656	402
ENSG00000(	0	0	0	2.247227	0	3.28786	-1.5293	0.25888	NA	AC072052.	chr7	-	6530424	6530729	306
ENSG00000(	1.035792	0	0	0.749076	0	2.465895	-0.63474	0.6383	NA	AL592284.	chr1	+	1.44E+08	1.45E+08	1073
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-715I4	chr3	-	13094467	13094622	156
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-148B	chr1	+	94713464	94715048	212
ENSG00000(	195.7647	215.5675	195.2732	168.542	121.497	111.7872	0.58729	0.008696	0.020499	RP11-418J1	chr1	+	1.2E+08	1.2E+08	2469
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC016995.	chr2	-	38633861	38742882	1156
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-466A	chr9	+	80071211	80141613	605
ENSG00000(	0	0	2.638828	0	0.920432	0	0.55591	0.6721	NA	NDUFAF4P4	chr1	-	1.75E+08	1.75E+08	502
ENSG00000(	0	0	1.319414	0	0.920432	4.93179	-1.1451	0.39703	0.52808	RNF2P1	chr9	-	6668999	6670008	1010
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	FGF12-AS1	chr3	+	1.92E+08	1.92E+08	580
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	AC007919.	chr3	+	1.72E+08	1.72E+08	511
ENSG00000(	2.071584	0	5.277655	99.62705	87.44104	106.8554	-5.0746	3.50E-17	3.09E-16	HLA-DPA1	chr6	-	33032346	33048552	5025
ENSG00000(	1.035792	0	5.277655	0	0	0.821965	1.5001	0.26711	0.38717	RP11-331F	chr9	+	35642511	35643514	679
ENSG00000(	2.071584	19.2686	2.638828	1.498151	1.840864	0.821965	2.0596	0.048616	0.0947	AC124914.	chr3	-	23920472	23920989	518
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-375N	chr10	+	99034769	99037854	365
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC023481.	chr3	-	8406393	8408078	938
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC099344.	chr2	-	11528149	11530493	626
ENSG00000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	CTA-992D9	chr22	+	27539439	27555840	473

ENSG00000(	9.322127	14.45145	27.70769	5.243529	8.283888	9.041614	1.1048	0.10073	0.17649	RP11-576I2	chr1	-	1.7E+08	1.71E+08	2080
ENSG00000(	0	0	0	2.247227	0	0.821965	-0.85594	0.51054	NA	RP11-83J1(	chr15	+	35235281	35235595	315
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTC-490G2	chr19	-	43833447	43835582	301
ENSG00000(	0	3.612863	2.638828	1.498151	0	1.64393	0.61715	0.63428	0.74375	AC016700.	chr2	-	70480987	70481142	156
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-422P	chr1	+	1.54E+08	1.54E+08	329
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	AC006050.	chr17	-	28900489	28904018	1351
ENSG00000(	6.214751	2.408575	0	0	0	0	2.4198	0.073366	0.13503	RP1-45C12	chr1	-	1.71E+08	1.71E+08	500
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	RP5-899B1	chr6	+	1.4E+08	1.4E+08	956
ENSG00000(	2.071584	1.204288	0	0	1.840864	6.575719	-0.88037	0.49035	0.61939	RP11-343N	chr1	+	1.21E+08	1.21E+08	529
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-144L	chr1	+	1.58E+08	1.58E+08	2167
ENSG00000(	5.17896	0	0	1.498151	10.12475	0	-0.76354	0.54308	0.66563	WASIR2	chr16	+	72910	75123	1080
ENSG00000(	1.035792	3.612863	1.319414	0	0	0	1.9913	0.14206	0.23358	RP11-467I2	chr1	-	2.41E+08	2.41E+08	675
ENSG00000(	3.107376	2.408575	5.277655	6.74168	6.443024	7.397684	-0.82316	0.36131	0.49097	RP11-472N	chr6	+	56708800	56728876	551
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	LARP1BP1	chr4	+	64215832	64217190	1359
ENSG00000(	5.17896	0	1.319414	8.988907	10.12475	4.93179	-1.5423	0.12042	0.20437	AC024937.	chr3	+	1.96E+08	1.96E+08	1242
ENSG00000(	0	0	0	12.73428	11.96562	13.9734	-4.5572	6.48E-05	0.000217	TIMM8AP1	chr2	-	1.63E+08	1.63E+08	295
ENSG00000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	AC097359.	chr3	+	37237695	37238157	463
ENSG00000(	1.035792	0	0	10.48706	8.283888	9.041614	-3.3928	0.002652	0.006918	AC018470.	chr2	+	1.75E+08	1.75E+08	3123
ENSG00000(	0	0	1.319414	6.74168	1.840864	2.465895	-2.0244	0.11169	0.19195	LINC00032	chr9	-	27245682	27282791	2913
ENSG00000(	0	0	0	2.247227	8.283888	15.61733	-3.8887	0.001343	0.003693	RP11-321L	chr9	+	23829668	23849912	1430
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC024937.	chr3	+	1.96E+08	1.96E+08	1242
ENSG00000(	14.50109	6.021439	13.19414	8.988907	6.443024	0.821965	0.94332	0.25087	0.36834	CTA-246H3	chr22	-	25745510	25746289	780
ENSG00000(	6.214751	13.24716	7.916483	6.74168	8.283888	20.54912	-0.35252	0.62644	0.73774	PRDX3P2	chr1	-	28852830	28853739	611
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	HMGN2P34	chr10	-	74396255	74396523	269
ENSG00000(	0	3.612863	1.319414	0	1.840864	1.64393	0.31197	0.81271	0.87847	LINC00441	chr13	-	48870649	48877797	1143
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	AC141930.	chr2	-	1576326	1584083	555
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP4-535B2	chr1	-	65532310	65533420	310
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RP1-251M9	chr10	+	11002114	11012779	537
ENSG00000(	42612.48	43615.69	30929.7	20870.74	18959.06	24831.56	0.85509	2.51E-09	1.33E-08	RPS18	chr6	+	33239787	33244287	1109
ENSG00000(	0	0	1.319414	0.749076	0.920432	3.28786	-1.0653	0.42959	0.55972	RP11-118B	chr12	-	9392582	9392927	346
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-134P	chr1	+	2.03E+08	2.03E+08	775
ENSG00000(	0	0	2.638828	0	0	1.64393	0.26729	0.84149	NA	RP11-452K	chr10	-	99152954	99153304	351
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-574F	chr9	+	5584490	5588994	758
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-261C	chr1	-	2.43E+08	2.43E+08	823
ENSG00000(	1.035792	1.204288	0	4.494453	0	0.821965	-0.72705	0.58575	0.70317	AC007285.	chr7	-	30109274	30114731	518
ENSG00000(	0	0	0	0	6.443024	0	-1.5465	0.25144	0.36902	RP11-244N	chr9	-	1E+08	1E+08	285
ENSG00000(	2.071584	0	0	2.996302	1.840864	2.465895	-1.1199	0.38695	0.51775	RP11-374N	chr9	+	45108392	45112532	931
ENSG00000(	0	0	1.319414	0	2.761296	0	-0.44505	0.73801	NA	FAM225A	chr9	+	1.16E+08	1.16E+08	6100
ENSG00000(	4.143168	8.430014	9.235896	8.988907	7.363456	9.863579	-0.2562	0.73718	0.8238	RP11-187A	chr13	-	42617863	42618383	363
ENSG00000(	0	0	0	2.247227	4.60216	1.64393	-2.2377	0.09376	0.16632	LINC00278	chrY	+	2870953	2970313	587
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RSL24D1P1	chr18	+	55505708	55506198	491
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	USMG5P1	chrX	+	73393725	73393901	177
ENSG00000(	0	2.408575	0	0	0	2.465895	-0.0181	0.98928	NA	PTCHD3P2	chr2	-	1.71E+08	1.71E+08	1205
ENSG00000(	2.071584	3.612863	3.958241	2.996302	5.522592	0	0.1406	0.90042	0.93808	RP11-495P	chr1	+	1.48E+08	1.48E+08	1555

ENSG00000(	0	0	0	0.749076	0.920432	4.93179	-1.8442	0.17319	0.27452	RSL24D1P3	chr7	-	64800087	64800581	495
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP3-354J5.	chr6	+	1.09E+08	1.09E+08	247
ENSG00000(	0	0	2.638828	1.498151	8.283888	0	-1.2183	0.34862	0.4783	RP11-508N	chr9	-	1.1E+08	1.1E+08	779
ENSG00000(	9.322127	10.83859	13.19414	23.22134	17.48821	18.08323	-0.78684	0.17775	0.28006	RP11-245P	chr1	+	2.29E+08	2.29E+08	283
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	EIF4A1P11	chr1	+	1.79E+08	1.79E+08	222
ENSG00000(	14.50109	0	9.235896	25.46857	37.73771	37.81039	-1.9475	0.002191	0.005797	RP5-1158E	chrX	-	45707328	45710920	1960
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-399L	chr10	-	89167801	89168015	215
ENSG00000(	4.143168	6.021439	6.597069	0	0	0.821965	2.979	0.013714	0.030933	RP11-91K9	chr3	+	1.78E+08	1.78E+08	2957
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	RP11-162K	chr10	+	95868873	95880864	446
ENSG00000(	1.035792	1.204288	1.319414	0	0	0.821965	0.9823	0.4689	NA	RP11-278J(	chr5	+	1.43E+08	1.43E+08	635
ENSG00000(	25.8948	14.45145	5.277655	20.22504	14.72691	29.59074	-0.45819	0.44722	0.57694	FAHD2CP	chr2	+	96676299	96689128	965
ENSG00000(	10.35792	13.24716	11.87472	13.48336	16.56778	17.26126	-0.39466	0.51193	0.63898	RP11-334J(	chr9	+	1.34E+08	1.34E+08	86
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC009110.	chr16	+	62630276	62632353	558
ENSG00000(	6.214751	1.204288	17.15238	15.73059	11.04518	9.041614	-0.51229	0.51025	0.63759	AC005224.	chr17	+	14113805	14121239	1537
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	RP11-445P	chr1	+	1.87E+08	1.87E+08	424
ENSG00000(	93.22127	152.9445	114.789	126.5938	158.3143	156.9953	-0.29091	0.24347	0.35945	DLEU2	chr13	-	50601269	50699856	1294
ENSG00000(	11.39371	21.67718	9.235896	16.47966	18.40864	3.28786	0.14025	0.83916	0.89721	AC009501.	chr2	-	63271057	63275775	2069
ENSG00000(	18.64425	15.65574	17.15238	26.96672	16.56778	27.94681	-0.45859	0.37536	0.50594	AP006216.	chr11	-	1.17E+08	1.17E+08	598
ENSG00000(	8.286335	8.430014	2.638828	0	0	0	3.8335	0.002077	0.005521	RP11-522N	chr1	-	2.46E+08	2.46E+08	447
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP5-943J3.	chr1	+	90254473	90256051	509
ENSG00000(	0	2.408575	1.319414	0	0	1.64393	0.57532	0.67154	NA	RP11-296C	chr1	-	1.73E+08	1.73E+08	1337
ENSG00000(	8.286335	0	3.958241	0.749076	2.761296	0	1.3164	0.27998	0.40221	RP11-575L	chr9	+	86446501	86483335	1434
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC013264.	chr2	+	1.98E+08	1.98E+08	455
ENSG00000(	2.071584	0	0	0.749076	0	0	0.47431	0.71145	NA	RP4-700A9	chr1	+	65620163	65620333	171
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	CTD-2104P	chr17	+	19519102	19537138	1150
ENSG00000(	8.286335	4.817151	5.277655	0	11.04518	2.465895	0.39491	0.69396	0.7913	RP3-355L5	chr6	+	1.06E+08	1.06E+08	1198
ENSG00000(	1.035792	4.817151	10.55531	0	0.920432	0.821965	2.3728	0.044449	0.087673	RP11-82L1	chr9	-	91624949	91625393	445
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	LINC00283	chr13	+	1.03E+08	1.03E+08	1947
ENSG00000(	3.107376	0	1.319414	0	0.920432	0	1.1063	0.4148	NA	AGBL5-AS1	chr2	-	27272551	27273132	407
ENSG00000(	9.322127	3.612863	9.235896	0.749076	1.840864	0.821965	2.2352	0.029598	0.061423	AC011738.	chr7	-	43548327	43562141	2916
ENSG00000(	6.214751	0	0	0	0	0	1.7844	0.18526	0.28968	GHc-210E9	chrX	-	1E+08	1E+08	295
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AC025627.	chr17	-	20415873	20420792	1220
ENSG00000(	2.071584	2.408575	2.638828	0	1.840864	0	1.2541	0.33659	0.46499	AC008174.	chr2	-	1.87E+08	1.87E+08	689
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-372N	chr1	+	2.1E+08	2.1E+08	727
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	SPATA31B1	chr9	-	84672562	84678597	4016
ENSG00000(	0	1.204288	1.319414	0	1.840864	0.821965	-0.04333	0.97449	NA	DLG3-AS1	chrX	-	69672808	69675844	432
ENSG00000(	6.214751	2.408575	0	0	0	0	2.4198	0.073366	0.13503	RP11-553A	chr6	-	74405258	74405854	341
ENSG00000(	0	6.021439	1.319414	2.247227	0.920432	4.93179	-0.11871	0.92018	0.95145	AC011742.	chr2	-	26363132	26364133	352
ENSG00000(	12.4295	14.45145	2.638828	11.23613	10.12475	6.575719	0.083647	0.91093	0.9453	RP5-827C2	chr1	-	2.35E+08	2.35E+08	575
ENSG00000(	4.143168	7.225726	1.319414	0.749076	0	0	2.5706	0.042195	0.083855	OGFOD1P1	chr13	-	49784558	49786430	1592
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-404C	chr1	-	1.58E+08	1.58E+08	834
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	RP11-368D	chrX	+	64808261	64820630	539
ENSG00000(	24.85901	18.06432	31.66593	0.749076	0	2.465895	4.0143	9.85E-07	4.09E-06	DIRC3	chr2	-	2.18E+08	2.19E+08	3078
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AP003774.	chr11	-	64161814	64163303	985

ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	RP11-416K	chr1	+	1.82E+08	1.82E+08	339
ENSG00000(	0	1.204288	1.319414	3.745378	2.761296	5.753754	-1.6893	0.15689	0.25296	RP1-203P1	chrX	-	1.46E+08	1.46E+08	988
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RPL21P43	chr3	-	1.69E+08	1.69E+08	472
ENSG00000(	0	0	2.638828	3.745378	3.681728	2.465895	-1.3555	0.27657	0.39811	AC068718.	chr2	-	1.89E+08	1.89E+08	881
ENSG00000(	3.107376	0	2.638828	0	0.920432	0	1.3903	0.30396	0.42915	LINC00574	chr6	+	1.7E+08	1.7E+08	2318
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-203F	chr1	+	2.04E+08	2.04E+08	446
ENSG00000(	4.143168	4.817151	5.277655	1.498151	0	4.93179	0.90658	0.40275	0.53388	NANOGP5	chr9	+	1.03E+08	1.03E+08	879
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AP002856.	chr11	+	1.31E+08	1.31E+08	584
ENSG00000(	2.071584	1.204288	0	0	1.840864	0	0.43378	0.74914	NA	AC020550.	chr2	+	1.98E+08	1.98E+08	163
ENSG00000(	2.071584	1.204288	0	2.996302	0.920432	4.93179	-0.98987	0.42062	0.55131	RP11-54O7	chr1	-	943456	943609	154
ENSG00000(	2.071584	2.408575	1.319414	0	0.920432	0	1.4927	0.26608	0.38612	RP4-669H2	chr20	-	52014199	52029448	3280
ENSG00000(	1.035792	1.204288	2.638828	2.996302	0	2.465895	-0.13427	0.91491	0.94808	AC004895.	chr7	+	6120734	6132716	547
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-432J	chr10	+	1.34E+08	1.34E+08	297
ENSG00000(	3.107376	3.612863	2.638828	0	0.920432	1.64393	1.3372	0.2752	0.39658	PABPC1P1	chr4	+	39975064	39975958	591
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP5-857K2	chr1	-	521369	523833	842
ENSG00000(	12.4295	16.86003	17.15238	0	0	0.821965	4.4972	1.68E-05	6.08E-05	RP11-398F	chr22	-	46436146	46440733	2584
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	AF064860.	chr21	+	41099682	41102607	1542
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-568A	chr6	-	1.68E+08	1.68E+08	579
ENSG00000(	27.96638	27.69862	46.17948	7.490755	3.681728	4.109825	2.58	1.13E-05	4.17E-05	AC058791.	chr7	-	1.31E+08	1.31E+08	3505
ENSG00000(	1.035792	0	0	0.749076	0.920432	0	-0.14603	0.91115	NA	RP11-573D	chr3	+	1.87E+08	1.87E+08	540
ENSG00000(	2.071584	0	0	0	2.761296	0	-0.15346	0.90925	NA	HMGN2P38	chr11	+	73291298	73291562	265
ENSG00000(	3.107376	13.24716	7.916483	5.243529	5.522592	8.219649	0.30923	0.70512	0.8	LL0XNC01-	chrX	-	1.03E+08	1.03E+08	1229
ENSG00000(	0	2.408575	1.319414	0	0.920432	0	0.92035	0.49653	NA	ARHGEF9-I1	chrX	-	62890076	62891382	394
ENSG00000(	17.60846	18.06432	17.15238	13.48336	15.64734	18.90519	0.13276	0.80898	0.87599	AC010976.	chr2	+	1.28E+08	1.28E+08	1007
ENSG00000(	6.214751	4.817151	1.319414	2.996302	2.761296	4.93179	0.18818	0.85134	0.90521	RP6-206I17	chr1	+	1.44E+08	1.44E+08	1523
ENSG00000(	5.17896	0	0	1.498151	0	2.465895	0.24898	0.85114	0.90513	TSPAN19	chr12	-	85408094	85430055	3829
ENSG00000(	0	3.612863	0	0.749076	0.920432	0	0.5439	0.68847	NA	RP11-213G	chr9	+	88549503	88551514	1468
ENSG00000(	1.035792	2.408575	2.638828	4.494453	3.681728	11.50751	-1.425	0.1588	0.25562	RP11-112L	chr20	+	48789087	48793096	573
ENSG00000(	0	1.204288	2.638828	0	2.761296	3.28786	-0.43779	0.73545	0.823	RP11-164H	chr9	-	1.27E+08	1.27E+08	607
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC079922.	chr2	-	1.13E+08	1.13E+08	359
ENSG00000(	5.17896	2.408575	5.277655	8.239831	12.88605	5.753754	-0.94141	0.26462	0.38444	EMBP1	chr1	+	1.21E+08	1.21E+08	903
ENSG00000(	11.39371	7.225726	19.79121	1.498151	3.681728	1.64393	2.2267	0.008769	0.020653	RP11-183I6	chr9	+	16473186	16476235	414
ENSG00000(	8.286335	3.612863	1.319414	4.494453	7.363456	4.93179	-0.27013	0.77252	0.85055	RP11-350J2	chr6	-	1.5E+08	1.5E+08	1117
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-354K	chr6	+	77370203	77372487	2285
ENSG00000(	0	0	0	108.616	134.3831	170.1467	-7.7513	5.59E-15	4.41E-14	DLX6-AS1	chr7	-	96594839	96643377	4978
ENSG00000(	1.035792	3.612863	3.958241	1.498151	3.681728	2.465895	0.12842	0.90783	0.94329	MIR4426	chr1	+	1.93E+08	1.93E+08	471
ENSG00000(	4.143168	0	1.319414	0	0	0	1.7539	0.19459	NA	RP5-855F1	chr1	-	2.35E+08	2.35E+08	2860
ENSG00000(	0	0	0	0	3.681728	2.465895	-1.6477	0.22446	0.33686	RP1-8B1.4	chr6	-	46064830	46097443	462
ENSG00000(	15.53688	15.65574	21.11062	46.44268	8.283888	30.4127	-0.68066	0.24006	0.35527	TMEM44-AS	chr3	+	1.94E+08	1.94E+08	1119
ENSG00000(	4.143168	15.65574	2.638828	2.996302	1.840864	6.575719	0.83685	0.37015	0.50061	RP11-147C	chrX	+	21911718	21920026	7619
ENSG00000(	8.286335	3.612863	3.958241	0	0	0.821965	2.8946	0.017793	0.039083	RP1-90L14	chr6	-	85130746	85265870	504
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	AC090960.	chr3	+	17374618	17374923	306
ENSG00000(	8.286335	2.408575	6.597069	8.239831	14.72691	10.68554	-0.86287	0.26388	0.38372	DBIL5P	chr17	+	655900	658576	2677
ENSG00000(	0	3.612863	2.638828	0	0	0	1.93	0.15472	0.25026	RP11-370B	chrX	-	1.03E+08	1.03E+08	433

ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RPL31P50	chr12	-	31750048	31750343	296
ENSG00000(	31.07376	22.88147	34.30476	29.21395	23.93123	39.45432	-0.07017	0.87343	0.92056	RP11-558F	chr1	-	9732484	9747613	939
ENSG00000(	43.50326	52.98866	43.54065	7.490755	11.04518	20.54912	1.7853	0.000178	0.00056	DOC2GP	chr11	-	67380124	67383728	1163
ENSG00000(	1.035792	0	3.958241	0	0	0	1.6134	0.2311	NA	AC009542.	chr7	+	1.35E+08	1.35E+08	1810
ENSG00000(	2.071584	0	3.958241	1.498151	0	3.28786	0.21031	0.86892	0.91759	ITCH-IT1	chr20	+	33038735	33042357	208
ENSG00000(	0	0	0	3.745378	0	4.109825	-1.998	0.13991	0.23065	RP13-93L1	chr9	+	92064473	92065669	1197
ENSG00000(	0	3.612863	0	0	0	0.821965	0.85103	0.52479	NA	AC009502.	chr2	-	2.21E+08	2.21E+08	766
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-317B	chr9	-	91099767	91100240	474
ENSG00000(	3.107376	3.612863	3.958241	9.737982	5.522592	4.109825	-0.75393	0.41244	0.54296	RP11-342C	chr9	+	97320996	97330312	1080
ENSG00000(	1.035792	0	0	0	0	3.28786	-0.59917	0.65385	NA	RP3-527G5	chr6	-	4345977	4347271	329
ENSG00000(	0	0	1.319414	0.749076	0	3.28786	-0.81202	0.54946	NA	AC005326.	chr7	+	97515180	97515386	207
ENSG00000(	0	0	0	18.72689	13.80648	9.041614	-4.6485	4.41E-05	0.000151	RP11-189B	chr13	-	47029472	47060641	1125
ENSG00000(	1.035792	3.612863	3.958241	7.490755	0.920432	3.28786	-0.38306	0.7216	0.81285	AC019097.	chr2	+	99718481	99719215	735
ENSG00000(	0	0	0	4.494453	8.283888	4.109825	-3.2851	0.008763	0.020643	AC016735.	chr2	-	43254992	43266686	2156
ENSG00000(	0	1.204288	1.319414	0	1.840864	1.64393	-0.26493	0.84426	0.90064	RP11-216N	chr1	+	1.54E+08	1.54E+08	2040
ENSG00000(	0	0	0	1.498151	7.363456	0.821965	-2.37	0.075274	0.13803	RP11-310E	chr10	-	96901682	96928182	420
ENSG00000(	1.035792	0	0	0	1.840864	3.28786	-1.0892	0.42171	0.55228	XX-FW8312	chrX	-	1.54E+08	1.54E+08	341
ENSG00000(	0	0	0	0	0.920432	4.93179	-1.5674	0.24723	NA	MTHFD1P1	chrX	-	57419079	57421842	2764
ENSG00000(	0	8.430014	0	2.996302	4.60216	0.821965	0.001227	0.99919	0.99936	RP11-206F	chr4	+	1.54E+08	1.54E+08	762
ENSG00000(	0	0	0	0	6.443024	0	-1.5465	0.25144	0.36902	RP11-527F	chr6	+	1.26E+08	1.27E+08	583
ENSG00000(	2.071584	0	2.638828	0	7.363456	1.64393	-0.6385	0.60874	0.72279	HMGB3P14	chr3	+	1.34E+08	1.34E+08	599
ENSG00000(	6.214751	3.612863	0	2.247227	0	2.465895	0.76851	0.52684	0.65163	UBE2V2P4	chr1	-	36707499	36707757	259
ENSG00000(	7.250543	6.021439	6.597069	1.498151	6.443024	7.397684	0.33935	0.69965	0.79573	AC104655.	chr2	-	1.06E+08	1.06E+08	565
ENSG00000(	0	3.612863	0	0	0.920432	0	0.81649	0.54246	NA	CYP21A2	chr6	+	32006042	32009447	2182
ENSG00000(	1.035792	1.204288	1.319414	15.73059	6.443024	2.465895	-2.2648	0.03096	0.063901	RP11-327P	chr13	+	52378433	52387356	569
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC067945.	chr2	+	1.92E+08	1.92E+08	490
ENSG00000(	0	0	0	0	0.920432	4.93179	-1.5674	0.24723	NA	AC007875.	chr7	+	97535741	97536134	394
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	OR5K2	chr3	+	98216448	98217496	1049
ENSG00000(	14.50109	26.49433	14.51355	0.749076	16.56778	6.575719	1.1344	0.12794	0.21458	SIK3-IT1	chr11	-	1.17E+08	1.17E+08	2472
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	KRT17P3	chr17	-	28894718	28898766	1262
ENSG00000(	5.17896	0	0	0	0	1.64393	0.83898	0.5363	0.66034	IPO9-AS1	chr1	-	2.02E+08	2.02E+08	839
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-346E	chrX	+	80618767	80619669	903
ENSG00000(	1.035792	2.408575	11.87472	2.996302	1.840864	2.465895	0.84506	0.42266	0.55313	RP11-177F	chr1	+	2.39E+08	2.39E+08	2900
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	SNRPFP1	chr20	-	48346128	48346379	252
ENSG00000(	0	0	0	0	5.522592	0	-1.3606	0.30939	NA	NDUFB1P1	chr3	+	48223037	48223216	180
ENSG00000(	2.071584	1.204288	1.319414	3.745378	0.920432	0	-0.02029	0.98738	0.99245	MTND5P15	chr3	-	1.77E+08	1.77E+08	349
ENSG00000(	121.1877	114.4073	106.8725	137.8299	96.64536	96.1699	0.048897	0.84788	0.90301	TRAF3IP2-A	chr6	+	1.12E+08	1.12E+08	2191
ENSG00000(	26.93059	44.55865	19.79121	3.745378	4.60216	9.041614	2.2669	0.000196	0.000613	AC093391.	chr2	+	1.37E+08	1.37E+08	1394
ENSG00000(	1.035792	0	0	0.749076	1.840864	2.465895	-1.1429	0.39687	0.52793	SETP10	chr1	+	1.79E+08	1.79E+08	814
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	GAPDHP37	chr22	-	41069488	41070455	968
ENSG00000(	0	0	2.638828	0.749076	4.60216	7.397684	-1.629	0.18526	0.28968	IDH1-AS1	chr2	+	2.09E+08	2.09E+08	489
ENSG00000(	4.143168	1.204288	1.319414	0	0	0	2.1615	0.11037	0.19002	AC007682.	chr2	+	51259739	52635055	3939
ENSG00000(	1.035792	0	0	0	1.840864	5.753754	-1.5183	0.25776	0.37643	NEBL-AS1	chr10	+	21462943	21463977	661
ENSG00000(	0	0	0	40.45008	21.16994	34.52253	-5.8364	4.50E-08	2.14E-07	PSG1	chr19	-	43370616	43383974	2830

ENSG0000(	1977.327	1870.259	1614.962	905.6323	910.3072	873.7487	1.0207	1.37E-16	1.18E-15	TAPBP	chr6	-	33267471	33282164	3759
ENSG0000(	1.035792	1.204288	0	1.498151	0	0	0.24225	0.85676	NA	AC102953.	chr7	-	1548291	1549063	242
ENSG0000(	1.035792	3.612863	0	0	0	0	1.5346	0.25314	NA	HMGB3P31	chrX	-	1.34E+08	1.34E+08	595
ENSG0000(	0	1.204288	0	1.498151	2.761296	6.575719	-2.0156	0.11502	0.19688	RPS7P3	chr1	-	2.33E+08	2.33E+08	580
ENSG0000(	1.035792	0	2.638828	0.749076	0.920432	1.64393	0.081282	0.9509	0.97057	RP13-923C	chr8	+	82720007	82720961	955
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	PHKA1-AS1	chrX	+	71908800	71932190	598
ENSG0000(	3.107376	0	3.958241	0	1.840864	0	1.1687	0.37941	0.51017	HS1BP3-IT1	chr2	-	20790535	20792308	600
ENSG0000(	4.143168	1.204288	0	7.490755	3.681728	4.109825	-1.168	0.28417	0.40715	AC018648.	chr7	+	32852369	32878182	915
ENSG0000(	49.71801	52.98866	43.54065	45.69361	40.49901	41.09825	0.19718	0.57507	0.69347	AC007383.	chr2	+	2.07E+08	2.07E+08	1411
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-67C2	chr10	-	45940018	45948569	462
ENSG0000(	8.286335	4.817151	10.55531	1.498151	7.363456	4.109825	0.77735	0.37518	0.50575	AF131215.	chr8	+	11032560	11033079	520
ENSG0000(	1.035792	0	0	0	0	1.64393	-0.12526	0.92174	NA	RP11-12M	chr1	-	1.8E+08	1.8E+08	353
ENSG0000(	3.107376	0	0	0	0	2.465895	0.17171	0.89908	NA	RP11-12D2	chr9	-	5356312	5356525	214
ENSG0000(	3.107376	3.612863	2.638828	0.749076	0	0	2.1796	0.093159	0.16542	AC144449.	chr2	+	1.5E+08	1.51E+08	1022
ENSG0000(	23.82321	9.634302	14.51355	4.494453	3.681728	9.041614	1.3717	0.054225	0.10432	RP11-452K	chr10	+	99160872	99179281	548
ENSG0000(	1.035792	0	0	1.498151	1.840864	0.821965	-0.93518	0.49005	NA	RP11-557H	chr6	-	1.35E+08	1.35E+08	1360
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	LINC00202	chr10	+	26932098	26942383	6037
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP5-963E2	chr20	-	61798149	61812255	542
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-132G	chr1	+	22094762	22095068	307
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RPL7L1P12	chr13	-	99601973	99602701	729
ENSG0000(	24.85901	25.29004	23.74945	14.23244	24.85166	6.575719	0.67197	0.23031	0.34369	RP11-573D	chr3	+	1.87E+08	1.87E+08	330
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-82L2	chr1	+	72036639	72039241	170
ENSG0000(	0	0	1.319414	2.247227	0	0	-0.3289	0.80275	NA	PPP1R2P3	chr5	+	1.56E+08	1.56E+08	1991
ENSG0000(	123.2592	151.7403	98.95603	126.5938	100.3271	142.1999	0.018583	0.94176	0.9649	ANXA2P2	chr9	+	33624223	33625532	1310
ENSG0000(	7.250543	8.430014	2.638828	5.992604	3.681728	15.61733	-0.40833	0.62786	0.73868	RP1-85F18	chr22	-	41570595	41593460	457
ENSG0000(	1.035792	16.86003	9.235896	0	0	0	4.2515	0.000522	0.001531	RP11-111F	chr9	+	46577620	46578220	601
ENSG0000(	0	0	0	0	1.840864	2.465895	-1.2108	0.36631	NA	FAM27D1	chr9	+	46389110	46391556	2447
ENSG0000(	0	6.021439	5.277655	4.494453	20.2495	3.28786	-1.1288	0.24139	0.35684	RP5-1007M	chr1	-	90048800	90098453	851
ENSG0000(	1.035792	0	0	0	0.920432	0.821965	-0.16752	0.89839	NA	CAP1P2	chr10	-	44100291	44101699	1409
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC005537.	chr7	-	42993734	43087661	1238
ENSG0000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	AP001059.	chr21	+	45670696	45671403	523
ENSG0000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	AC107021.	chr3	+	1.46E+08	1.46E+08	1799
ENSG0000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-181C	chr1	+	78319040	78319578	251
ENSG0000(	10.35792	16.86003	7.916483	24.71949	23.93123	36.16646	-1.2156	0.026302	0.055415	LEF1-AS1	chr4	+	1.09E+08	1.09E+08	3360
ENSG0000(	0	0	0	1.498151	1.840864	0.821965	-1.2806	0.34348	NA	RP5-1109J	chr1	+	46897801	46911374	1267
ENSG0000(	4.143168	10.83859	10.55531	4.494453	3.681728	8.219649	0.56165	0.49402	0.62282	LSM12P1	chr8	-	35382694	35383281	588
ENSG0000(	8.286335	0	2.638828	2.247227	4.60216	3.28786	0.11086	0.91863	0.9507	RP11-275F	chr1	+	51837942	51838896	955
ENSG0000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	AC007391.	chr2	+	37552483	37553940	504
ENSG0000(	3.107376	1.204288	1.319414	0	0	0	1.9243	0.1561	NA	RP5-991C6	chr6	-	82434439	82446070	471
ENSG0000(	3.107376	0	0	0	0	0.821965	0.7418	0.57612	NA	AC079781.	chr7	+	97537568	97537736	169
ENSG0000(	13.46529	26.49433	14.51355	0	1.840864	0	4.1702	1.31E-05	4.80E-05	AC092168.	chr2	+	1.01E+08	1.01E+08	717
ENSG0000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	GS1-115G2	chr1	+	1.85E+08	1.85E+08	1325
ENSG0000(	15.53688	44.55865	19.79121	73.4094	56.14635	41.09825	-1.0711	0.015528	0.034537	SCAND3	chr6	-	28539407	28583989	4877
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-45J1.	chrX	+	1.19E+08	1.19E+08	400

ENSG00000(	13.46529	22.88147	13.19414	0	2.761296	4.93179	2.4238	0.003228	0.008304	RP4-530I15	chr20	-	49187512	49194578	4587
ENSG00000(	2.071584	7.225726	3.958241	1.498151	1.840864	0	1.5117	0.18935	0.29449	AC073479.	chr2	+	6072819	6141407	3329
ENSG00000(	0	0	0	0	2.761296	3.28786	-1.6293	0.2296	0.34285	AC007392.	chr2	+	66801162	66957289	682
ENSG00000(	0	6.021439	2.638828	0	0.920432	0	1.8648	0.16059	0.25797	AC009784.	chr7	+	1.36E+08	1.36E+08	889
ENSG00000(	0	0	6.597069	0	0	0	1.83	0.17508	0.27674	NPM1P34	chrX	+	1.23E+08	1.23E+08	893
ENSG00000(	2.071584	1.204288	2.638828	0.749076	3.681728	0.821965	0.1358	0.91122	0.94547	RP11-173A	chr1	-	2.45E+08	2.45E+08	291
ENSG00000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	RP11-255N	chr9	-	30558878	30559479	602
ENSG00000(	2.071584	3.612863	5.277655	0.749076	0	0.821965	1.9235	0.1177	0.20067	RP11-307E	chr9	+	97094758	97123230	2162
ENSG00000(	1.035792	0	0	4.494453	6.443024	4.93179	-2.6005	0.032871	0.067287	AC023797.	chr3	-	1.96E+08	1.96E+08	348
ENSG00000(	1.035792	0	2.638828	1.498151	0.920432	1.64393	-0.10768	0.93418	0.96038	TMEM253	chr14	+	21567096	21571883	1526
ENSG00000(	4.143168	0	1.319414	0	0	0	1.7539	0.19459	NA	RP1-302D9	chr22	+	33560049	33562425	567
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	MRPL35P2	chr10	-	65394077	65394587	511
ENSG00000(	4.143168	2.408575	0	0.749076	0	3.28786	0.47341	0.71196	0.80531	RP11-452J	chr1	+	1.93E+08	1.93E+08	779
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	AL035610.	chr21	+	29420733	29509930	1754
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	LARGE-IT1	chr22	-	34119818	34120898	558
ENSG00000(	9.322127	8.430014	10.55531	2.996302	0	1.64393	2.186	0.022229	0.047668	RPS6KA2-IT	chr6	-	1.67E+08	1.67E+08	579
ENSG00000(	1.035792	0	0	2.996302	0	0	-0.53136	0.68956	NA	RPL31P7	chr17	-	78576349	78576741	393
ENSG00000(	5.17896	0	2.638828	6.74168	13.80648	16.4393	-1.9326	0.029767	0.061741	RP11-307C	chr1	-	1.55E+08	1.55E+08	822
ENSG00000(	5.17896	0	0	0.749076	3.681728	0.821965	0.023872	0.98526	0.99132	AC079781.	chr7	-	97567751	97568106	356
ENSG00000(	223.7311	246.879	187.3568	113.1104	155.553	152.8855	0.64181	0.003259	0.008373	CTD-2619J	chr19	-	58915605	58919851	3059
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC108059.	chr2	-	1.29E+08	1.29E+08	151
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	MTCO3P2	chr13	-	24340073	24340243	171
ENSG00000(	2.071584	2.408575	3.958241	1.498151	3.681728	4.93179	-0.2152	0.84028	0.89775	RP11-509J	chr9	+	3526723	3671646	552
ENSG00000(	9.322127	12.04288	7.916483	5.992604	0.920432	1.64393	1.533	0.084535	0.15256	RP11-149I	chr10	+	91043522	91051882	603
ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	RP11-126C	chrX	+	9370791	9382606	11812
ENSG00000(	196.8005	201.116	157.0102	374.5378	221.8241	267.1386	-0.63384	0.004323	0.010843	TMA7	chr3	+	48481667	48485616	688
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-123G	chr10	-	59866184	59866640	457
ENSG00000(	2.071584	7.225726	0	1.498151	0	2.465895	0.85376	0.49165	0.62077	RP11-187C	chr9	+	45484572	45488153	935
ENSG00000(	1.035792	0	0	0.749076	0	0.821965	-0.11768	0.9281	NA	RP11-490N	chr13	-	30726023	30733758	6852
ENSG00000(	1.035792	1.204288	0	3.745378	0.920432	2.465895	-1.0837	0.39745	0.52849	BACH1-AS1	chr21	-	30742340	30743547	241
ENSG00000(	653.5847	755.0884	663.6651	957.3186	799.8554	767.7152	-0.28499	0.045191	0.088907	MCTS1	chrX	+	1.2E+08	1.2E+08	1130
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	AP001057.	chr21	+	45621173	45622579	799
ENSG00000(	0	4.817151	3.958241	2.247227	0	2.465895	0.61119	0.62	0.73225	AC011385.	chr5	+	1.38E+08	1.38E+08	195
ENSG00000(	3.107376	0	0	2.247227	0	0.821965	0.021745	0.98719	0.9923	RP1-293L8	chr6	-	1.26E+08	1.26E+08	501
ENSG00000(	2.071584	3.612863	0	0.749076	0	1.64393	0.7652	0.56186	0.68183	RP11-544K	chr1	-	2.2E+08	2.2E+08	388
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	DUXAP7	chr20	-	18623426	18624278	689
ENSG00000(	0	1.204288	0	3.745378	0	2.465895	-1.2708	0.34576	0.47523	LINC00867	chr10	+	1.2E+08	1.2E+08	580
ENSG00000(	1.035792	0	0	2.247227	0	0	-0.31629	0.80869	NA	RP11-367H	chr10	-	71958744	71958995	252
ENSG00000(	0	3.612863	1.319414	3.745378	0.920432	0	0.032302	0.98023	0.98847	FERP1	chrX	+	1.23E+08	1.23E+08	793
ENSG00000(	1.035792	2.408575	3.958241	2.247227	3.681728	3.28786	-0.26419	0.81012	0.87679	ST13P4	chr13	+	50746225	50747317	1093
ENSG00000(	0	4.817151	0	2.996302	1.840864	1.64393	-0.29781	0.81412	0.87932	RP11-277L	chr1	+	1.5E+08	1.5E+08	5730
ENSG00000(	27.96638	30.10719	21.11062	23.97042	14.72691	21.37109	0.38332	0.43147	0.56126	RP5-842K2	chrX	+	1.31E+08	1.32E+08	3474
ENSG00000(	5.17896	4.817151	1.319414	0	2.761296	0	1.4696	0.23322	0.34697	USP12-AS1	chr13	+	27736992	27743272	268
ENSG00000(	2.071584	9.634302	14.51355	3.745378	0	2.465895	1.7072	0.085614	0.1543	RPLP1P13	chr13	+	23947562	23948200	299

ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	RP11-146N	chr9	-	19200333	19201044	712
ENSG00000(	8.286335	8.430014	10.55531	5.243529	6.443024	3.28786	0.7826	0.32692	0.45462	RP11-311P	chrX	-	74546607	74547834	1228
ENSG00000(	11.39371	10.83859	18.47179	11.98521	2.761296	5.753754	0.89129	0.22246	0.33444	FTH1P7	chr13	-	23270162	23270713	552
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-134D	chr16	+	87091390	87097597	4083
ENSG00000(	43.50326	44.55865	43.54065	5.243529	7.363456	3.28786	2.9355	4.06E-08	1.94E-07	RP11-62I2:	chr1	-	2.45E+08	2.45E+08	810
ENSG00000(	0	0	0	2.996302	5.522592	7.397684	-3.1918	0.011453	0.026259	RP1-313L4	chr1	+	1.68E+08	1.68E+08	718
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	MTRNR2L4	chr16	-	3421053	3422283	1231
ENSG00000(	5.17896	4.817151	2.638828	0	0	0	3.172	0.014447	0.032394	AC098824.	chr2	-	43053462	43054757	980
ENSG00000(	8.286335	3.612863	0	0	0	4.93179	0.89807	0.47015	0.59927	PHBP15	chr7	-	74155796	74156460	665
ENSG00000(	0	0	0	2.247227	1.840864	4.93179	-2.3302	0.079788	0.14505	RP11-395D	chr9	+	89247062	89311411	530
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-430I1	chr1	+	2.48E+08	2.48E+08	940
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	FTLP8	chr13	-	98639204	98639470	267
ENSG00000(	5.17896	8.430014	1.319414	1.498151	5.522592	6.575719	0.12925	0.89386	0.93429	RP1-149A1	chr22	+	32782655	32782855	201
ENSG00000(	21.75163	15.65574	13.19414	2.247227	4.60216	6.575719	1.7825	0.012766	0.028954	LINC00202	chr10	-	27220135	27230930	3620
ENSG00000(	1.035792	1.204288	0	0	3.681728	0	-0.34221	0.80082	NA	RP11-77O7	chr2	-	69821873	69822190	318
ENSG00000(	8.286335	1.204288	5.277655	8.988907	5.522592	4.93179	-0.3396	0.70571	0.80057	RP11-573D	chr3	-	1.87E+08	1.87E+08	1832
ENSG00000(	0	3.612863	0	1.498151	0	0	0.55191	0.68269	NA	ASCL5	chr1	-	2.01E+08	2.01E+08	2026
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CSF2RBP1	chr22	-	37346571	37349764	391
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-4C20	chr10	-	1.3E+08	1.3E+08	748
ENSG00000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	BTF3L4P1	chr21	-	18890841	18891311	471
ENSG00000(	8.286335	3.612863	2.638828	0.749076	3.681728	0	1.3616	0.2282	0.34146	INTS4L2	chr7	+	65112777	65180636	1403
ENSG00000(	1.035792	6.021439	2.638828	2.247227	1.840864	0.821965	0.7396	0.52113	0.64678	FTH1P1	chr1	+	38010364	38010895	532
ENSG00000(	9.322127	9.634302	15.83297	14.98151	23.0108	10.68554	-0.46139	0.46057	0.59001	RP11-782C	chr1	-	1.43E+08	1.43E+08	5783
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	MTND1P32	chrX	+	1.02E+08	1.02E+08	938
ENSG00000(	65.25489	54.19295	75.20659	14.23244	30.37426	23.01502	1.501	0.000148	0.000472	GNG12-AS1	chr1	+	68297986	68668670	2232
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	TCEB2P3	chr2	+	49007741	49008034	294
ENSG00000(	2.071584	1.204288	1.319414	2.996302	1.840864	0.821965	-0.21069	0.86395	0.91402	RP1-292B1	chr6	-	1.51E+08	1.51E+08	396
ENSG00000(	224.7668	214.3632	249.3692	89.13999	88.36147	53.42772	1.563	1.07E-10	6.35E-10	RP11-154D	chr6	-	71931160	72037931	946
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-10N1	chr1	-	24634046	24648391	856
ENSG00000(	5.17896	3.612863	1.319414	0	4.60216	3.28786	0.30223	0.78981	0.86243	FAM215B	chr17	-	44636196	44640161	2183
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-132A	chr7	+	1.01E+08	1.01E+08	756
ENSG00000(	4.143168	4.817151	3.958241	2.247227	0.920432	3.28786	0.8082	0.44237	0.57203	RP11-205N	chr9	-	32566146	32567124	979
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC012485.	chr2	-	2.39E+08	2.39E+08	563
ENSG00000(	0	0	0	2.996302	2.761296	0.821965	-1.8697	0.16674	0.26571	RP11-557H	chr6	-	1.35E+08	1.35E+08	892
ENSG00000(	0	0	0	2.996302	0	3.28786	-1.6956	0.21138	0.32124	RP1-249I4.	chr6	+	1.1E+08	1.1E+08	465
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP1-124C6	chr6	-	1.14E+08	1.14E+08	524
ENSG00000(	5.17896	2.408575	14.51355	2.247227	4.60216	0	1.3998	0.17223	0.27331	AC009299.	chr2	-	1.62E+08	1.62E+08	513
ENSG00000(	3.107376	0	0	2.996302	7.363456	0.821965	-1.2411	0.31504	0.44164	AC008440.	chr19	+	54368017	54369394	555
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	AC093627.	chr7	-	70972	71835	759
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-395C	chr4	-	81307332	81309870	2539
ENSG00000(	0	2.408575	0	0	0	1.64393	0.21935	0.86915	NA	RPS27AP2	chr20	+	17497488	17497952	465
ENSG00000(	8.286335	2.408575	9.235896	0	0	0	3.8663	0.001868	0.005007	RP11-47G1	chr10	-	1.26E+08	1.26E+08	525
ENSG00000(	2.071584	4.817151	0	1.498151	0	4.109825	0.20581	0.86924	0.91789	RP11-46O2	chr10	-	76265890	76289096	897
ENSG00000(	15.53688	7.225726	13.19414	13.48336	6.443024	8.219649	0.32486	0.63857	0.74678	AC087163.	chr17	+	17913957	17915136	853

ENSG00000(	7.250543	3.612863	1.319414	4.494453	16.56778	18.08323	-1.472	0.077294	0.14111	RP11-488L	chr1	-	2.47E+08	2.47E+08	706
ENSG00000(	3.107376	1.204288	2.638828	0.749076	0	0.821965	1.3555	0.29535	0.41972	U73167.7	chr3	-	50304073	50304803	338
ENSG00000(	0	0	0	5.992604	3.681728	5.753754	-3.1585	0.012451	0.028337	VIPR1-AS1	chr3	-	42548016	42574098	810
ENSG00000(	0	0	0	0	1.840864	2.465895	-1.2108	0.36631	NA	RP5-955M2	chr20	+	49615907	49626556	802
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC104777.	chr2	-	1.51E+08	1.51E+08	568
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	RP1-102D2	chr22	-	45831744	45844624	545
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP5-882O7	chr1	-	45453906	45454397	492
ENSG00000(	30.03797	20.47289	14.51355	17.97781	34.05598	41.09825	-0.48612	0.3311	0.45898	RP11-504P	chr1	-	2.24E+08	2.24E+08	360
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	MTCYBP3	chr13	+	96346823	96347959	1137
ENSG00000(	1.035792	6.021439	1.319414	0	0	0	2.4683	0.066378	0.12397	GPR79	chr3	-	1.59E+08	1.59E+08	1086
ENSG00000(	2.071584	1.204288	2.638828	0	0	0.821965	1.5471	0.2493	0.36656	AC016910.	chr2	+	1.45E+08	1.45E+08	1046
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-308D	chrX	-	1.36E+08	1.36E+08	386
ENSG00000(	11.39371	24.08575	7.916483	16.47966	7.363456	4.109825	0.57978	0.41659	0.54716	RPS3AP25	chr7	-	94324339	94325131	793
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	SKA2P1	chr9	+	1.26E+08	1.26E+08	390
ENSG00000(	511.6812	409.4578	436.726	384.2758	333.1964	526.0575	0.12674	0.49687	0.62537	LINC00493	chr20	+	18548064	18550207	505
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	RP11-134K	chr6	-	71317937	71319037	1101
ENSG00000(	3.107376	2.408575	3.958241	0.749076	2.761296	0	1.0569	0.38139	0.51206	TMPRSS11(	chr4	-	68632198	68639572	683
ENSG00000(	0	0	5.277655	0	4.60216	3.28786	-0.40015	0.75517	0.83804	RP11-234K	chr20	-	34738335	34743655	2701
ENSG00000(	2.071584	7.225726	0	0	0	0	2.5144	0.062241	0.11725	AC009495.	chr2	-	1.67E+08	1.67E+08	506
ENSG00000(	0	1.204288	0	0	1.840864	0.821965	-0.461	0.73167	NA	RP1-315G1	chrX	-	1.23E+08	1.23E+08	326
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-380N	chr6	+	73696036	73697473	1438
ENSG00000(	2.071584	0	0	0.749076	0	2.465895	-0.29388	0.82852	NA	AC105396.	chr2	+	1.84E+08	1.84E+08	338
ENSG00000(	266.1985	272.169	234.8557	30.7121	54.30549	32.05663	2.7108	6.44E-26	8.24E-25	C9orf172	chr9	+	1.4E+08	1.4E+08	2931
ENSG00000(	0	2.408575	5.277655	0	0	1.64393	1.3035	0.32586	0.45353	RP11-487I5	chr10	+	76884975	76885620	326
ENSG00000(	12.4295	8.430014	9.235896	0	10.12475	4.109825	0.96861	0.27988	0.40219	RPL18AP7	chr3	-	38568293	38568816	524
ENSG00000(	69.39806	59.0101	63.33186	89.88907	58.90765	56.71558	-0.10068	0.75236	0.83611	CTD-3184A	chr20	+	62258580	62260177	801
ENSG00000(	0	0	1.319414	0	0	4.109825	-0.74763	0.58005	NA	AC010745.	chr2	-	16497592	16500834	740
ENSG00000(	13.46529	8.430014	19.79121	131.0882	96.64536	120.0069	-3.0113	2.78E-15	2.23E-14	RP11-132A	chr7	+	1.01E+08	1.01E+08	705
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-416N	chr20	+	10160883	10166423	446
ENSG00000(	7.250543	2.408575	11.87472	8.239831	10.12475	1.64393	0.090734	0.91716	0.94971	RP4-730K3	chr1	-	1.14E+08	1.14E+08	748
ENSG00000(	12.4295	7.225726	6.597069	4.494453	0	0	2.0489	0.048251	0.094084	RP4-794H1	chr1	-	59348540	59362375	1211
ENSG00000(	3.107376	1.204288	0	1.498151	1.840864	5.753754	-0.75313	0.53177	0.65636	RP11-3J10.	chr9	+	37836041	37836391	351
ENSG00000(	0	1.204288	0	0	1.840864	0	-0.18234	0.88799	NA	LARS2-AS1	chr3	-	45525466	45551037	575
ENSG00000(	3.107376	2.408575	5.277655	2.996302	3.681728	4.93179	-0.09471	0.92443	0.95429	RP11-583F	chr17	+	62936720	62952664	1059
ENSG00000(	9.322127	0	0	0	0	0	2.3486	0.083387	0.15069	AC005029.	chr7	-	41004266	41019537	3263
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	BMPR1APS	chr11	-	1.21E+08	1.21E+08	1014
ENSG00000(	0	0	0	0	3.681728	3.28786	-1.8162	0.1806	0.28356	RP11-644C	chr3	-	1.76E+08	1.77E+08	678
ENSG00000(	0	0	0	0	4.60216	2.465895	-1.83	0.17727	0.27944	RP11-337A	chr9	-	26880176	26880547	372
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	TMA16P2	chr1	-	46312666	46313266	601
ENSG00000(	4.143168	1.204288	0	5.243529	1.840864	6.575719	-1.0235	0.36041	0.49	RP11-313D	chr10	+	1.13E+08	1.13E+08	401
ENSG00000(	38.3243	22.88147	34.30476	35.20655	17.48821	32.05663	0.16396	0.71954	0.81111	EEF1B2P3	chrX	-	24806509	24807186	678
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	NCKAP5-IT1	chr2	-	1.34E+08	1.34E+08	554
ENSG00000(	0	1.204288	2.638828	1.498151	2.761296	4.93179	-0.93625	0.43958	0.56936	AC010900.	chr2	+	2.04E+08	2.04E+08	1296
ENSG00000(	1030.613	1023.645	1686.211	28.46487	61.66894	64.11326	4.4951	6.42E-28	8.94E-27	RP11-224C	chr1	-	2.19E+08	2.19E+08	557

ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP4-654C1	chr1	+	23737325	23738639	426
ENSG00000(	7.250543	0	1.319414	2.247227	2.761296	13.15144	-0.84536	0.42932	0.5595	AC098820.	chr2	-	2.17E+08	2.17E+08	750
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	RP11-18B3	chr9	+	1.09E+08	1.09E+08	2434
ENSG00000(	12.4295	16.86003	5.277655	0	4.60216	0.821965	2.3255	0.014591	0.03268	RASA3-IT1	chr13	-	1.15E+08	1.15E+08	380
ENSG00000(	6.214751	1.204288	1.319414	0	0.920432	5.753754	0.30205	0.80155	0.87083	MFAP1P1	chr13	-	31115780	31117034	1255
ENSG00000(	0	2.408575	1.319414	0	7.363456	2.465895	-0.96429	0.44182	0.57155	OSBPL10-A	chr3	+	31745550	31763144	575
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP4-756H1	chr7	+	66021203	66022052	850
ENSG00000(	6.214751	0	6.597069	1.498151	0	0.821965	1.7205	0.15977	0.25696	NPM1P13	chr7	-	18988521	18989385	865
ENSG00000(	0	0	1.319414	0	4.60216	0.821965	-1.0585	0.43446	0.56417	RPL12P11	chr20	+	40176061	40176561	501
ENSG00000(	5.17896	7.225726	2.638828	7.490755	8.283888	4.109825	-0.34773	0.68954	0.78803	RP11-512F	chr1	+	1.14E+08	1.14E+08	1029
ENSG00000(	1.035792	0	0	0.749076	0	4.93179	-1.1903	0.37953	0.51027	AC105053.	chr2	+	86116403	86118103	783
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC112198.	chr5	-	54104038	54168379	6996
ENSG00000(	3.107376	0	0	0.749076	0	0.821965	0.47233	0.72731	NA	AC074366.	chr2	-	38895830	38898563	552
ENSG00000(	1.035792	2.408575	0	2.996302	1.840864	0.821965	-0.47149	0.71241	0.80558	RP11-29H2	chr1	-	1.56E+08	1.56E+08	448
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	AC012507.	chr2	+	2.32E+08	2.32E+08	1765
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC025750.	chr2	-	42690279	42691137	859
ENSG00000(	456.7842	392.5978	394.5047	126.5938	78.23672	105.2115	1.9883	2.13E-22	2.38E-21	RP11-14N7	chr1	+	1.49E+08	1.49E+08	605
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP4-673D2	chr20	-	1748603	1760641	1367
ENSG00000(	0	2.408575	1.319414	2.996302	2.761296	0.821965	-0.57745	0.64645	0.75329	RP1-102K2	chr22	+	30635183	30636527	808
ENSG00000(	0	0	1.319414	0	1.840864	1.64393	-0.68367	0.61391	NA	AC027612.	chr2	-	91935966	91937021	1056
ENSG00000(	151.2256	142.106	142.4967	122.0993	76.39586	92.06007	0.57636	0.021406	0.046106	AC093673.	chr7	-	1.43E+08	1.43E+08	648
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	OR5H8P	chr3	+	98030757	98031687	931
ENSG00000(	0	0	0	0.749076	2.761296	6.575719	-2.4505	0.064705	0.1212	RP11-74C1	chr1	+	1.52E+08	1.52E+08	526
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RPL36P19	chr13	+	43968661	43968961	301
ENSG00000(	27.96638	19.2686	36.94359	1.498151	11.04518	7.397684	1.9745	0.001987	0.005296	KB-318B8.1	chr22	+	24497652	24499317	558
ENSG00000(	17.60846	14.45145	10.55531	7.490755	16.56778	18.08323	0.027737	0.9644	0.97945	RP11-458F	chr7	+	66313483	66323123	298
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC006026.	chr7	-	23624681	23625974	1294
ENSG00000(	143.9751	215.5675	117.4278	123.5975	155.553	193.9837	0.013224	0.95964	0.97639	GS1-124K5	chr7	-	66010634	66057373	958
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	C21orf37	chr21	+	18811208	18821503	714
ENSG00000(	29.00217	44.55865	46.17948	32.21025	14.72691	20.54912	0.79008	0.082206	0.14884	GTF2IP1	chr7	-	74602783	74653438	2629
ENSG00000(	10.35792	15.65574	15.83297	7.490755	10.12475	13.9734	0.37802	0.55646	0.67705	RP4-591N1	chr22	+	40917804	40922711	1932
ENSG00000(	0	0	0	0	0.920432	5.753754	-1.7332	0.2014	0.30905	AC093038.	chr2	-	1.87E+08	1.87E+08	501
ENSG00000(	148.1182	191.4817	121.3861	113.1104	69.0324	146.3098	0.48171	0.09124	0.16263	RPL3P4	chr14	-	99439216	99439638	423
ENSG00000(	2.071584	0	1.319414	0	0.920432	0	0.84841	0.52989	NA	CTC-303L1.	chr5	+	93928473	93930496	2021
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTD-3105H	chr19	+	12615479	12615704	226
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-397C	chr13	+	1.02E+08	1.02E+08	429
ENSG00000(	7.250543	2.408575	1.319414	2.247227	4.60216	7.397684	-0.28853	0.773	0.85085	RP11-46A1	chr1	-	1.81E+08	1.81E+08	1440
ENSG00000(	3.107376	0	7.916483	3.745378	4.60216	2.465895	0.011818	0.99118	0.99478	EEF1A1P3	chr13	+	28788650	28790034	1385
ENSG00000(	35.21692	42.15007	32.98534	17.97781	11.04518	24.65895	1.0025	0.032625	0.066877	RP11-258C	chrX	+	53123327	53196196	1196
ENSG00000(	0	0	2.638828	0.749076	1.840864	0.821965	-0.22632	0.86669	0.91598	RP1-161N1	chrX	-	1.24E+08	1.24E+08	534
ENSG00000(	9.322127	15.65574	5.277655	2.247227	4.60216	13.15144	0.54253	0.50511	0.63283	AC084125.	chr8	+	1.46E+08	1.46E+08	555
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC010090.	chr2	+	1.45E+08	1.45E+08	362
ENSG00000(	1.035792	8.430014	2.638828	2.247227	0.920432	0	1.4002	0.2407	0.35606	TIMM9P2	chr21	+	40588550	40589432	266
ENSG00000(	56.96855	60.21439	56.73479	40.45008	20.2495	34.52253	0.84439	0.025616	0.054111	RP11-1114	chrX	-	1.36E+08	1.36E+08	3018

ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AC007386.	chr2	-	65257861	65280151	1018
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-439L	chr6	+	1.43E+08	1.43E+08	554
ENSG00000(	1.035792	6.021439	1.319414	0	2.761296	0	1.0745	0.40299	0.53403	AP000266.	chr21	-	33678775	33681048	582
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP11-175B	chr1	+	2.02E+08	2.02E+08	1171
ENSG00000(	5.17896	0	1.319414	2.996302	0	0	0.66973	0.61353	0.72694	AC021876.	chr7	+	23405237	23405595	359
ENSG00000(	4.143168	0	3.958241	0	0.920432	4.109825	0.48273	0.69906	0.79535	RP11-365C	chr1	-	2.24E+08	2.24E+08	790
ENSG00000(	11.39371	14.45145	13.19414	23.22134	14.72691	31.23467	-0.7947	0.15646	0.25251	PRPS1P2	chr9	+	1.28E+08	1.28E+08	937
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	MTND2P23	chr2	+	2.13E+08	2.13E+08	651
ENSG00000(	5.17896	2.408575	2.638828	2.247227	0	0.821965	1.2478	0.29901	0.42399	CTD-2201G	chr5	+	1.13E+08	1.13E+08	3361
ENSG00000(	3.107376	0	7.916483	0	0	0	2.7683	0.0385	0.077422	NEFLP1	chrY	-	23382992	23383975	984
ENSG00000(	54.89697	51.78437	67.2901	31.46117	73.63456	33.70056	0.32447	0.40436	0.53529	WI2-3658N	chr1	-	1.46E+08	1.46E+08	5496
ENSG00000(	17.60846	16.86003	15.83297	48.68991	27.61296	27.12484	-1.0074	0.038903	0.078091	RP1-266L2	chr6	-	1.7E+08	1.7E+08	403
ENSG00000(	1.035792	2.408575	3.958241	0	0	0	2.3061	0.087354	0.1569	AC008073.	chr2	-	24388753	24397874	792
ENSG00000(	3.107376	0	9.235896	2.247227	4.60216	4.93179	0.044774	0.96599	0.98015	RP3-322G1	chr20	-	23337231	23338753	514
ENSG00000(	6.214751	13.24716	5.277655	0	0	0.821965	3.5423	0.002063	0.005487	RP11-344N	chr10	+	74824884	74825225	214
ENSG00000(	14.50109	18.06432	7.916483	20.97412	16.56778	19.72716	-0.47192	0.41249	0.54297	RP11-367N	chr4	-	1.84E+08	1.84E+08	559
ENSG00000(	0	0	0	2.247227	2.761296	0	-1.3959	0.30129	NA	RP5-834N1	chr1	+	1.2E+08	1.2E+08	442
ENSG00000(	8.286335	4.817151	13.19414	0	0.920432	4.109825	1.9915	0.046893	0.091786	GOLGA8N	chr15	+	32885657	32896179	1997
ENSG00000(	3.107376	0	0	4.494453	9.20432	0	-1.4323	0.24941	0.36667	IDI2-AS1	chr10	+	1068606	1090138	1054
ENSG00000(	0	0	2.638828	0	2.761296	4.93179	-0.97206	0.46016	0.58962	LDHBP1	chr13	+	1.14E+08	1.14E+08	1119
ENSG00000(	0	2.408575	0	4.494453	3.681728	4.93179	-1.7647	0.14219	0.23371	RP11-126K	chr1	-	1.51E+08	1.51E+08	622
ENSG00000(	149.154	169.8046	120.0667	879.4147	666.3928	697.8482	-2.3408	9.60E-38	1.86E-36	LINC00665	chr19	-	36803969	36822620	2732
ENSG00000(	22.78742	27.69862	7.916483	0	0	0	5.5065	8.24E-07	3.44E-06	RP11-400N	chr1	-	2.22E+08	2.22E+08	562
ENSG00000(	8.286335	8.430014	13.19414	0.749076	0.920432	1.64393	2.6835	0.005279	0.013019	RP11-388P	chr10	+	61815632	61820501	1546
ENSG00000(	2.071584	0	1.319414	2.996302	0.920432	0.821965	-0.30787	0.81277	0.87847	ATP11A-AS	chr13	-	1.13E+08	1.13E+08	2192
ENSG00000(	9.322127	0	2.638828	1.498151	1.840864	1.64393	0.97867	0.39745	0.52849	ARID4B-IT1	chr1	-	2.35E+08	2.35E+08	463
ENSG00000(	0	0	0	5.992604	8.283888	0	-2.8415	0.030651	0.063334	RP11-561I	chr1	-	2.42E+08	2.42E+08	462
ENSG00000(	12.4295	3.612863	11.87472	7.490755	0.920432	4.93179	0.92642	0.28804	0.41168	AP001596.	chr21	+	27750871	27844017	1078
ENSG00000(	4.143168	0	2.638828	2.996302	0	0.821965	0.54064	0.67315	0.77541	AC012370.	chr2	-	65600834	65607819	530
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC017006.	chr2	-	46305154	46305967	464
ENSG00000(	0	3.612863	1.319414	0	0	0	1.6005	0.2346	NA	AP001058.	chr21	-	45626408	45627282	463
ENSG00000(	0	0	2.638828	2.996302	0	0.821965	-0.31504	0.81597	0.88068	RP3-437C1	chr6	-	51274879	51275335	457
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	NUTMHP	chr10	+	52439351	52446086	1698
ENSG00000(	0	0	2.638828	2.247227	5.522592	2.465895	-1.3845	0.26617	0.38615	MARK2P9	chr10	+	94178424	94180632	1727
ENSG00000(	10.35792	14.45145	14.51355	0.749076	9.20432	3.28786	1.436	0.076647	0.14016	RP4-669P1	chr22	-	42532442	42535938	667
ENSG00000(	8.286335	7.225726	6.597069	2.996302	0	0	2.2478	0.037662	0.075945	RP4-777D9	chr20	-	21134664	21198927	5369
ENSG00000(	1.035792	3.612863	1.319414	1.498151	2.761296	0	0.33791	0.78871	0.86174	AC010733.	chr2	-	61165339	61165739	401
ENSG00000(	2.071584	0	6.597069	0	0	0	2.3978	0.076093	0.13933	AC016831.	chr7	-	1.31E+08	1.31E+08	1723
ENSG00000(	1.035792	6.021439	6.597069	0	0	0	3.2318	0.012718	0.028861	TRIM51JP	chr2	+	96240647	96246512	1320
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-13J8.	chr2	+	2.02E+08	2.02E+08	1269
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-403I	chr1	+	1.49E+08	1.49E+08	1073
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	AC111186.	chr17	+	73070401	73075644	2848
ENSG00000(	4.143168	8.430014	1.319414	0.749076	1.840864	0	1.8203	0.12142	0.20586	U52111.14	chrX	-	1.53E+08	1.53E+08	914
ENSG00000(	30.03797	26.49433	35.62417	3.745378	6.443024	6.575719	2.3477	5.28E-05	0.000179	AC083884.	chr7	-	74103273	74143339	1268

ENSG00000(	1.035792	1.204288	3.958241	14.98151	14.72691	9.041614	-2.3526	0.007599	0.018159	AC073043.	chr2	-	2.01E+08	2.01E+08	982
ENSG00000(	3.107376	3.612863	1.319414	5.992604	0.920432	2.465895	-0.18043	0.8702	0.91845	RP11-25G1	chr10	+	15279491	15283766	794
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	AC062020.	chr2	-	1.24E+08	1.24E+08	584
ENSG00000(	1.035792	1.204288	14.51355	3.745378	1.840864	0.821965	1.0762	0.32445	0.45197	RHOQP2	chr2	+	1.32E+08	1.32E+08	600
ENSG00000(	0	0	1.319414	2.247227	0	0	-0.3289	0.80275	NA	ANKRD20A	chr1	+	1.43E+08	1.43E+08	1746
ENSG00000(	4.143168	1.204288	3.958241	0	0.920432	0	2.0879	0.10796	0.18672	RP11-177A	chr1	-	1.79E+08	1.79E+08	344
ENSG00000(	1.035792	4.817151	1.319414	0.749076	0	0	1.7912	0.17914	0.28185	RP1-85F18	chr22	-	41565194	41579148	357
ENSG00000(	0	0	0	0.749076	2.761296	2.465895	-1.7341	0.2007	0.30828	RP5-1185I1	chr7	+	77619701	77624488	1965
ENSG00000(	1.035792	1.204288	1.319414	0	1.840864	0	0.52252	0.69958	NA	ETF1P1	chr6	+	29999490	30000780	984
ENSG00000(	4.143168	1.204288	1.319414	8.988907	8.283888	11.50751	-1.7955	0.050156	0.097393	AC002480.	chr7	+	22602956	22613615	2432
ENSG00000(	0	6.021439	3.958241	0.749076	7.363456	1.64393	0.025343	0.9822	0.98984	RP4-784A1	chr1	+	53770208	53773134	752
ENSG00000(	0	2.408575	2.638828	1.498151	0	0	0.90396	0.50381	0.63148	RP11-201C	chr1	+	31523719	31523881	163
ENSG00000(	22.78742	22.88147	15.83297	4.494453	4.60216	7.397684	1.7862	0.005782	0.014142	RP11-47I22	chr14	+	62037258	62125414	1655
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	MRPL51P2	chr21	-	44535444	44535819	376
ENSG00000(	6.214751	1.204288	0	0	1.840864	0.821965	0.98323	0.44885	0.5786	RPL23AP5(	chr6	+	1.08E+08	1.08E+08	455
ENSG00000(	0	4.817151	1.319414	0	4.60216	0	0.2666	0.83964	0.8974	AC078883.	chr2	-	1.73E+08	1.73E+08	754
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	AC053503.	chr2	-	2.2E+08	2.2E+08	114
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	AC006481.	chr7	+	20875050	21062767	447
ENSG00000(	0	1.204288	0	0	0.920432	0.821965	-0.17164	0.89643	NA	FTH1P25	chr1	-	1.85E+08	1.85E+08	469
ENSG00000(	7.250543	13.24716	10.55531	2.247227	0.920432	0	2.7351	0.005236	0.012925	DNAJC19P8	chr1	-	2.45E+08	2.45E+08	259
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	SCAND3P1	chr13	+	35759431	35760816	1060
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-204N	chr9	+	42037568	42037913	346
ENSG00000(	0	0	0	3.745378	0	1.64393	-1.4934	0.26982	NA	CRYGFP	chr2	+	2.1E+08	2.1E+08	633
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-93B1	chr20	-	61294371	61298076	1420
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-536K	chr10	-	5979079	5987863	640
ENSG00000(	0	0	1.319414	10.48706	0.920432	0	-1.8925	0.14923	0.24295	TNF	chr6	+	31543344	31546113	1676
ENSG00000(	20.71584	22.88147	7.916483	16.47966	15.64734	5.753754	0.42491	0.50647	0.63412	RP11-96K1	chr1	+	1.11E+08	1.11E+08	2359
ENSG00000(	8.286335	0	1.319414	4.494453	9.20432	0	-0.36502	0.75085	0.8347	COL4A2-AS	chr13	-	1.11E+08	1.11E+08	540
ENSG00000(	30.03797	21.67718	21.11062	38.95193	40.49901	46.03004	-0.7584	0.069545	0.12902	RP11-764K	chr9	-	68413482	68414196	715
ENSG00000(	23.82321	15.65574	15.83297	38.20285	19.32907	23.83698	-0.53416	0.29644	0.42086	RPS2P32	chr7	+	23530092	23530983	892
ENSG00000(	78.72018	98.75159	58.05421	59.92604	60.74851	41.09825	0.53661	0.10104	0.17693	AC003986.	chr7	+	19152097	19153894	1711
ENSG00000(	0	0	2.638828	0	0.920432	0.821965	0.26148	0.84655	NA	RP11-401A	chr1	-	1.98E+08	1.98E+08	408
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-211N	chr9	+	46826492	46833319	3321
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AF196970.	chrX	-	48557354	48595570	925
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	RP11-144C	chr3	+	1.01E+08	1.01E+08	406
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	LMLN-AS1	chr3	-	1.98E+08	1.98E+08	542
ENSG00000(	8.286335	15.65574	3.958241	29.21395	18.40864	20.54912	-1.2147	0.04985	0.096855	FAM27E3	chr9	-	67784944	67786624	1506
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AF064858.	chr21	-	40346355	40349700	1598
ENSG00000(	0	1.204288	0	2.247227	0	0	-0.3239	0.80512	NA	AC098592.	chr7	-	17072713	17073102	390
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	SLC25A6P3	chr1	+	52174734	52175612	879
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	CTA-215D1	chr1	-	8117305	8118523	800
ENSG00000(	0	2.408575	1.319414	0	3.681728	0	0.015586	0.99078	0.99468	AL590708.	chr9	+	1.31E+08	1.31E+08	696
ENSG00000(	1.035792	0	1.319414	0.749076	0	0	0.56083	0.6714	NA	CICP4	chr20	-	62921540	62924351	2812
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	LUZP4P1	chr10	+	21536681	21537024	344

ENSG00000(	8.286335	20.47289	9.235896	0	0	0	4.8805	2.44E-05	8.64E-05	AF131217.	chr21	-	29816870	30047170	900
ENSG00000(	45.57484	37.33292	26.38828	19.47596	10.12475	12.32947	1.3312	0.006973	0.0168	LYRM9	chr17	-	26205340	26221778	2824
ENSG00000(	11.39371	4.817151	22.43003	3.745378	7.363456	3.28786	1.2939	0.10137	0.17745	SMG7-AS1	chr1	-	1.83E+08	1.83E+08	2246
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	RP4-665N4	chr1	-	36545667	36547923	898
ENSG00000(	4.143168	1.204288	1.319414	0	0	0	2.1615	0.11037	0.19002	SEC1P	chr19	+	49141328	49184461	1511
ENSG00000(	3.107376	7.225726	2.638828	0	2.761296	0.821965	1.431	0.21723	0.3284	CTAGE3P	chr13	-	52482354	52484757	2404
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	RP11-135A	chr3	-	1.94E+08	1.94E+08	430
ENSG00000(	6.214751	1.204288	1.319414	0	0	2.465895	1.2124	0.34401	0.47322	HMGN2P3!	chr10	-	98675390	98675659	270
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	CTA-212D2	chr6	+	1.35E+08	1.35E+08	790
ENSG00000(	0	0	0	2.247227	0.920432	0.821965	-1.2297	0.36205	NA	RP11-544N	chr1	+	1.61E+08	1.61E+08	173
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	RP3-453C1	chr20	-	44016987	44017345	359
ENSG00000(	6.214751	0	3.958241	0	0	0.821965	2.137	0.10375	0.18082	PHKA1P1	chr1	-	91358549	91359169	621
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	GPC5-AS2	chr13	-	92992047	92992856	401
ENSG00000(	46.61064	62.62296	48.81831	12.73428	16.56778	20.54912	1.6257	0.000117	0.000379	RPS11P5	chr12	+	1.33E+08	1.33E+08	486
ENSG00000(	0	0	0	0	3.681728	2.465895	-1.6477	0.22446	0.33686	RP11-136K	chr6	+	1.51E+08	1.51E+08	378
ENSG00000(	0	0	1.319414	0	0	2.465895	-0.38078	0.77353	NA	RP11-267N	chr1	+	1.63E+08	1.63E+08	2633
ENSG00000(	6.214751	7.225726	2.638828	14.98151	3.681728	0.821965	-0.241	0.80003	0.86975	CYCSP10	chr3	-	10042331	10042624	294
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP13-137A	chr10	-	1.35E+08	1.35E+08	2619
ENSG00000(	3.107376	0	2.638828	5.243529	4.60216	11.50751	-1.5565	0.12682	0.21305	RP11-746P	chr7	+	64820847	64822089	1243
ENSG00000(	14.50109	4.817151	7.916483	6.74168	15.64734	10.68554	-0.23984	0.74077	0.82663	RP5-977B1	chr20	-	35136563	35201794	749
ENSG00000(	6.214751	7.225726	9.235896	0.749076	2.761296	0.821965	2.0175	0.042781	0.08489	RP3-510O8	chr6	-	35701644	35704724	669
ENSG00000(	0	7.225726	0	2.247227	1.840864	1.64393	0.22757	0.85534	0.90803	RP5-1115A	chr1	+	8484705	8494898	516
ENSG00000(	1.035792	4.817151	1.319414	0	0	0.821965	1.7611	0.18608	0.29062	RP11-429H	chr10	-	95841707	95868571	1612
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	AC097721.	chr2	-	1.39E+08	1.39E+08	1253
ENSG00000(	1.035792	0	0	2.247227	0	0	-0.31629	0.80869	NA	HMGN2P2	chr5	-	1.16E+08	1.16E+08	270
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	AC000078.	chr22	+	19874812	19875493	682
ENSG00000(	4.143168	4.817151	2.638828	0	3.681728	1.64393	0.89038	0.43424	0.564	DDX3YP1	chrX	+	73340847	73351758	1950
ENSG00000(	249.6258	254.1047	139.8579	74.15848	71.7937	69.04505	1.5699	1.80E-09	9.66E-09	LINC00342	chr2	-	96472866	96481963	2351
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-80H5	chr10	+	91405039	91410424	563
ENSG00000(	9.322127	2.408575	5.277655	7.490755	1.840864	7.397684	0.022611	0.98016	0.98845	AC139099.	chr17	+	81174666	81188573	2256
ENSG00000(	4.143168	8.430014	1.319414	1.498151	3.681728	6.575719	0.21125	0.83256	0.8928	HCG25	chr6	+	33217311	33222766	759
ENSG00000(	0	0	0	2.247227	3.681728	0	-1.606	0.23624	0.35065	RP11-390F	chr9	+	6675284	6675614	331
ENSG00000(	3.107376	1.204288	2.638828	1.498151	0	0.821965	1.0366	0.41655	0.54713	HSPA8P18	chr3	-	19981761	19984802	1928
ENSG00000(	346.9903	446.7907	275.7575	515.364	426.16	530.1674	-0.45788	0.014112	0.031741	SNHG15	chr7	-	45022622	45026560	3116
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	HMGN2P2(	chr2	+	24553271	24553543	273
ENSG00000(	3.107376	4.817151	3.958241	2.247227	0	0.821965	1.4313	0.22159	0.3333	POLHP1	chr2	-	2.17E+08	2.17E+08	470
ENSG00000(	40.39588	31.31148	47.4989	9.737982	19.32907	12.32947	1.4857	0.001947	0.005199	CYP1B1-AS	chr2	+	38302791	38408997	1757
ENSG00000(	31.07376	28.90291	54.09597	23.97042	8.283888	11.50751	1.3124	0.011259	0.02588	LINC00327	chr13	+	24040710	24061603	2087
ENSG00000(	2.071584	0	0	0	0	1.64393	0.14412	0.91322	NA	RP11-146N	chr9	-	19291335	19292574	409
ENSG00000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	AC051649.	chr11	+	2012326	2014699	722
ENSG00000(	5.17896	0	1.319414	2.247227	0	0	0.89268	0.50325	0.63121	RPL7P14	chr2	+	2.04E+08	2.04E+08	741
ENSG00000(	16.57267	16.86003	14.51355	38.95193	30.37426	18.90519	-0.8472	0.097201	0.17127	RP11-267N	chr1	-	1.63E+08	1.63E+08	1441
ENSG00000(	3.107376	0	1.319414	23.97042	27.61296	21.37109	-3.5548	1.31E-05	4.78E-05	AC034220.	chr5	-	1.32E+08	1.32E+08	1792
ENSG00000(	0	0	2.638828	6.74168	5.522592	0	-1.5172	0.23055	0.34396	RP11-475C	chr1	-	84041459	84326706	3177

ENSG00000(	3.107376	1.204288	0	1.498151	0	0	0.77471	0.56777	NA	NALCN-AS1	chr13	+	1.01E+08	1.02E+08	2846
ENSG00000(	1.035792	3.612863	2.638828	0	2.761296	1.64393	0.52346	0.6709	0.77365	RPEP4	chr22	+	30004889	30005490	602
ENSG00000(	0	0	2.638828	0	6.443024	4.109825	-1.3252	0.30237	0.42747	HDAC1P2	chr1	+	2.21E+08	2.21E+08	1398
ENSG00000(	8.286335	3.612863	3.958241	0.749076	2.761296	1.64393	1.3464	0.19973	0.30742	FAM157B	chr9	+	1.41E+08	1.41E+08	1795
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	SLC25A6P1	chr20	-	21722941	21723715	775
ENSG00000(	2897.11	2796.356	2224.532	1530.361	1438.635	1789.418	0.73312	7.61E-08	3.53E-07	SNHG7	chr9	-	1.4E+08	1.4E+08	2357
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP5-908M:	chr20	+	61004604	61006568	477
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP4-597N1	chr1	-	2.35E+08	2.35E+08	226
ENSG00000(	1.035792	0	1.319414	2.996302	0.920432	0	-0.4173	0.75669	0.83898	RP11-490E	chr10	+	483501	487110	558
ENSG00000(	1.035792	1.204288	0	0.749076	0	0	0.55357	0.6746	NA	PKD1P1	chr16	-	18451943	18473188	1547
ENSG00000(	12.4295	10.83859	1.319414	1.498151	5.522592	1.64393	1.3131	0.16993	0.27006	CRYZP1	chr7	-	1.03E+08	1.03E+08	947
ENSG00000(	2.071584	2.408575	0	0.749076	5.522592	0.821965	-0.43409	0.72755	0.81751	RP11-439A	chr1	+	1.21E+08	1.21E+08	3543
ENSG00000(	9.322127	20.47289	7.916483	5.243529	1.840864	5.753754	1.3966	0.077409	0.1413	RP11-196G	chr1	-	1.5E+08	1.5E+08	3543
ENSG00000(	3.107376	0	0	0.749076	0	0.821965	0.47233	0.72731	NA	CASK-AS1	chrX	+	41379289	41381589	515
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	FAM204BP	chr1	-	1.98E+08	1.98E+08	701
ENSG00000(	0	2.408575	2.638828	0	0	0	1.6365	0.22501	NA	RP1-137K2	chr6	-	1.57E+08	1.57E+08	423
ENSG00000(	2.071584	0	0	2.247227	3.681728	0	-0.83162	0.53462	0.65901	AC097523.	chr2	+	1.39E+08	1.39E+08	637
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RP5-1069C	chr20	-	12845850	12933167	3033
ENSG00000(	10.35792	9.634302	10.55531	69.66403	87.44104	90.41614	-2.941	4.20E-12	2.75E-11	ERVH48-1	chr21	-	44336913	44345756	2790
ENSG00000(	4.143168	1.204288	9.235896	9.737982	1.840864	0.821965	0.17066	0.86881	0.91759	AC046143.	chr3	+	1.94E+08	1.94E+08	2680
ENSG00000(	0	0	2.638828	0.749076	0	0	0.57076	0.66213	NA	AC016700.	chr2	+	70316853	70323232	448
ENSG00000(	3.107376	1.204288	6.597069	0.749076	4.60216	6.575719	-0.10867	0.91737	0.94983	TTLL7-IT1	chr1	-	84444801	84449983	2921
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP3-380B8	chr6	+	5851739	5870453	411
ENSG00000(	0	0	0	4.494453	0	0.821965	-1.4611	0.2797	NA	RP11-40F8	chrX	-	22407432	23082236	718
ENSG00000(	0	0	2.638828	0.749076	0.920432	1.64393	-0.20682	0.87815	0.92389	ZFY-AS1	chrY	-	2834885	2870667	500
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RP11-487E	chr1	-	21330043	21330427	385
ENSG00000(	0	1.204288	0	0	1.840864	1.64393	-0.67765	0.61688	NA	AC005009.	chr7	-	86413542	86415986	687
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	AL023583.	chr6	+	13817713	13817966	252
ENSG00000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	RP11-290F	chr20	-	48927248	48937879	2250
ENSG00000(	0	4.817151	0	0.749076	1.840864	0.821965	0.30687	0.81654	0.88106	RP11-440G	chr9	+	94188520	94189426	474
ENSG00000(	3.107376	0	1.319414	2.996302	0.920432	1.64393	-0.216	0.86401	0.91404	AL672183.	chr1	+	2.49E+08	2.49E+08	463
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	XXyac-YX65	chr6	-	1.7E+08	1.7E+08	654
ENSG00000(	0	1.204288	0	0.749076	9.20432	0	-1.7404	0.18937	0.2945	RP11-375C	chr9	-	82120719	82147257	1788
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC073869.	chr2	-	1.32E+08	1.32E+08	3666
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-520A	chr3	-	41012032	41013069	670
ENSG00000(	0	0	5.277655	122.8484	103.0884	104.3895	-5.683	9.05E-18	8.25E-17	RP11-344E	chr17	+	20771746	20905589	3727
ENSG00000(	2.071584	0	5.277655	0	0	0	2.1617	0.11093	0.19077	RP11-375A	chr1	-	77811731	77815270	377
ENSG00000(	1.035792	7.225726	2.638828	95.13259	103.0884	128.2265	-4.7272	1.31E-18	1.24E-17	HOXB-AS3	chr17	+	46626992	46683776	743
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	RP11-524P	chrX	-	41907136	41914089	478
ENSG00000(	1.035792	0	1.319414	0	0.920432	0	0.55201	0.67753	NA	AC006042.	chr7	-	7997814	8009534	568
ENSG00000(	3.107376	3.612863	0	0	0	0	2.0594	0.12904	0.21592	RP11-22C8	chr8	+	49826419	49826939	465
ENSG00000(	0	0	0	5.243529	3.681728	2.465895	-2.689	0.039185	0.078612	RP11-301L	chr4	+	1.87E+08	1.87E+08	1789
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RAB1C	chr9	-	37636685	37637290	606
ENSG00000(	1.035792	3.612863	0	0	0	0	1.5346	0.25314	NA	RP4-533D7	chr1	+	46570622	46570847	226

ENSG00000(	25.8948	16.86003	14.51355	6.74168	0.920432	7.397684	1.7698	0.013134	0.02971	LINC00702	chr10	-	4277752	4285981	446
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	VN1R20P	chr3	+	13968310	13969275	966
ENSG00000(	7.250543	18.06432	9.235896	3.745378	29.45382	13.15144	-0.38475	0.59342	0.70949	CTAGE7P	chr10	+	1.32E+08	1.32E+08	2823
ENSG00000(	1.035792	0	1.319414	1.498151	0.920432	0	-0.02384	0.98598	NA	RP11-199B	chr13	-	97824723	97831876	692
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP5-837O2	chr1	-	94400035	94400800	766
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC104451.	chr3	-	17747550	17747725	176
ENSG00000(	922.8906	1018.827	1186.153	313.8627	358.9685	320.5663	1.6498	3.78E-29	5.56E-28	RP11-220I:	chr9	+	37079893	37090398	4375
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AC009492.	chr2	+	2.18E+08	2.18E+08	557
ENSG00000(	0	0	1.319414	0	0.920432	2.465895	-0.65854	0.62673	NA	RP11-537A	chr10	+	75141191	75143254	401
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	UBE2E2-AS:	chr3	-	23236561	23244069	499
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP4-655J1:	chr1	-	1.17E+08	1.17E+08	621
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	HMGA1P8	chr2	-	74645249	74645569	321
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP3-388M:	chr22	-	44155079	44155790	712
ENSG00000(	0	3.612863	0	0	0.920432	0	0.81649	0.54246	NA	RP11-259F	chr10	-	70921286	70921662	377
ENSG00000(	2.071584	4.817151	5.277655	25.46857	11.04518	8.219649	-1.7241	0.029212	0.060746	ADIRF-AS1	chr10	-	88725496	88729158	718
ENSG00000(	8.286335	2.408575	7.916483	5.992604	14.72691	11.50751	-0.71029	0.36362	0.4934	RP11-863K	chr8	-	37604854	37605522	669
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-12A2	chr9	+	67789674	67789866	193
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	CTD-2020K	chr17	-	43315395	43319101	2003
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	OR7E157P	chr8	+	7449528	7450438	911
ENSG00000(	112.9013	104.773	120.0667	74.15848	37.73771	50.96182	1.0316	0.000669	0.001929	RP11-421L	chr1	+	1.01E+08	1.02E+08	1531
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-307I:	chr9	-	4803788	4804972	1185
ENSG00000(	0	0	1.319414	0	2.761296	0	-0.44505	0.73801	NA	RP11-122F	chr10	-	86148926	86149382	457
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-460H	chr10	-	32520777	32521173	397
ENSG00000(	0	0	5.277655	0.749076	1.840864	0	0.57019	0.6715	0.77389	GS1-304P7	chr1	-	1.87E+08	1.87E+08	677
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	TMEM256P	chr10	-	71283067	71283406	340
ENSG00000(	7.250543	8.430014	5.277655	3.745378	6.443024	13.9734	-0.17963	0.82393	0.88633	RNF224	chr9	+	1.4E+08	1.4E+08	1503
ENSG00000(	0	1.204288	1.319414	0	2.761296	0	-0.06147	0.96386	NA	AC006028.	chr7	+	2804242	2815134	544
ENSG00000(	0	0	0	4.494453	3.681728	3.28786	-2.7058	0.037623	0.075872	RP11-67L3	chr1	+	55353236	55354523	515
ENSG00000(	0	2.408575	0	0.749076	0	3.28786	-0.40143	0.76683	0.84621	AC108479.	chr2	+	88272175	88272601	427
ENSG00000(	1.035792	1.204288	7.916483	0	0	0	2.73	0.040531	0.080979	AP000472.	chr21	-	23381263	23470778	897
ENSG00000(	3.107376	0	0	0.749076	0	0	0.76338	0.56438	NA	RP11-414C	chr1	-	58694354	58694675	322
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	MROH3P	chr1	+	2.01E+08	2.01E+08	2625
ENSG00000(	1.035792	1.204288	1.319414	10.48706	1.840864	4.93179	-1.7981	0.1029	0.17957	SNX18P16	chr1	-	1.43E+08	1.43E+08	547
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-89N1	chr7	-	33908113	33913843	380
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	LINC00167	chr11	+	1.3E+08	1.3E+08	1419
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AC133785.	chr2	-	1.32E+08	1.32E+08	2824
ENSG00000(	37.28851	40.94578	25.06886	36.7047	36.81728	55.89361	-0.31344	0.43624	0.5659	AC113189.	chr17	-	7485282	7487390	679
ENSG00000(	0	2.408575	0	0	0.920432	0.821965	0.212	0.87508	NA	HIST1H2AM	chr6	-	27860477	27860963	487
ENSG00000(	0	3.612863	1.319414	1.498151	1.840864	5.753754	-0.66063	0.58152	0.69939	AC004987.	chr7	+	39872813	39874544	1731
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CNOT7P1	chrX	-	69157016	69157867	852
ENSG00000(	69.39806	71.05298	72.56776	38.20285	62.58938	33.70056	0.65811	0.054725	0.10515	AC079807.	chr2	+	48132817	48134949	656
ENSG00000(	32.10955	13.24716	18.47179	8.239831	17.48821	4.109825	1.0487	0.10399	0.18112	RP4-655C5	chr6	+	1.67E+08	1.67E+08	904
ENSG00000(	1.035792	0	3.958241	1.498151	0	3.28786	0.019276	0.98813	0.99282	NPIPL1	chr16	-	28467693	28481868	1406
ENSG00000(	18.64425	15.65574	38.263	50.18806	45.10117	38.63235	-0.87278	0.048803	0.095017	LINC00472	chr6	-	72054047	72130472	2958

ENSG0000(	0	0	0	0	4.60216	0.821965	-1.4643	0.27877	NA	RP11-399F	chr9	-	43027748	43032877	783
ENSG0000(	5.17896	6.021439	10.55531	0.749076	1.840864	0	2.4659	0.021467	0.046216	RP11-415J	chr1	+	33815953	33828846	490
ENSG0000(	0	0	1.319414	0.749076	1.840864	3.28786	-1.2451	0.35207	0.48182	GS1-257G1	chrX	+	14262325	14263544	1220
ENSG0000(	3.107376	1.204288	2.638828	4.494453	1.840864	0	0.092584	0.93878	0.9628	RP3-339A1	chrX	-	53459670	53459979	218
ENSG0000(	7.250543	8.430014	5.277655	59.92604	36.81728	58.35951	-2.7712	9.95E-08	4.57E-07	AC007743.	chr2	-	56400669	56412905	3075
ENSG0000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RPL21P134	chrX	+	74604181	74604663	483
ENSG0000(	0	0	0	2.247227	0	2.465895	-1.3312	0.32317	NA	AC019181.	chr2	+	1.66E+08	1.66E+08	567
ENSG0000(	4.143168	6.021439	2.638828	1.498151	0	0.821965	1.7994	0.12625	0.21231	AC006042.	chr7	+	8019943	8021859	1469
ENSG0000(	3.107376	7.225726	1.319414	0.749076	0	0	2.4468	0.055528	0.10642	HMGB1P31	chr2	+	54278471	54278897	427
ENSG0000(	0	0	2.638828	5.243529	6.443024	13.15144	-2.5921	0.017771	0.039043	SNRPEP4	chr19	-	5576671	5576949	279
ENSG0000(	1.035792	0	6.597069	0	0	0	2.1847	0.10719	0.18573	AC009238.	chr2	+	96100507	96100861	355
ENSG0000(	6667.392	6429.692	5087.66	4809.814	3952.335	4693.42	0.43359	0.00091	0.002565	GPX1	chr3	-	49394609	49396033	1146
ENSG0000(	33.14534	40.94578	121.3861	0.749076	18.40864	4.109825	2.5877	0.008858	0.020833	CRYBG3	chr3	+	97540884	97594132	4261
ENSG0000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-341B	chr10	+	90898801	90899215	415
ENSG0000(	2.071584	2.408575	1.319414	0	0	0	1.9715	0.14607	NA	RP11-410N	chr20	+	31148895	31161690	469
ENSG0000(	1.035792	1.204288	1.319414	0.749076	2.761296	3.28786	-0.65376	0.59706	0.71279	AC092159.	chr2	+	677186	697371	1943
ENSG0000(	8.286335	1.204288	13.19414	0	0	0	4.0086	0.001227	0.003392	RASA4DP	chr7	-	1.02E+08	1.02E+08	1199
ENSG0000(	4.143168	0	0	0	3.681728	1.64393	-0.1859	0.88835	0.9307	XXYLT1-AS1	chr3	+	1.95E+08	1.95E+08	431
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	OSTN-AS1	chr3	-	1.91E+08	1.91E+08	515
ENSG0000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-500G	chr10	-	1.32E+08	1.32E+08	472
ENSG0000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	H2BFXP	chrX	+	1.03E+08	1.03E+08	364
ENSG0000(	2.071584	0	0	1.498151	0.920432	0.821965	-0.3171	0.81476	NA	RP11-482E	chr10	-	3529086	3545030	832
ENSG0000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	MIPEPP3	chr13	+	21872398	21880512	444
ENSG0000(	2.071584	0	0	4.494453	1.840864	0.821965	-1.0833	0.4065	0.53736	USP32P2	chr17	-	18414535	18445234	4735
ENSG0000(	5.17896	1.204288	9.235896	6.74168	17.48821	14.79537	-1.2011	0.1307	0.21823	PFN1P1	chr1	-	1.72E+08	1.72E+08	423
ENSG0000(	0	2.408575	2.638828	0	1.840864	0.821965	0.55733	0.67451	0.77646	RP1-12G14	chr6	-	1.5E+08	1.5E+08	340
ENSG0000(	2.071584	3.612863	6.597069	0	5.522592	4.109825	0.28292	0.79384	0.86525	RP11-464C	chr10	+	1.26E+08	1.26E+08	1491
ENSG0000(	8.286335	12.04288	14.51355	8.988907	11.96562	18.90519	-0.1891	0.77047	0.84912	UBE2FP3	chr1	+	1.12E+08	1.12E+08	524
ENSG0000(	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	TLR8-AS1	chrX	-	12920936	12926452	1349
ENSG0000(	2.071584	0	3.958241	0	3.681728	0	0.44714	0.73536	0.82299	AC018878.	chr2	+	1.07E+08	1.07E+08	433
ENSG0000(	0	0	0	0	2.761296	3.28786	-1.6293	0.2296	0.34285	RP11-25C1	chr10	-	1.14E+08	1.14E+08	358
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	ATP6V1G1F	chr10	+	35447234	35447568	335
ENSG0000(	0	7.225726	2.638828	0	1.840864	0	1.5423	0.23614	0.35057	ERP29P1	chr20	-	50726883	50727588	706
ENSG0000(	0	2.408575	1.319414	2.247227	0	0	0.35636	0.79265	0.86445	RP1-69D17	chr6	-	1.3E+08	1.3E+08	391
ENSG0000(	0	0	1.319414	0.749076	2.761296	0.821965	-0.93317	0.49046	NA	CHRM3-AS2	chr1	-	2.4E+08	2.4E+08	2431
ENSG0000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP1-209A6	chr6	-	22744624	23032009	871
ENSG0000(	0	0	0	3.745378	2.761296	0	-1.7329	0.20153	0.30918	RP11-202K	chr1	-	1.03E+08	1.03E+08	657
ENSG0000(	0	4.817151	0	2.247227	1.840864	1.64393	-0.17283	0.89246	0.93347	Z83844.1	chr22	-	38037839	38054384	1945
ENSG0000(	0	0	2.638828	0	0	3.28786	-0.16812	0.90128	NA	RP11-307L	chr9	-	6415145	6449558	638
ENSG0000(	114.9729	166.1917	141.1773	43.44638	42.33987	44.38611	1.6775	1.49E-09	8.05E-09	RP11-396K	chr7	+	72569033	72619657	2629
ENSG0000(	0	0	0	5.992604	5.522592	0.821965	-2.7569	0.03466	0.070533	RP11-318G	chr13	-	78513297	78519009	902
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AK4P3	chr12	-	31768702	31769373	672
ENSG0000(	0	4.817151	0	18.72689	20.2495	25.48091	-3.317	1.00E-04	0.000326	NKAPP1	chrX	-	1.19E+08	1.19E+08	4940
ENSG0000(	4.143168	10.83859	5.277655	0	0.920432	4.93179	1.4601	0.16456	0.26295	RP11-100E	chr1	-	2.25E+08	2.25E+08	403

ENSG00000(	23.82321	20.47289	5.277655	0	0	0	5.2521	3.89E-06	1.51E-05	AC104809.	chr2	-	2.42E+08	2.42E+08	2274
ENSG00000(	0	0	0	40.45008	34.05598	13.15144	-5.6764	1.57E-07	7.07E-07	AP000688.	chr21	+	37477179	37481988	2336
ENSG00000(	14.50109	18.06432	19.79121	5.243529	4.60216	4.109825	1.7707	0.009705	0.022638	RP11-458D	chr1	-	1.45E+08	1.45E+08	872
ENSG00000(	2.071584	2.408575	1.319414	2.996302	0	2.465895	0.052429	0.96608	0.98018	RP11-296A	chr1	-	51716270	51717144	870
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	AC012065.	chr2	-	20806040	20806414	375
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	RP5-875O1	chr1	-	16860381	16862144	1548
ENSG00000(	24.85901	49.3758	36.94359	25.46857	26.69253	31.23467	0.39931	0.3544	0.48417	EIF3FP3	chr2	+	58478575	58479703	1086
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP1-212P9	chr1	-	29196995	29203848	1085
ENSG00000(	102.5434	86.70872	72.56776	63.67142	55.22592	63.2913	0.51968	0.075694	0.13872	HOTAIRM1	chr7	+	27135266	27139884	889
ENSG00000(	5.17896	0	0	0	1.840864	1.64393	0.36786	0.78266	0.85692	RP11-403I1	chr1	-	1.49E+08	1.49E+08	537
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-63N8	chr1	+	21912965	21917680	821
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP1-296G1	chrX	-	1.2E+08	1.2E+08	1600
ENSG00000(	0	2.408575	1.319414	0	0.920432	0	0.92035	0.49653	NA	AGGF1P2	chr10	+	1.35E+08	1.35E+08	809
ENSG00000(	10.35792	8.430014	17.15238	20.97412	7.363456	5.753754	0.055081	0.93772	0.9623	BTBD18	chr11	-	57510986	57519253	3044
ENSG00000(	6.214751	14.45145	0	0	2.761296	0.821965	1.9657	0.084573	0.15262	AC109829.	chr2	+	27760253	27790011	825
ENSG00000(	16.57267	12.04288	17.15238	1.498151	8.283888	0	2.0098	0.017961	0.039389	STXBP5-AS1	chr6	-	1.47E+08	1.48E+08	2927
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RPL35AP31	chr13	+	72420113	72420449	337
ENSG00000(	31.07376	50.58008	27.70769	89.88907	59.82808	55.89361	-0.89564	0.01658	0.036673	RP11-295G	chr1	-	2.32E+08	2.32E+08	465
ENSG00000(	2.071584	6.021439	0	5.243529	0	2.465895	0.04353	0.97119	0.98327	ST6GALNAC	chr13	-	20392261	20392759	499
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC000094.	chr22	+	19245043	19246329	1287
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-218D	chr10	+	28288717	28338544	469
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-520H	chr1	-	1.59E+08	1.59E+08	663
ENSG00000(	455.7484	484.1237	451.2395	280.9033	208.9381	249.0554	0.90695	7.14E-08	3.32E-07	EEF1A1P6	chr7	-	22550231	22551618	1386
ENSG00000(	8.286335	2.408575	1.319414	0	0	0	3.0453	0.020333	0.04402	RP1-187B2	chr1	-	25971035	25985602	2224
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP11-78O9	chr1	+	94610667	94611175	352
ENSG00000(	0	0	1.319414	1.498151	0	9.041614	-1.8199	0.16582	0.26453	CTD-2020K	chr17	-	43322553	43326203	579
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-74B2	chrX	-	83658906	83659032	127
ENSG00000(	4.143168	10.83859	9.235896	25.46857	26.69253	36.98842	-1.8063	0.001879	0.005032	RP11-181E	chr2	-	1.12E+08	1.12E+08	2044
ENSG00000(	12.4295	3.612863	7.916483	0	0	0	4.1685	0.000611	0.001773	AC010091.	chr7	-	81205702	81255532	4571
ENSG00000(	0	6.021439	11.87472	62.92235	85.60018	81.37453	-3.6008	1.46E-11	9.19E-11	TMEM238	chr19	-	55890613	55895966	1000
ENSG00000(	0	1.204288	0	0	0	1.64393	-0.12916	0.91993	NA	SYNJ2-IT1	chr6	+	1.58E+08	1.58E+08	599
ENSG00000(	0	0	0	0.749076	0	4.109825	-1.3462	0.31758	NA	SRGAP2-AS	chr1	-	2.07E+08	2.07E+08	2178
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-288G	chr6	-	7481327	7482827	1501
ENSG00000(	6.214751	6.021439	6.597069	5.992604	1.840864	6.575719	0.3297	0.70913	0.80335	ZNF197-AS	chr3	-	44658620	44666289	623
ENSG00000(	2.071584	3.612863	0	0.749076	0	0.821965	1.0769	0.41927	0.54998	RP1-128O3	chr6	+	1.09E+08	1.09E+08	187
ENSG00000(	1.035792	4.817151	2.638828	0	0	0	2.5113	0.061109	0.11541	RP11-132N	chr6	-	85397069	85398465	495
ENSG00000(	0	0	0	1.498151	2.761296	0	-1.199	0.3707	NA	RP11-570P	chr1	-	44587825	44588184	360
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP11-177F	chr1	-	2.41E+08	2.41E+08	316
ENSG00000(	4.143168	9.634302	6.597069	2.247227	0	0	2.4048	0.031448	0.064777	RP5-1172A	chr22	-	27617310	27620688	637
ENSG00000(	3.107376	3.612863	0	0	0	0	2.0594	0.12904	0.21592	RANP8	chr13	-	21321174	21322196	713
ENSG00000(	35.21692	56.60152	36.94359	29.96302	48.7829	50.13986	0.000733	0.99851	0.99905	AC092295.	chr19	+	37063972	37085610	1033
ENSG00000(	44.53905	31.31148	31.66593	2.247227	13.80648	9.041614	2.024	0.000438	0.001299	LINC00460	chr13	+	1.07E+08	1.07E+08	739
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-867G	chr11	+	94371204	94373999	712
ENSG00000(	8.286335	4.817151	0	2.247227	8.283888	3.28786	-0.03318	0.9741	0.98485	AC017104.	chr2	+	2.32E+08	2.32E+08	568

ENSG00000(	3.107376	1.204288	2.638828	0	4.60216	2.465895	-0.00039	0.99974	0.99974	RP11-57H1	chr10	-	1.15E+08	1.15E+08	460
ENSG00000(	1.035792	0	0	0	0	2.465895	-0.37334	0.77636	NA	RP11-335H	chr9	-	16775571	16775843	273
ENSG00000(	8.286335	14.45145	6.597069	17.22874	11.96562	17.26126	-0.62513	0.33225	0.46038	RP11-326F	chr9	+	33166973	33179981	843
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	NFU1P2	chr1	+	98542556	98543024	469
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	RP3-486I3.	chr6	-	1.17E+08	1.17E+08	623
ENSG00000(	20.71584	14.45145	15.83297	11.23613	7.363456	7.397684	0.91513	0.14545	0.238	AC016831.	chr7	+	1.31E+08	1.31E+08	1616
ENSG00000(	13.46529	1.204288	1.319414	5.243529	10.12475	13.9734	-0.73401	0.40908	0.53984	KRT8P39	chr12	+	69099414	69100846	1433
ENSG00000(	0	0	0	0	3.681728	1.64393	-1.4596	0.2805	NA	RP11-548N	chr1	+	1.83E+08	1.83E+08	684
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	RP11-545D	chrX	-	34224842	34433654	526
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP3-462D8	chr22	-	25675496	25679061	568
ENSG00000(	1.035792	0	0	2.247227	0.920432	3.28786	-1.4278	0.28462	0.40765	RP5-1022P	chr20	+	5529486	5530127	642
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	KRT8P15	chr2	-	2.04E+08	2.04E+08	1451
ENSG00000(	0	0	0	4.494453	7.363456	3.28786	-3.1175	0.013969	0.031454	AC069155.	chr2	+	2.17E+08	2.17E+08	575
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP4-635A2	chr1	-	1.85E+08	1.85E+08	1152
ENSG00000(	0	0	0	2.996302	1.840864	4.109825	-2.3265	0.080173	0.14563	AC115617.	chrX	-	48634408	48635385	978
ENSG00000(	3.107376	3.612863	6.597069	0	0	0	3.2434	0.01198	0.027356	CYP51P2	chr13	-	29296523	29298158	1499
ENSG00000(	0	0	5.277655	0	0.920432	2.465895	0.35899	0.78831	0.8615	RP4-694A7	chr1	+	68944812	68949222	960
ENSG00000(	21.75163	18.06432	15.83297	5.992604	9.20432	5.753754	1.3379	0.035608	0.072224	RP4-665J2	chr1	-	91295104	91317207	2986
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	RP11-343B	chr3	-	1.42E+08	1.42E+08	576
ENSG00000(	7.250543	14.45145	3.958241	1.498151	12.88605	8.219649	0.17772	0.83247	0.89276	ERI3-IT1	chr1	-	44709080	44709945	619
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	JTBP1	chr22	+	41194043	41194289	247
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC073628.	chr2	+	78143060	78145135	635
ENSG00000(	3.107376	1.204288	0	0	0	0	1.4526	0.27741	NA	AC068610.	chr7	-	1.15E+08	1.15E+08	565
ENSG00000(	454.7126	481.7151	393.1853	8.239831	17.48821	16.4393	4.9489	6.70E-72	3.02E-70	TWIST2	chr2	+	2.4E+08	2.4E+08	1176
ENSG00000(	0	0	9.235896	0	0	8.219649	0.054747	0.966	0.98015	RP11-62H7	chr8	+	8818710	8836535	722
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC079135.	chr2	+	2.37E+08	2.37E+08	768
ENSG00000(	5.17896	12.04288	2.638828	7.490755	6.443024	5.753754	0.012781	0.98789	0.99279	DCUN1D2-/	chr13	+	1.14E+08	1.14E+08	330
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	DDX11L10	chr16	+	61553	64093	1653
ENSG00000(	0	0	0	2.247227	0	0.821965	-0.85594	0.51054	NA	AC006328.	chrY	-	27633431	27633809	379
ENSG00000(	7.250543	13.24716	6.597069	7.490755	10.12475	12.32947	-0.13171	0.85407	0.90713	RP11-422J	chr1	-	37920480	37940012	1395
ENSG00000(	18.64425	39.74149	31.66593	7.490755	8.283888	13.15144	1.5621	0.004881	0.012116	CYP2T2P	chr19	-	41314430	41317295	1285
ENSG00000(	0	0	0	3.745378	5.522592	4.109825	-2.9378	0.021961	0.047171	PGAM1P11	chr1	+	10118729	10119706	680
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	RP5-905G1	chr20	-	17868007	17868804	632
ENSG00000(	8.286335	0	0	2.247227	2.761296	1.64393	0.25659	0.83335	0.89318	RP11-565J	chr1	+	2.12E+08	2.12E+08	386
ENSG00000(	0	3.612863	7.916483	5.243529	0	1.64393	0.52233	0.65864	0.76322	RP11-457N	chr6	-	26634611	26637008	530
ENSG00000(	3.107376	0	0	0	0	2.465895	0.17171	0.89908	NA	AC037445.	chr17	-	61271291	61416414	491
ENSG00000(	0	6.021439	7.916483	0	0	0	3.1275	0.017638	0.038775	AC018730.	chr2	-	1.05E+08	1.05E+08	747
ENSG00000(	4.143168	0	0	0.749076	0	0	1.0202	0.44849	NA	RP11-491H	chr10	-	63541503	63581004	510
ENSG00000(	1.035792	0	1.319414	0	0	0.821965	0.54471	0.68089	NA	ARHGEF7-I1	chr13	+	1.12E+08	1.12E+08	804
ENSG00000(	3.107376	3.612863	0	0	0	0	2.0594	0.12904	0.21592	OR52T1P	chr11	-	5587908	5588846	939
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-8J9.1	chr1	-	47131582	47132047	466
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC010095.	chr2	-	1.09E+08	1.09E+08	144
ENSG00000(	1.035792	0	0	12.73428	5.522592	3.28786	-2.9984	0.011238	0.025844	AC093388.	chr2	+	1.91E+08	1.91E+08	404
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	SPIN4-AS1	chrX	+	62569525	62572057	426

ENSG00000(	0	7.225726	7.916483	1.498151	0.920432	1.64393	1.4416	0.20476	0.31327	RP11-571F	chr9	-	34223982	34224626	645
ENSG00000(	13.46529	16.86003	15.83297	3.745378	7.363456	6.575719	1.2953	0.059665	0.11316	RNASEH2B-	chr13	-	51450822	51484848	794
ENSG00000(	0	6.021439	2.638828	0.749076	0.920432	1.64393	0.96305	0.43687	0.56654	RP11-184I:	chr1	+	44209142	44209412	271
ENSG00000(	1.035792	0	0	0	1.840864	0	-0.17777	0.89006	NA	RP11-13P5	chr6	+	1.6E+08	1.6E+08	385
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP5-1106H	chr7	-	1.01E+08	1.01E+08	213
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC079779.	chr2	+	317912	342118	853
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-108K	chr10	-	1.35E+08	1.35E+08	910
ENSG00000(	3.107376	3.612863	5.277655	0	0	0	3.0852	0.01784	0.039172	EBAG9P1	chr10	-	1.01E+08	1.01E+08	543
ENSG00000(	0	0	3.958241	0	3.681728	0.821965	-0.11768	0.92998	0.95795	RP11-506C	chr1	-	1.65E+08	1.65E+08	1963
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC007365.	chr2	+	64834109	64843616	1722
ENSG00000(	3.107376	1.204288	2.638828	2.247227	0	0	1.0135	0.43628	0.5659	GAS6-AS1	chr13	+	1.15E+08	1.15E+08	773
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	AC107083.	chr2	-	62734680	62734958	279
ENSG00000(	0	1.204288	0	10.48706	3.681728	4.109825	-2.7418	0.022342	0.04788	SLC26A4-A:	chr7	-	1.07E+08	1.07E+08	3687
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP4-798P1	chr1	-	1.78E+08	1.78E+08	811
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	AC074367.	chr2	-	63459588	63460712	1125
ENSG00000(	0	0	0	8.239831	13.80648	12.32947	-4.3723	0.000158	0.0005	MYCNOS	chr2	-	16061159	16082371	1313
ENSG00000(	5.17896	13.24716	11.87472	3.745378	1.840864	3.28786	1.5536	0.069721	0.12931	AC007092.	chr2	+	58654934	59290901	4077
ENSG00000(	12.4295	8.430014	5.277655	0	0	0.821965	3.6377	0.001395	0.00382	LINC00284	chr13	+	44482850	44604597	3208
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-219F	chr2	+	24557381	24558021	317
ENSG00000(	4.143168	2.408575	0	0.749076	6.443024	0.821965	-0.17849	0.88206	0.92636	RP11-34P1	chr1	+	131025	134836	3812
ENSG00000(	10.35792	10.83859	35.62417	1.498151	10.12475	12.32947	1.1464	0.1194	0.20291	AC092835.	chr2	+	95873283	95881351	1096
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC004947.	chr7	+	26591441	26596819	2781
ENSG00000(	23.82321	22.88147	15.83297	13.48336	11.04518	17.26126	0.55896	0.31012	0.43627	AC007969.	chr2	-	1.72E+08	1.72E+08	484
ENSG00000(	1.035792	1.204288	2.638828	0	0	0	1.7123	0.20641	NA	RP11-154P	chr9	+	70662044	70663084	635
ENSG00000(	7.250543	2.408575	2.638828	0	0.920432	0	2.4846	0.048801	0.095017	AC098617.	chr2	+	1.93E+08	1.93E+08	1207
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	PSMA6P3	chr21	-	47491999	47492162	164
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	CICP5	chr1	+	2.24E+08	2.24E+08	2215
ENSG00000(	0	0	2.638828	0	1.840864	0	0.2163	0.87177	NA	RP4-811H2	chr1	-	32814795	32816264	687
ENSG00000(	8.286335	6.021439	9.235896	5.992604	9.20432	6.575719	0.10649	0.89025	0.93185	AP001442.	chr21	+	27306401	27315001	1573
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP13-314C	chrX	-	23791109	23801073	672
ENSG00000(	0	0	0	0.749076	1.840864	0	-0.68825	0.58858	NA	UFL1-AS1	chr6	-	96806250	96969545	548
ENSG00000(	5.17896	2.408575	10.55531	0	4.60216	3.28786	0.99633	0.33782	0.46645	AC139887.	chr4	-	758275	758862	286
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-295G	chr9	+	1.36E+08	1.36E+08	526
ENSG00000(	8.286335	18.06432	6.597069	2.247227	3.681728	7.397684	1.1774	0.1492	0.24291	AC131097.	chr2	+	2.43E+08	2.43E+08	843
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC139426.	chr15	-	32694108	32695493	1386
ENSG00000(	0	0	0	7.490755	0.920432	0	-2.0459	0.1308	0.2183	IFNA13	chr9	-	21367371	21368075	705
ENSG00000(	3.107376	20.47289	9.235896	3.745378	0.920432	3.28786	1.7621	0.050535	0.098023	RP11-168K	chr9	+	1.16E+08	1.16E+08	3043
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AP000695.	chr21	+	37818029	37904706	715
ENSG00000(	1.035792	0	0	11.23613	3.681728	3.28786	-2.7645	0.022205	0.047629	RP11-535N	chr9	+	99488172	99489751	1262
ENSG00000(	3.107376	4.817151	0	4.494453	1.840864	3.28786	-0.21291	0.84906	0.90389	ENOX1-AS1	chr13	+	44118054	44122192	3907
ENSG00000(	44.53905	18.06432	39.58241	10.48706	47.86246	35.34449	0.12959	0.80469	0.87332	HIST1H2BN	chr6	+	27806323	27819974	707
ENSG00000(	0	0	1.319414	4.494453	2.761296	6.575719	-2.3418	0.05802	0.11056	RP11-135A	chr10	+	32635427	32636107	383
ENSG00000(	4.143168	0	1.319414	0	0	0	1.7539	0.19459	NA	AC017078.	chr2	-	46231081	46231448	368
ENSG00000(	12.4295	7.225726	13.19414	14.23244	11.96562	9.041614	-0.09638	0.88427	0.92775	AC073150.	chr7	-	27497782	27498468	687

ENSG00000(	0	0	0	9.737982	13.80648	22.19305	-4.7794	2.33E-05	8.26E-05	AC005083.	chr7	+	20257200	20261323	740
ENSG00000(	0	0	1.319414	14.98151	17.48821	12.32947	-4.0315	0.000129	0.000413	RP11-255H	chr19	+	23945746	24016116	1931
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	EIF3LP2	chr10	+	43062125	43062931	807
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	DPH3P1	chr20	+	61476490	61477543	1054
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	PCDH9-AS4	chr13	+	67565018	67576139	436
ENSG00000(	0	0	0	1.498151	0.920432	1.64393	-1.2565	0.35231	NA	CYCSP48	chrY	+	28546758	28547377	323
ENSG00000(	0	2.408575	2.638828	1.498151	0	0	0.90396	0.50381	0.63148	KCNQ5-IT1	chr6	+	73340223	73388282	563
ENSG00000(	5.17896	0	3.958241	0	1.840864	1.64393	0.98132	0.43206	0.56189	AC093732.	chr2	-	47262418	47267663	504
ENSG00000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	AC104113.	chr5	+	60213317	60215400	408
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP3-348I23	chr6	-	20756334	20800925	614
ENSG00000(	0	0	0	2.247227	0	1.64393	-1.1086	0.40518	NA	LATS2-AS1	chr13	+	21579296	21592261	632
ENSG00000(	0	3.612863	1.319414	0.749076	0	0	1.2665	0.35059	NA	AC005304.	chr17	-	13836037	13843911	405
ENSG00000(	0	0	0	2.996302	3.681728	1.64393	-2.2168	0.097064	0.1711	POU6F2-AS	chr7	-	39023843	39053151	514
ENSG00000(	45.57484	32.51577	40.90183	0.749076	0.920432	0.821965	5.0041	2.05E-10	1.19E-09	AC026904.	chr8	+	49502961	49507181	3549
ENSG00000(	1.035792	0	1.319414	0	0.920432	2.465895	-0.28162	0.83495	NA	RP11-359D	chr4	-	77678113	77679627	555
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	AC016907.	chr2	-	30273932	30366670	3563
ENSG00000(	255.8406	260.1261	271.7992	271.9144	370.9341	354.2669	-0.33752	0.062219	0.11723	TTTY15	chrY	+	14774265	14804162	5284
ENSG00000(	0	1.204288	0	0	1.840864	0.821965	-0.461	0.73167	NA	AC009302.	chr2	+	2.23E+08	2.23E+08	390
ENSG00000(	0	0	5.277655	9.737982	2.761296	5.753754	-1.4479	0.19382	0.29979	DLG5-AS1	chr10	+	79687130	79689582	487
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC005033.	chr2	-	74845983	74848106	813
ENSG00000(	0	3.612863	2.638828	0	0	0	1.93	0.15472	0.25026	RP11-182I1	chr1	+	65407662	65408048	387
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC073133.	chr7	-	1.56E+08	1.56E+08	2698
ENSG00000(	6.214751	21.67718	6.597069	2.247227	7.363456	1.64393	1.4487	0.091517	0.16303	YEATS2-AS1	chr3	-	1.84E+08	1.84E+08	1868
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AL353698.	chrX	+	56100757	56102014	1258
ENSG00000(	5.17896	2.408575	6.597069	0	7.363456	3.28786	0.35137	0.73869	0.82493	PAIP1P1	chr6	-	30154575	30156391	1203
ENSG00000(	0	0	0	0	3.681728	4.93179	-2.1075	0.1187	0.20199	EZR-AS1	chr6	+	1.59E+08	1.59E+08	217
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP4-650F1	chr1	+	74933879	74935227	497
ENSG00000(	22.78742	12.04288	26.38828	6.74168	20.2495	13.9734	0.55875	0.34997	0.47976	RP1-122P2	chr20	+	19738352	19790319	677
ENSG00000(	0	8.430014	7.916483	1.498151	0.920432	2.465895	1.3489	0.22505	0.33765	RP4-742C1	chr22	-	39532704	39537189	2364
ENSG00000(	44.53905	48.17151	27.70769	34.45748	8.283888	13.15144	1.055	0.043032	0.085314	RP11-65J3.	chr9	+	1.32E+08	1.32E+08	901
ENSG00000(	13.46529	3.612863	0	15.73059	9.20432	25.48091	-1.3738	0.087317	0.15686	Z83851.4	chr22	+	42672361	42673057	544
ENSG00000(	0	0	0	0	5.522592	4.109825	-2.2636	0.092421	0.16428	RP11-315I1	chr9	-	23671786	23672397	237
ENSG00000(	10.35792	15.65574	0	6.74168	0	2.465895	1.2176	0.24188	0.3575	AC026202.	chr3	-	5198590	5229014	672
ENSG00000(	27.96638	32.51577	31.66593	26.96672	11.04518	32.8786	0.35753	0.46349	0.59278	CTC-575D1	chr5	+	1.68E+08	1.68E+08	743
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	ZDHHC20P	chr6	-	29675902	29676324	423
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP11-372H	chr3	-	41203778	41210038	610
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP5-1061H	chr1	-	2.29E+08	2.29E+08	792
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AL133493.	chr21	+	47013568	47017005	821
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	AL160471.	chr14	-	55471531	55472405	875
ENSG00000(	2.071584	0	0	0	1.840864	1.64393	-0.34884	0.79706	NA	RP11-154D	chr9	+	84304628	84391815	1449
ENSG00000(	17703.76	16381.93	11270.43	9151.456	9205.24	11397.37	0.60634	8.48E-05	0.000279	RPS28	chr19	+	8386042	8388224	1523
ENSG00000(	0	0	0	7.490755	25.7721	12.32947	-4.7438	3.08E-05	0.000107	RP11-305F	chrX	+	33744625	33960397	495
ENSG00000(	3.107376	0	1.319414	0.749076	0	1.64393	0.51931	0.698	0.79445	MT1XP1	chr1	-	16567708	16567893	186
ENSG00000(	0	2.408575	0	6.74168	13.80648	10.68554	-2.9653	0.004721	0.011753	RP13-25N2	chr11	+	1592583	1620414	2265

ENSG00000(	27.96638	37.33292	50.13772	11.98521	40.49901	56.71558	0.076481	0.87676	0.92284	CTC-338M1	chr5	+	1.81E+08	1.81E+08	1000
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-336N	chr9	+	80793179	80794428	1250
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	FTLP15	chr7	-	46037139	46037670	532
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	AC009970.	chr2	+	60722821	60727099	432
ENSG00000(	48.68222	42.15007	17.15238	17.97781	25.7721	37.81039	0.40243	0.4011	0.53229	RP11-169K	chr1	-	16133679	16134194	516
ENSG00000(	0	1.204288	2.638828	2.996302	1.840864	7.397684	-1.2838	0.27328	0.39425	BTF3P6	chr21	-	34890917	34891415	499
ENSG00000(	25.8948	31.31148	35.62417	26.96672	23.93123	22.19305	0.32967	0.4566	0.58636	RP11-87H9	chr9	+	69065655	69084989	457
ENSG00000(	11.39371	9.634302	22.43003	13.48336	18.40864	13.15144	-0.05588	0.92653	0.95578	UBE2SP1	chr17	-	15607546	15608214	669
ENSG00000(	38.3243	68.6444	38.263	16.47966	11.04518	20.54912	1.5423	0.000737	0.002114	RP11-250B	chr6	+	81153061	81175644	682
ENSG00000(	21.75163	28.90291	42.22124	6.74168	36.81728	12.32947	0.70582	0.22087	0.33269	RP11-823P	chr5	-	21481436	21484120	2685
ENSG00000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	AC016735.	chr2	-	43268332	43270921	569
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	AC002553.	chr17	+	15987356	15987695	340
ENSG00000(	2.071584	0	0	0	2.761296	0	-0.15346	0.90925	NA	RP3-380E1	chr6	+	14005151	14007132	386
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	RP11-297H	chr1	+	1.7E+08	1.7E+08	760
ENSG00000(	1.035792	0	3.958241	0	0	0	1.6134	0.2311	NA	RP11-401E	chr10	-	7875581	7875920	340
ENSG00000(	23.82321	27.69862	22.43003	0.749076	2.761296	1.64393	3.5404	2.47E-06	9.81E-06	AC116050.	chr2	+	91777536	91809447	1804
ENSG00000(	2.071584	1.204288	2.638828	0	0	0	1.9938	0.14152	NA	RP11-379J	chr20	-	18655039	18679353	1695
ENSG00000(	0	2.408575	6.597069	0	0	0	2.4461	0.070095	0.12986	GDI2P2	chr1	+	72740235	72740842	608
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AC013439.	chr2	-	1.9E+08	1.9E+08	1239
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AP000475.	chr21	+	23119293	23169735	760
ENSG00000(	2.071584	2.408575	5.277655	0.749076	5.522592	4.109825	-0.07335	0.94511	0.9671	SETP5	chr9	-	1.41E+08	1.41E+08	562
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	CTD-3105H	chr19	+	12617063	12618844	621
ENSG00000(	1.035792	1.204288	0	2.247227	0	0	-0.00597	0.99648	NA	RP11-543B	chr1	+	2.11E+08	2.11E+08	375
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	GAPDHP22	chr13	-	99842833	99843245	413
ENSG00000(	3.107376	0	0	1.498151	0	6.575719	-0.83856	0.52093	0.64664	DDX39B-AS	chr6	+	31510081	31510915	516
ENSG00000(	48.68222	43.35436	47.4989	53.93344	17.48821	73.97684	-0.06215	0.88758	0.93006	AL049757.	chr22	-	43172412	43173302	891
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-295J	chr10	-	1.28E+08	1.28E+08	199
ENSG00000(	0	6.021439	1.319414	0	1.840864	0	1.1857	0.37338	0.50388	RP11-214N	chr10	-	1.14E+08	1.14E+08	241
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	RP11-236P	chrX	-	53122892	53124040	615
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	CHIAP3	chr1	-	1.12E+08	1.12E+08	1133
ENSG00000(	1.035792	0	2.638828	1.498151	1.840864	0	0.074303	0.95562	0.97381	AC008278.	chr2	+	15704294	15713992	409
ENSG00000(	2.071584	4.817151	1.319414	0	0.920432	0	1.9166	0.14465	0.23689	RP11-257K	chr6	-	73867240	73867862	623
ENSG00000(	0	0	0	5.243529	3.681728	7.397684	-3.2403	0.009959	0.023171	RP11-310E	chr10	-	96988000	96990901	663
ENSG00000(	22.78742	4.817151	21.11062	18.72689	9.20432	6.575719	0.45978	0.5002	0.62844	AC062029.	chr2	+	88927057	88931337	1614
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	TMEM97P1	chr21	+	45203004	45203454	451
ENSG00000(	0	3.612863	2.638828	0	0	1.64393	1.0804	0.42044	0.5512	RPS3AP44	chr13	+	27151023	27151812	790
ENSG00000(	0	7.225726	0	0	0	0	1.9679	0.14595	0.2386	AP001044.	chr21	-	40285093	40287072	407
ENSG00000(	11.39371	21.67718	25.06886	7.490755	11.96562	3.28786	1.2686	0.055745	0.10676	RP11-123J	chr4	-	77880013	77880322	310
ENSG00000(	8.286335	7.225726	7.916483	5.243529	0.920432	0	1.5829	0.11486	0.19668	RP11-254B	chr12	-	69020650	69020967	318
ENSG00000(	0	4.817151	5.277655	0	0	0	2.6348	0.049808	0.096782	RP11-345I	chr1	+	1.79E+08	1.79E+08	171
ENSG00000(	3.107376	2.408575	1.319414	0	0	0	2.2119	0.10183	0.17802	RP11-452D	chr9	+	68298799	68299489	691
ENSG00000(	1.035792	2.408575	1.319414	2.996302	2.761296	9.041614	-1.3038	0.2321	0.34568	RP11-56M	chr10	-	92912362	92913106	745
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	LL0XNC01-	chrX	-	1.02E+08	1.02E+08	628
ENSG00000(	0	3.612863	0	0.749076	5.522592	0	-0.47354	0.72104	0.8124	AC007969.	chr2	+	1.72E+08	1.72E+08	191

ENSG00000(	18.64425	21.67718	7.916483	28.46487	24.85166	26.30288	-0.68574	0.19192	0.29761	RP11-308D	chrX	+	1.36E+08	1.36E+08	2222
ENSG00000(	2.071584	0	2.638828	0	0.920432	5.753754	-0.33463	0.79374	0.86523	MTND4P26	chr2	+	1.21E+08	1.21E+08	1359
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	TAS2R62P	chr7	+	1.43E+08	1.43E+08	940
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	PAGE2	chrX	+	55115441	55119275	551
ENSG00000(	146.0467	191.4817	133.2608	489.1463	383.8201	341.1154	-1.3592	4.27E-11	2.59E-10	AC074117.	chr2	+	27579113	27590489	3060
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AC011816.	chr3	-	36921675	36922220	546
ENSG00000(	5.17896	8.430014	10.55531	0	9.20432	3.28786	0.82958	0.38293	0.51355	RP3-388E2	chr6	+	1.36E+08	1.36E+08	577
ENSG00000(	1.035792	3.612863	0	0	0	0.821965	1.1852	0.38234	NA	AL391994.	chr1	-	2.35E+08	2.35E+08	375
ENSG00000(	0	2.408575	1.319414	0	0	0	1.2548	0.34239	NA	RP11-353N	chr10	+	13771383	13798200	474
ENSG00000(	7.250543	2.408575	6.597069	1.498151	2.761296	6.575719	0.50245	0.60455	0.71953	RP11-269F	chr1	-	45245998	45246387	390
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	KRT19P4	chr10	+	70020314	70021256	943
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-288E	chr11	+	93268634	93268982	349
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-145A	chr1	+	2.26E+08	2.26E+08	301
ENSG00000(	0	6.021439	2.638828	0	2.761296	0	1.06	0.41619	0.54682	RPL13AP6	chr10	-	1.13E+08	1.13E+08	612
ENSG00000(	0	0	0	0	3.681728	1.64393	-1.4596	0.2805	NA	RHBDF1P1	chr3	-	14614359	14616299	1941
ENSG00000(	960.1791	814.0985	952.6168	742.3339	911.2277	849.9117	0.12389	0.36918	0.49955	TRIM26	chr6	-	30152232	30181204	3478
ENSG00000(	5.17896	1.204288	5.277655	5.992604	14.72691	10.68554	-1.2636	0.13558	0.22485	RP11-120D	chrX	-	10988011	11129234	1071
ENSG00000(	2.071584	3.612863	2.638828	0	4.60216	0.821965	0.47038	0.69591	0.79281	AC005154.	chr7	-	30586782	30590397	353
ENSG00000(	0	6.021439	7.916483	0	0.920432	0	2.5068	0.049543	0.096311	RP11-383C	chr10	-	1.27E+08	1.27E+08	300
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RPL23AP8	chrX	-	56269370	56269842	473
ENSG00000(	6.214751	6.021439	10.55531	1.498151	1.840864	0.821965	2.0556	0.037932	0.076431	AC055764.	chr3	-	1.98E+08	1.98E+08	473
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP4-550H1	chr20	+	34660363	34673182	458
ENSG00000(	0	0	0	1.498151	1.840864	0	-0.93652	0.47589	NA	AC009473.	chr7	-	7989484	7990340	692
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	RP5-1044H	chr1	-	65764438	65764663	226
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	NAP1L4P3	chr13	+	48337595	48338741	1147
ENSG00000(	16.57267	21.67718	10.55531	0.749076	1.840864	2.465895	2.9337	0.000413	0.001229	RP3-460G2	chr6	-	1.41E+08	1.41E+08	453
ENSG00000(	6.214751	8.430014	9.235896	2.247227	1.840864	2.465895	1.6075	0.080848	0.14671	RP11-30P6	chr6	-	86096937	86099904	2513
ENSG00000(	4.143168	0	0	4.494453	0	3.28786	-0.57062	0.6585	0.7631	RBPMSLP	chr21	-	17116323	17117399	502
ENSG00000(	123.2592	139.6974	154.3714	117.6049	105.8497	132.3364	0.22471	0.33401	0.46205	RP11-613N	chr9	+	37509147	37510296	289
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-479G	chr10	-	33312296	33312575	280
ENSG00000(	0	0	0	5.243529	17.48821	0.821965	-3.6526	0.00336	0.008618	AC114877.	chr3	+	26753798	26754855	582
ENSG00000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	TCEB2P4	chr10	-	34777511	34777806	296
ENSG00000(	185.4068	197.5032	127.9831	282.4015	303.7426	387.9674	-0.92173	1.48E-05	5.39E-05	AC108488.	chr2	+	3606082	3609324	1207
ENSG00000(	0	0	0	1.498151	1.840864	0	-0.93652	0.47589	NA	AC016683.	chr2	-	1.14E+08	1.14E+08	583
ENSG00000(	2.071584	0	1.319414	0.749076	4.60216	1.64393	-0.68846	0.58542	0.70292	RP11-730A	chr10	-	13181196	13181533	338
ENSG00000(	0	6.021439	0	4.494453	3.681728	0	-0.30227	0.81185	0.878	HSPA8P1	chrX	-	1.2E+08	1.2E+08	1833
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	AC004854.	chr7	+	44888015	44889167	281
ENSG00000(	2.071584	1.204288	2.638828	5.992604	0.920432	0	-0.1753	0.88655	0.92923	RP5-1132H	chr7	-	65584590	65629998	404
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AIMP1P1	chr20	+	14108046	14108982	937
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-157D	chrX	-	39260506	39294078	786
ENSG00000(	0	1.204288	0	1.498151	0	2.465895	-0.80408	0.55336	NA	AC097461.	chr2	-	2.24E+08	2.24E+08	537
ENSG00000(	3.107376	0	1.319414	0	0.920432	0	1.1063	0.4148	NA	ETV5-AS1	chr3	+	1.86E+08	1.86E+08	560
ENSG00000(	6.214751	9.634302	2.638828	2.996302	1.840864	4.109825	0.89498	0.34894	0.47862	AC092431.	chr2	+	69871557	70008692	905
ENSG00000(	0	0	5.277655	0	3.681728	0.821965	0.1308	0.92148	0.95241	AC010982.	chr2	+	1.15E+08	1.15E+08	844

ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	U82671.8	chrX	+	1.52E+08	1.52E+08	938
ENSG00000(	9.322127	1.204288	0	0	0.920432	1.64393	1.4002	0.26824	0.38858	RP5-1050D	chr17	+	4876146	4877976	439
ENSG00000(	18.64425	1.204288	7.916483	0	0.920432	0	3.5971	0.001902	0.005086	RP1-67A8.3	chr6	-	1.08E+08	1.08E+08	338
ENSG00000(	1.035792	3.612863	0	0	0	1.64393	0.7866	0.56136	0.68149	CTA-256D1	chr22	-	29909878	29931379	289
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC006372.	chr7	+	1.57E+08	1.57E+08	4049
ENSG00000(	0	2.408575	3.958241	0	1.840864	0	1.0371	0.43845	0.56806	RP5-942I1(	chr7	-	69060944	69062434	691
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	RP11-454L	chr1	+	2.08E+08	2.08E+08	680
ENSG00000(	17.60846	28.90291	23.74945	8.239831	5.522592	7.397684	1.6317	0.006607	0.015971	RP11-315I2	chr1	-	1.45E+08	1.46E+08	919
ENSG00000(	0	0	0	56.92974	65.35067	75.62077	-6.81	2.69E-11	1.66E-10	TMEM229A	chr7	-	1.24E+08	1.24E+08	2551
ENSG00000(	2.071584	13.24716	7.916483	0	0.920432	0	3.3744	0.003924	0.009934	RP4-704D2	chr1	-	1.46E+08	1.46E+08	727
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-308N	chr9	+	1.09E+08	1.09E+08	2054
ENSG00000(	3.107376	3.612863	0	1.498151	2.761296	0	0.46284	0.71543	0.80806	ZFX-AS1	chrX	-	24164342	24167771	417
ENSG00000(	34.18113	40.94578	25.06886	26.21764	11.04518	12.32947	0.97022	0.055345	0.10614	AC093616.	chr2	+	88000503	88038766	2095
ENSG00000(	1.035792	0	0	2.247227	0	2.465895	-1.0179	0.45303	NA	RP11-353N	chr1	-	1.5E+08	1.5E+08	537
ENSG00000(	0	0	0	5.992604	4.60216	4.109825	-3.0862	0.015074	0.033638	KCNH1-IT1	chr1	-	2.11E+08	2.11E+08	626
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	BOK-AS1	chr2	-	2.42E+08	2.42E+08	643
ENSG00000(	0	2.408575	0	0	1.840864	1.64393	-0.27261	0.84063	NA	AL162431.	chr1	+	1.81E+08	1.81E+08	168
ENSG00000(	0	0	2.638828	0	0.920432	3.28786	-0.38418	0.77626	0.85302	RP4-775C1	chr20	+	6194346	6196028	1683
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-799C	chr10	-	6933419	6962434	299
ENSG00000(	4.143168	13.24716	11.87472	5.243529	6.443024	8.219649	0.49711	0.5198	0.64576	AC007308.	chr22	+	21077335	21080208	2400
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	SOD2P1	chr1	-	1.04E+08	1.04E+08	562
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CTC-507E1(	chr5	+	1.19E+08	1.19E+08	884
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP11-146I2	chr6	-	14977019	15090234	1017
ENSG00000(	0	0	0	5.992604	0.920432	1.64393	-2.2242	0.096806	0.17077	RP3-325F2	chr6	+	1.37E+08	1.37E+08	505
ENSG00000(	0	0	7.916483	7.490755	2.761296	12.32947	-1.263	0.23564	0.35	RP4-694A7	chr1	+	68962359	69004310	1247
ENSG00000(	1.035792	0	5.277655	2.247227	0	0	0.83652	0.53141	0.65612	AP000936.	chr11	-	1.17E+08	1.17E+08	255
ENSG00000(	1.035792	0	0	2.247227	3.681728	1.64393	-1.6224	0.21862	0.3301	RP1-138B7	chr20	-	42151901	42152212	312
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	AC079790.	chr2	+	1.53E+08	1.53E+08	291
ENSG00000(	0	0	5.277655	0	0.920432	4.109825	0.024042	0.98548	0.99136	COX7BP2	chr20	-	34438596	34438837	242
ENSG00000(	1.035792	6.021439	5.277655	0.749076	8.283888	9.863579	-0.52668	0.59305	0.70922	AC007970.	chr2	+	2.11E+08	2.11E+08	864
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-495P	chr1	-	1.48E+08	1.48E+08	420
ENSG00000(	41.43168	30.10719	19.79121	21.72319	32.21512	32.05663	0.096939	0.83147	0.89203	ZNF879	chr5	+	1.78E+08	1.78E+08	3304
ENSG00000(	0	0	0	1.498151	2.761296	0.821965	-1.5229	0.26162	NA	AC006026.	chr7	-	23719814	23720405	143
ENSG00000(	19.68005	16.86003	10.55531	8.988907	13.80648	18.90519	0.17697	0.76979	0.84862	RP11-761N	chr3	+	40803036	40803290	255
ENSG00000(	0	2.408575	0	3.745378	0	1.64393	-0.6727	0.61611	0.72901	H2BFS	chr21	+	44985070	44985529	460
ENSG00000(	9.322127	0	7.916483	0.749076	3.681728	1.64393	1.2179	0.26336	0.38313	AC116366.	chr5	-	1.32E+08	1.32E+08	3730
ENSG00000(	2.071584	7.225726	3.958241	0	1.840864	0	2.0461	0.09343	0.16581	RP11-213H	chr5	-	90575914	90576959	1046
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	BACH1-IT3	chr21	+	30868367	30872706	406
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-54D1	chr9	+	15055055	15056050	996
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	LINC00229	chr22	-	45002819	45021299	500
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-432J1	chr10	-	1.34E+08	1.34E+08	1013
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP4-771M4	chr1	+	63361680	63367310	447
ENSG00000(	0	0	0	4.494453	0	0	-1.1446	0.38559	NA	RPS12P2	chr10	-	81975607	81975875	269
ENSG00000(	3.107376	4.817151	2.638828	2.247227	0	0	1.5194	0.22055	0.33229	RP11-381C	chr9	+	66954107	66954749	643

ENSG00000(	1.035792	0	0	1.498151	1.840864	0.821965	-0.93518	0.49005	NA	ST13P18	chrX	-	92542732	92543758	1027
ENSG00000(	1.035792	1.204288	2.638828	2.996302	0.920432	0	0.18765	0.88435	0.92779	RP11-308N	chr9	+	1.09E+08	1.09E+08	1686
ENSG00000(	2.071584	3.612863	0	0.749076	0.920432	0.821965	0.77326	0.55178	0.67278	RPL9P2	chr17	+	15346953	15347505	553
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	MRPS10P2	chr3	-	4456264	4456644	381
ENSG00000(	2.071584	13.24716	11.87472	42.69731	9.20432	23.01502	-1.3856	0.043661	0.086382	AC012146.	chr17	+	5014763	5018299	1646
ENSG00000(	5.17896	2.408575	7.916483	1.498151	2.761296	4.109825	0.74569	0.45459	0.58424	RP11-767N	chr1	-	46116711	46117498	788
ENSG00000(	1.035792	0	0	1.498151	0.920432	4.109825	-1.4326	0.28327	0.4061	BCAS2P2	chr1	-	1.01E+08	1.01E+08	674
ENSG00000(	0	0	6.597069	1.498151	0	0	1.0877	0.42155	0.55216	RP11-241I2	chr10	-	32391450	32392221	772
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	JAZF1-AS1	chr7	+	28219941	28283536	3684
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	RP11-297L	chr16	+	52689216	52689962	747
ENSG00000(	19.68005	9.634302	25.06886	5.992604	30.37426	32.05663	-0.3094	0.61632	0.72914	RP11-797H	chr7	-	64295658	64297260	1603
ENSG00000(	4.143168	3.612863	1.319414	6.74168	4.60216	5.753754	-0.76506	0.42753	0.55776	LL0XNC01-	chrX	-	1.03E+08	1.03E+08	1048
ENSG00000(	0	0	1.319414	4.494453	5.522592	0	-1.7832	0.17404	0.27559	AC007405.	chr2	-	1.72E+08	1.72E+08	2026
ENSG00000(	2.071584	0	1.319414	0	0.920432	0	0.84841	0.52989	NA	AC009264.	chr7	-	1.36E+08	1.37E+08	2160
ENSG00000(	3.107376	8.430014	6.597069	2.247227	4.60216	3.28786	0.72309	0.43996	0.56964	AP000347.	chr22	-	23980679	23982949	906
ENSG00000(	1.035792	0	10.55531	3.745378	0.920432	1.64393	0.6315	0.58914	0.70612	RPS26P47	chr13	-	1.01E+08	1.01E+08	440
ENSG00000(	0	0	3.958241	0	0	0.821965	0.91937	0.49384	NA	AC003080.	chr7	-	1.12E+08	1.12E+08	767
ENSG00000(	3.107376	0	3.958241	0	0	0.821965	1.6682	0.2144	0.32488	RP11-52J3.	chr6	-	1.58E+08	1.58E+08	681
ENSG00000(	23.82321	14.45145	36.94359	0	0	0	5.8815	6.86E-08	3.20E-07	AC104654.	chr2	-	42158739	42160863	769
ENSG00000(	11.39371	12.04288	14.51355	0	7.363456	2.465895	1.7495	0.044289	0.087416	PFN1P3	chr1	+	1.48E+08	1.48E+08	402
ENSG00000(	3.107376	0	2.638828	4.494453	0	0.821965	0.064504	0.95974	0.97645	TATDN1P1	chr10	+	64981915	64982805	891
ENSG00000(	0	0	0	16.47966	50.62376	11.50751	-5.4794	6.69E-07	2.82E-06	SNX18P7	chr9	+	33576378	33577012	635
ENSG00000(	3.107376	3.612863	3.958241	0.749076	2.761296	11.50751	-0.40862	0.69012	0.78851	RNF219-AS	chr13	+	79152611	79193239	4001
ENSG00000(	38.3243	36.12863	23.74945	2.247227	13.80648	11.50751	1.7625	0.00275	0.007151	AP000330.	chr21	+	36118054	36157183	2632
ENSG00000(	0	2.408575	0	2.247227	2.761296	4.109825	-1.2995	0.30292	0.42804	RP11-40F6	chr10	+	81993420	82005123	635
ENSG00000(	13.46529	24.08575	21.11062	8.988907	11.96562	12.32947	0.77513	0.18555	0.28998	CTBP2P8	chr1	-	68627444	68628773	1330
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC007278.	chr2	+	1.03E+08	1.03E+08	1327
ENSG00000(	9.322127	13.24716	6.597069	2.247227	9.20432	17.26126	0.027791	0.97143	0.9834	AF238380.	chrX	-	49641892	49643844	1610
ENSG00000(	2.071584	3.612863	1.319414	1.498151	0	0.821965	1.044	0.41303	0.54352	RP11-211N	chr10	-	1.15E+08	1.15E+08	692
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-181G	chr1	+	2143962	2152177	326
ENSG00000(	9.322127	0	0	1.498151	7.363456	0	0.081321	0.94786	0.9686	LL0XNC01-	chrX	+	1.03E+08	1.03E+08	632
ENSG00000(	15.53688	8.430014	2.638828	1.498151	1.840864	4.93179	1.4699	0.11316	0.19415	AC006547.	chr22	-	20135970	20138399	1266
ENSG00000(	1.035792	2.408575	6.597069	0	0	0	2.7473	0.03877	0.077892	RBMY1A1	chrY	+	23673258	23711212	1921
ENSG00000(	97.36444	127.6545	109.5113	62.92235	85.60018	70.68898	0.60532	0.02546	0.053835	ZNF37BP	chr10	-	43015073	43048270	2929
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	SLC25A5P4	chr13	+	57888873	57890043	869
ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	UBE2WP1	chr1	+	96884150	96884489	340
ENSG00000(	0	0	1.319414	0	0	1.64393	-0.1317	0.91874	NA	AC019118.	chr2	-	2898820	3129798	2344
ENSG00000(	3.107376	1.204288	6.597069	1.498151	3.681728	2.465895	0.41066	0.70324	0.79851	RP11-666F	chr12	+	26776302	26802412	876
ENSG00000(	32.10955	49.3758	42.22124	114.6086	108.611	106.8554	-1.4046	3.19E-06	1.25E-05	AC007283.	chr2	+	2.02E+08	2.02E+08	445
ENSG00000(	29.00217	48.17151	36.94359	17.97781	38.65814	50.13986	0.094269	0.83314	0.89318	AC092171.	chr7	-	5465916	5468558	2643
ENSG00000(	0	0	0	2.247227	19.32907	8.219649	-4.0606	0.000731	0.002097	ZNF736	chr7	+	63767837	63810017	2098
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP11-706C	chrX	-	3771051	3800358	2198
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	AC005534.	chr7	+	1.56E+08	1.56E+08	433
ENSG00000(	275.5206	367.3078	362.8388	168.542	222.7445	188.23	0.79118	4.79E-05	0.000163	MAGI2-AS3	chr7	+	79082198	79100524	4505

ENSG00000(	1.035792	0	1.319414	0	0	0.821965	0.54471	0.68089	NA	AC006960.	chr7	+	36345240	36345513	153
ENSG00000(	0	3.612863	1.319414	0	0	0	1.6005	0.2346	NA	AC002064.	chr7	-	89895348	89899530	289
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	XXyac-YM2	chr9	+	90479081	90481205	452
ENSG00000(	38.3243	6.021439	11.87472	17.22874	16.56778	38.63235	-0.3297	0.59695	0.71269	PINLYP	chr19	+	44080952	44088116	2587
ENSG00000(	0	4.817151	2.638828	0.749076	8.283888	3.28786	-0.56655	0.61642	0.72921	ZNF101P2	chr1	-	1.93E+08	1.93E+08	1229
ENSG00000(	0	1.204288	0	0	0.920432	2.465895	-0.65251	0.6297	NA	RP11-496N	chr1	-	2.26E+08	2.26E+08	656
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	AC004231.	chr17	+	39077682	39132178	815
ENSG00000(	0	4.817151	11.87472	1.498151	3.681728	4.93179	0.57767	0.58011	0.69826	RP11-275I2	chr1	+	2.26E+08	2.26E+08	535
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	AC096664.	chr2	+	63911439	63911844	406
ENSG00000(	5.17896	1.204288	0	0	5.522592	9.041614	-0.86338	0.45935	0.58894	RPL34-AS1	chr4	-	1.09E+08	1.1E+08	3713
ENSG00000(	0	0	0	10.48706	8.283888	10.68554	-4.1504	0.000409	0.00122	GS1-421I3.	chrX	-	1.19E+08	1.19E+08	772
ENSG00000(	20.71584	26.49433	17.15238	12.73428	16.56778	7.397684	0.77833	0.17396	0.2755	AC003665.	chr17	-	45974696	46018776	1738
ENSG00000(	1.035792	4.817151	1.319414	31.46117	12.88605	12.32947	-2.6817	0.00111	0.00309	RPL13AP2(	chr12	+	13028433	13029044	612
ENSG00000(	21.75163	38.53721	15.83297	6.74168	17.48821	13.15144	0.98814	0.087136	0.15662	GS1-124K5	chr7	+	65976543	66010053	712
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	FYTTD1P1	chr9	-	1.04E+08	1.04E+08	921
ENSG00000(	4.143168	0	3.958241	0	0	2.465895	1.0742	0.41176	0.54245	AP000253.	chr21	-	33025906	33031813	2233
ENSG00000(	4.143168	0	5.277655	2.996302	3.681728	1.64393	0.14078	0.89993	0.9378	PTGES3P1	chr1	-	89569968	89570450	483
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP3-495K2	chr6	+	1.69E+08	1.69E+08	393
ENSG00000(	0	3.612863	1.319414	1.498151	0	0	0.87932	0.51595	0.64256	AC018464.	chr7	-	1.13E+08	1.13E+08	687
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	NDUFB1P2	chr1	+	2.23E+08	2.23E+08	176
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	RP11-37L2	chr13	+	34185104	34185659	385
ENSG00000(	4.143168	1.204288	6.597069	0	10.12475	3.28786	-0.12511	0.90756	0.94309	AC096582.	chr7	+	45813194	45822756	386
ENSG00000(	12.4295	7.225726	1.319414	3.745378	0	0	1.9027	0.090238	0.16113	RP11-100G	chr9	+	94894680	94900911	1863
ENSG00000(	240.3037	286.6205	306.104	438.2092	388.4223	406.8726	-0.56757	0.000699	0.002011	FAM133B	chr7	-	92190107	92219708	2434
ENSG00000(	11.39371	6.021439	3.958241	1.498151	7.363456	4.109825	0.65556	0.46756	0.59689	RP3-510D1	chr1	+	9242271	9243855	269
ENSG00000(	4.143168	0	0	1.498151	0	0	0.68397	0.6136	NA	RP1-164F3	chrX	-	1.01E+08	1.01E+08	397
ENSG00000(	1.035792	2.408575	0	0	0	2.465895	0.25271	0.85215	NA	API5P1	chrX	-	1.15E+08	1.15E+08	1510
ENSG00000(	0	1.204288	0	0	4.60216	0	-0.85017	0.52991	NA	TPMTP2	chr3	-	42187138	42187863	726
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RPL7AP71	chrX	+	54249757	54250495	739
ENSG00000(	0	0	0	0.749076	1.840864	0	-0.68825	0.58858	NA	RP1-283K1	chr6	-	1.34E+08	1.34E+08	317
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC007880.	chr2	-	65073264	65090760	1977
ENSG00000(	1.035792	1.204288	5.277655	0.749076	0	0	1.8363	0.16751	0.26679	CTSL1P8	chr9	+	90459067	90462229	967
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	SYNE1-AS1	chr6	+	1.53E+08	1.53E+08	553
ENSG00000(	2.071584	6.021439	2.638828	0	0	0	2.8917	0.028261	0.058971	AC019186.	chr2	-	1.59E+08	1.59E+08	545
ENSG00000(	32.10955	51.78437	36.94359	49.43899	45.10117	41.09825	-0.16695	0.65616	0.76109	CCT6P3	chr7	+	64498732	64535091	3702
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	FABP5P14	chr2	-	2.18E+08	2.18E+08	393
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	MCIDAS	chr5	-	54515442	54523143	2091
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	RP1-206D1	chr1	-	1.69E+08	1.69E+08	100
ENSG00000(	2.071584	9.634302	2.638828	2.247227	0.920432	7.397684	0.35623	0.72942	0.81867	RP11-5P18	chr1	+	16296127	16296689	563
ENSG00000(	72.50543	65.03154	98.95603	80.15108	74.55499	95.34793	-0.08418	0.77181	0.85002	MAPKAPK5	chr12	-	1.12E+08	1.12E+08	2285
ENSG00000(	0	4.817151	0	10.48706	23.0108	10.68554	-2.741	0.00346	0.008848	AL450992.	chr1	+	1.52E+08	1.52E+08	506
ENSG00000(	795.4882	810.4856	866.8549	631.4707	783.2876	724.9731	0.20861	0.12641	0.21252	JRK	chr8	-	1.44E+08	1.44E+08	8937
ENSG00000(	2.071584	0	5.277655	0.749076	0.920432	0	1.3127	0.31726	0.4442	SNRK-AS1	chr3	-	43391136	43393454	750
ENSG00000(	9.322127	2.408575	3.958241	13.48336	17.48821	10.68554	-1.2642	0.093968	0.16657	RPSAP9	chr9	+	79013615	79014502	888

ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP1-149A1	chr22	-	32723158	32739092	361
ENSG00000(	36.25272	43.35436	15.83297	15.73059	25.7721	13.9734	0.76542	0.13559	0.22485	LL22NC03-	chr22	+	22648098	22649159	524
ENSG00000(	52.82539	45.76293	31.66593	44.19546	39.57858	41.92021	0.056109	0.88065	0.92529	LINC00849	chr10	-	70237756	70240521	1779
ENSG00000(	0	1.204288	1.319414	0.749076	0	9.863579	-1.3757	0.28275	0.40547	MED14-AS1	chrX	+	40594652	40597950	897
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP11-360J	chr9	-	78339138	78339491	354
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC097523.	chr2	-	1.39E+08	1.39E+08	765
ENSG00000(	22.78742	16.86003	19.79121	3.745378	6.443024	6.575719	1.7239	0.007988	0.018981	AL162151.	chr14	+	99439651	99439808	158
ENSG00000(	12.4295	6.021439	11.87472	2.247227	2.761296	0	2.2302	0.018381	0.040216	PCCA-AS1	chr13	-	1.01E+08	1.01E+08	474
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	OR7E155P	chr13	-	42013952	42015035	1084
ENSG00000(	1.035792	4.817151	0	0	0	0	1.8349	0.17548	NA	AC104820.	chr2	+	1.82E+08	1.82E+08	1771
ENSG00000(	36.25272	33.72006	38.263	34.45748	53.38506	51.78379	-0.35729	0.34903	0.47866	HMGN2P5	chr15	+	30022917	30023189	273
ENSG00000(	3.107376	8.430014	19.79121	5.992604	3.681728	4.109825	1.0367	0.21513	0.32584	RP11-262H	chr9	-	66513488	66553911	1602
ENSG00000(	2.071584	2.408575	2.638828	0	0	0	2.2753	0.091747	0.16332	RP11-242F	chr6	-	1.48E+08	1.48E+08	446
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-337A	chr9	-	26955778	26956293	405
ENSG00000(	7.250543	4.817151	7.916483	3.745378	6.443024	20.54912	-0.55943	0.48936	0.6184	RP11-465N	chr1	-	2.02E+08	2.02E+08	788
ENSG00000(	40.39588	25.29004	47.4989	14.98151	18.40864	37.81039	0.64665	0.17661	0.2786	SDCBP2-AS	chr20	+	1306065	1358827	1811
ENSG00000(	0	0	0	3.745378	4.60216	0.821965	-2.3295	0.080339	0.14587	NUS1P2	chr13	+	23489790	23490662	873
ENSG00000(	0	0	1.319414	2.247227	0	0	-0.3289	0.80275	NA	LINC00444	chr13	-	48479464	48481492	215
ENSG00000(	2.071584	1.204288	0	5.243529	3.681728	2.465895	-1.3023	0.26909	0.38945	AC073283.	chr2	-	47419544	47572213	1892
ENSG00000(	2.071584	10.83859	0	0	0	0	2.9952	0.024127	0.051358	RP4-530I15	chr20	+	49262008	49278812	638
ENSG00000(	6.214751	0	2.638828	1.498151	7.363456	5.753754	-0.55881	0.6003	0.71574	RP1-92O14	chr1	-	43820355	43824329	661
ENSG00000(	2.071584	2.408575	0	0.749076	0	0	1.1924	0.3794	NA	RP11-112L	chr20	+	48782899	48788279	425
ENSG00000(	0	0	0	5.243529	0.920432	2.465895	-2.2485	0.09265	0.16463	AC004478.	chrX	-	91237654	91238504	851
ENSG00000(	0	3.612863	0	2.247227	0.920432	0	0.094959	0.94398	0.96648	HMGA1P4	chr9	-	1.31E+08	1.31E+08	334
ENSG00000(	1.035792	2.408575	2.638828	0	1.840864	0	1.0594	0.42361	0.55412	RP11-745C	chr7	+	54827118	54872621	481
ENSG00000(	0	3.612863	1.319414	1.498151	1.840864	3.28786	-0.31474	0.79827	0.86851	UPF3AP3	chr9	-	1.03E+08	1.03E+08	769
ENSG00000(	0	0	0	1.498151	5.522592	2.465895	-2.3902	0.071608	0.13235	AC060834.	chr7	+	9776951	9809142	618
ENSG00000(	6.214751	2.408575	0	0	0	1.64393	1.4705	0.26323	0.38297	AC007161.	chr7	-	7778165	7782204	1050
ENSG00000(	0	0	0	0.749076	7.363456	0.821965	-2.23	0.09643	0.17025	RP11-166B	chr16	-	12021230	12070500	1194
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	ATP5A1P8	chr9	-	41799259	41800556	1298
ENSG00000(	2.071584	0	2.638828	0	1.840864	0	0.7447	0.58184	0.69955	HDAC1P1	chr10	+	95897505	95899257	1445
ENSG00000(	4.143168	0	2.638828	5.992604	0	0.821965	-0.01133	0.99275	0.99538	KRT18P15	chr3	+	32300432	32301722	1291
ENSG00000(	1.035792	3.612863	3.958241	0.749076	0.920432	4.93179	0.27909	0.80897	0.87599	RP11-272P	chr9	-	13274509	13279186	457
ENSG00000(	6586.601	7136.609	5057.313	3677.961	3051.232	3773.641	0.83623	2.39E-09	1.27E-08	GAS5	chr1	-	1.74E+08	1.74E+08	1698
ENSG00000(	13.46529	7.225726	17.15238	3.745378	2.761296	1.64393	1.9778	0.016222	0.035937	AC144530.	chr3	-	1.98E+08	1.98E+08	555
ENSG00000(	2.071584	1.204288	1.319414	2.996302	2.761296	4.109825	-0.83682	0.46427	0.59343	EIF5AP4	chr10	-	82006975	82007439	465
ENSG00000(	110.8297	97.54731	126.6637	43.44638	50.62376	45.20807	1.2531	1.11E-05	4.11E-05	HLA-B	chr6	-	31321649	31324965	1547
ENSG00000(	6.214751	16.86003	7.916483	23.22134	16.56778	17.26126	-0.83938	0.17683	0.27891	CTD-2666L	chr19	+	12395152	12396000	849
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	AP002381.	chr11	+	72651543	72652157	615
ENSG00000(	4.143168	0	1.319414	8.239831	3.681728	13.9734	-1.8337	0.068119	0.12676	RP11-328N	chr6	-	41462591	41516359	575
ENSG00000(	3.107376	2.408575	3.958241	1.498151	1.840864	0	1.0993	0.36059	0.49018	RP11-421L	chr1	-	2.22E+08	2.22E+08	4340
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-120C	chr10	+	64049280	64063792	706
ENSG00000(	0	0	1.319414	0	1.840864	0.821965	-0.46629	0.72905	NA	RP11-38O1	chr1	-	2.03E+08	2.03E+08	1239
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC008132.	chr22	+	18821207	18821951	745

ENSG00000(	45.57484	38.53721	23.74945	71.16218	46.94203	37.81039	-0.51418	0.20211	0.3099	WASH4P	chr16	-	64043	69452	4243
ENSG00000(	89.0781	75.87013	73.88717	96.63075	137.1444	129.0485	-0.59206	0.026193	0.055227	RP11-395P	chr9	-	1.31E+08	1.31E+08	3801
ENSG00000(	0	0	0	5.243529	1.840864	0	-1.8401	0.17492	0.27673	RP11-428C	chr13	-	27810419	27810948	420
ENSG00000(	1.035792	0	7.916483	0.749076	1.840864	4.109825	0.29198	0.80639	0.87431	CTD-2666L	chr19	+	12305830	12348582	917
ENSG00000(	14.50109	7.225726	9.235896	0	5.522592	2.465895	1.7252	0.061326	0.11574	C11orf94	chr11	-	45928085	45928833	369
ENSG00000(	32.10955	45.76293	21.11062	18.72689	15.64734	12.32947	1.0464	0.035745	0.07249	RP11-62F2	chr9	+	16726812	16727522	428
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	RP11-182I	chr1	+	65384126	65384366	241
ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	LINC00458	chr13	-	54689924	54707001	1054
ENSG00000(	0	0	0	3.745378	0.920432	3.28786	-2.1393	0.11086	0.19074	HSPA8P3	chr10	+	27003551	27004761	780
ENSG00000(	3.107376	2.408575	0	2.247227	4.60216	1.64393	-0.43743	0.71057	0.80433	RP11-483H	chr9	+	1.32E+08	1.32E+08	470
ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	AC007275.	chrY	-	7610636	7677302	1033
ENSG00000(	95.29286	137.2888	109.5113	101.1252	59.82808	139.734	0.17956	0.5575	0.67797	RPS3AP6	chr15	+	60060543	60061347	805
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	PCMTD1P3	chr7	-	23760930	23761401	472
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	MORF4	chr4	-	1.75E+08	1.75E+08	971
ENSG00000(	1.035792	1.204288	0	4.494453	6.443024	5.753754	-2.1551	0.059103	0.11225	RP11-9E13	chr10	+	70184317	70184754	438
ENSG00000(	5.17896	15.65574	9.235896	0	0	0	4.5184	0.000138	0.000442	RP11-466L	chr1	+	56046710	56200675	4063
ENSG00000(	12.4295	24.08575	21.11062	1.498151	10.12475	0.821965	2.0375	0.008824	0.020762	SVILP1	chr10	+	30960495	31006195	2592
ENSG00000(	0	1.204288	1.319414	1.498151	0	0	0.30687	0.81977	NA	U91328.2	chr6	+	26044217	26044585	369
ENSG00000(	2.071584	1.204288	3.958241	6.74168	4.60216	3.28786	-0.85244	0.40758	0.53837	RP3-400B1	chr6	+	4136306	4157619	2277
ENSG00000(	2.071584	6.021439	10.55531	1.498151	0	0.821965	2.2771	0.042092	0.083686	AC092687.	chr2	+	10729292	10744956	565
ENSG00000(	0	0	0	1.498151	2.761296	0	-1.199	0.3707	NA	XRCC6P2	chrX	-	1.49E+08	1.49E+08	1822
ENSG00000(	2.071584	2.408575	0	0	1.840864	1.64393	0.24481	0.85273	0.90607	RP3-322G1	chr20	-	23327578	23332123	814
ENSG00000(	2.071584	0	0	0	0.920432	2.465895	-0.32781	0.80908	NA	PHBP13	chr13	+	35825207	35825966	760
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC005251.	chr7	+	20883246	20883580	335
ENSG00000(	41.43168	31.31148	42.22124	1.498151	0	2.465895	4.4187	9.98E-10	5.47E-09	RP11-399D	chr9	+	22646199	22824212	2347
ENSG00000(	1.035792	0	0	1.498151	0	2.465895	-0.83868	0.53629	NA	RP11-119H	chr4	+	1.14E+08	1.14E+08	1301
ENSG00000(	1.035792	0	0	0	1.840864	1.64393	-0.70101	0.60446	NA	CTD-3105H	chr19	+	12561749	12571519	695
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP11-513M	chr9	-	19383215	19383885	345
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	LINC00676	chr13	+	1.1E+08	1.1E+08	474
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	RP11-831H	chr11	-	62457747	62494856	4001
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC003958.	chr17	+	39558668	39581301	3890
ENSG00000(	6.214751	9.634302	11.87472	2.996302	0.920432	4.109825	1.5487	0.081543	0.14776	RP3-439F8	chr22	+	46937392	46944093	2949
ENSG00000(	0	3.612863	3.958241	0	2.761296	4.109825	0.091695	0.94028	0.96401	LINC00163	chr21	-	46409779	46414001	2155
ENSG00000(	0	0	3.958241	1.498151	0	0	0.61337	0.65027	NA	PIGFP2	chr9	+	1.27E+08	1.27E+08	651
ENSG00000(	5.17896	6.021439	7.916483	7.490755	11.96562	7.397684	-0.44873	0.5628	0.68256	EIF3EP1	chr6	+	74001685	74003000	1316
ENSG00000(	41.43168	43.35436	23.74945	12.73428	16.56778	13.9734	1.2918	0.007504	0.017957	MIR155HG	chr21	+	26934221	26947480	1600
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	CTA-407F1	chr22	-	25957084	25960429	488
ENSG00000(	2.071584	0	1.319414	0	2.761296	0.821965	-0.02526	0.98493	0.99109	MTND5P26	chrX	+	1.02E+08	1.02E+08	1752
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	OR7E62P	chr2	+	71282657	71283133	477
ENSG00000(	1.035792	6.021439	5.277655	5.992604	11.96562	18.90519	-1.4319	0.085248	0.15371	AC005152.	chr17	-	70033455	70217977	3032
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP1-278O2	chr20	-	10733926	10745934	729
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC007879.	chr2	-	2.08E+08	2.08E+08	823
ENSG00000(	4.143168	3.612863	6.597069	7.490755	5.522592	1.64393	-0.03519	0.97011	0.98249	TEX21P	chr14	-	64812889	64841384	1476
ENSG00000(	176.0846	150.536	168.885	122.0993	83.75931	122.4728	0.58651	0.01354	0.030563	LINC00338	chr17	+	75082798	75091068	2139

ENSG00000(	3.107376	2.408575	3.958241	1.498151	0	0	1.7186	0.17654	0.27852	XXbac-B47(	chr22	-	18487036	18490074	2493
ENSG00000(	3.107376	6.021439	1.319414	7.490755	7.363456	4.109825	-0.73369	0.43479	0.56453	RP5-994D1	chr1	+	43144406	43147325	596
ENSG00000(	3.107376	13.24716	5.277655	4.494453	0	2.465895	1.3341	0.18764	0.29237	RP11-254B	chr12	-	69036299	69036773	475
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	CDC42P1	chr20	-	32989955	32990502	548
ENSG00000(	2.071584	4.817151	3.958241	0	0.920432	2.465895	1.2412	0.29642	0.42085	AC010883.	chr2	+	43456712	43460533	398
ENSG00000(	1.035792	8.430014	3.958241	0	1.840864	0	2.0311	0.098633	0.17341	RP11-101C	chr1	+	1.56E+08	1.56E+08	941
ENSG00000(	0	4.817151	5.277655	0	2.761296	1.64393	0.85549	0.485	0.61421	AC092839.	chr2	-	54772505	54773814	377
ENSG00000(	4.143168	10.83859	5.277655	10.48706	7.363456	4.93179	-0.16023	0.84339	0.90015	AC109828.	chr2	+	27558409	27565466	863
ENSG00000(	1.035792	0	1.319414	0.749076	0	0	0.56083	0.6714	NA	SDHCP3	chr2	+	24166716	24167221	506
ENSG00000(	0	1.204288	0	0	3.681728	0	-0.65196	0.62789	NA	AC104667.	chr2	+	2.38E+08	2.39E+08	1301
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-356I2	chr6	-	1.38E+08	1.38E+08	737
ENSG00000(	30.03797	28.90291	17.15238	60.67512	31.29469	49.3179	-0.86585	0.045054	0.088697	FABP5P7	chr11	-	59548786	59549195	408
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	SHISA8	chr22	-	42307297	42310570	486
ENSG00000(	1.035792	2.408575	0	1.498151	2.761296	0	-0.17373	0.89572	0.93537	RP13-33H1	chrX	+	73289111	73290667	1182
ENSG00000(	12.4295	7.225726	3.958241	8.988907	20.2495	11.50751	-0.70378	0.32445	0.45197	TBC1D3C	chr17	-	34580902	34757050	2653
ENSG00000(	11.39371	2.408575	11.87472	8.988907	1.840864	4.109825	0.6764	0.43979	0.56955	FTH1P2	chr1	+	2.29E+08	2.29E+08	412
ENSG00000(	3.107376	1.204288	3.958241	0	0	0	2.4855	0.063943	0.12003	AC074389.	chr7	-	1731542	1732086	454
ENSG00000(	1.035792	0	6.597069	25.46857	9.20432	11.50751	-2.3259	0.008484	0.020045	RP11-423C	chr1	-	1.43E+08	1.43E+08	1742
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-534L	chr1	+	2.07E+08	2.07E+08	792
ENSG00000(	10.35792	1.204288	3.958241	0	0	0	3.4357	0.007505	0.017957	RP11-3L10	chr7	-	1.21E+08	1.21E+08	428
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	XX-C2158C	chr6	+	1.71E+08	1.71E+08	806
ENSG00000(	0	0	1.319414	2.247227	1.840864	0.821965	-1.0697	0.42719	0.55742	AC013429.	chr7	-	1.38E+08	1.38E+08	781
ENSG00000(	1.035792	0	2.638828	9.737982	11.96562	16.4393	-2.8854	0.002502	0.006551	RP11-480I1	chr1	+	2.03E+08	2.03E+08	2321
ENSG00000(	3.107376	3.612863	0	0	1.840864	0	1.1244	0.39884	0.52986	AC016745.	chr2	+	1.14E+08	1.14E+08	508
ENSG00000(	0	0	1.319414	0.749076	0	5.753754	-1.2572	0.35105	0.48075	AC004016.	chr7	-	24945754	24946213	460
ENSG00000(	1.035792	2.408575	0	2.996302	0	5.753754	-0.90991	0.47099	0.59994	EIF4A1P2	chrY	-	5205786	5207005	1220
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-157D	chr1	-	42878069	42878465	397
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP3-497J2	chr6	-	1.67E+08	1.67E+08	1746
ENSG00000(	20.71584	37.33292	18.47179	23.22134	21.16994	35.34449	-0.0586	0.90414	0.94074	RP11-493K	chr3	-	50153455	50193518	2755
ENSG00000(	0	0	1.319414	2.247227	0	0.821965	-0.59149	0.66171	NA	RP11-11M2	chr20	-	60612485	60613012	528
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-109I1	chr10	-	18523097	18550123	793
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-439E	chr1	+	2.47E+08	2.47E+08	522
ENSG00000(	0	0	0	19.47596	21.16994	15.61733	-5.0983	3.81E-06	1.48E-05	AC066593.	chr2	-	1.16E+08	1.16E+08	730
ENSG00000(	11.39371	7.225726	13.19414	0	3.681728	9.863579	1.0841	0.22569	0.33838	AC068580.	chr11	+	1781578	1783716	2015
ENSG00000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	RP4-813D1	chr20	+	55789928	55790922	436
ENSG00000(	0	6.021439	0	0	0.920432	0	1.3099	0.33429	0.46228	RP11-61I13	chr6	-	39856566	39865156	638
ENSG00000(	4.143168	1.204288	3.958241	2.996302	2.761296	2.465895	0.14524	0.89285	0.93378	RP5-1099D	chr20	-	10593509	10594877	1369
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC098820.	chr2	-	2.17E+08	2.17E+08	666
ENSG00000(	26.93059	37.33292	9.235896	33.7084	25.7721	27.94681	-0.23545	0.64167	0.74925	TECRP1	chr4	-	87870818	87871276	459
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	PPIAP3	chr20	+	36158441	36158945	505
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP5-1096D	chr12	-	2038368	2045740	2350
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	MLIP-AS1	chr6	-	53893975	53944524	1534
ENSG00000(	0	2.408575	1.319414	4.494453	0	2.465895	-0.6186	0.62963	0.73982	RP1-150O5	chr1	-	23875630	23877406	456
ENSG00000(	3.107376	7.225726	1.319414	0.749076	6.443024	0	0.55295	0.63155	0.7416	VDAC1P4	chr1	+	1.8E+08	1.8E+08	835

ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RPL24P2	chr20	+	21095364	21095838	475
ENSG00000(	2.071584	0	5.277655	2.996302	0.920432	0.821965	0.42876	0.72766	0.81759	AC009303.	chr2	+	1.19E+08	1.19E+08	853
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC068138.	chr2	-	2.27E+08	2.27E+08	1134
ENSG00000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	AC012074.	chr2	-	25592042	25598714	419
ENSG00000(	1.035792	0	1.319414	2.996302	0.920432	0	-0.4173	0.75669	0.83898	GAPDHP52	chr13	+	21932512	21933453	942
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC073842.	chr7	+	99728587	99738062	342
ENSG00000(	2.071584	4.817151	2.638828	3.745378	1.840864	1.64393	0.30577	0.77977	0.85496	AC142528.	chr2	+	3523046	3526968	974
ENSG00000(	2.071584	6.021439	2.638828	2.247227	8.283888	13.15144	-0.98689	0.28819	0.41177	ZRANB2-AS	chr1	+	71514538	71532867	607
ENSG00000(	1.035792	2.408575	1.319414	8.239831	4.60216	4.109825	-1.4941	0.15656	0.25258	AC010492.	chr19	+	54732911	54734088	901
ENSG00000(	1.035792	3.612863	5.277655	0	0.920432	9.041614	-0.01597	0.98895	0.99347	RP11-179G	chr1	+	1.6E+08	1.6E+08	304
ENSG00000(	2.071584	2.408575	1.319414	0	1.840864	0	1.0187	0.44268	0.57231	CHCHD2P6	chr1	+	15931077	15931538	462
ENSG00000(	0	3.612863	0	1.498151	0	2.465895	-0.08537	0.94933	0.96942	AC091153.	chr17	+	4578674	4600126	384
ENSG00000(	2.071584	3.612863	1.319414	0	0.920432	0.821965	1.3097	0.31084	0.43705	RP4-620E1	chr20	-	40087994	40090584	323
ENSG00000(	0	0	2.638828	0	1.840864	0	0.2163	0.87177	NA	RPL7L1P3	chr7	+	75552073	75552761	689
ENSG00000(	2.071584	0	0	0.749076	0	0	0.47431	0.71145	NA	WI2-85898	chr22	-	46271879	46283628	805
ENSG00000(	7.250543	6.021439	0	4.494453	0.920432	2.465895	0.60199	0.58164	0.69945	AC011747.	chr2	-	8806766	8821993	953
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-1217	chr7	-	57215693	57218054	1980
ENSG00000(	5.17896	2.408575	5.277655	0	0	0	3.1932	0.013698	0.030905	RP11-83A1	chr1	+	2.46E+08	2.46E+08	703
ENSG00000(	5.17896	3.612863	7.916483	12.73428	12.88605	9.041614	-0.97064	0.19963	0.3073	ANKRD65	chr1	-	1353800	1357149	2014
ENSG00000(	6.214751	0	0	3.745378	7.363456	7.397684	-1.2039	0.26818	0.38855	RP11-80H5	chr10	-	91426938	91459428	1298
ENSG00000(	2.071584	2.408575	2.638828	0	0	4.109825	0.52984	0.67702	0.77848	RP11-329A	chr1	+	48901639	48902895	1257
ENSG00000(	985.0381	821.3242	832.5501	355.0618	389.3427	329.6079	1.2949	7.59E-19	7.30E-18	LINC00094	chr9	+	1.37E+08	1.37E+08	5179
ENSG00000(	42.46747	61.41867	40.90183	53.93344	53.38506	52.60575	-0.14157	0.68145	0.78194	ZSCAN31	chr6	-	28292470	28324048	3551
ENSG00000(	5.17896	3.612863	0	5.243529	1.840864	2.465895	-0.08135	0.94167	0.9649	RP11-628K	chr1	+	21487968	21488574	296
ENSG00000(	0	0	0	3.745378	0	1.64393	-1.4934	0.26982	NA	RP11-229P	chr9	+	1.4E+08	1.4E+08	697
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-9M1(	chr9	-	1.17E+08	1.17E+08	173
ENSG00000(	6.214751	16.86003	10.55531	0	7.363456	1.64393	1.6703	0.071046	0.13146	RP11-90L2	chr1	-	2.02E+08	2.02E+08	1809
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC128709.	chr3	-	1.97E+08	1.97E+08	558
ENSG00000(	3.107376	0	1.319414	0.749076	0	4.109825	-0.07618	0.95352	0.97227	AC013474.	chr2	+	1.27E+08	1.27E+08	799
ENSG00000(	3.107376	1.204288	0	0	0	0	1.4526	0.27741	NA	FABP7P2	chr2	-	96034255	96034633	379
ENSG00000(	4.143168	14.45145	13.19414	1.498151	4.60216	18.90519	0.30235	0.71752	0.80984	RP11-374P	chr9	+	1.37E+08	1.37E+08	2112
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC003984.	chr7	+	84161792	84213638	4104
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP5-1092K	chr10	-	7337068	7337252	185
ENSG00000(	3.107376	0	1.319414	0	0	0.821965	1.1429	0.39948	NA	RP11-533E	chr1	+	1.8E+08	1.8E+08	821
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-45I2(	chr4	+	1.87E+08	1.87E+08	549
ENSG00000(	0	0	0	0.749076	1.840864	0.821965	-1.0455	0.43461	NA	RP5-865N1	chr1	+	2.32E+08	2.32E+08	818
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	TMEM30C	chr3	+	99904531	99913035	454
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP6-109B7	chr22	-	46463236	46465771	867
ENSG00000(	739.5554	699.6912	778.4541	3155.106	2448.349	2783.995	-1.9154	2.14E-49	5.82E-48	C12orf75	chr12	+	1.06E+08	1.06E+08	1366
ENSG00000(	6.214751	9.634302	0	6.74168	8.283888	8.219649	-0.46927	0.59934	0.71468	RP11-425N	chr20	-	36120874	36137633	714
ENSG00000(	9.322127	18.06432	10.55531	5.992604	10.12475	32.8786	-0.34495	0.61605	0.72901	SMIM1	chr1	+	3689352	3692546	546
ENSG00000(	0	0	0	2.996302	1.840864	0.821965	-1.6683	0.21867	NA	CTB-114C7	chr5	+	1.7E+08	1.7E+08	983
ENSG00000(	51.7896	49.3758	42.22124	107.1178	97.56579	78.08667	-0.96422	0.001557	0.004226	FAM203A	chr8	+	1.45E+08	1.45E+08	2531
ENSG00000(	89.0781	104.773	102.9143	39.701	40.49901	108.4994	0.63963	0.079335	0.14433	RPL39P3	chr6	-	74082831	74082986	156

ENSG00000(	14.50109	8.430014	7.916483	0	0.920432	0	3.868	0.000475	0.001401	LINC00601	chr10	-	1.28E+08	1.28E+08	1168
ENSG00000(	0	0	1.319414	2.247227	0.920432	0	-0.61221	0.65083	NA	RP11-613C	chr17	+	47872705	47873031	327
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP5-1056L	chr1	-	19918296	19923326	207
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP4-537K2	chrX	-	1.29E+08	1.29E+08	526
ENSG00000(	0	3.612863	0	0	3.681728	0.821965	-0.17437	0.89661	0.93585	NUCB1-AS1	chr19	-	49414187	49422148	433
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	AC009495.	chr2	+	1.67E+08	1.67E+08	779
ENSG00000(	104.615	107.1816	105.5531	70.4131	76.39586	73.97684	0.51934	0.045398	0.089275	PPP1R3E	chr14	-	23765112	23772057	4513
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	TBC1D3P3	chr17	-	20446794	20454276	1080
ENSG00000(	25.8948	19.2686	27.70769	0.749076	9.20432	4.109825	2.2368	0.00123	0.003399	RP11-121A	chr9	-	1.27E+08	1.27E+08	308
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	TATDN2P3	chr13	+	23817659	23821323	3665
ENSG00000(	1.035792	7.225726	3.958241	0	0	0	3.0594	0.019495	0.04241	CTA-150C2	chr22	+	39317232	39320713	678
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	OR6E1P	chr14	+	23171352	23172274	923
ENSG00000(	1.035792	0	0	2.996302	0.920432	0	-0.82044	0.545	NA	FAM83C-AS	chr20	+	33873054	33873559	352
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-145N	chr1	-	59521671	59543788	317
ENSG00000(	141.9035	126.4502	102.9143	58.42789	67.19154	88.77221	0.78798	0.004212	0.010598	TSPY26P	chr20	-	30774280	30778330	3884
ENSG00000(	0	0	2.638828	0.749076	0	0	0.57076	0.66213	NA	IGKV1OR-1	chr2	+	92005797	92006650	354
ENSG00000(	3.107376	0	0	1.498151	2.761296	3.28786	-0.8138	0.52248	0.64788	RP13-131K	chr3	-	49017351	49021418	555
ENSG00000(	9.322127	3.612863	3.958241	8.988907	2.761296	12.32947	-0.44548	0.60235	0.71748	SUMO2P1	chr6	-	29603837	29604120	284
ENSG00000(	6.214751	0	5.277655	0	1.840864	1.64393	1.2517	0.30407	0.42927	RP11-108N	chr1	+	17215590	17216097	508
ENSG00000(	8.286335	6.021439	17.15238	2.247227	4.60216	4.109825	1.3616	0.1018	0.17801	RP11-761E	chrX	-	1.15E+08	1.15E+08	2445
ENSG00000(	29.00217	27.69862	14.51355	6.74168	23.93123	19.72716	0.4906	0.39118	0.52198	RP11-122K	chr10	-	1.35E+08	1.35E+08	626
ENSG00000(	0	2.408575	0	0	2.761296	2.465895	-0.6284	0.63995	0.74795	RP1-5O6.5	chr22	+	38627326	38628254	297
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP11-384B	chr1	-	87510618	87511554	937
ENSG00000(	1.035792	8.430014	14.51355	8.239831	9.20432	7.397684	-0.066	0.93597	0.96146	AC010240.	chr5	+	1.32E+08	1.32E+08	1205
ENSG00000(	2.071584	0	0	1.498151	0	0	0.18632	0.88758	NA	TMEM185A	chrX	+	1.49E+08	1.49E+08	546
ENSG00000(	12.4295	34.92434	23.74945	27.7158	41.41944	32.05663	-0.49832	0.29823	0.42312	AC093415.	chr3	-	37786923	37903271	3139
ENSG00000(	1.035792	3.612863	5.277655	0.749076	0	0	2.2186	0.087422	0.15698	AC115115.	chr2	-	1.13E+08	1.13E+08	366
ENSG00000(	0	0	0	2.996302	0.920432	0.821965	-1.4343	0.28996	NA	KDM5C-IT1	chrX	-	53241590	53243861	755
ENSG00000(	3.107376	3.612863	1.319414	0	0	1.64393	1.4597	0.25989	0.37876	AC074117.	chr2	+	27678023	27678729	397
ENSG00000(	0	0	0	2.996302	0.920432	0.821965	-1.4343	0.28996	NA	KDM4E	chr11	+	94758422	94760760	2339
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	AL162759.	chr14	-	54235660	54317600	602
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP1-90L6.3	chr22	+	27299255	27316574	517
ENSG00000(	0	8.430014	1.319414	3.745378	0.920432	4.109825	0.1021	0.92916	0.95732	FAM103A2	chr6	-	1.67E+08	1.67E+08	354
ENSG00000(	0	0	1.319414	0	0.920432	2.465895	-0.65854	0.62673	NA	AF127577.	chr21	+	16290855	16319417	781
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	ZNF652P1	chr3	-	50824105	50825716	1309
ENSG00000(	0	0	1.319414	5.992604	5.522592	4.93179	-2.5936	0.031343	0.064589	MCF2L-AS1	chr13	-	1.14E+08	1.14E+08	712
ENSG00000(	0	0	6.597069	0	1.840864	4.93179	-0.04272	0.9735	0.98465	SNORD62A	chr9	+	1.34E+08	1.34E+08	86
ENSG00000(	4.143168	4.817151	3.958241	1.498151	0.920432	0.821965	1.5425	0.16928	0.26922	AP000925.	chr11	-	1.12E+08	1.12E+08	1449
ENSG00000(	6.214751	0	6.597069	0	1.840864	1.64393	1.3828	0.25006	0.3674	HLA-W	chr6	+	29924373	29926347	771
ENSG00000(	0	6.021439	5.277655	0	0	0	2.8073	0.03554	0.072118	AC137723.	chr17	+	79899745	79905477	691
ENSG00000(	1.035792	2.408575	1.319414	2.247227	0.920432	0.821965	0.16298	0.89738	0.93632	FAUP1	chr18	-	72057119	72057532	414
ENSG00000(	0	4.817151	0	0	0	0.821965	1.1172	0.40901	NA	RP11-575L	chr9	+	86587148	86590692	390
ENSG00000(	4.143168	1.204288	1.319414	0	0	0	2.1615	0.11037	0.19002	MRPL53P1	chr1	-	1.13E+08	1.13E+08	319
ENSG00000(	1.035792	4.817151	1.319414	2.996302	6.443024	5.753754	-0.89023	0.39072	0.52154	RP11-82K1	chr1	+	89389053	89389527	475

ENSG00000(	19.68005	15.65574	27.70769	8.239831	13.80648	20.54912	0.53878	0.34687	0.47644	HM13-IT1	chr20	+	30150969	30151879	356
ENSG00000(	12.4295	3.612863	5.277655	3.745378	0.920432	0.821965	1.6202	0.10779	0.18657	AC017116.	chr7	+	44078770	44081905	2590
ENSG00000(	54.89697	50.58008	65.97069	22.47227	44.18074	32.8786	0.77414	0.041826	0.083234	DUSP8P5	chr10	+	75491582	75493396	1815
ENSG00000(	0	0	2.638828	0	0	4.93179	-0.48536	0.72032	0.81178	AC012360.	chr2	+	1.06E+08	1.06E+08	674
ENSG00000(	1.035792	4.817151	0	0	0	0	1.8349	0.17548	NA	RP11-509J	chr9	+	3674546	3691814	537
ENSG00000(	0	1.204288	1.319414	0.749076	0	0	0.61214	0.64459	NA	AC006946.	chr22	-	17574502	17574829	328
ENSG00000(	0	0	2.638828	0	5.522592	0.821965	-0.74976	0.57468	0.69333	RP11-165F	chr9	+	477750	478423	674
ENSG00000(	0	1.204288	0	0	2.761296	0	-0.43954	0.74062	NA	AC016723.	chr2	-	1.69E+08	1.69E+08	643
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	AC114765.	chr2	+	2.21E+08	2.21E+08	347
ENSG00000(	1.035792	0	2.638828	0.749076	0.920432	0	0.59434	0.66077	NA	RP1-37M3.	chr22	-	46188298	46189516	1219
ENSG00000(	5.17896	0	2.638828	0	2.761296	5.753754	-0.07435	0.9507	0.97041	AC114730.	chr2	-	2.43E+08	2.43E+08	584
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	RP11-399E	chr1	+	41708045	41750533	709
ENSG00000(	53.86118	63.82725	54.09597	146.0697	143.5874	101.9236	-1.1764	2.66E-05	9.36E-05	SNRPGP10	chr1	+	2.05E+08	2.05E+08	225
ENSG00000(	2.071584	1.204288	2.638828	0	0.920432	2.465895	0.54134	0.67162	0.77391	RPL36AP15	chr2	-	48024965	48025230	266
ENSG00000(	13.46529	8.430014	6.597069	0	0	0	4.4621	0.000172	0.000542	CSPG4P5	chr15	-	84953014	84966399	8752
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP4-764D2	chr1	+	2.36E+08	2.36E+08	2310
ENSG00000(	27.96638	26.49433	15.83297	9.737982	26.69253	21.37109	0.28443	0.59836	0.71383	RP11-206L	chr1	-	677193	685396	4860
ENSG00000(	8.286335	6.021439	7.916483	7.490755	12.88605	7.397684	-0.28774	0.70104	0.79683	SSR4P1	chr21	-	46491648	46494080	967
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	RP11-332C	chr10	+	1.05E+08	1.05E+08	2130
ENSG00000(	4.143168	3.612863	0	1.498151	0	1.64393	0.87739	0.48969	0.6187	MRPS10P1	chr1	+	1.7E+08	1.7E+08	130
ENSG00000(	18.64425	22.88147	11.87472	45.69361	26.69253	36.16646	-0.98832	0.03925	0.078701	RP11-477D	chr6	-	1.56E+08	1.56E+08	3088
ENSG00000(	12.4295	12.04288	10.55531	2.996302	5.522592	5.753754	1.1932	0.11598	0.19826	GS1-600G8	chrX	-	13284167	13321571	1497
ENSG00000(	1.035792	2.408575	0	1.498151	1.840864	3.28786	-0.63752	0.61202	0.72563	RP11-397A	chr1	+	2.47E+08	2.47E+08	105
ENSG00000(	3.107376	0	5.277655	1.498151	5.522592	0	0.1917	0.8747	0.92133	RP11-327L	chr9	+	35909480	35911683	1612
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP11-134K	chr9	-	8700595	8701552	486
ENSG00000(	14.50109	16.86003	17.15238	4.494453	11.04518	14.79537	0.64112	0.32018	0.44735	EPN2-AS1	chr17	-	19199909	19209574	1190
ENSG00000(	3.107376	0	5.277655	5.243529	6.443024	9.041614	-1.1104	0.25789	0.37658	LINC00623	chr1	-	1.44E+08	1.44E+08	2084
ENSG00000(	7.250543	9.634302	11.87472	9.737982	11.96562	13.15144	-0.26528	0.69446	0.79169	SNORA71B	chr20	-	37053843	37053978	136
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	RP11-397C	chr10	+	14116283	14129604	790
ENSG00000(	0	2.408575	1.319414	0	0	0.821965	0.95657	0.47938	NA	AC007041.	chr2	-	20439653	20440807	1155
ENSG00000(	0	1.204288	5.277655	0	3.681728	1.64393	0.1836	0.88523	0.92834	RP11-414P	chr4	+	17913297	17914599	979
ENSG00000(	4.143168	0	1.319414	0	1.840864	0	0.89572	0.50629	0.63393	AC010149.	chr2	-	2.31E+08	2.31E+08	571
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	AP005136.	chr18	-	2593673	2594912	909
ENSG00000(	34.18113	52.98866	46.17948	36.7047	48.7829	42.74218	0.053661	0.88517	0.92832	RP11-282C	chr12	-	1.24E+08	1.24E+08	1110
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC112211.	chr3	+	33118696	33118983	288
ENSG00000(	20.71584	20.47289	15.83297	0.749076	7.363456	1.64393	2.3611	0.002081	0.005529	RP11-342N	chr10	+	81142084	81169030	511
ENSG00000(	4.143168	0	1.319414	2.247227	2.761296	0	0.10137	0.93703	0.96179	AC006159.	chr7	-	1.16E+08	1.16E+08	386
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	WI2-2998D	chr1	-	2.24E+08	2.24E+08	886
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	AC083875.	chr7	-	1.33E+08	1.33E+08	405
ENSG00000(	0	0	0	2.996302	0	2.465895	-1.5141	0.2635	NA	DPY19L2P4	chr7	+	89748714	89754914	2335
ENSG00000(	48.68222	37.33292	75.20659	54.68252	67.19154	60.00344	-0.1751	0.61489	0.72803	RP11-357C	chrX	-	62729822	62780929	529
ENSG00000(	1.035792	3.612863	3.958241	2.247227	2.761296	4.109825	-0.08081	0.94042	0.96402	RP11-214J9	chr2	-	26324186	26325005	820
ENSG00000(	0	0	1.319414	1.498151	6.443024	1.64393	-1.8161	0.16041	0.25776	XXbac-B47(	chr22	-	18465971	18466385	361
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-74K1	chr1	-	69709055	69715106	434

ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP1-279N1	chrX	-	75875899	75876960	1062
ENSG00000(	2.071584	6.021439	3.958241	0	0	0	3.0775	0.01832	0.040098	RP11-3L8.3	chr9	-	12700100	12814344	799
ENSG00000(	0	0	5.277655	0	0.920432	0	1.1592	0.39256	0.52329	RP11-480I1	chr1	-	2.03E+08	2.03E+08	190
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-142A	chr7	-	91010093	91186163	202
ENSG00000(	2.071584	4.817151	7.916483	6.74168	8.283888	16.4393	-0.99757	0.22342	0.33563	TOPORS-AS	chr9	+	32551142	32567003	1000
ENSG00000(	7.250543	0	2.638828	0.749076	6.443024	13.9734	-0.87599	0.4009	0.53215	RP11-678B	chr7	+	53929926	53931032	1107
ENSG00000(	0	0	0	2.247227	1.840864	0	-1.1573	0.3864	NA	RP5-928E2.	chrX	+	84465712	84474704	1135
ENSG00000(	0	0	0	0	0.920432	3.28786	-1.1769	0.37857	NA	TAB3P1	chrY	-	15265842	15274125	1634
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-513D	chr1	+	2.43E+08	2.43E+08	634
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	EIF4A1P7	chr13	+	29172970	29174189	1220
ENSG00000(	8.286335	14.45145	11.87472	5.243529	8.283888	13.15144	0.34646	0.62234	0.73431	RP11-166C	chr7	+	66800963	66805011	489
ENSG00000(	151.2256	149.3317	154.3714	112.3613	99.40666	115.0751	0.47227	0.034959	0.071074	RP11-122G	chr1	+	1.61E+08	1.61E+08	1806
ENSG00000(	3.107376	1.204288	0	0	0.920432	2.465895	0.23267	0.86084	0.91151	AC006946.	chr22	+	17602476	17612994	1175
ENSG00000(	2.071584	2.408575	5.277655	0.749076	8.283888	0.821965	-0.00416	0.997	0.99811	RP11-133C	chr9	-	33785948	33818793	647
ENSG00000(	1.035792	0	0	0.749076	2.761296	0.821965	-0.96388	0.47679	NA	RPL21P135	chr3	+	37789601	37790391	791
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	GYG2-AS1	chrX	-	2770781	2771801	515
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC114755.	chr2	+	1.07E+08	1.07E+08	831
ENSG00000(	3.107376	6.021439	6.597069	2.247227	2.761296	9.863579	0.06016	0.94876	0.96918	JARID2-AS1	chr6	-	15248046	15248865	455
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	DBF4P1	chr10	-	65928715	65930611	1892
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AC097499.	chr2	+	1.26E+08	1.27E+08	668
ENSG00000(	0	0	0	2.247227	0	7.397684	-2.268	0.091934	0.1636	AC092415.	chr3	-	28038701	28070095	755
ENSG00000(	0	0	0	3.745378	3.681728	0	-1.9109	0.15856	0.25533	RP11-498P	chr9	+	99995483	99997296	281
ENSG00000(	5.17896	6.021439	15.83297	1.498151	32.21512	4.109825	-0.4281	0.61947	0.7318	AC073046.	chr2	+	74212259	74213470	390
ENSG00000(	38.3243	50.58008	34.30476	17.22874	22.09037	23.01502	0.96102	0.025769	0.05439	RP4-639F2	chr1	+	95393122	95428826	952
ENSG00000(	10.35792	12.04288	3.958241	0	0	0	4.3225	0.000325	0.000984	RP11-693N	chr11	-	1.05E+08	1.05E+08	3530
ENSG00000(	5.17896	2.408575	3.958241	9.737982	11.96562	3.28786	-0.96871	0.27387	0.39495	RPS2P7	chr20	-	44269125	44270009	885
ENSG00000(	9.322127	8.430014	26.38828	4.494453	1.840864	3.28786	1.9611	0.014114	0.031741	RP4-756G2	chr22	-	41605126	41613631	2500
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	AC011196.	chr15	-	26902177	26903910	595
ENSG00000(	5.17896	10.83859	3.958241	0	4.60216	0.821965	1.5562	0.14184	0.23337	AC009505.	chr2	-	1.06E+08	1.06E+08	890
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP5-1028L	chr1	-	1.11E+08	1.11E+08	508
ENSG00000(	8.286335	1.204288	0	1.498151	1.840864	4.93179	0.17867	0.87665	0.92281	RP5-1073C	chr1	-	1.14E+08	1.14E+08	2117
ENSG00000(	11.39371	7.225726	1.319414	2.996302	19.32907	19.72716	-0.94325	0.24503	0.36137	AGAP1-IT1	chr2	+	2.36E+08	2.36E+08	664
ENSG00000(	4.143168	9.634302	6.597069	11.98521	24.85166	24.65895	-1.4978	0.023672	0.050454	AC087294.	chr17	+	21117644	21133348	1152
ENSG00000(	5.17896	10.83859	10.55531	1.498151	0	0	3.1631	0.003628	0.009242	RP11-383H	chr8	+	72740402	73030628	4220
ENSG00000(	2.071584	0	0	1.498151	0	0.821965	-0.06236	0.96323	NA	LINC00402	chr13	+	74805594	74834113	3340
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	FECHP1	chr3	+	34914133	34915346	1214
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC009411.	chr2	-	21853420	21859181	539
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RPS11P1	chr20	-	11326031	11326503	473
ENSG00000(	5.17896	1.204288	5.277655	5.243529	8.283888	6.575719	-0.67769	0.4573	0.58705	RP11-230B	chr1	+	63154153	63176365	1228
ENSG00000(	142.9393	239.6533	184.7179	140.8262	141.7465	230.1502	0.14241	0.57736	0.69565	RPL6P27	chr18	-	6462143	6463014	867
ENSG00000(	3.107376	1.204288	6.597069	0	0.920432	2.465895	1.2325	0.30417	0.42936	AC005822.	chr17	-	16520162	16521195	1034
ENSG00000(	0	0	2.638828	2.996302	1.840864	0.821965	-0.71043	0.58981	0.70665	NOL5BP	chr6	-	28751410	28751781	372
ENSG00000(	3.107376	14.45145	2.638828	19.47596	26.69253	16.4393	-1.518	0.02887	0.060125	AC002310.	chr16	+	30546073	30548465	1445
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AP000477.	chr21	-	25333220	25339588	778

ENSG00000(	1.035792	3.612863	0	0.749076	0.920432	4.109825	-0.21009	0.86804	0.91711	RP11-86H7	chr1	-	95086707	95089740	2272
ENSG00000(	0	0	1.319414	1.498151	3.681728	6.575719	-2.098	0.097144	0.17123	NFAM1	chr22	-	42776416	42828401	5602
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP3-412A9	chr22	+	31509003	31509382	380
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP4-800F2	chr1	+	1.69E+08	1.69E+08	368
ENSG00000(	0	0	0	0.749076	2.761296	0.821965	-1.3133	0.33155	NA	AC007283.	chr2	-	2.02E+08	2.02E+08	197
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-448G	chr1	+	1.98E+08	1.98E+08	472
ENSG00000(	9.322127	3.612863	3.958241	13.48336	17.48821	11.50751	-1.2017	0.10075	0.17651	AC011247.	chr2	+	38828740	38829320	233
ENSG00000(	1.035792	4.817151	1.319414	5.992604	0.920432	4.93179	-0.58719	0.5932	0.70931	GAPDHP65	chrX	-	46299144	46300149	1006
ENSG00000(	15.53688	19.2686	7.916483	15.73059	31.29469	26.30288	-0.73253	0.19027	0.29564	GNAS-AS1	chr20	-	57393974	57425958	1156
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	RBMS3-AS1	chr3	-	29968302	29975647	554
ENSG00000(	4.143168	0	2.638828	0	0	0	2.0639	0.1282	0.21482	AC013402.	chr2	+	1.05E+08	1.05E+08	3778
ENSG00000(	5.17896	7.225726	6.597069	0.749076	1.840864	0.821965	2.0278	0.05291	0.10203	POU5F1P3	chr12	-	8286372	8287447	670
ENSG00000(	62.14751	62.62296	88.40072	14.23244	22.09037	21.37109	1.8498	1.62E-06	6.57E-06	AF127936.	chr21	-	16193529	16254296	1997
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP1-158P9	chr1	+	56611393	56620896	731
ENSG00000(	1.035792	0	6.597069	4.494453	0.920432	6.575719	-0.53326	0.6385	0.74678	NSRP1P1	chr1	+	78312795	78314487	1693
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	AJ239322.:	chr2	-	1.33E+08	1.33E+08	2209
ENSG00000(	3.107376	12.04288	10.55531	7.490755	8.283888	4.93179	0.27137	0.73299	0.8214	XXbac-B47(	chr22	+	18584378	18584654	277
ENSG00000(	6.214751	1.204288	5.277655	0.749076	0	0.821965	2.1125	0.081818	0.14819	RP11-324H	chr10	-	51780942	51827563	2177
ENSG00000(	8.286335	0	5.277655	0	1.840864	0	1.9779	0.11552	0.19767	RP11-156G	chr9	+	35507561	35507870	310
ENSG00000(	0	0	3.958241	6.74168	1.840864	4.109825	-1.2789	0.28369	0.40661	SNRPFP4	chr3	+	48202666	48202907	242
ENSG00000(	0	4.817151	1.319414	2.247227	4.60216	0	-0.11188	0.92883	0.95719	AC016644.	chr5	+	56237134	56242979	434
ENSG00000(	3.107376	2.408575	3.958241	2.247227	6.443024	0	0.10639	0.92491	0.95453	NUS1P1	chrX	-	47372001	47372882	882
ENSG00000(	4.143168	2.408575	1.319414	1.498151	0	0.821965	1.1871	0.34621	0.47576	LINC00484	chr9	+	93922051	93927858	2745
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	MXRA5P1	chrY	+	14077914	14108092	8000
ENSG00000(	4.143168	1.204288	3.958241	2.247227	4.60216	6.575719	-0.43266	0.67025	0.77303	AC064850.	chr2	-	1.36E+08	1.36E+08	1398
ENSG00000(	7.250543	9.634302	7.916483	0	7.363456	0	1.4638	0.16064	0.25799	RP11-545I9	chr6	+	1.46E+08	1.46E+08	715
ENSG00000(	410.1736	451.6079	328.534	723.607	549.4979	644.4205	-0.68473	4.52E-05	0.000155	H3F3AP4	chr2	+	1.76E+08	1.76E+08	1022
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	LINC00345	chr13	-	53058296	53058815	285
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	SAPCD1-AS	chr6	-	31732087	31733365	461
ENSG00000(	0	2.408575	0	6.74168	2.761296	1.64393	-1.5366	0.21551	0.32621	AC005682.	chr7	-	22928990	22980809	675
ENSG00000(	1.035792	3.612863	2.638828	0	0	0.821965	1.7946	0.17647	0.27846	AC009502.	chr2	+	2.21E+08	2.21E+08	361
ENSG00000(	0	1.204288	0	3.745378	6.443024	3.28786	-2.3286	0.060658	0.11473	AC004593.	chr7	-	29239156	29248586	798
ENSG00000(	4.143168	0	0	4.494453	1.840864	0.821965	-0.50142	0.69357	0.79114	AC090286.	chr17	+	18811592	18812178	587
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-109P	chr1	+	38306658	38307348	691
ENSG00000(	2.071584	2.408575	9.235896	2.996302	4.60216	4.109825	0.17753	0.85672	0.90907	NPM1P26	chr10	+	98319942	98320679	738
ENSG00000(	20.71584	6.021439	25.06886	14.98151	9.20432	15.61733	0.35306	0.57485	0.69339	AC008746.	chr19	+	54958008	54958225	218
ENSG00000(	1.035792	9.634302	0	0	0.920432	0	2.1063	0.10946	0.18874	AC018442.	chr8	+	1.01E+08	1.01E+08	2061
ENSG00000(	0	0	5.277655	0.749076	2.761296	7.397684	-0.78115	0.52155	0.64717	AC116614.	chr2	-	945320	945960	532
ENSG00000(	1.035792	0	1.319414	5.243529	3.681728	3.28786	-1.7236	0.14893	0.24252	RP11-395P	chr3	+	47705116	47705424	309
ENSG00000(	4.143168	1.204288	2.638828	1.498151	0.920432	0	1.1757	0.34995	0.47975	CYCSP52	chr1	+	1.57E+08	1.57E+08	310
ENSG00000(	6.214751	8.430014	2.638828	0	2.761296	0	2.0458	0.075935	0.13906	PCBP2P1	chr21	-	40543056	40544032	977
ENSG00000(	108.7581	134.8802	81.80365	29.21395	82.83888	43.56414	1.055	0.00332	0.008521	RP13-507I2	chrX	+	1.49E+08	1.49E+08	3414
ENSG00000(	1.035792	0	0	0.749076	0	1.64393	-0.39004	0.77029	NA	AC023490.	chr22	+	20377669	20378803	853
ENSG00000(	25.8948	33.72006	13.19414	34.45748	30.37426	35.34449	-0.44085	0.34049	0.46923	DICER1-AS1	chr14	+	95623982	95646263	2323

ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-323A	chr9	-	78016805	78017908	1104
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP5-1097F	chr1	-	2.31E+08	2.31E+08	2293
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-340I(	chr7	+	63353664	63355019	1356
ENSG0000(	1.035792	8.430014	0	0	0	0	2.506	0.063419	0.11921	AC009299.	chr2	-	1.62E+08	1.62E+08	1072
ENSG0000(	2.071584	4.817151	6.597069	0	4.60216	1.64393	0.88572	0.42519	0.55556	AC010148.	chr2	-	2.36E+08	2.36E+08	1652
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-29O6	chrX	+	1.43E+08	1.43E+08	343
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	OR2AF1P	chrX	+	1.31E+08	1.31E+08	889
ENSG0000(	2.071584	9.634302	3.958241	9.737982	10.12475	9.863579	-0.84164	0.29969	0.4246	HMGN1P3(	chr2	+	98443711	98444013	303
ENSG0000(	1.035792	0	0	0.749076	2.761296	0	-0.70185	0.6039	NA	RP11-436I2	chr6	-	1.44E+08	1.44E+08	1699
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CTBP2P2	chr10	-	96406121	96407753	1334
ENSG0000(	1.035792	2.408575	2.638828	5.243529	0.920432	0	-0.03518	0.97728	0.98673	RP11-32D1	chr1	-	1.97E+08	1.97E+08	560
ENSG0000(	0	0	0	11.98521	4.60216	9.863579	-3.9683	0.000899	0.002539	KIAA0040	chr1	-	1.75E+08	1.75E+08	4564
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	MAGI2-IT1	chr7	-	78530591	78629614	574
ENSG0000(	3.107376	1.204288	1.319414	0	2.761296	5.753754	-0.41803	0.72841	0.81801	AC138655.	chr2	+	47754676	47762338	434
ENSG0000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	SNRPGP5	chr10	-	13146574	13146793	220
ENSG0000(	94.25706	116.8159	145.1355	0	0	0	7.9872	6.45E-16	5.37E-15	LINC00607	chr2	-	2.16E+08	2.17E+08	3690
ENSG0000(	0	6.021439	2.638828	0.749076	5.522592	3.28786	-0.11237	0.92163	0.95253	AP001625.	chr21	-	43980484	43982044	575
ENSG0000(	1.035792	0	0	1.498151	1.840864	1.64393	-1.1367	0.39915	0.53025	AC000089.	chr22	+	19779817	19780617	801
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC079779.	chr2	-	305111	314367	1200
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	XXbac-BPG	chr6	+	30484043	30486994	851
ENSG0000(	1.035792	7.225726	1.319414	2.247227	0	0	1.3575	0.28705	0.4106	HNRNPA1P	chr13	-	94047230	94048108	879
ENSG0000(	1.035792	6.021439	1.319414	5.243529	3.681728	0	-0.07563	0.9481	0.96872	ZNRF3-IT1	chr22	+	29388709	29414608	674
ENSG0000(	8.286335	10.83859	6.597069	3.745378	13.80648	0.821965	0.44426	0.61162	0.72533	RP11-73M7	chr1	+	32110590	32125539	872
ENSG0000(	9.322127	1.204288	6.597069	2.247227	0	2.465895	1.466	0.17927	0.28197	RP11-421L	chr1	+	1.01E+08	1.01E+08	671
ENSG0000(	3.107376	2.408575	3.958241	0	0	6.575719	0.37868	0.75451	0.83767	HCFC1-AS1	chrX	+	1.53E+08	1.53E+08	350
ENSG0000(	1.035792	0	1.319414	0.749076	4.60216	0	-0.68392	0.60811	0.72223	RP4-646N3	chrX	+	38629584	38658911	1180
ENSG0000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	MYL6P2	chr21	+	40860253	40860686	434
ENSG0000(	3.107376	0	0	0	0	0.821965	0.7418	0.57612	NA	ADAM21P1	chr14	-	70712208	70714518	2170
ENSG0000(	3.107376	7.225726	2.638828	0	0	0	3.1955	0.013699	0.030905	RP11-308B	chrX	+	1.34E+08	1.34E+08	938
ENSG0000(	8.286335	2.408575	0	0.749076	0	3.28786	1.0051	0.41455	0.54502	PRELID1P3	chr10	+	65187057	65187713	657
ENSG0000(	58.00435	56.60152	60.69303	72.66033	77.31629	72.33291	-0.33864	0.25483	0.37301	LINC00263	chr10	+	1.02E+08	1.02E+08	2551
ENSG0000(	2.071584	0	1.319414	0	0.920432	0.821965	0.51734	0.70267	NA	TBCAP2	chr1	-	15018625	15019109	326
ENSG0000(	5.17896	1.204288	1.319414	19.47596	6.443024	0.821965	-1.4733	0.14467	0.23691	BHLHE40-A	chr3	-	4938493	5021646	2356
ENSG0000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	RP1-60N8.:	chrX	+	17546558	17605281	1554
ENSG0000(	10.35792	1.204288	1.319414	4.494453	11.96562	0.821965	-0.31822	0.75653	0.83898	AC073333.	chr7	-	16735496	16759523	648
ENSG0000(	8.286335	12.04288	5.277655	9.737982	16.56778	7.397684	-0.35662	0.61984	0.73213	RP11-356I2	chr6	-	1.38E+08	1.38E+08	1025
ENSG0000(	2.071584	0	0	2.247227	0	1.64393	-0.45565	0.73665	0.82369	RP13-16H1	chr10	+	27006564	27007707	485
ENSG0000(	1.035792	8.430014	0	2.247227	0.920432	2.465895	0.54663	0.64658	0.7533	RMDN2-AS:	chr2	-	38177144	38294184	859
ENSG0000(	3.107376	1.204288	0	0	0	0	1.4526	0.27741	NA	HS6ST2-AS:	chrX	+	1.32E+08	1.32E+08	550
ENSG0000(	2.071584	0	0	0	4.60216	6.575719	-1.5244	0.23494	0.34918	AC005540.	chr2	-	1.92E+08	1.92E+08	919
ENSG0000(	5.17896	4.817151	5.277655	59.92604	35.89685	46.03004	-3.0702	5.03E-08	2.38E-07	AC006978.	chr7	+	30410987	30412357	1234
ENSG0000(	17.60846	7.225726	11.87472	20.22504	34.05598	20.54912	-0.96585	0.089349	0.15982	B3GALT4	chr6	+	33244917	33246602	1686
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	HSPA8P6	chr2	-	2.1E+08	2.1E+08	1552
ENSG0000(	306.5944	281.8033	245.411	17.22874	59.82808	60.00344	2.5798	2.79E-16	2.36E-15	GSN-AS1	chr9	-	1.24E+08	1.24E+08	4763

ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP1-102G2	chr1	-	1.75E+08	1.75E+08	334
ENSG00000(	2.071584	0	0	2.247227	0.920432	0	-0.28364	0.8344	NA	RP11-335C	chr12	-	68052771	68064699	777
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	ARHGEF7-A	chr13	-	1.12E+08	1.12E+08	777
ENSG00000(	17.60846	13.24716	25.06886	2.996302	3.681728	3.28786	2.2982	0.001372	0.003765	AP001468.	chr21	-	47612391	47613673	804
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-59O6	chr9	-	267966	273002	406
ENSG00000(	83.89914	81.89156	97.63662	92.88537	76.39586	96.1699	-0.01469	0.95647	0.97426	RP11-77I2	chr12	+	30947977	30955645	1645
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC023115.	chr2	+	67313578	67523207	1074
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	AF064858.	chr21	-	40360633	40378079	1412
ENSG00000(	14.50109	15.65574	7.916483	2.247227	11.04518	9.863579	0.67605	0.36016	0.48975	TSPEAR-AS1	chr21	+	45926690	45935738	1388
ENSG00000(	2.071584	3.612863	0	0	0	0	1.8175	0.17961	NA	RP11-460E	chr9	+	70348573	70349113	541
ENSG00000(	4.143168	1.204288	6.597069	1.498151	4.60216	0.821965	0.63572	0.56069	0.68112	TM4SF19-A	chr3	+	1.96E+08	1.96E+08	1829
ENSG00000(	0	0	0	0.749076	0.920432	1.64393	-1.0185	0.44577	NA	RP11-626E	chr4	+	1.87E+08	1.87E+08	618
ENSG00000(	5.17896	1.204288	9.235896	3.745378	10.12475	9.863579	-0.53562	0.54084	0.66385	CPB2-AS1	chr13	+	46627037	46687467	747
ENSG00000(	1.035792	1.204288	7.916483	5.992604	10.12475	8.219649	-1.1173	0.23056	0.34396	RBMS3-AS3	chr3	-	29305685	29332217	613
ENSG00000(	0	2.408575	0	0.749076	4.60216	0	-0.63728	0.6358	0.74472	RP4-580O1	chr1	-	33977608	33978343	736
ENSG00000(	8.286335	4.817151	2.638828	3.745378	0.920432	12.32947	-0.08642	0.92801	0.95677	RHOA-IT1	chr3	-	49402578	49404439	517
ENSG00000(	3.107376	3.612863	0	0	0.920432	0.821965	1.213	0.35705	0.48654	AP006216.	chr11	+	1.17E+08	1.17E+08	563
ENSG00000(	1.035792	2.408575	0	0.749076	0.920432	2.465895	-0.15898	0.90336	0.94026	RP1-159A1	chr1	+	27975930	27976121	192
ENSG00000(	6.214751	1.204288	0	0.749076	0	0	1.75	0.19303	0.29886	RP11-39K2	chr9	+	5098341	5099325	680
ENSG00000(	29.00217	22.88147	31.66593	53.93344	23.0108	42.74218	-0.51079	0.24953	0.36676	ASH1L-AS1	chr1	+	1.56E+08	1.56E+08	1955
ENSG00000(	1.035792	0	0	0	1.840864	0	-0.17777	0.89006	NA	AC073109.	chr7	-	11859943	11860920	978
ENSG00000(	10.35792	14.45145	3.958241	1.498151	3.681728	4.93179	1.345	0.12276	0.20778	NEXN-AS1	chr1	-	78347033	78355224	2292
ENSG00000(	0	2.408575	2.638828	0	0	0	1.6365	0.22501	NA	AC008280.	chr2	-	54256689	54257819	412
ENSG00000(	2.071584	0	1.319414	0	0.920432	0	0.84841	0.52989	NA	MTND1P21	chr10	+	21093222	21093506	285
ENSG00000(	19.68005	28.90291	27.70769	14.98151	19.32907	23.01502	0.39559	0.42463	0.55514	ZNF815P	chr7	+	5862791	5894066	2750
ENSG00000(	4.143168	1.204288	0	0	1.840864	4.93179	-0.20606	0.87056	0.91862	AC002543.	chr7	-	1.17E+08	1.17E+08	1954
ENSG00000(	9.322127	12.04288	9.235896	5.243529	10.12475	4.109825	0.60529	0.42328	0.55375	LL0XNC01-	chrX	-	1.03E+08	1.03E+08	496
ENSG00000(	167.7983	210.7504	151.7326	128.841	95.72493	142.1999	0.5259	0.02721	0.057094	TTC28-AS1	chr22	+	28315364	28404569	5859
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC096582.	chr7	-	45855815	45858615	2801
ENSG00000(	0	0	0	0.749076	3.681728	0	-1.2286	0.35939	NA	COX7CP1	chr13	-	49761615	49761806	192
ENSG00000(	8.286335	2.408575	2.638828	4.494453	3.681728	13.9734	-0.61808	0.49857	0.62686	UBOX5-AS1	chr20	+	3087559	3131513	1792
ENSG00000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	AC009237.	chr2	-	96305929	96306352	424
ENSG00000(	7.250543	1.204288	2.638828	1.498151	0	0.821965	1.5981	0.18904	0.29411	PNMA6C	chrX	+	1.52E+08	1.52E+08	2255
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	COX5BP3	chr7	-	1.33E+08	1.33E+08	367
ENSG00000(	0	6.021439	0	0	0.920432	0.821965	0.99518	0.45994	0.5894	VN2R19P	chr19	-	58523957	58537294	1052
ENSG00000(	2.071584	1.204288	2.638828	0	0	0	1.9938	0.14152	NA	AC007875.	chr7	+	97512594	97513107	514
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	GPC5-AS1	chr13	-	93353642	93373867	393
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-495P	chr1	-	1.48E+08	1.48E+08	331
ENSG00000(	92.18548	144.5145	133.2608	133.3354	112.2927	90.41614	0.13236	0.6174	0.72983	MORC2-AS	chr22	+	31318295	31328436	2170
ENSG00000(	0	1.204288	1.319414	6.74168	0	3.28786	-1.3587	0.28399	0.40694	RP11-323D	chr1	+	2.42E+08	2.42E+08	421
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP3-470B2	chr6	-	1.68E+08	1.68E+08	1016
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	UBE2V1P6	chr2	+	1.7E+08	1.7E+08	422
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-97N1	chr20	-	19193496	19194121	366
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC109642.	chr2	+	30569525	30575297	2952

ENSG00000(	39.36009	30.10719	17.15238	76.40571	27.61296	35.34449	-0.66078	0.16078	0.25818	RP11-403I:	chr1	+	1.49E+08	1.49E+08	1986
ENSG00000(	7.250543	8.430014	7.916483	4.494453	8.283888	3.28786	0.50509	0.53892	0.6626	CTB-75G16	chr17	-	34930301	34931164	864
ENSG00000(	1.035792	2.408575	0	0	1.840864	1.64393	0.005027	0.997	0.99811	AC007050.	chr22	-	20876357	20878157	652
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	AC011747.	chr2	-	8699963	8723922	8839
ENSG00000(	0	0	5.277655	0.749076	4.60216	0	-0.02212	0.98662	0.99181	RP3-332B2	chr6	+	1.4E+08	1.4E+08	1252
ENSG00000(	17.60846	7.225726	9.235896	11.23613	3.681728	5.753754	0.65762	0.38438	0.51514	AC011290.	chr7	-	39608975	39609797	823
ENSG00000(	5.17896	8.430014	6.597069	8.988907	16.56778	0.821965	-0.33718	0.69682	0.79353	RP1-3J17.3	chr6	+	86340080	86340995	916
ENSG00000(	79.75598	67.44011	30.34652	35.95563	61.66894	73.97684	0.058127	0.88277	0.92678	ASMTL-AS1	chrX	+	1520662	1532921	840
ENSG00000(	8.286335	8.430014	6.597069	5.243529	2.761296	4.109825	0.83416	0.32773	0.45549	RP4-814D1	chr7	-	1.57E+08	1.57E+08	766
ENSG00000(	1.035792	2.408575	1.319414	1.498151	2.761296	3.28786	-0.4935	0.67711	0.77848	RP11-195C	chr1	+	1.76E+08	1.76E+08	579
ENSG00000(	5.17896	3.612863	5.277655	0	0	0	3.3468	0.009021	0.021191	RP11-483H	chr9	-	1.32E+08	1.32E+08	429
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	PATE3	chr11	+	1.26E+08	1.26E+08	1336
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AL953854.	chr9	-	47295855	47314322	4523
ENSG00000(	1.035792	0	5.277655	5.992604	0	0	0.022878	0.98598	0.99155	RP11-108N	chr1	+	1.87E+08	1.87E+08	858
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-269F	chr1	+	2.44E+08	2.44E+08	751
ENSG00000(	0	4.817151	6.597069	3.745378	0	2.465895	0.62694	0.59513	0.71099	RP11-90O2	chr1	-	2.04E+08	2.04E+08	792
ENSG00000(	8.286335	2.408575	1.319414	5.243529	0	0.821965	0.74367	0.52101	0.6467	AC019117.	chr7	-	17474101	17500296	589
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CHIAP1	chr1	+	1.12E+08	1.12E+08	995
ENSG00000(	1.035792	0	1.319414	0.749076	0	1.64393	-0.01859	0.98907	NA	FABP5P2	chr13	+	52540878	52541285	408
ENSG00000(	6.214751	4.817151	0	0	0	0	2.803	0.03585	0.072671	RP3-467K1	chr1	-	15660662	15661960	727
ENSG00000(	1.035792	1.204288	1.319414	0	0.920432	2.465895	0.046007	0.97227	0.98387	AC073410.	chr2	+	2.03E+08	2.03E+08	589
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	AC013470.	chr7	+	12510978	12512171	1194
ENSG00000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	AC104777.	chr2	-	1.51E+08	1.51E+08	2528
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	MYCBP2-AS	chr13	+	77649649	77672677	834
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-423C	chr1	-	1.43E+08	1.43E+08	593
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	GAPDHP14	chr21	+	30594642	30595578	937
ENSG00000(	1.035792	0	3.958241	0.749076	0	0	1.2761	0.34694	NA	RP11-215A	chr10	-	1.21E+08	1.21E+08	549
ENSG00000(	0	1.204288	2.638828	0.749076	1.840864	1.64393	-0.10771	0.93395	0.96031	HSPB1P1	chr9	-	74622797	74623052	256
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP6-191P2	chrX	-	1.07E+08	1.07E+08	2090
ENSG00000(	1.035792	0	1.319414	0	1.840864	2.465895	-0.49225	0.71368	0.80659	RP1-117O3	chr1	+	33452676	33498070	1680
ENSG00000(	2.071584	2.408575	5.277655	2.996302	5.522592	4.109825	-0.31979	0.75082	0.8347	RP11-389C	chr1	+	1.14E+08	1.14E+08	436
ENSG00000(	18.64425	12.04288	21.11062	2.996302	0	1.64393	3.0493	0.000274	0.000839	RP5-1011C	chr1	+	1.92E+08	1.93E+08	684
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-281B	chrX	+	34405839	34406581	743
ENSG00000(	3.107376	0	13.19414	1.498151	2.761296	0.821965	1.3035	0.24605	0.3626	AC074389.	chr7	-	1778266	1781927	637
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-217L	chr11	-	1.31E+08	1.31E+08	149
ENSG00000(	7.250543	7.225726	3.958241	0	0.920432	0	3.0951	0.00935	0.021887	OR13E1P	chr9	-	35859059	35859980	922
ENSG00000(	160.5477	183.0517	171.5238	86.14369	90.20234	87.12828	0.96024	2.05E-05	7.33E-05	COX10-AS1	chr17	-	13659795	13972812	2998
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	LDHAP3	chr2	+	42046887	42047894	1008
ENSG00000(	0	2.408575	2.638828	0	1.840864	0	0.79984	0.55362	0.67452	RP3-473B4	chrX	+	1.34E+08	1.34E+08	961
ENSG00000(	2.071584	1.204288	0	0.749076	0	2.465895	0.026614	0.98418	0.99091	RP11-49O1	chr9	+	97662711	97667036	779
ENSG00000(	2.071584	0	7.916483	0.749076	1.840864	2.465895	0.71871	0.54511	0.66734	RP11-148B	chr1	-	94784035	94790125	592
ENSG00000(	593.5088	657.5411	584.5003	223.2245	249.4371	324.6761	1.1986	3.03E-12	2.01E-11	ZBTB22	chr6	-	33282183	33285719	2651
ENSG00000(	0	0	0	3.745378	4.60216	1.64393	-2.481	0.060152	0.11399	AC010729.	chr2	+	5866581	5870474	1746
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC010127.	chr2	+	1.67E+08	1.67E+08	2305

ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-383G	chr1	+	2.05E+08	2.05E+08	305
ENSG0000(	3.107376	0	3.958241	0	0	1.64393	1.2286	0.35606	0.48557	RP11-517P	chr10	+	44018704	44020665	1962
ENSG0000(	0	3.612863	0	0.749076	0	0	0.87856	0.51086	NA	RP11-62C3	chr9	+	94967638	94972440	333
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC064853.	chr2	-	2.28E+08	2.28E+08	540
ENSG0000(	0	0	2.638828	2.247227	0	0	0.077345	0.95422	NA	RP11-733C	chrX	-	5571462	5644346	860
ENSG0000(	5.17896	1.204288	0	2.247227	5.522592	0.821965	-0.28117	0.81304	0.87865	CTA-440B3	chr22	-	32212365	32213477	477
ENSG0000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	ADORA2BP	chr1	+	2.1E+08	2.1E+08	842
ENSG0000(	1.035792	0	3.958241	2.996302	5.522592	15.61733	-1.8785	0.072196	0.13322	RP11-27K1	chr1	-	1.18E+08	1.18E+08	1814
ENSG0000(	10.35792	21.67718	14.51355	1.498151	3.681728	2.465895	2.3713	0.002726	0.007094	RP11-413E	chr3	+	75718082	75719336	1255
ENSG0000(	0	4.817151	0	2.996302	0	4.109825	-0.37435	0.77221	0.85025	RP11-89F3	chr1	-	1.48E+08	1.48E+08	381
ENSG0000(	33.14534	36.12863	51.45714	134.8336	138.0648	174.2566	-1.8767	1.19E-10	7.02E-10	AD000090.	chr19	-	36031640	36036931	3911
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-65J3.	chr9	-	1.32E+08	1.32E+08	335
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	MRPS36P1	chr3	-	6814724	6815030	307
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC104076.	chr2	-	1.82E+08	1.82E+08	265
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-343J:	chr10	+	71335563	71336910	503
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-231P	chr1	+	26536232	26556331	2108
ENSG0000(	14.50109	7.225726	6.597069	4.494453	5.522592	14.79537	0.18525	0.81019	0.87681	CHCHD4P3	chr9	+	37434174	37434583	410
ENSG0000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-187C	chr9	-	45424050	45424634	585
ENSG0000(	0	0	1.319414	0.749076	0.920432	0	-0.15244	0.90808	NA	RP3-343K2	chr20	-	35794177	35794715	539
ENSG0000(	1.035792	0	2.638828	0.749076	0	10.68554	-1.1347	0.36569	0.49558	PRADC1P1	chr3	+	37017807	37018331	525
ENSG0000(	1.035792	3.612863	2.638828	0	0	0	2.2878	0.090046	0.16086	RP3-523C2	chr6	+	1.32E+08	1.32E+08	552
ENSG0000(	0	2.408575	1.319414	0	0	0	1.2548	0.34239	NA	RP1-182D1	chr6	-	1.7E+08	1.7E+08	694
ENSG0000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	SSU72P6	chr11	+	4299935	4300422	488
ENSG0000(	0	1.204288	0	0	3.681728	0	-0.65196	0.62789	NA	RP11-297K	chr3	-	1.89E+08	1.89E+08	754
ENSG0000(	2.071584	12.04288	6.597069	10.48706	8.283888	6.575719	-0.27624	0.73318	0.82147	TCEA1P4	chr9	-	32979558	32980401	844
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	GJA6P	chrX	+	18553199	18554240	1042
ENSG0000(	0	0	3.958241	0	3.681728	1.64393	-0.27102	0.83828	0.89652	PRKX-AS1	chrX	+	3577528	3586233	516
ENSG0000(	3.107376	1.204288	2.638828	0.749076	2.761296	4.93179	-0.20762	0.85515	0.90791	AC003104.	chr17	-	40422535	40424701	855
ENSG0000(	1.035792	0	0	0	3.681728	0	-0.68494	0.60991	NA	AC002429.	chr7	-	94784025	94843644	2569
ENSG0000(	12.4295	2.408575	11.87472	1.498151	2.761296	1.64393	1.8756	0.047917	0.093534	RP11-264I:	chr9	-	2041900	2046023	420
ENSG0000(	12.4295	19.2686	19.79121	19.47596	15.64734	16.4393	-0.01118	0.98379	0.99079	KDM4A-AS:	chr1	-	44165436	44173809	833
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	GRM7-AS1	chr3	-	7561428	7602020	430
ENSG0000(	8.286335	2.408575	5.277655	5.992604	2.761296	5.753754	0.12325	0.89305	0.93379	AC092594.	chr2	-	19167729	19546509	1949
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-400N	chr1	-	2.22E+08	2.23E+08	675
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC017048.	chr2	-	1.77E+08	1.77E+08	822
ENSG0000(	5.17896	4.817151	2.638828	0.749076	2.761296	0.821965	1.236	0.26631	0.3863	RP11-12A2	chr9	+	67792167	67794649	2483
ENSG0000(	16.57267	10.83859	1.319414	2.247227	0	4.93179	1.6809	0.089009	0.1593	AC091132.	chr17	+	43530210	43541431	769
ENSG0000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	AC093106.	chr7	+	1.31E+08	1.31E+08	352
ENSG0000(	0	0	0	3.745378	3.681728	2.465895	-2.4805	0.059957	0.11364	GPC5-IT1	chr13	+	93136859	93162347	658
ENSG0000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	MYO16-AS1	chr13	-	1.1E+08	1.1E+08	580
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-15J1(	chr9	-	70113593	70124467	1263
ENSG0000(	55.93276	43.35436	48.81831	42.69731	40.49901	45.20807	0.20426	0.561	0.68128	AC009404.	chr2	+	1.19E+08	1.19E+08	3090
ENSG0000(	2.071584	1.204288	3.958241	9.737982	5.522592	4.109825	-1.2136	0.21782	0.32919	DIAPH2-AS:	chrX	-	96686257	96897588	1128
ENSG0000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	SHANK2-AS	chr11	+	70492270	70493667	356

ENSG00000(	4.143168	3.612863	1.319414	6.74168	0.920432	1.64393	-0.03203	0.97676	0.9865	RPL26P30	chr11	-	2356362	2357006	645
ENSG00000(	0	0	0	1.498151	0.920432	0.821965	-0.99775	0.45448	NA	RP11-170N	chr1	-	83439565	83451891	1526
ENSG00000(	25.8948	49.3758	13.19414	1.498151	7.363456	9.863579	2.1092	0.001559	0.004229	ENO1-IT1	chr1	-	8935847	8938066	744
ENSG00000(	2.071584	0	2.638828	0	0.920432	4.93179	-0.20512	0.87357	0.92056	RP4-728D4	chr1	+	35975343	35977039	1003
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	AC093106.	chr7	-	1.31E+08	1.31E+08	507
ENSG00000(	574.8645	600.9396	723.0388	704.131	601.9625	549.0726	0.031506	0.83825	0.89652	ZBED5	chr11	-	10833621	10880343	3677
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	EEF1GP7	chr1	+	53038786	53039488	703
ENSG00000(	8.286335	9.634302	9.235896	11.98521	10.12475	17.26126	-0.50483	0.44956	0.57942	GUSBP5	chr4	+	1.44E+08	1.45E+08	1989
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-175P	chr3	-	1.93E+08	1.93E+08	735
ENSG00000(	19.68005	10.83859	11.87472	0	2.761296	0	3.3948	0.000423	0.001257	AP001189.	chr11	+	76368100	76374910	1426
ENSG00000(	18.64425	3.612863	5.277655	5.243529	4.60216	14.79537	0.15993	0.84464	0.90085	RP11-126L	chr7	-	1E+08	1E+08	369
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	RP11-33G1	chr9	+	25780054	25784560	463
ENSG00000(	0	2.408575	2.638828	7.490755	4.60216	5.753754	-1.5075	0.15528	0.25103	AC104651.	chr2	+	1.13E+08	1.13E+08	430
ENSG00000(	1.035792	2.408575	9.235896	7.490755	4.60216	10.68554	-0.76512	0.40454	0.53542	RP11-316N	chr10	+	1.02E+08	1.02E+08	578
ENSG00000(	0	1.204288	2.638828	0	0	0	1.2853	0.33195	NA	AC005027.	chr7	-	41706766	41744933	386
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-348H	chr1	-	2.13E+08	2.13E+08	192
ENSG00000(	34.18113	25.29004	14.51355	0	0	0	5.8715	7.17E-08	3.33E-07	AC019117.	chr7	+	17414491	17506288	837
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CTD-2033D	chr17	-	53604325	53638938	669
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	RP3-403L1	chr6	-	1.58E+08	1.58E+08	372
ENSG00000(	0	1.204288	0	1.498151	0.920432	0	-0.40353	0.76332	NA	RP11-759F	chr1	+	1.54E+08	1.54E+08	271
ENSG00000(	24.85901	24.08575	25.06886	180.5272	238.3919	269.6045	-3.1787	1.75E-27	2.40E-26	TRHDE-AS1	chr12	-	72647288	72668687	4733
ENSG00000(	0	3.612863	3.958241	10.48706	14.72691	16.4393	-2.2147	0.010081	0.023426	FMR1-IT1	chrX	+	1.47E+08	1.47E+08	343
ENSG00000(	15.53688	18.06432	21.11062	2.996302	1.840864	3.28786	2.5126	0.000674	0.001941	RP11-59D5	chr6	+	64516729	64532535	1454
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-346D	chr6	+	1.14E+08	1.14E+08	597
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	PSMC1P10	chr2	+	17566358	17567684	1327
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	SUCLG2P2	chr12	+	94942017	94943312	1296
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-349C	chr13	-	39107480	39119436	791
ENSG00000(	2.071584	1.204288	0	4.494453	9.20432	4.93179	-1.9302	0.077135	0.14086	RP11-525G	chr1	-	1.66E+08	1.66E+08	347
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-440G	chr6	-	1.43E+08	1.43E+08	2293
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP5-865N1	chr1	-	2.32E+08	2.32E+08	2241
ENSG00000(	3.107376	3.612863	2.638828	0	0	5.753754	0.50398	0.67927	0.78006	POU5F1P5	chr10	-	69770184	69770601	418
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC084809.	chr17	+	31232680	31233602	512
ENSG00000(	75.61281	49.3758	48.81831	4.494453	8.283888	14.79537	2.5779	1.16E-07	5.26E-07	LINC00854	chr17	-	41368960	41383338	980
ENSG00000(	0	0	0	0	4.60216	1.64393	-1.6592	0.22125	0.33301	LINC00479	chr21	-	43131680	43135935	2033
ENSG00000(	8.286335	0	1.319414	0	0	0	2.5459	0.059133	0.11229	RP11-114N	chr3	-	1.77E+08	1.77E+08	723
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC009518.	chr7	+	1.32E+08	1.32E+08	253
ENSG00000(	2.071584	0	3.958241	0	0	0	1.8862	0.16413	0.26236	ITCH-AS1	chr20	-	33029397	33029830	299
ENSG00000(	4.143168	2.408575	5.277655	2.247227	2.761296	4.109825	0.31029	0.76083	0.84189	RP11-25B7	chr1	-	2.02E+08	2.02E+08	579
ENSG00000(	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	AC092573.	chr2	-	1.74E+08	1.74E+08	336
ENSG00000(	1.035792	0	3.958241	2.996302	8.283888	0.821965	-0.97054	0.40739	0.53818	RP11-320G	chrX	+	40122170	40146973	3000
ENSG00000(	44.53905	19.2686	52.77655	94.38352	80.99802	70.68898	-1.06	0.003877	0.009825	DDX11L2	chr2	-	1.14E+08	1.14E+08	1651
ENSG00000(	21.75163	15.65574	21.11062	63.67142	69.0324	52.60575	-1.6235	4.73E-05	0.000162	RP11-125B	chr9	-	2422702	2641395	3167
ENSG00000(	0	3.612863	0	3.745378	2.761296	0.821965	-0.68603	0.59106	0.70756	NRADDP	chr3	+	47053032	47054636	691
ENSG00000(	0	1.204288	2.638828	0.749076	1.840864	0	0.31478	0.81488	0.8797	NDUFAF4P2	chr3	-	37831412	37831936	525

ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	CTSL1P1	chr10	-	89146442	89149960	1002
ENSG00000(	26.93059	20.47289	18.47179	32.21025	35.89685	45.20807	-0.75336	0.087802	0.15755	RP13-15E1	chr1	+	3816936	3833789	3059
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AC090018.	chr3	-	1.95E+08	1.95E+08	366
ENSG00000(	3.107376	0	1.319414	0.749076	0	3.28786	0.090315	0.94534	0.9672	RP11-79M:	chr10	-	1.21E+08	1.21E+08	706
ENSG00000(	0	0	0	3.745378	0.920432	1.64393	-1.8144	0.1802	0.28308	RP11-107N	chr1	+	1.52E+08	1.52E+08	397
ENSG00000(	0	1.204288	1.319414	3.745378	1.840864	5.753754	-1.5832	0.19069	0.29614	KRT8P29	chr1	-	2.04E+08	2.04E+08	1371
ENSG00000(	24.85901	14.45145	14.51355	14.98151	8.283888	9.041614	0.69746	0.25416	0.37222	AC097662.	chr2	-	2.28E+08	2.28E+08	2568
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-296A	chr1	-	51730588	51731746	435
ENSG00000(	46.61064	38.53721	56.73479	30.7121	64.43024	59.18147	-0.11622	0.76104	0.84198	FAM157A	chr3	+	1.98E+08	1.98E+08	2168
ENSG00000(	17.60846	21.67718	23.74945	11.98521	10.12475	13.15144	0.79462	0.1554	0.25118	RP11-175B	chr1	-	2.02E+08	2.02E+08	322
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	UBE2L5P	chr13	+	31002084	31002656	573
ENSG00000(	2.071584	0	1.319414	0	1.840864	0.821965	0.21443	0.87358	0.92056	ATG10-IT1	chr5	+	81287814	81288300	487
ENSG00000(	11.39371	33.72006	14.51355	1.498151	2.761296	1.64393	3.0244	0.000138	0.00044	AC018890.	chr2	+	1.75E+08	1.76E+08	2400
ENSG00000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	AC067956.	chr2	+	2.21E+08	2.22E+08	2062
ENSG00000(	0	2.408575	1.319414	0	0	0	1.2548	0.34239	NA	AC003092.	chr7	+	93652145	93695973	743
ENSG00000(	5.17896	13.24716	10.55531	1.498151	3.681728	0.821965	1.9768	0.032245	0.066209	AC005154.	chr7	-	30617128	30625588	1405
ENSG00000(	1.035792	3.612863	0	0	0	0	1.5346	0.25314	NA	AC130689.	chr17	-	2118776	2119309	323
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-523L	chr9	-	1.18E+08	1.18E+08	1525
ENSG00000(	2.071584	1.204288	0	0	0.920432	1.64393	0.21609	0.87277	NA	LINC00427	chr13	-	30890497	30894040	430
ENSG00000(	21.75163	15.65574	21.11062	4.494453	15.64734	4.93179	1.1646	0.07521	0.13794	RP11-443A	chr10	+	78647802	78740382	3566
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-104D	chr1	+	1.99E+08	1.99E+08	1335
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AF127577.	chr21	+	16439391	16440158	446
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	AC002401.	chr17	+	48212951	48223541	468
ENSG00000(	0	1.204288	0	0	5.522592	0	-1.0223	0.45107	0.58069	GCNT1P1	chr20	-	18400804	18402098	1295
ENSG00000(	2.071584	0	2.638828	0	0	0	1.5584	0.24658	NA	TRIM26BP	chr6	+	30206078	30210056	753
ENSG00000(	11.39371	9.634302	5.277655	12.73428	22.09037	24.65895	-1.0933	0.082853	0.14987	AC012513.	chr2	-	2.17E+08	2.17E+08	1137
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	PKMP1	chr1	+	1.15E+08	1.15E+08	1523
ENSG00000(	1.035792	0	1.319414	2.996302	1.840864	1.64393	-0.95747	0.45631	0.58607	CTD-3105H	chr19	+	12613489	12614920	841
ENSG00000(	0	0	1.319414	0	4.60216	0	-0.82615	0.54181	NA	RP11-537I:	chr3	+	1.85E+08	1.85E+08	299
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP13-565C	chrX	-	1.34E+08	1.34E+08	730
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	EIF2S2P3	chr10	-	94428502	94429500	999
ENSG00000(	3.107376	4.817151	6.597069	2.996302	6.443024	5.753754	-0.06112	0.9467	0.96779	RP11-89N1	chr7	-	33832780	33842768	1589
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-255J:	chr9	-	2875442	2876427	986
ENSG00000(	15.53688	10.83859	2.638828	7.490755	11.04518	8.219649	0.12724	0.8661	0.91552	AC107081.	chr2	+	62095567	62113217	802
ENSG00000(	1.035792	1.204288	3.958241	0	0	0	2.0343	0.13352	0.22221	EM:AC006:	chr22	+	20194100	20194706	607
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP1-63P18	chr1	+	41029206	41029331	126
ENSG00000(	1.035792	0	7.916483	0	0	0	2.4101	0.074732	0.13721	RPL21P13:	chrX	+	1.34E+08	1.34E+08	476
ENSG00000(	0	0	0	2.247227	11.04518	2.465895	-3.1203	0.01447	0.032436	AC011284.	chr7	-	3682447	3683416	856
ENSG00000(	1.035792	0	1.319414	1.498151	1.840864	1.64393	-0.67375	0.60745	0.7217	RP3-336K2	chr6	+	7620655	7621111	457
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-162G	chr10	+	38146668	38148038	826
ENSG00000(	1.035792	1.204288	0	1.498151	8.283888	8.219649	-2.2159	0.054253	0.10437	AL773604.	chr21	+	46222492	46224632	1031
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	GPC6-AS1	chr13	-	94806447	94840245	698
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-134F	chr3	-	1.86E+08	1.86E+08	534
ENSG00000(	5.17896	18.06432	13.19414	2.247227	9.20432	5.753754	0.98872	0.20764	0.31693	RP4-742J2	chr20	-	11890052	11899325	1831

ENSG00000(	1.035792	2.408575	1.319414	0	0.920432	0.821965	0.8709	0.51283	0.6398	ARF4P2	chr20	-	61503602	61504428	526
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP1-125I3.	chr1	+	26186104	26189911	849
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP13-254B	chr7	+	65305199	65305583	385
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC097711.	chr4	+	81000686	81002276	1591
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	AL035610.	chr21	-	29488413	29600986	4486
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	AC009413.	chr2	-	42077343	42077741	399
ENSG00000(	0	1.204288	0	0.749076	0	0	0.1572	0.90001	NA	H3F3BP1	chr13	+	72249199	72249601	403
ENSG00000(	3.107376	4.817151	1.319414	2.996302	0.920432	3.28786	0.2805	0.80035	0.86991	RC3H1-IT1	chr1	-	1.74E+08	1.74E+08	448
ENSG00000(	4.143168	1.204288	5.277655	2.247227	4.60216	4.109825	-0.03376	0.97371	0.98475	AC003986.	chr7	+	19159556	19161539	692
ENSG00000(	23.82321	38.53721	44.86007	9.737982	25.7721	23.01502	0.84554	0.087801	0.15755	RP11-732M	chr6	+	1.59E+08	1.59E+08	424
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	RP11-215I2	chr1	-	1.79E+08	1.79E+08	9714
ENSG00000(	48.68222	55.39724	40.90183	36.7047	41.41944	48.49593	0.19462	0.58838	0.70554	AC006547.	chr22	-	20050503	20058045	930
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	MED28P7	chr20	-	25650493	25651022	530
ENSG00000(	0	1.204288	3.958241	1.498151	2.761296	2.465895	-0.29649	0.80881	0.87589	AP001619.	chr21	+	43290742	43292163	587
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP1-118J2:	chr1	+	40363417	40364770	785
ENSG00000(	8.286335	13.24716	10.55531	2.247227	6.443024	4.109825	1.2087	0.13106	0.21865	RP11-510H	chr6	-	1.25E+08	1.25E+08	4507
ENSG00000(	1.035792	1.204288	0	3.745378	0.920432	0.821965	-0.79376	0.54531	0.66745	AC079807.	chr2	+	48110594	48111048	455
ENSG00000(	357.3482	410.6621	286.3128	191.0143	144.5078	259.7409	0.81849	0.000234	0.000724	RPL13AP5	chr10	+	98510045	98510675	612
ENSG00000(	0	3.612863	5.277655	1.498151	0	0	1.5307	0.24376	0.35975	ASNSP3	chr13	-	1.01E+08	1.01E+08	1306
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	AC115115.	chr2	+	1.13E+08	1.13E+08	248
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-443C	chr10	+	61041907	61042595	336
ENSG00000(	0	0	0	0	0.920432	7.397684	-2.0204	0.1358	0.22509	AC138655.	chr2	-	47713153	47715691	2007
ENSG00000(	7.250543	0	2.638828	5.992604	2.761296	9.041614	-0.68591	0.49942	0.62778	RP11-243J:	chr20	+	30274019	30304628	374
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-396M	chr4	+	66959844	66960244	399
ENSG00000(	16.57267	12.04288	18.47179	8.988907	24.85166	13.9734	-0.01291	0.98284	0.99026	HNRNPA3P	chr13	-	66362064	66362896	833
ENSG00000(	1.035792	0	2.638828	0	2.761296	1.64393	-0.1601	0.90357	0.94038	RP11-39K2	chr9	+	5110913	5112849	1937
ENSG00000(	2.071584	4.817151	6.597069	1.498151	5.522592	0	0.7517	0.49582	0.62449	RP11-22B1	chrX	+	51600064	51601162	1099
ENSG00000(	2.071584	0	2.638828	0	0.920432	0.821965	0.81976	0.54181	0.66459	SNRPGP14	chr13	+	50063106	50063500	219
ENSG00000(	2.071584	2.408575	0	0	0	0	1.5041	0.26224	NA	RP11-95P9	chr7	-	1.14E+08	1.14E+08	316
ENSG00000(	5.17896	6.021439	13.19414	6.74168	2.761296	1.64393	0.96794	0.27882	0.40091	STARD13-A	chr13	+	33851690	33855471	900
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	PRPF38AP2	chr10	+	17619361	17620211	851
ENSG00000(	1.035792	7.225726	7.916483	0.749076	0	0	2.8838	0.019542	0.042499	AP004290.	chr8	-	1E+08	1E+08	1412
ENSG00000(	10.35792	4.817151	10.55531	1.498151	0	0.821965	2.7689	0.007916	0.01884	RP11-162J:	chr6	-	1.49E+08	1.49E+08	130
ENSG00000(	1.035792	0	2.638828	5.992604	5.522592	8.219649	-1.9597	0.067818	0.12636	RANP1	chr6	+	30453717	30454367	651
ENSG00000(	50.7538	42.15007	46.17948	82.39831	58.90765	64.11326	-0.55491	0.092067	0.16381	ZNF853	chr7	+	6655248	6663921	3857
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AP000343.	chr22	+	23668803	23670680	346
ENSG00000(	4.143168	0	1.319414	0	4.60216	4.93179	-0.54773	0.65469	0.76006	RP11-46H1	chr12	+	1.33E+08	1.33E+08	555
ENSG00000(	6.214751	1.204288	0	5.243529	1.840864	5.753754	-0.5957	0.58982	0.70665	PITPNA-AS1	chr17	+	1420225	1421390	542
ENSG00000(	41.43168	51.78437	47.4989	69.66403	34.05598	49.3179	-0.12624	0.73509	0.82279	CCDC163P	chr1	-	45959538	45965751	2229
ENSG00000(	0	2.408575	1.319414	0	0	0	1.2548	0.34239	NA	RP11-211A	chr1	-	2.27E+08	2.27E+08	432
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	CTA-221G9	chr22	+	25608709	25609652	482
ENSG00000(	0	3.612863	1.319414	3.745378	0	4.93179	-0.58985	0.63446	0.74381	RP11-175D	chr9	+	1.28E+08	1.28E+08	617
ENSG00000(	0	1.204288	2.638828	2.996302	16.56778	7.397684	-2.3166	0.026657	0.056093	AC104801.	chr2	+	1.73E+08	1.73E+08	950
ENSG00000(	0	2.408575	0	2.247227	1.840864	0	-0.41398	0.75953	0.84108	AC079780.	chr7	+	23520372	23520578	207

ENSG00000(	3.107376	0	2.638828	1.498151	0	0	1.0543	0.43346	0.56318	AP001631.	chr21	-	44560633	44561202	422
ENSG00000(	0	1.204288	0	0	0	4.109825	-0.75943	0.57378	NA	RP11-85O2	chr9	-	1.27E+08	1.27E+08	2146
ENSG00000(	9.322127	12.04288	2.638828	8.239831	3.681728	11.50751	0.035335	0.96511	0.97979	KRT18P5	chr22	-	20837102	20838392	1291
ENSG00000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	PRKG1-AS1	chr10	-	53990502	54073888	1111
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-69I8.	chr6	+	1.32E+08	1.32E+08	2305
ENSG00000(	138.7961	143.3102	122.7055	24.71949	35.89685	68.22309	1.6289	1.09E-06	4.53E-06	MTX1P1	chr1	+	1.55E+08	1.55E+08	838
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-296P	chr9	+	19026890	19028127	1238
ENSG00000(	5.17896	4.817151	7.916483	3.745378	2.761296	4.109825	0.64605	0.48182	0.61098	AC068282.	chr2	+	1.28E+08	1.28E+08	2690
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	BZW1P1	chr3	-	1.72E+08	1.72E+08	1240
ENSG00000(	10.35792	3.612863	5.277655	10.48706	21.16994	23.01502	-1.3784	0.046589	0.091282	EIF1AXP1	chr1	-	17012116	17012550	435
ENSG00000(	1.035792	0	1.319414	5.243529	5.522592	3.28786	-1.9041	0.10402	0.18114	ARHGEF38	chr4	+	1.06E+08	1.07E+08	5454
ENSG00000(	0	0	0	4.494453	11.04518	11.50751	-3.993	0.000815	0.002319	AC073316.	chr7	-	3303664	3342084	982
ENSG00000(	3.107376	2.408575	0	5.243529	0.920432	1.64393	-0.35692	0.76684	0.84621	DAPK1-IT1	chr9	+	90168369	90169374	702
ENSG00000(	0	6.021439	2.638828	0	0.920432	1.64393	1.1605	0.36438	0.49419	AC108448.	chr11	-	3105623	3106673	730
ENSG00000(	9.322127	8.430014	6.597069	0	2.761296	0.821965	2.3166	0.02384	0.050789	SMAD9-AS1	chr13	-	37423503	37424183	504
ENSG00000(	2.071584	9.634302	5.277655	0.749076	0	0	2.9844	0.014438	0.032383	AC005592.	chr5	+	1.42E+08	1.42E+08	2237
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-100G	chr9	-	94912664	94919727	210
ENSG00000(	3.107376	1.204288	0	0	0	0	1.4526	0.27741	NA	RP11-359I:	chr3	+	58497037	58497403	367
ENSG00000(	3.107376	0	3.958241	0	0	0	2.1194	0.11819	0.20137	RP11-252N	chr9	+	3875584	3878809	243
ENSG00000(	0	0	6.597069	0	0	0	1.83	0.17508	0.27674	AC094019.	chr3	-	32192575	32193387	472
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	GRIFIN	chr7	-	2514360	2516528	648
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RPL31P63	chrX	+	67819926	67820315	390
ENSG00000(	2.071584	0	6.597069	0	2.761296	0	1.0597	0.41629	0.54691	RP11-370B	chr9	+	22747699	22748233	535
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP4-560B9	chr1	+	1.72E+08	1.72E+08	451
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	RP11-168C	chr10	-	57007515	57356993	439
ENSG00000(	0	1.204288	0	2.996302	1.840864	8.219649	-2.2622	0.071382	0.132	YRDCP2	chr9	+	99717102	99717743	642
ENSG00000(	0	1.204288	6.597069	0	0	0	2.2118	0.10284	0.17949	AC009237.	chr2	-	96307382	96307728	347
ENSG00000(	0	1.204288	0	7.490755	15.64734	5.753754	-3.3865	0.002683	0.006996	RP1-30G7.:	chrX	-	46185359	46187080	626
ENSG00000(	42.46747	51.78437	27.70769	23.97042	25.7721	10.68554	0.98612	0.036732	0.07428	AC018642.	chr7	-	1.31E+08	1.31E+08	2043
ENSG00000(	0	0	0	0.749076	4.60216	3.28786	-2.2366	0.094412	0.1672	AC004019.	chr22	-	18062923	18071958	1838
ENSG00000(	0	4.817151	0	0	1.840864	1.64393	0.27734	0.83578	0.8949	DNAJC9-AS	chr10	+	75006946	75036742	3037
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	AC007251.	chr2	-	1.03E+08	1.04E+08	708
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CTAGE9	chr6	-	1.32E+08	1.32E+08	2626
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	TRMT112P4	chr9	-	1.04E+08	1.04E+08	379
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	RP11-1029	chr3	-	48162159	48162705	547
ENSG00000(	6.214751	14.45145	7.916483	2.247227	1.840864	1.64393	2.0059	0.027739	0.058049	RP5-1184F	chr20	+	31037558	31041410	986
ENSG00000(	5.17896	0	0	0	0	0	1.5469	0.24589	NA	RP11-365C	chr1	-	2.24E+08	2.24E+08	231
ENSG00000(	2.071584	2.408575	2.638828	0	0	0	2.2753	0.091747	0.16332	RP11-213P	chr1	+	57004124	57004583	460
ENSG00000(	14.50109	25.29004	11.87472	8.239831	17.48821	13.9734	0.36768	0.54392	0.66625	INTS6-AS1	chr13	+	52026503	52126500	906
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	RP11-430C	chr1	-	2.04E+08	2.04E+08	848
ENSG00000(	0	1.204288	1.319414	2.996302	0.920432	0	-0.37942	0.77795	0.85376	LINC00299	chr2	-	8147901	8523751	2342
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-462B	chr9	-	32836573	32869593	1184
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	SPA17P1	chr10	-	77142151	77142602	452
ENSG00000(	1.035792	0	3.958241	0	0	3.28786	0.33699	0.80142	0.87078	RP11-383C	chr10	+	1.17E+08	1.17E+08	344

ENSG00000(	16.57267	3.612863	9.235896	8.988907	15.64734	6.575719	-0.06124	0.93409	0.96038	RP11-373A	chr9	+	72832111	72832584	474
ENSG00000(	2.071584	0	0	0	1.840864	0	0.093542	0.94384	NA	RPS3AP12	chr1	-	1.2E+08	1.2E+08	753
ENSG00000(	0	0	1.319414	7.490755	2.761296	9.041614	-2.796	0.018656	0.040757	SNX25P1	chr1	+	2.12E+08	2.12E+08	834
ENSG00000(	10.35792	26.49433	5.277655	11.23613	18.40864	8.219649	0.15045	0.82575	0.8877	RP5-886K2	chr1	-	24086872	24104777	1074
ENSG00000(	1.035792	3.612863	9.235896	2.247227	1.840864	3.28786	0.7226	0.49251	0.62151	GAPDHP2	chr20	+	13373324	13374321	998
ENSG00000(	6.214751	1.204288	1.319414	5.992604	0.920432	10.68554	-0.81044	0.43414	0.56393	RP11-446E	chr8	-	56962597	56963766	1170
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	ANKRD20A	chr9	-	44076368	44118444	2414
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	ARL5AP2	chr10	-	1.01E+08	1.01E+08	533
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-137J	chr6	+	1.42E+08	1.42E+08	222
ENSG00000(	72.50543	52.98866	75.20659	67.4168	61.66894	41.09825	0.2338	0.48125	0.61035	BCYRN1	chr2	+	47558199	47571656	13458
ENSG00000(	3.107376	0	6.597069	2.996302	1.840864	2.465895	0.30435	0.78838	0.86153	Z97634.5	chr16	+	432097	442960	1715
ENSG00000(	4.143168	0	2.638828	13.48336	15.64734	29.59074	-2.7627	0.000714	0.002052	CBR3-AS1	chr21	-	37504065	37528605	4651
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AC024560.	chr3	-	1.97E+08	1.97E+08	1471
ENSG00000(	0	2.408575	1.319414	0	0	0	1.2548	0.34239	NA	AC090617.	chr17	+	2116991	2117708	404
ENSG00000(	24.85901	28.90291	27.70769	0	2.761296	0	4.3992	1.78E-07	7.97E-07	AC007750.	chr2	+	1.63E+08	1.63E+08	3694
ENSG00000(	0	0	0	3.745378	2.761296	0	-1.7329	0.20153	0.30918	AC091633.	chr3	+	1.95E+08	1.95E+08	474
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-401L	chr7	-	1.03E+08	1.03E+08	265
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-151D	chr9	-	75486644	75489025	628
ENSG00000(	371.8493	369.7163	299.5069	304.8737	327.6738	305.7709	0.15171	0.36331	0.49313	LL22NC03-	chr22	+	22657589	22677203	1776
ENSG00000(	6.214751	7.225726	5.277655	0	0	0	3.8068	0.002177	0.005764	RP11-503K	chr9	-	18717972	18718524	553
ENSG00000(	75.61281	51.78437	47.4989	56.92974	69.0324	60.8254	-0.08481	0.79563	0.8666	AC018737.	chr2	+	1.22E+08	1.22E+08	1273
ENSG00000(	2.071584	9.634302	10.55531	5.243529	3.681728	1.64393	0.91307	0.3235	0.45091	AC006378.	chr7	+	93598754	93640425	563
ENSG00000(	2.071584	0	2.638828	0	2.761296	1.64393	0.072233	0.95576	0.97381	RPL23AP23	chr1	+	2.35E+08	2.35E+08	471
ENSG00000(	6.214751	8.430014	10.55531	0.749076	0.920432	4.93179	1.6458	0.083844	0.15144	RP3-522J7.	chr22	+	50210896	50211360	465
ENSG00000(	2.071584	2.408575	7.916483	0.749076	6.443024	1.64393	0.39704	0.71108	0.80473	RP11-944L	chr3	-	44598849	44727145	456
ENSG00000(	89.0781	98.75159	50.13772	30.7121	38.65814	60.00344	0.86788	0.017871	0.039228	LINC00106	chrX	+	1515320	1518295	370
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	DDX11L5	chr9	+	11987	14522	1488
ENSG00000(	2.071584	1.204288	1.319414	1.498151	0	0	0.87726	0.51481	0.64148	TMSB4XP1	chr1	-	42965876	42966067	192
ENSG00000(	0	6.021439	3.958241	0.749076	2.761296	3.28786	0.41541	0.71899	0.81066	AC012363.	chr2	+	1.21E+08	1.21E+08	662
ENSG00000(	2.071584	0	5.277655	0.749076	5.522592	3.28786	-0.29192	0.80065	0.87013	C5orf27	chr5	+	95187936	95195837	2052
ENSG00000(	0	0	2.638828	0	6.443024	1.64393	-1.0106	0.44237	0.57203	XXbac-B47(	chr22	-	18564232	18564441	210
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-482E	chr10	-	3574286	3579223	430
ENSG00000(	1.035792	10.83859	0	0.749076	20.2495	5.753754	-0.95282	0.36025	0.48982	RP11-535C	chr9	-	1.01E+08	1.01E+08	402
ENSG00000(	0	0	0	0	2.761296	1.64393	-1.2339	0.35779	NA	TIMM9P1	chr10	-	76104308	76104563	256
ENSG00000(	67.32647	49.3758	67.2901	89.88907	204.3359	133.9803	-1.1978	0.00016	0.000506	MIR600HG	chr9	-	1.26E+08	1.26E+08	5984
ENSG00000(	0	4.817151	1.319414	0	0	0	1.8904	0.16312	0.26107	RP11-348H	chr1	+	2.13E+08	2.13E+08	479
ENSG00000(	0	0	0	0	0.920432	3.28786	-1.1769	0.37857	NA	RP5-1063N	chr12	+	3427884	3434509	3004
ENSG00000(	6.214751	18.06432	9.235896	10.48706	12.88605	12.32947	-0.08939	0.89425	0.93463	RP11-1008	chr15	-	38361682	38365160	967
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-408N	chr9	-	22203989	22214671	443
ENSG00000(	0	0	0	1.498151	2.761296	0.821965	-1.5229	0.26162	NA	RP11-390F	chr9	+	6645956	6670635	526
ENSG00000(	1.035792	2.408575	0	1.498151	0	0	0.56582	0.67651	NA	RP11-792A	chr7	-	65899621	65900465	521
ENSG00000(	0	4.817151	6.597069	0	1.840864	1.64393	1.2212	0.31792	0.44484	RP11-439A	chr1	-	1.21E+08	1.21E+08	754
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	AP003774.	chr11	-	64092522	64096976	672
ENSG00000(	2.071584	4.817151	1.319414	2.247227	0	0	1.1984	0.35068	0.48033	RP3-329E2	chr1	+	21592575	21593744	723

ENSG00000(	1.035792	0	3.958241	0	0.920432	0	1.2088	0.37284	NA	PTGES3P4	chr10	+	1.05E+08	1.05E+08	356
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC003092.	chr7	-	93701071	93706469	446
ENSG00000(	9.322127	6.021439	9.235896	0	0	0	4.2351	0.00044	0.001304	C8orf56	chr8	-	1.04E+08	1.04E+08	496
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-98D1	chr1	+	1.52E+08	1.52E+08	462
ENSG00000(	1.035792	0	1.319414	0.749076	0	1.64393	-0.01859	0.98907	NA	RP11-366N	chr4	+	1.66E+08	1.66E+08	1360
ENSG00000(	0	1.204288	0	0	1.840864	0.821965	-0.461	0.73167	NA	RP11-6B6.3	chr1	+	2.06E+08	2.06E+08	353
ENSG00000(	7.250543	10.83859	11.87472	10.48706	14.72691	17.26126	-0.4787	0.46029	0.58975	RP11-640N	chr1	-	1.44E+08	1.45E+08	2073
ENSG00000(	4.143168	2.408575	0	0	2.761296	1.64393	0.41478	0.74439	0.82968	RP11-98G7	chr1	-	1.56E+08	1.56E+08	675
ENSG00000(	3.107376	4.817151	5.277655	0.749076	5.522592	0.821965	0.73808	0.49169	0.62078	ZDHHC20-I	chr13	-	21951116	21952013	440
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-264A	chr10	-	56624434	56628882	207
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP1-261G2	chr6	-	43690523	43705571	348
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP4-749H3	chr1	-	20687072	20757727	2993
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-298E	chr10	+	3266008	3269599	597
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	GGT8P	chr2	+	91963970	91969195	532
ENSG00000(	0	0	0	2.247227	0	0.821965	-0.85594	0.51054	NA	GAPDHP51	chr1	-	52172810	52173809	1000
ENSG00000(	0	0	0	5.992604	5.522592	3.28786	-3.0907	0.014949	0.033385	RP5-1065P	chr1	-	2.29E+08	2.29E+08	599
ENSG00000(	1.035792	0	2.638828	0.749076	0	0.821965	0.62335	0.64544	NA	ANKRD44-I	chr2	-	1.98E+08	1.98E+08	1069
ENSG00000(	9.322127	0	2.638828	0	3.681728	0	1.1919	0.34417	0.47341	LINC00614	chr10	-	27232252	27233347	645
ENSG00000(	11.39371	3.612863	5.277655	4.494453	4.60216	6.575719	0.34272	0.69085	0.78917	RP11-544A	chr9	-	1.34E+08	1.34E+08	931
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC109309.	chr11	+	3297275	3297620	346
ENSG00000(	4.143168	13.24716	10.55531	3.745378	1.840864	8.219649	0.89065	0.29534	0.41972	RP11-383C	chr10	-	1.27E+08	1.27E+08	712
ENSG00000(	1.035792	3.612863	3.958241	0	0	0.821965	2.0059	0.12612	0.21212	RPL12L3	chr20	-	19804087	19804587	501
ENSG00000(	0	0	0	0	4.60216	4.109825	-2.1232	0.11583	0.19807	GAPDHP21	chr10	-	57427101	57428110	1010
ENSG00000(	2.071584	1.204288	0	1.498151	0	0	0.53227	0.69456	NA	RP11-203L	chr9	-	71403223	71404586	1248
ENSG00000(	4.143168	0	0	0	0.920432	0	0.95689	0.47805	NA	WASF3-AS1	chr13	-	27180681	27215501	734
ENSG00000(	3.107376	0	0	2.996302	0	0	0.032759	0.98073	0.98877	RP4-612C1	chr1	-	93656297	93656617	321
ENSG00000(	9.322127	15.65574	18.47179	34.45748	37.73771	28.76877	-1.1865	0.017181	0.037884	ZNRF2P1	chr7	+	32768181	32768623	443
ENSG00000(	0	0	1.319414	0	2.761296	0	-0.44505	0.73801	NA	KRT18P52	chr2	-	32047660	32048505	846
ENSG00000(	2.071584	8.430014	5.277655	0	0	0	3.491	0.006134	0.014933	GLIS3-AS1	chr9	+	3898642	3901248	734
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC010987.	chr2	-	68023186	68052694	725
ENSG00000(	6.214751	6.021439	0	14.23244	19.32907	18.08323	-1.861	0.014991	0.033472	CTA-984G1	chr22	+	29656878	29658026	385
ENSG00000(	7.250543	18.06432	9.235896	2.996302	4.60216	21.37109	0.22804	0.77065	0.84912	AC012314.	chr19	-	54622891	54628722	4158
ENSG00000(	1.035792	3.612863	1.319414	2.247227	5.522592	0	-0.27099	0.82274	0.88559	RP3-486I3.	chr6	+	1.17E+08	1.17E+08	2081
ENSG00000(	0	7.225726	0	2.996302	1.840864	1.64393	0.10375	0.93317	0.95995	RP1-315G1	chrX	-	1.23E+08	1.23E+08	707
ENSG00000(	0	0	0	0.749076	1.840864	0	-0.68825	0.58858	NA	RP11-328P	chr7	-	64696164	64697097	312
ENSG00000(	0	3.612863	0	0	0.920432	0	0.81649	0.54246	NA	RP11-16C1	chr6	-	90270594	90276763	811
ENSG00000(	1.035792	1.204288	0	0.749076	0.920432	0	0.21038	0.87653	NA	RP11-144L	chr13	+	1.13E+08	1.13E+08	435
ENSG00000(	47.64643	33.72006	56.73479	5.243529	12.88605	5.753754	2.454	2.06E-06	8.25E-06	ZEB1-AS1	chr10	-	31596646	31608810	585
ENSG00000(	27.96638	32.51577	46.17948	9.737982	9.20432	2.465895	2.2045	0.000111	0.000361	NDUFA6-AS	chr22	+	42486937	42533614	2811
ENSG00000(	2.071584	8.430014	6.597069	2.996302	0	6.575719	0.6724	0.51444	0.64123	AC018738.	chr2	+	2.32E+08	2.32E+08	210
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	AC007679.	chr2	+	2.07E+08	2.07E+08	414
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RPL34P1	chr1	+	1.68E+08	1.68E+08	354
ENSG00000(	4.143168	1.204288	2.638828	0.749076	3.681728	4.109825	-0.059	0.95789	0.97513	PRMT5-AS1	chr14	+	23388665	23396105	2104
ENSG00000(	0	0	0	0	5.522592	15.61733	-1.4447	0.26128	0.38055	RP11-956J	chr8	-	73996022	73998114	480

ENSG00000(	0	0	0	2.996302	2.761296	0	-1.5727	0.24592	NA	NANOGP4	chr7	+	29251916	29252816	901
ENSG00000(	6.214751	6.021439	9.235896	0	0	0	4.0182	0.001024	0.002867	AC005550.	chr7	+	15707572	15721605	3743
ENSG00000(	2.071584	0	0	0	4.60216	0.821965	-0.72555	0.59028	0.70695	RP11-168K	chr9	-	1.16E+08	1.16E+08	395
ENSG00000(	0	0	10.55531	0	5.522592	0	0.31267	0.80758	0.87507	RP11-497H	chr5	+	69783429	69786959	3531
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	AC007272.	chr2	+	2.02E+08	2.02E+08	126
ENSG00000(	0	1.204288	2.638828	0	0	2.465895	0.32319	0.81142	0.8777	EHMT2-AS1	chr6	+	31851538	31851831	223
ENSG00000(	0	0	5.277655	12.73428	21.16994	17.26126	-2.925	0.001113	0.003097	COX5BP6	chr13	-	1.01E+08	1.01E+08	211
ENSG00000(	0	0	0	2.247227	1.840864	0.821965	-1.4859	0.2733	NA	AC068134.	chr2	-	2.33E+08	2.33E+08	576
ENSG00000(	0	7.225726	0	0	1.840864	0	1.0898	0.41901	0.5497	RP11-73E6	chr9	+	20532550	20533337	788
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	PCNPP4	chrX	-	74757382	74758537	517
ENSG00000(	30.03797	34.92434	18.47179	35.20655	22.09037	23.83698	0.039775	0.93209	0.95928	RP4-669L1	chr1	+	317720	453948	2661
ENSG00000(	2.071584	0	3.958241	5.243529	4.60216	4.93179	-1.052	0.32716	0.45479	RP11-365C	chr1	+	2.24E+08	2.24E+08	1323
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC018890.	chr2	-	1.76E+08	1.76E+08	1879
ENSG00000(	2.071584	0	1.319414	0.749076	4.60216	0	-0.38624	0.76937	0.84835	RP1-131F1	chr6	-	1.32E+08	1.32E+08	2433
ENSG00000(	24.85901	40.94578	18.47179	1.498151	3.681728	0	3.698	1.23E-06	5.08E-06	CYP2F1P	chr19	-	41324626	41332677	1056
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	PIEZO1P2	chr20	-	57315588	57358877	2180
ENSG00000(	0	0	0	0.749076	6.443024	0.821965	-2.0857	0.12153	0.20601	MTND2P11	chr9	+	1.12E+08	1.12E+08	648
ENSG00000(	678.4437	676.8097	771.8571	21.72319	32.21512	23.01502	4.7702	2.70E-106	2.28E-104	RP11-471J	chr4	+	1.74E+08	1.75E+08	5278
ENSG00000(	18.64425	7.225726	17.15238	5.992604	11.96562	14.79537	0.37578	0.57131	0.69031	AC073254.	chr2	-	2.33E+08	2.33E+08	1244
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-351N	chr10	-	28721937	28784742	273
ENSG00000(	0	0	0	0	0.920432	3.28786	-1.1769	0.37857	NA	MRPS6P2	chr1	+	51312140	51312509	370
ENSG00000(	3.107376	3.612863	0	0	0	1.64393	1.184	0.37488	0.5055	AC020594.	chr2	-	33780114	33788614	338
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	DDX10P1	chr10	-	31207941	31210164	1933
ENSG00000(	1.035792	2.408575	1.319414	0	1.840864	3.28786	-0.06871	0.9568	0.97447	C4orf51	chr4	+	1.47E+08	1.47E+08	846
ENSG00000(	0	0	2.638828	2.247227	0	1.64393	-0.33245	0.80579	0.8741	AP000260.	chr21	-	33393279	33394095	616
ENSG00000(	0	3.612863	0	0	0	4.109825	-0.10129	0.9404	0.96402	RP11-137L	chr10	+	75297561	75298149	284
ENSG00000(	142.9393	132.4716	122.7055	40.45008	34.97642	51.78379	1.6272	7.72E-09	3.92E-08	ZNF503-AS	chr10	+	77160759	77168738	2024
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	DLEU7-AS1	chr13	+	51381992	51423190	955
ENSG00000(	0	0	0	0	3.681728	4.93179	-2.1075	0.1187	0.20199	RP11-472F	chr9	+	6568844	6569360	517
ENSG00000(	1.035792	0	2.638828	0	0	0.821965	0.94405	0.48501	NA	RP11-296L	chr9	+	34568013	34582827	892
ENSG00000(	6.214751	4.817151	18.47179	5.992604	15.64734	8.219649	-0.02228	0.9764	0.98634	RP11-32B5	chr15	-	21936560	21938111	1549
ENSG00000(	0	3.612863	1.319414	0	0	0	1.6005	0.2346	NA	RP11-443F	chr2	+	63167051	63167417	367
ENSG00000(	1.035792	0	0	0	2.761296	0	-0.44657	0.73574	NA	AC128709.	chr3	+	1.97E+08	1.97E+08	626
ENSG00000(	0	3.612863	0	0	6.443024	0.821965	-0.61377	0.64128	0.74899	RP11-323F	chr4	+	4508805	4509504	584
ENSG00000(	464.0348	473.2851	386.5882	38.20285	23.0108	24.65895	3.9036	6.77E-61	2.42E-59	B3GNT9	chr16	-	67182008	67185117	2917
ENSG00000(	0	0	2.638828	0	0	1.64393	0.26729	0.84149	NA	AC019080.	chr2	+	1.78E+08	1.78E+08	394
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC007392.	chr2	-	66924257	66930359	765
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	AC147651.	chr7	+	642822	648119	731
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	RP11-229A	chr3	-	57516072	57516694	623
ENSG00000(	276.5564	307.0934	278.3963	17.22874	34.05598	27.94681	3.4262	3.90E-39	7.88E-38	RP11-65F1	chr5	-	92746995	92921354	2868
ENSG00000(	46.61064	22.88147	40.90183	26.96672	23.0108	28.76877	0.47552	0.27822	0.40019	RP11-337C	chr1	+	1.47E+08	1.47E+08	1057
ENSG00000(	429.8536	502.188	360.2	895.1453	802.6167	974.8504	-1.0441	2.34E-11	1.45E-10	CDKN2AIPN	chr5	-	1.34E+08	1.34E+08	1223
ENSG00000(	0	0	0	1.498151	0.920432	4.109825	-1.8535	0.1707	0.27109	FAM27E1	chr9	-	46385691	46387031	1341
ENSG00000(	1.035792	1.204288	5.277655	2.247227	1.840864	0	0.60035	0.62838	0.73907	ZBTB40-IT1	chr1	+	22843967	22846201	273

ENSG00000(	1.035792	9.634302	7.916483	4.494453	6.443024	1.64393	0.47286	0.62063	0.73278	IMPDH1P4	chrX	-	43137374	43138907	1534
ENSG00000(	0	0	0	2.247227	0	1.64393	-1.1086	0.40518	NA	RP11-12M9	chr22	+	41460056	41460640	585
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	AC008074.	chr2	+	64677230	64677658	429
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	PPEF1-AS1	chrX	-	18706762	18709723	430
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	SULT1C2P1	chr2	+	1.09E+08	1.09E+08	1875
ENSG00000(	0	2.408575	1.319414	0	1.840864	1.64393	0.055561	0.96676	0.98045	OR13K1P	chrX	+	1.31E+08	1.31E+08	975
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RPS3AP39	chr11	-	3570975	3571749	775
ENSG00000(	0	0	0	5.992604	11.96562	8.219649	-3.957	0.000911	0.002568	RP5-1155K	chr1	-	62673808	62674114	307
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	KRTAP2-5P	chr17	+	39228198	39228593	396
ENSG00000(	2.071584	0	5.277655	2.996302	0.920432	0	0.58919	0.64398	0.7512	ZNF295-AS	chr21	+	43429303	43445060	2869
ENSG00000(	13.46529	4.817151	9.235896	0	0	0	4.3941	0.000237	0.000733	RP1-142L7	chr6	+	1.12E+08	1.12E+08	777
ENSG00000(	109.7939	134.8802	109.5113	44.94453	49.70333	60.8254	1.1756	2.84E-05	9.95E-05	RP11-236F	chr9	-	67327775	67334983	1120
ENSG00000(	6.214751	12.04288	14.51355	0	2.761296	0	2.986	0.003353	0.008602	AC022173.	chr7	+	1.38E+08	1.38E+08	577
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-118B	chr12	+	9392599	9395635	2459
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP1-102G2	chr1	+	1.75E+08	1.75E+08	395
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC072061.	chr7	+	39856148	39907739	771
ENSG00000(	3.107376	0	0	0	0.920432	0.821965	0.42346	0.75471	NA	RP11-322A	chrX	+	75443036	75443496	461
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-666A	chr1	+	1.49E+08	1.49E+08	365
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	TRBV30	chr7	-	1.43E+08	1.43E+08	447
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	MTND2P8	chr9	-	81356636	81357660	1025
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	AC073069.	chr2	+	1.77E+08	1.77E+08	441
ENSG00000(	1.035792	3.612863	0	2.996302	3.681728	0.821965	-0.48471	0.69264	0.79034	MAPK6PS3	chr13	-	42643068	42645229	2162
ENSG00000(	9.322127	6.021439	11.87472	2.996302	0	0	2.5355	0.014875	0.033255	FTH1P11	chr8	-	82433917	82434467	551
ENSG00000(	6.214751	0	0	0	0	0	1.7844	0.18526	0.28968	RP11-402P	chrX	-	70882845	70885603	697
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RBMY2TP	chrY	-	23592583	23599131	947
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RSL24D1P8	chr19	+	12207239	12207730	492
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-575C	chr9	+	6195934	6197248	1004
ENSG00000(	14.50109	10.83859	11.87472	4.494453	3.681728	5.753754	1.2999	0.081915	0.14836	ANO7P1	chr1	-	16542404	16554522	1720
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP4-631H1	chr1	-	53409208	53409602	395
ENSG00000(	7.250543	1.204288	7.916483	0	3.681728	4.109825	0.87809	0.41106	0.54181	RP11-96C2	chr10	+	88873711	88875280	688
ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	AC021016.	chr2	-	2.19E+08	2.19E+08	535
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	LINC00851	chr20	+	18359693	18362128	727
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-316I3	chr1	-	1.89E+08	1.89E+08	733
ENSG00000(	0	0	0	33.7084	27.61296	33.70056	-5.8342	4.03E-08	1.93E-07	CKMT1B	chr15	+	43885252	43891604	2396
ENSG00000(	0	2.408575	1.319414	0.749076	5.522592	1.64393	-0.76001	0.54202	0.66469	RP11-782C	chr1	+	1.43E+08	1.43E+08	605
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-540K	chr1	+	1.81E+08	1.81E+08	542
ENSG00000(	9.322127	4.817151	30.34652	5.243529	8.283888	4.93179	1.1532	0.13036	0.21774	SMG1P1	chr16	+	22448329	22503541	4223
ENSG00000(	23.82321	19.2686	23.74945	26.96672	28.53339	27.12484	-0.29558	0.52208	0.64757	TTN-AS1	chr2	+	1.79E+08	1.8E+08	4592
ENSG00000(	4.143168	0	2.638828	0	0	1.64393	1.1875	0.3736	0.50408	RP11-522L	chrX	+	1.02E+08	1.02E+08	500
ENSG00000(	0	2.408575	7.916483	0	0	4.93179	0.70699	0.57682	0.69512	RP4-680D5	chr1	-	15912631	15930121	2845
ENSG00000(	4.143168	0	2.638828	0	0.920432	0	1.5854	0.23844	0.35335	RP11-118F	chr9	+	94789780	94790106	327
ENSG00000(	2.071584	0	13.19414	0.749076	4.60216	9.041614	0.055406	0.95839	0.9755	SRRM1P3	chrX	-	1.36E+08	1.36E+08	2678
ENSG00000(	13.46529	13.24716	14.51355	17.22874	11.04518	13.15144	-0.01214	0.9839	0.99083	GS1-124K5	chr7	+	65958693	65960461	540
ENSG00000(	3.107376	1.204288	0	3.745378	1.840864	2.465895	-0.62647	0.60495	0.71977	AP000563.	chr21	+	32824779	32825536	758

ENSG00000(	2.071584	6.021439	7.916483	2.247227	12.88605	3.28786	-0.17583	0.84988	0.90441	RAI1-AS1	chr17	-	17662468	17674135	724
ENSG00000(	2.071584	10.83859	2.638828	0	3.681728	2.465895	1.0752	0.32796	0.45567	RP11-201C	chr1	+	31509581	31510087	507
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RNF223	chr1	-	1007126	1009687	1122
ENSG00000(	5.17896	7.225726	6.597069	2.996302	0.920432	0	1.811	0.089273	0.1597	XIAP-AS1	chrX	-	1.23E+08	1.23E+08	482
ENSG00000(	7.250543	0	2.638828	1.498151	0	0	1.6787	0.1975	0.30458	RP11-230L	chr9	+	1.26E+08	1.26E+08	722
ENSG00000(	1.035792	2.408575	1.319414	0	1.840864	0	0.80071	0.55085	0.67206	FTCD-AS1	chr21	+	47571528	47572561	500
ENSG00000(	4.143168	0	0	0	0	1.64393	0.64085	0.63628	NA	AC004461.	chr22	+	19043314	19044025	403
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP5-1065J.	chr1	-	1.1E+08	1.1E+08	283
ENSG00000(	1.035792	3.612863	2.638828	2.996302	5.522592	13.9734	-1.3843	0.15823	0.25481	CDC42P6	chr4	-	22728998	22729573	576
ENSG00000(	8.286335	6.021439	11.87472	2.247227	3.681728	13.15144	0.40502	0.6278	0.73868	CTD-2522E	chrX	-	47016037	47017598	1248
ENSG00000(	0	0	0	0	3.681728	1.64393	-1.4596	0.2805	NA	PATE4	chr11	+	1.26E+08	1.26E+08	1983
ENSG00000(	1.035792	14.45145	1.319414	2.996302	3.681728	12.32947	-0.1545	0.87427	0.92104	AL163953.	chr14	+	53635772	54153976	566
ENSG00000(	0	1.204288	0	7.490755	1.840864	0.821965	-1.9066	0.14119	0.2324	RP11-475I.	chr9	+	44401766	44404440	2579
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-509J.	chr9	+	3647335	3648338	728
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC010907.	chr2	-	3650987	3651832	693
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	RP13-152C	chr20	+	62688156	62688437	188
ENSG00000(	1.035792	0	1.319414	0	2.761296	0	-0.09868	0.94199	NA	BRWD1-IT1	chr21	-	40589019	40591731	489
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC005703.	chr17	-	15179879	15182794	343
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CBX1P3	chr1	+	2.04E+08	2.04E+08	527
ENSG00000(	113.9371	134.8802	147.7743	0	0	0	8.1331	1.19E-16	1.02E-15	HOXD-AS2	chr2	-	1.77E+08	1.77E+08	999
ENSG00000(	2.071584	1.204288	0	2.247227	6.443024	2.465895	-1.2606	0.28872	0.41239	RPL21P121	chr17	+	18216074	18216847	465
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	CTA-407F1.	chr22	-	25976208	25977349	660
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-402L	chr10	-	44126330	44127012	411
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	HLA-DPA3	chr6	-	33098993	33111102	229
ENSG00000(	33.14534	38.53721	17.15238	15.73059	21.16994	13.9734	0.78452	0.12133	0.20574	PITRM1-AS	chr10	+	3183824	3210164	3823
ENSG00000(	4.143168	1.204288	1.319414	0.749076	1.840864	2.465895	0.31316	0.79453	0.86569	NDUFA9P1	chr22	-	36293318	36294452	1135
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-226L	chr1	+	1.6E+08	1.6E+08	428
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AP001092.	chr11	+	64413871	64427153	469
ENSG00000(	10.35792	13.24716	15.83297	0	0	0	4.9624	1.45E-05	5.28E-05	RP11-183N	chr1	+	78695283	78835149	1993
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-321L	chr9	-	23894988	23898052	687
ENSG00000(	0	1.204288	1.319414	0	4.60216	7.397684	-1.5546	0.21336	0.32365	RP11-465K	chr1	-	95302304	95320982	697
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	XRCC6P1	chr10	-	94966614	94969384	1805
ENSG00000(	4.143168	2.408575	15.83297	6.74168	11.96562	5.753754	-0.12758	0.87794	0.92375	AC069257.	chr3	-	1.96E+08	1.96E+08	155
ENSG00000(	12.4295	16.86003	5.277655	12.73428	28.53339	14.79537	-0.64314	0.30907	0.43522	FOXD2-AS1	chr1	-	47897805	47900313	2509
ENSG00000(	2.071584	4.817151	2.638828	0.749076	1.840864	0	1.3452	0.27259	0.39337	RP1-159A1	chr1	+	27852316	27857072	283
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-15P1	chr9	+	20331444	20332275	832
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-147C	chr1	+	96403457	96488436	943
ENSG00000(	1.035792	0	1.319414	11.98521	12.88605	15.61733	-3.3847	0.000619	0.001795	RP11-312B	chr1	-	6843952	6844903	415
ENSG00000(	32.10955	14.45145	15.83297	4.494453	5.522592	9.863579	1.5572	0.017345	0.03821	ASS1P12	chr9	+	32945994	32947220	1227
ENSG00000(	0	0	0	2.996302	3.681728	0	-1.7656	0.19313	0.299	CECR7	chr22	+	17517460	17539682	2726
ENSG00000(	137.7603	139.6974	146.4549	127.3428	169.3595	140.556	-0.04282	0.84794	0.90301	ZNF737	chr19	-	20718631	20748615	2867
ENSG00000(	445.3905	452.8122	442.0036	699.6366	749.2316	802.2378	-0.74597	5.62E-08	2.64E-07	RGL2	chr6	-	33259431	33267101	3278
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AC009223.	chr2	+	41383738	41384695	958
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CDK2AP2P2	chr9	+	66500642	66501008	367

ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	AC074212.	chr19	+	46236509	46267792	2749
ENSG00000(	1.035792	4.817151	1.319414	0	0	0	2.2478	0.09633	0.17012	RP11-154D	chr3	-	62109878	62110282	405
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-547I	chr1	+	1.9E+08	1.9E+08	526
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-554F	chr9	-	1.02E+08	1.03E+08	1544
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-280C	chr1	-	1.65E+08	1.66E+08	2400
ENSG00000(	1.035792	0	2.638828	0	0	0.821965	0.94405	0.48501	NA	AC073115.	chr7	+	46009256	46019790	555
ENSG00000(	0	0	1.319414	7.490755	4.60216	4.93179	-2.6394	0.027976	0.058466	XXbac-B13	chr22	+	21311380	21318967	684
ENSG00000(	2.071584	0	0	0	0.920432	0.821965	0.13309	0.92108	NA	RP4-803J1	chr1	+	2.29E+08	2.29E+08	640
ENSG00000(	1.035792	0	2.638828	0.749076	0	0	0.96773	0.47383	NA	RP11-423E	chr3	-	1.72E+08	1.72E+08	445
ENSG00000(	0	1.204288	0	0	5.522592	1.64393	-1.3958	0.29863	0.42361	SGOL1-AS1	chr3	+	20215736	20227919	819
ENSG00000(	12.4295	18.06432	9.235896	5.243529	11.96562	8.219649	0.61053	0.3741	0.50456	RP11-500G	chr10	-	1.32E+08	1.32E+08	2843
ENSG00000(	39.36009	15.65574	23.74945	20.22504	17.48821	17.26126	0.5061	0.3263	0.45398	RP11-206L	chr1	+	714162	745440	1873
ENSG00000(	15.53688	15.65574	14.51355	2.996302	11.04518	5.753754	1.1376	0.10404	0.18117	RP11-603J	chr12	-	56374216	56374819	604
ENSG00000(	6.214751	0	2.638828	28.46487	11.96562	14.79537	-2.3417	0.0039	0.009877	RP11-356I	chr6	-	1.38E+08	1.38E+08	963
ENSG00000(	6.214751	1.204288	9.235896	2.996302	0	0	1.8124	0.12088	0.20507	RP1-12G14	chr6	-	1.5E+08	1.5E+08	660
ENSG00000(	0	1.204288	1.319414	3.745378	4.60216	0.821965	-1.3011	0.29737	0.42193	RP11-76N2	chr1	-	89003196	89150887	3542
ENSG00000(	52.82539	48.17151	52.77655	71.16218	46.0216	65.75719	-0.25008	0.45422	0.58392	RPSAP15	chrX	-	86958277	86959307	1031
ENSG00000(	8.286335	21.67718	32.98534	5.992604	6.443024	19.72716	0.89543	0.17826	0.28075	UNC5B-AS1	chr10	-	72976981	72977985	647
ENSG00000(	7.250543	7.225726	14.51355	0	0	0	4.4745	0.000162	0.000513	RP11-325F	chr7	+	1.05E+08	1.05E+08	891
ENSG00000(	82.86335	63.82725	80.48424	632.9688	587.2356	587.7049	-2.9765	3.58E-57	1.18E-55	SHISA9	chr16	+	12995477	13334272	6726
ENSG00000(	6.214751	10.83859	10.55531	11.23613	15.64734	32.05663	-1.036	0.10929	0.18854	DGCR5	chr22	+	18958027	19018755	5492
ENSG00000(	5.17896	13.24716	7.916483	0.749076	2.761296	1.64393	2.0246	0.033527	0.068471	NONOP2	chr2	-	61163954	61165184	1231
ENSG00000(	7.250543	19.2686	23.74945	157.3059	145.4283	125.7606	-3.0669	2.83E-17	2.51E-16	LINC00857	chr10	+	81967466	81979413	2161
ENSG00000(	8.286335	8.430014	1.319414	0	0	0	3.6864	0.003513	0.008968	AC012668.	chr2	+	2.16E+08	2.17E+08	1642
ENSG00000(	0	2.408575	0	0	0.920432	0.821965	0.212	0.87508	NA	RP11-439K	chr9	+	85891291	85894414	527
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP3-449H6	chr6	+	44492996	44494491	473
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	GS1-594A7	chrX	-	15664290	15664998	611
ENSG00000(	3.107376	2.408575	1.319414	0	0	0	2.2119	0.10183	0.17802	RP11-58A1	chr9	+	69146939	69149621	681
ENSG00000(	0	13.24716	3.958241	0	0	2.465895	1.9689	0.1073	0.18589	TTLL11-IT1	chr9	-	1.25E+08	1.25E+08	1052
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AC092570.	chr2	-	1.02E+08	1.02E+08	693
ENSG00000(	2.071584	1.204288	0	2.996302	0	1.64393	-0.30009	0.82029	0.88407	RPL9P9	chr15	-	82664459	82748784	673
ENSG00000(	4.143168	7.225726	3.958241	7.490755	5.522592	21.37109	-1.0524	0.19444	0.30065	PYY2	chr17	+	26553589	26555091	1076
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	AC093166.	chr2	+	1.12E+08	1.12E+08	318
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-442J	chr13	+	45225948	45275152	295
ENSG00000(	1.035792	6.021439	3.958241	0	0	0	2.9047	0.02768	0.05795	RP11-383J	chr8	+	1.25E+08	1.25E+08	490
ENSG00000(	3.107376	0	1.319414	1.498151	0	2.465895	0.10464	0.9365	0.96168	RP11-66D1	chr1	-	1.57E+08	1.57E+08	4120
ENSG00000(	5.17896	1.204288	0	0	0	0	1.9695	0.14647	0.23926	IGKV1OR1(	chr10	+	42680787	42681239	329
ENSG00000(	7.250543	0	15.83297	14.98151	30.37426	26.30288	-1.5248	0.031699	0.065219	AP000251.	chr21	+	32931537	32932800	843
ENSG00000(	8.286335	2.408575	1.319414	0.749076	1.840864	2.465895	0.9987	0.37339	0.50388	RP11-112L	chr20	-	48780001	48782639	733
ENSG00000(	6.214751	4.817151	15.83297	0	0	0	4.3289	0.000321	0.000972	RP13-143G	chr6	-	1.36E+08	1.37E+08	824
ENSG00000(	0	4.817151	0	0.749076	0	4.109825	-0.01365	0.99179	0.99508	RP11-343H	chr1	-	2.07E+08	2.07E+08	358
ENSG00000(	16.57267	16.86003	13.19414	15.73059	14.72691	24.65895	-0.22834	0.68303	0.78314	AL353898.	chr1	-	54565641	54565897	255
ENSG00000(	0	0	0	1.498151	2.761296	2.465895	-1.9136	0.15629	0.25228	OXCT2P1	chr1	+	39980628	39982162	1535
ENSG00000(	5.17896	0	0	0	0	1.64393	0.83898	0.5363	0.66034	RP11-522L	chrX	+	1.02E+08	1.02E+08	598

ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	UQCRHP2	chr2	+	26217663	26217950	288
ENSG00000(	3.107376	0	5.277655	1.498151	0	0.821965	1.1973	0.35016	0.47987	RP11-72B4	chr9	+	98680418	98680986	569
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	FRY-AS1	chr13	-	32599451	32605776	1115
ENSG00000(	4.143168	2.408575	1.319414	0.749076	0	0.821965	1.5108	0.23806	0.35291	RP11-690I2	chr2	-	2.33E+08	2.33E+08	407
ENSG00000(	2.071584	1.204288	5.277655	1.498151	0	1.64393	0.99668	0.41844	0.54904	HLCS-IT1	chr21	-	38176285	38178585	531
ENSG00000(	503.3949	455.2208	442.0036	2071.194	2047.961	2149.438	-2.1561	3.10E-70	1.35E-68	KIFC1	chr6	+	33359313	33377701	2706
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RNASEH2CI	chrY	+	2657868	2658369	502
ENSG00000(	0	0	0	0	0.920432	3.28786	-1.1769	0.37857	NA	RP11-169L	chrX	-	40691097	40691815	719
ENSG00000(	0	1.204288	0	0.749076	1.840864	0	-0.44385	0.74106	NA	DNAJC19P7	chr1	-	52717734	52718445	344
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	LINC00316	chr21	-	46758505	46761905	455
ENSG00000(	1.035792	3.612863	0	0	0	1.64393	0.7866	0.56136	0.68149	HCG4P3	chr6	-	29973898	29974893	996
ENSG00000(	22.78742	22.88147	13.19414	5.243529	3.681728	9.041614	1.6031	0.015216	0.033911	KRR1P1	chr13	-	20644390	20646276	803
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	GSTA7P	chr6	-	52604388	52609454	448
ENSG00000(	0	0	5.277655	0	1.840864	0	0.76764	0.57145	0.69031	RP11-307E	chr9	-	97049981	97050832	852
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP3-514P1	chrX	-	1.01E+08	1.01E+08	1792
ENSG00000(	64.2191	65.03154	47.4989	217.981	181.3251	138.0901	-1.5841	5.13E-09	2.64E-08	AL627309.	chr1	-	134901	139379	2661
ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	RP11-360C	chr6	-	10511269	10514779	1475
ENSG00000(	3.107376	7.225726	2.638828	0	0	4.109825	1.2209	0.30457	0.42988	RP5-1120P	chr6	-	43963460	44042389	2232
ENSG00000(	1.035792	3.612863	0	0	0	0	1.5346	0.25314	NA	AC007064.	chr22	+	17350368	17352016	500
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	IRGM	chr5	+	1.5E+08	1.5E+08	1659
ENSG00000(	2.071584	1.204288	0	2.996302	1.840864	0	-0.33095	0.80187	0.87107	LINC00312	chr3	+	8613468	8615561	2094
ENSG00000(	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	AP004289.	chr8	-	1E+08	1E+08	1457
ENSG00000(	0	1.204288	3.958241	0.749076	0.920432	2.465895	0.18962	0.88247	0.92661	AC008937.	chr5	-	56137843	56157991	619
ENSG00000(	4.143168	0	3.958241	0	0.920432	2.465895	0.85634	0.49986	0.62814	RP11-445C	chrX	-	57095347	57096118	772
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-39K2	chr9	+	5100236	5101009	774
ENSG00000(	2.071584	0	5.277655	0	0	1.64393	1.2611	0.34291	0.472	AC006000.	chr7	-	13378826	13404674	842
ENSG00000(	1.035792	3.612863	1.319414	0	0	0	1.9913	0.14206	0.23358	P4HA2-AS1	chr5	+	1.32E+08	1.32E+08	839
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP3-400B1	chr6	-	4186858	4188343	266
ENSG00000(	5.17896	0	3.958241	0	2.761296	12.32947	-0.55084	0.62836	0.73907	AC009095.	chr16	-	67648284	67649245	522
ENSG00000(	11.39371	1.204288	7.916483	5.992604	9.20432	8.219649	-0.15829	0.84947	0.9042	RP1-179N1	chr6	-	36059768	36060423	656
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-386C	chr1	+	71716682	71717802	518
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC002075.	chr7	-	93299138	93299389	252
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RNGTTP1	chr21	+	27015801	27016528	728
ENSG00000(	6.214751	0	5.277655	13.48336	11.96562	23.01502	-1.8652	0.019427	0.042277	AC010980.	chr2	+	2.23E+08	2.23E+08	1345
ENSG00000(	0	0	0	0	3.681728	2.465895	-1.6477	0.22446	0.33686	RP11-298E	chr9	+	27391732	27397561	708
ENSG00000(	5.17896	3.612863	0	6.74168	4.60216	2.465895	-0.51035	0.62762	0.73857	DCTN1-AS1	chr2	+	74612613	74621009	2145
ENSG00000(	3.107376	0	1.319414	0	0	1.64393	0.74833	0.5808	0.69888	RNF216-IT1	chr7	-	5702063	5720092	337
ENSG00000(	1.035792	1.204288	0	0	0.920432	0	0.54457	0.68095	NA	AC002368.	chrX	-	1.48E+08	1.48E+08	388
ENSG00000(	0	0	0	2.996302	0.920432	0.821965	-1.4343	0.28996	NA	RP11-624M	chr6	-	1.26E+08	1.26E+08	708
ENSG00000(	4.143168	0	1.319414	0	0	0.821965	1.3656	0.31367	0.44014	UQCRBP1	chrX	-	56763675	56764010	336
ENSG00000(	0	0	0	1.498151	3.681728	5.753754	-2.6053	0.047097	0.092155	AC007740.	chr2	+	1.64E+08	1.64E+08	2999
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC007040.	chr2	+	71115001	71117089	625
ENSG00000(	24.85901	30.10719	13.19414	8.988907	11.04518	14.79537	0.92991	0.10545	0.18316	AC079922.	chr2	-	1.13E+08	1.13E+08	2022
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	RP11-77M5	chr1	+	1.63E+08	1.63E+08	469

ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	EEF1A1P30	chrX	-	1.19E+08	1.19E+08	1335
ENSG00000(	4.143168	9.634302	3.958241	0	7.363456	13.15144	-0.17431	0.85653	0.90907	BANF1P3	chr2	-	2.32E+08	2.32E+08	261
ENSG00000(	0	0	1.319414	0	1.840864	1.64393	-0.68367	0.61391	NA	RP11-3B12	chr7	+	1.25E+08	1.25E+08	1453
ENSG00000(	372.8851	397.4149	393.1853	816.4923	664.5519	640.3107	-0.86511	1.30E-08	6.45E-08	FAM200B	chr4	+	15683285	15707188	2962
ENSG00000(	0	2.408575	1.319414	2.247227	2.761296	5.753754	-1.1486	0.33293	0.46096	RP11-512G	chr12	-	67659622	67660746	1125
ENSG00000(	6.214751	1.204288	0	0.749076	1.840864	2.465895	0.42443	0.7292	0.81854	RP11-344N	chr10	+	74831053	74833766	291
ENSG00000(	0	0	0	0.749076	0	4.93179	-1.5344	0.25706	NA	AC092620.	chr2	+	1.39E+08	1.39E+08	680
ENSG00000(	1.035792	1.204288	0	0	1.840864	0	0.14661	0.91336	NA	AC003075.	chr7	-	17319458	17338981	720
ENSG00000(	2.071584	3.612863	3.958241	0	0	0.821965	2.1817	0.091658	0.16323	RP11-129B	chr12	+	95519536	95520165	630
ENSG00000(	8.286335	7.225726	0	3.745378	1.840864	1.64393	0.89553	0.40233	0.53353	RP11-54A4	chr1	-	1.51E+08	1.51E+08	663
ENSG00000(	3.107376	0	0	0.749076	0	0	0.76338	0.56438	NA	GFOD1-AS1	chr6	+	13486526	13487084	332
ENSG00000(	1.035792	3.612863	2.638828	2.996302	0	0.821965	0.6235	0.61658	0.72934	RP5-1041C	chr20	+	48445662	48447622	1653
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-472N	chr10	-	31982012	31996316	347
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC010894.	chr2	+	1.75E+08	1.75E+08	457
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AMDP1	chrX	-	1.55E+08	1.55E+08	992
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	LINC00211	chr2	-	38053390	38103417	1923
ENSG00000(	2.071584	0	2.638828	0	1.840864	0.821965	0.50427	0.70472	0.79966	AC015849.	chr17	+	34195971	34212867	662
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-400K	chr8	-	54427731	54436491	2387
ENSG00000(	0	0	0	2.247227	1.840864	2.465895	-1.8839	0.16313	0.26107	AC002066.	chr7	-	1.16E+08	1.16E+08	699
ENSG00000(	2.071584	9.634302	1.319414	0	1.840864	2.465895	1.2189	0.29395	0.41831	AC007000.	chr7	-	76689662	76689796	135
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RPS3AP29	chr7	-	97527659	97528427	769
ENSG00000(	5.17896	7.225726	2.638828	2.247227	2.761296	2.465895	0.85134	0.39602	0.52698	AC002454.	chr7	+	92465797	92546501	527
ENSG00000(	1.035792	0	3.958241	0.749076	1.840864	0.821965	0.34748	0.78888	0.86189	AC083873.	chr7	-	1.33E+08	1.33E+08	1099
ENSG00000(	8.286335	0	0	0	0.920432	0	1.6906	0.21004	0.31976	RP11-332C	chr10	-	1.05E+08	1.05E+08	400
ENSG00000(	6.214751	3.612863	1.319414	5.992604	0	1.64393	0.41813	0.71173	0.80522	PHKA2-AS1	chrX	+	18908414	18912615	656
ENSG00000(	8.286335	0	3.958241	5.243529	0.920432	6.575719	-0.0403	0.96969	0.98215	AC133680.	chr3	+	24729410	25215796	584
ENSG00000(	13.46529	9.634302	21.11062	2.996302	1.840864	0.821965	2.6248	0.001734	0.004669	FAM21FP	chr10	-	46201879	46217887	1131
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-110J	chr1	-	1.57E+08	1.57E+08	1531
ENSG00000(	2.071584	0	1.319414	0	1.840864	0	0.45539	0.73712	NA	RP5-940F7	chr1	-	2.36E+08	2.36E+08	740
ENSG00000(	143.9751	180.6432	141.1773	73.4094	55.22592	111.7872	0.94133	0.000791	0.002255	RP11-216N	chr9	+	42250840	42251545	706
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-739N	chr1	+	2.04E+08	2.04E+08	234
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP1-67K17	chr6	+	1.43E+08	1.43E+08	444
ENSG00000(	0	0	3.958241	1.498151	1.840864	1.64393	-0.2386	0.85491	0.90769	RP4-630A1	chr1	+	65952089	65959871	423
ENSG00000(	38.3243	32.51577	26.38828	23.97042	59.82808	55.89361	-0.49937	0.24758	0.36438	LINC00674	chr17	+	66098049	66111659	678
ENSG00000(	8.286335	8.430014	6.597069	26.21764	22.09037	34.52253	-1.7369	0.002777	0.007216	RP11-435C	chr9	-	98177116	98189078	1404
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP11-332L	chr1	+	1.97E+08	1.97E+08	1034
ENSG00000(	3.107376	3.612863	1.319414	0	0	0	2.4523	0.067889	0.12644	RP6-24A23	chrX	+	1.08E+08	1.08E+08	1142
ENSG00000(	7.250543	3.612863	5.277655	0	0	0	3.5634	0.004838	0.012018	AC073130.	chr7	-	1.16E+08	1.16E+08	1958
ENSG00000(	8.286335	1.204288	2.638828	2.247227	0	0	1.6758	0.17482	0.27665	POU5F1P4	chr1	+	1.55E+08	1.55E+08	1085
ENSG00000(	5.17896	2.408575	11.87472	6.74168	2.761296	4.93179	0.35781	0.69119	0.7894	AC097500.	chr2	-	1.87E+08	1.87E+08	1079
ENSG00000(	11.39371	10.83859	7.916483	12.73428	22.09037	6.575719	-0.4158	0.54064	0.66379	DGUOK-AS1	chr2	-	74174769	74208568	601
ENSG00000(	7.250543	12.04288	10.55531	6.74168	7.363456	11.50751	0.19894	0.78173	0.85631	RP11-611D	chr9	+	1.39E+08	1.39E+08	738
ENSG00000(	4.143168	3.612863	0	8.988907	5.522592	1.64393	-0.84216	0.42468	0.55518	AC092839.	chr2	+	54756480	54756938	459
ENSG00000(	8.286335	6.021439	1.319414	2.247227	5.522592	3.28786	0.44747	0.64583	0.75297	KLF7-IT1	chr2	-	2.08E+08	2.08E+08	655

ENSG00000(	7.250543	0	5.277655	10.48706	6.443024	8.219649	-0.86809	0.33862	0.46722	RP4-739H1	chr1	-	41134761	41153260	471
ENSG00000(	5.17896	6.021439	10.55531	2.996302	4.60216	5.753754	0.6188	0.4728	0.60187	RP3-404F1	chrX	+	1.19E+08	1.19E+08	433
ENSG00000(	1.035792	1.204288	0	6.74168	0	0	-0.90816	0.49744	0.62588	SRP68P3	chr17	-	20319105	20320010	344
ENSG00000(	2.071584	2.408575	5.277655	0.749076	0	0.821965	1.7674	0.15707	0.25319	RP11-537E	chr2	+	1.1E+08	1.1E+08	311
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	PARP4P1	chrY	-	28740998	28780799	2337
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP13-346H	chrX	+	50905696	50906509	814
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	RP3-393E1	chr6	-	1.6E+08	1.6E+08	2002
ENSG00000(	1.035792	4.817151	6.597069	0	0	0	3.0891	0.018102	0.039665	RP4-668G5	chr1	-	61405911	61436448	1275
ENSG00000(	7.250543	0	0	2.247227	3.681728	1.64393	-0.01215	0.99204	0.99518	RP11-467D	chr1	+	29550445	29551328	573
ENSG00000(	7.250543	13.24716	3.958241	0.749076	0	5.753754	1.5826	0.11853	0.2018	RP11-288I2	chr1	-	16049214	16063391	645
ENSG00000(	0	0	0	0	0.920432	4.93179	-1.5674	0.24723	NA	AC097523.	chr2	+	1.39E+08	1.39E+08	652
ENSG00000(	30.03797	39.74149	22.43003	4.494453	5.522592	4.93179	2.4973	2.65E-05	9.32E-05	AC093642.	chr2	+	2.43E+08	2.43E+08	2170
ENSG00000(	1.035792	2.408575	1.319414	92.88537	52.46462	59.18147	-5.0096	9.97E-13	6.83E-12	PRKCQ-AS1	chr10	+	6622381	6627641	1133
ENSG00000(	4.143168	1.204288	26.38828	35.20655	39.57858	40.27628	-1.7782	0.005414	0.013316	LINC00649	chr21	+	35287838	35349992	9124
ENSG00000(	0	7.225726	7.916483	0.749076	7.363456	4.93179	0.17055	0.87021	0.91845	RP11-7O11	chr1	-	44410042	44412223	494
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	PPIL1P1	chr2	+	26384925	26385423	499
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	RPL7AP73	chr13	+	23377435	23377787	353
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-1281	chr4	-	49239116	49247436	765
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	RP11-231N	chrX	-	64404898	64407145	1362
ENSG00000(	1.035792	2.408575	0	3.745378	2.761296	0.821965	-0.74474	0.55156	0.67269	TUBG1P	chr7	+	43958296	43959653	1358
ENSG00000(	586.2582	551.5638	631.9992	602.2567	468.4999	545.7847	0.12866	0.39081	0.52162	hsa-mir-67	chr1	+	566454	567996	1543
ENSG00000(	0	0	0	50.18806	51.54419	62.46933	-6.5666	1.91E-10	1.11E-09	FLG-AS1	chr1	+	1.52E+08	1.52E+08	2995
ENSG00000(	0	0	2.638828	0.749076	0	0	0.57076	0.66213	NA	RP11-126K	chr1	+	1.51E+08	1.51E+08	618
ENSG00000(	10.35792	7.225726	7.916483	23.22134	12.88605	21.37109	-1.1035	0.078747	0.14339	RP3-430N8	chr22	+	31298206	31298768	563
ENSG00000(	6.214751	3.612863	9.235896	5.243529	16.56778	11.50751	-0.73209	0.34455	0.47375	RP11-385J	chr3	-	1.78E+08	1.79E+08	964
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC007389.	chr2	-	65728127	65729272	793
ENSG00000(	1.035792	2.408575	6.597069	0	0	1.64393	1.703	0.18132	0.28449	RP11-338C	chr1	-	2.13E+08	2.13E+08	473
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-815I2	chr3	-	38311774	38312258	485
ENSG00000(	2.071584	3.612863	5.277655	2.247227	2.761296	3.28786	0.31909	0.76024	0.84152	PTENP1	chr9	-	33673502	33677497	3996
ENSG00000(	0	0	0	0	2.761296	4.93179	-1.9489	0.15029	0.24438	CELF2-AS2	chr10	-	11117094	11140436	853
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AP001046.	chr21	-	44778027	44782229	2798
ENSG00000(	2.071584	10.83859	6.597069	0	1.840864	0.821965	2.2637	0.041433	0.082542	RP11-432J9	chr10	-	72625245	72626128	884
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-465N	chr1	+	2.02E+08	2.02E+08	308
ENSG00000(	2.071584	1.204288	1.319414	0	0	4.93179	-0.06137	0.96256	0.9783	RP11-443B	chr1	-	2.35E+08	2.35E+08	889
ENSG00000(	4.143168	0	0	0	0.920432	0	0.95689	0.47805	NA	RP11-34P1	chr1	-	89295	133566	2748
ENSG00000(	16.57267	13.24716	19.79121	5.992604	11.96562	5.753754	1.0076	0.12348	0.20862	AC093110.	chr2	-	54888148	54889929	602
ENSG00000(	0	3.612863	1.319414	0	0	0	1.6005	0.2346	NA	RP11-732N	chr6	-	1.59E+08	1.59E+08	143
ENSG00000(	5.17896	0	0	0	0	0	1.5469	0.24589	NA	DDX39BP2	chr6	+	29960986	29961382	258
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	ZDHHC4P1	chr13	+	43507994	43509028	1035
ENSG00000(	76.6486	92.73015	64.65128	51.68621	72.71413	78.08667	0.2101	0.49379	0.62266	AC138035.	chr5	+	1.81E+08	1.81E+08	2661
ENSG00000(	1.035792	0	2.638828	0	0.920432	0	0.90832	0.50205	NA	AF011889.	chrX	-	1.49E+08	1.49E+08	655
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-59K5	chr11	+	56457941	56458199	259
ENSG00000(	4.143168	2.408575	2.638828	1.498151	0	0	1.6839	0.18715	0.29187	RP11-815N	chr1	-	2.22E+08	2.22E+08	720
ENSG00000(	3.107376	3.612863	0	1.498151	0.920432	4.93179	-0.08418	0.94362	0.96615	AC009133.	chr16	-	29819966	29823306	2440

ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	LL0XNC01-	chrX	-	1.03E+08	1.03E+08	268
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-554D	chr6	-	75303895	75304929	587
ENSG00000(	5.17896	0	3.958241	0	0.920432	3.28786	0.78877	0.52624	0.65104	RP1-128O3	chr6	+	1.09E+08	1.09E+08	326
ENSG00000(	0	13.24716	5.277655	0	0	2.465895	2.0732	0.086196	0.15511	ZEB2-AS1	chr2	+	1.45E+08	1.45E+08	1908
ENSG00000(	31.07376	15.65574	36.94359	26.21764	12.88605	36.98842	0.12604	0.80605	0.87427	RP11-432J	chr9	+	1.39E+08	1.39E+08	311
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP4-635A2	chr1	+	1.85E+08	1.85E+08	973
ENSG00000(	0	0	1.319414	1.498151	0	3.28786	-0.97147	0.47358	0.6027	AC105344.	chr2	-	2.32E+08	2.32E+08	3508
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	ZNF630-AS	chrX	+	47915699	47925971	396
ENSG00000(	0	3.612863	2.638828	1.498151	2.761296	6.575719	-0.62661	0.58419	0.70166	RP11-305N	chr7	-	1.29E+08	1.29E+08	258
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	MRPL48P1	chr6	-	10460139	10460774	636
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-198N	chr3	+	1.9E+08	1.9E+08	888
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	RP11-295N	chr1	+	2.21E+08	2.21E+08	962
ENSG00000(	1.035792	0	1.319414	0	4.60216	9.041614	-1.748	0.15746	0.25374	AC009948.	chr2	+	1.79E+08	1.79E+08	713
ENSG00000(	98.40023	56.60152	80.48424	47.19176	62.58938	41.92021	0.63096	0.057325	0.10941	LRRC37A2	chr17	+	44588877	44633016	5669
ENSG00000(	3.107376	9.634302	2.638828	3.745378	4.60216	0.821965	0.62405	0.53759	0.66147	PPP1R26P2	chr13	-	48890999	48894611	3613
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC006195.	chr7	+	33419576	33420498	923
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AC016745.	chr2	-	1.14E+08	1.14E+08	438
ENSG00000(	4.143168	2.408575	6.597069	2.247227	2.761296	5.753754	0.23785	0.81013	0.87679	ABCA17P	chr16	+	2389151	2476700	4188
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	RP11-12A2	chr6	-	1.4E+08	1.4E+08	490
ENSG00000(	16.57267	7.225726	11.87472	7.490755	0	2.465895	1.594	0.071206	0.1317	RPL9P7	chrX	-	23854761	23855459	640
ENSG00000(	3.107376	2.408575	1.319414	95.13259	66.2711	96.99186	-4.9036	1.45E-15	1.18E-14	GOLGA2B	chr12	-	1.01E+08	1.01E+08	5266
ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	RP11-495P	chr1	+	1.48E+08	1.48E+08	1918
ENSG00000(	4.143168	1.204288	3.958241	1.498151	0.920432	4.93179	0.26563	0.81219	0.87825	AC004893.	chr7	-	98596161	98597553	1393
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP11-350E	chr9	-	90559191	90559938	748
ENSG00000(	66.29068	79.48299	97.63662	74.15848	89.2819	64.11326	0.093062	0.7519	0.83563	RP11-262H	chr9	+	66457285	66469310	2877
ENSG00000(	4.143168	2.408575	3.958241	0	0	0	2.8785	0.028925	0.060214	AP004372.	chr11	-	1.32E+08	1.32E+08	509
ENSG00000(	5.17896	7.225726	6.597069	0	0	0	3.8276	0.002023	0.005387	CTA-941F9.	chr22	-	46000312	46001501	548
ENSG00000(	1.035792	1.204288	1.319414	0	0.920432	1.64393	0.2829	0.83225	0.89259	LINC00426	chr13	-	30914407	30951282	1589
ENSG00000(	30.03797	26.49433	25.06886	0.749076	8.283888	10.68554	1.9386	0.003033	0.007828	MID1IP1-A	chrX	-	38660821	38663136	376
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CASC4P1	chr13	-	20137729	20139040	1312
ENSG00000(	0	1.204288	3.958241	4.494453	4.60216	4.93179	-1.1698	0.29188	0.41596	MLK7-AS1	chr2	-	1.74E+08	1.74E+08	2538
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	ARPC3P2	chr1	+	2.12E+08	2.12E+08	533
ENSG00000(	1.035792	0	1.319414	0.749076	0	0.821965	0.26466	0.84506	NA	RP11-253A	chr1	+	51927393	51929088	678
ENSG00000(	0	0	3.958241	0	0	0.821965	0.91937	0.49384	NA	BRWD1-AS	chr21	+	40687633	40695144	691
ENSG00000(	5.17896	0	9.235896	5.243529	6.443024	10.68554	-0.5569	0.54676	0.66867	RP11-108N	chr1	-	17215033	17216144	406
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC104978.	chr11	-	28308782	28309172	391
ENSG00000(	0	1.204288	1.319414	3.745378	0	2.465895	-0.8304	0.52752	0.65227	MLLT10P1	chr20	-	29637799	29638060	262
ENSG00000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	AC116366.	chr5	-	1.32E+08	1.32E+08	767
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	OR7E117P	chr11	-	3620825	3621936	1112
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP3-395M2	chr1	-	2481359	2488470	3608
ENSG00000(	5.17896	1.204288	3.958241	2.996302	1.840864	6.575719	-0.11372	0.91246	0.94646	RP11-686G	chr12	+	1.12E+08	1.12E+08	429
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	AC068196.	chr2	-	1.82E+08	1.82E+08	833
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RPS2P35	chr9	-	1.03E+08	1.03E+08	897
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	RPL39P6	chr1	+	11293020	11293169	150

ENSG00000(	0	0	0	9.737982	16.56778	17.26126	-4.718	3.05E-05	0.000106	RP11-431J:	chrX	-	16171064	16188992	1037
ENSG00000(	0	0	0	1.498151	3.681728	0	-1.4292	0.2903	NA	RP11-169C	chr13	+	24993688	24995180	1070
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AHCYP2	chr9	+	1.23E+08	1.23E+08	1300
ENSG00000(	5.17896	7.225726	3.958241	5.992604	6.443024	4.109825	-0.01074	0.99019	0.99438	AC129929.	chr11	-	2349979	2399222	1460
ENSG00000(	2.071584	1.204288	3.958241	12.73428	14.72691	13.15144	-2.2314	0.00793	0.018864	RP11-656D	chr1	-	40981426	40982846	546
ENSG00000(	2.071584	1.204288	1.319414	0	0	0	1.6469	0.22376	NA	RP5-875H3	chrX	+	1.3E+08	1.3E+08	603
ENSG00000(	0	0	2.638828	0	0.920432	0	0.55591	0.6721	NA	ENOX1-AS2	chr13	+	44032601	44033259	248
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	HMGB1P15	chrX	-	50674114	50674548	435
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	CTA-503F6.	chr22	+	27600173	27601088	308
ENSG00000(	14.50109	4.817151	30.34652	17.22874	15.64734	14.79537	0.045472	0.94258	0.96532	PAXBP1-AS	chr21	+	34100426	34115433	3523
ENSG00000(	8.286335	14.45145	15.83297	8.239831	2.761296	9.863579	0.80042	0.27199	0.39263	RP11-31F1	chr1	-	1.14E+08	1.14E+08	2459
ENSG00000(	6.214751	0	0	2.996302	5.522592	4.109825	-0.73674	0.52295	0.64823	UBE2V2P3	chr1	-	11338673	11339408	437
ENSG00000(	75.61281	67.44011	83.12307	20.22504	14.72691	26.30288	1.8426	7.33E-07	3.08E-06	RP11-472B	chr4	+	39549456	39551432	608
ENSG00000(	0	1.204288	1.319414	0	0.920432	0	0.59762	0.65368	NA	AC009312.	chr2	-	1.19E+08	1.19E+08	592
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP13-210D	chrX	+	1.34E+08	1.34E+08	560
ENSG00000(	0	0	1.319414	1.498151	0	0	-0.08979	0.94423	NA	POLR2LP	chr6	+	31108504	31108690	187
ENSG00000(	0	0	0	0	5.522592	0	-1.3606	0.30939	NA	TARDBPP2	chr13	+	60848910	60850140	1231
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AP000275.	chr21	-	33996726	33997406	390
ENSG00000(	0	2.408575	0	0	1.840864	1.64393	-0.27261	0.84063	NA	RP11-69L1	chr6	+	7276264	7299105	500
ENSG00000(	3.107376	7.225726	1.319414	2.996302	0	0	1.363	0.26625	0.38623	RP11-522N	chr1	-	2.46E+08	2.46E+08	271
ENSG00000(	1462.538	1372.888	1220.458	1317.624	1453.362	1546.938	-0.08916	0.47927	0.60833	C9orf69	chr9	-	1.39E+08	1.39E+08	2844
ENSG00000(	11.39371	26.49433	3.958241	9.737982	10.12475	6.575719	0.61582	0.39433	0.52521	AC004967.	chr7	-	97576299	97577310	1012
ENSG00000(	3.107376	0	0	0.749076	1.840864	0	0.16218	0.90483	NA	RP11-460I:	chr1	-	28316669	28317035	367
ENSG00000(	5.17896	0	2.638828	0	0	0	2.2696	0.093866	0.16642	RP11-95P1	chr1	+	2.2E+08	2.2E+08	182
ENSG00000(	0	0	0	62.92235	32.21512	67.40112	-6.5306	3.18E-10	1.81E-09	OR2W3	chr1	+	2.48E+08	2.48E+08	1818
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	GABARAPL3	chr15	-	90890819	90892669	1851
ENSG00000(	0	6.021439	3.958241	14.23244	0	9.041614	-1.0128	0.34009	0.46884	MYO5BP2	chr9	+	66513032	66514308	1277
ENSG00000(	0	0	0	0.749076	1.840864	0.821965	-1.0455	0.43461	NA	RP11-575A	chr10	-	20359734	20380713	499
ENSG00000(	0	8.430014	0	1.498151	0.920432	3.28786	0.38812	0.75496	0.83789	ST6GAL2-IT	chr2	-	1.07E+08	1.07E+08	388
ENSG00000(	0	0	0	0	7.363456	1.64393	-2.1423	0.1127	0.19348	RP11-172F	chr9	+	99169566	99170079	514
ENSG00000(	12.4295	2.408575	13.19414	0.749076	0	0	3.71	0.00119	0.003295	RP11-342D	chr10	+	33500205	33502732	781
ENSG00000(	7.250543	0	2.638828	0	0	0	2.6157	0.051819	0.10018	AC067940.	chr2	-	1.69E+08	1.69E+08	300
ENSG00000(	4.143168	0	3.958241	0	3.681728	7.397684	-0.33292	0.77572	0.85283	RP11-46F1	chr1	-	3539754	3541307	622
ENSG00000(	24.85901	21.67718	22.43003	20.97412	23.93123	25.48091	-0.02542	0.95732	0.97479	RP11-435B	chr1	+	1.43E+08	1.43E+08	2495
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	LINC00707	chr10	+	6821560	6884868	3070
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-241K	chr3	-	39379620	39380370	476
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-229P	chr9	+	1.4E+08	1.4E+08	686
ENSG00000(	0	7.225726	0	0	0.920432	3.28786	0.49102	0.70775	0.80239	IFNWP19	chr9	+	21455483	21456048	566
ENSG00000(	21.75163	15.65574	6.597069	3.745378	13.80648	11.50751	0.57624	0.41039	0.5411	AC012360.	chr2	+	1.06E+08	1.06E+08	2008
ENSG00000(	6.214751	3.612863	2.638828	8.239831	8.283888	7.397684	-0.81793	0.33941	0.46804	LINC00340	chr6	+	22056775	22111157	327
ENSG00000(	136.7245	133.6759	120.0667	86.14369	93.88406	78.90863	0.59033	0.015487	0.034461	ALG1L6P	chr3	+	75464221	75471294	758
ENSG00000(	0	8.430014	0	0	0	0.821965	1.7274	0.20056	0.30811	BX470102.	chr1	+	1.54E+08	1.54E+08	531
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-436D	chr10	-	64553322	64565647	688
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP5-1164C	chr20	+	4456285	4505846	168

ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	MRPL50P2	chr2	-	2.04E+08	2.04E+08	482
ENSG00000(	5.17896	0	3.958241	0	3.681728	0	0.88818	0.48935	0.6184	SLC35E1P1	chr13	+	21181407	21182270	864
ENSG00000(	17.60846	21.67718	25.06886	10.48706	11.04518	10.68554	0.94911	0.092812	0.16487	RP11-656D	chr1	-	40958829	40974333	605
ENSG00000(	3.107376	0	0	2.247227	0	0	0.22117	0.87012	NA	RP11-100G	chr9	+	94872450	94872796	347
ENSG00000(	3.107376	0	3.958241	0	5.522592	2.465895	-0.11692	0.92344	0.95368	RP11-431K	chr1	+	8086798	8182762	2044
ENSG00000(	0	0	1.319414	0	0	1.64393	-0.1317	0.91874	NA	GAPDHP39	chr3	+	1.38E+08	1.38E+08	979
ENSG00000(	7.250543	24.08575	25.06886	7.490755	14.72691	12.32947	0.66172	0.29569	0.42005	RP11-85F1.	chr3	-	1.37E+08	1.37E+08	1194
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RPL27P12	chr12	-	1.24E+08	1.24E+08	394
ENSG00000(	24.85901	19.2686	15.83297	29.96302	36.81728	32.05663	-0.68941	0.13485	0.22398	RPS20P22	chr8	-	38291865	38293182	1318
ENSG00000(	1.035792	0	0	0	1.840864	0	-0.17777	0.89006	NA	RP11-12K1	chr3	+	1.67E+08	1.67E+08	167
ENSG00000(	16.57267	25.29004	17.15238	8.988907	23.93123	12.32947	0.37371	0.51899	0.64523	AC008280.	chr2	+	54197975	54307601	1330
ENSG00000(	4.143168	2.408575	0	2.247227	1.840864	1.64393	0.15971	0.89474	0.93492	RP11-464D	chr17	-	60593682	60594128	447
ENSG00000(	3.107376	3.612863	1.319414	0	0	0.821965	1.9375	0.14115	0.23236	RP11-365F	chr7	-	1.39E+08	1.39E+08	1751
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RBM43P1	chr3	-	69520603	69521683	1081
ENSG00000(	192.6573	160.1703	250.6886	51.68621	90.20234	41.92021	1.7004	5.57E-09	2.86E-08	TXNDC5	chr6	-	7881750	7911047	2964
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CLRN1-AS1	chr3	+	1.51E+08	1.51E+08	2223
ENSG00000(	9.322127	1.204288	7.916483	0.749076	4.60216	3.28786	0.93258	0.35275	0.48249	RP11-384F	chr3	-	1.17E+08	1.18E+08	554
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RPSAP4	chr14	+	95192625	95193512	888
ENSG00000(	0	3.612863	9.235896	1.498151	2.761296	1.64393	0.85659	0.44885	0.5786	RPL21P10	chr14	-	78149545	78150332	490
ENSG00000(	5.17896	4.817151	6.597069	3.745378	0.920432	4.109825	0.7646	0.43279	0.56268	RP11-271C	chr3	-	1.13E+08	1.13E+08	432
ENSG00000(	2.071584	0	0	0.749076	0.920432	4.109825	-0.84463	0.52461	0.64964	RPS29P2	chr8	+	41128950	41129085	136
ENSG00000(	17.60846	26.49433	9.235896	0.749076	2.761296	2.465895	2.862	0.000409	0.00122	GATSL3	chr22	-	30681106	30685616	1623
ENSG00000(	12.4295	15.65574	3.958241	1.498151	8.283888	1.64393	1.3387	0.12717	0.21352	RP5-867C2	chr17	-	45236557	45237359	803
ENSG00000(	5.17896	3.612863	13.19414	0	8.283888	9.863579	0.237	0.80259	0.87176	RP11-400L	chr2	+	9645574	9652541	491
ENSG00000(	147.0825	128.8588	155.6908	59.92604	96.64536	73.97684	0.90083	0.00058	0.001687	RNF103	chr2	-	86830516	86850989	4560
ENSG00000(	1084.474	926.0973	832.5501	2006.773	1673.345	1689.96	-0.91403	3.39E-11	2.07E-10	RBM14	chr11	+	66384053	66406124	2828
ENSG00000(	0	1.204288	1.319414	0	0.920432	0	0.59762	0.65368	NA	RP11-449H	chr5	+	1.46E+08	1.46E+08	238
ENSG00000(	0	0	0	3.745378	0.920432	0	-1.3029	0.33256	NA	AC007040.	chr2	-	71168947	71175740	1129
ENSG00000(	13.46529	8.430014	7.916483	1.498151	2.761296	4.93179	1.5169	0.076695	0.1402	AC016722.	chr2	+	47043836	47086146	2157
ENSG00000(	9.322127	2.408575	1.319414	8.988907	18.40864	8.219649	-1.2541	0.13381	0.22264	RP11-745C	chr12	+	66524531	66528229	623
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-771F	chr8	+	1.05E+08	1.05E+08	749
ENSG00000(	2.071584	1.204288	17.15238	7.490755	3.681728	8.219649	0.03897	0.96626	0.98027	NPM1P29	chr3	-	1.5E+08	1.5E+08	803
ENSG00000(	3.107376	2.408575	1.319414	0	1.840864	1.64393	0.69279	0.58038	0.69847	RP11-492E	chr9	+	1.32E+08	1.32E+08	382
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-407P	chr12	-	1.17E+08	1.17E+08	480
ENSG00000(	9.322127	6.021439	7.916483	1.498151	3.681728	12.32947	0.36675	0.67319	0.77541	RP4-584D1	chr7	-	1.5E+08	1.5E+08	420
ENSG00000(	25.8948	16.86003	29.0271	28.46487	31.29469	46.03004	-0.54418	0.22987	0.34316	ALKBH6	chr19	-	36500022	36505141	3326
ENSG00000(	10.35792	15.65574	10.55531	5.243529	8.283888	11.50751	0.51065	0.46242	0.59168	ASB14	chr3	-	57302375	57326710	3179
ENSG00000(	7.250543	8.430014	14.51355	1.498151	3.681728	3.28786	1.629	0.058394	0.11114	PCDHA13	chr5	+	1.4E+08	1.4E+08	5260
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-537H	chr9	-	34133155	34134694	1540
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	CTD-2301A	chr5	+	1.77E+08	1.77E+08	354
ENSG00000(	0	0	0	2.247227	2.761296	2.465895	-2.0693	0.1234	0.20854	TMED10P2	chr3	+	1.28E+08	1.28E+08	612
ENSG00000(	22.78742	20.47289	21.11062	2.996302	6.443024	1.64393	2.3781	0.000615	0.001784	LL0XNC01-	chrX	+	1.02E+08	1.02E+08	1133
ENSG00000(	35.21692	66.23582	62.01245	35.95563	37.73771	50.96182	0.37727	0.31507	0.44164	AP001469.	chr21	-	47671463	47674047	2014
ENSG00000(	5.17896	3.612863	1.319414	0	0	0	2.8008	0.034577	0.070376	PABPC1P1(	chr3	-	1.55E+08	1.55E+08	381

ENSG00000(	1.035792	0	3.958241	1.498151	2.761296	2.465895	-0.32139	0.7934	0.86496	ST3GAL6-A!	chr3	-	98433174	98451495	769
ENSG00000(	0	0	0	4.494453	11.96562	11.50751	-4.0408	0.000679	0.001954	RP11-561C	chr3	-	1.07E+08	1.07E+08	1776
ENSG00000(	8.286335	1.204288	0	0	0.920432	0	1.9812	0.13471	0.2238	CTD-2021J:	chr3	+	98621268	98737406	395
ENSG00000(	3.107376	3.612863	2.638828	1.498151	0	2.465895	0.90453	0.44683	0.5765	RP11-330L	chr15	-	64923308	64924113	485
ENSG00000(	6.214751	0	1.319414	11.98521	16.56778	16.4393	-2.2279	0.009283	0.021751	AC007405.	chr2	+	1.72E+08	1.72E+08	660
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	RP11-16F1	chr11	+	9681946	9682503	558
ENSG00000(	64.2191	55.39724	62.01245	0.749076	0	0	6.4525	6.97E-13	4.83E-12	KLHL41	chr2	+	1.7E+08	1.7E+08	2464
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	HYDIN2	chr1	+	1.46E+08	1.46E+08	1785
ENSG00000(	4.143168	1.204288	5.277655	5.992604	6.443024	6.575719	-0.72752	0.43354	0.56325	RP11-514P	chr7	-	1.02E+08	1.02E+08	541
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-90K6	chr3	+	1.12E+08	1.12E+08	1097
ENSG00000(	2.071584	3.612863	0	0.749076	2.761296	0.821965	0.28766	0.8199	0.88374	RPS15AP1(	chr3	-	1.29E+08	1.29E+08	361
ENSG00000(	22.78742	20.47289	27.70769	21.72319	17.48821	18.08323	0.29312	0.55419	0.67501	RP11-163E	chr7	-	1.02E+08	1.02E+08	338
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP11-101P	chr13	+	21834168	21867568	621
ENSG00000(	8.286335	1.204288	7.916483	0	0.920432	9.863579	0.55631	0.60643	0.721	MARK2P8	chr3	-	1.28E+08	1.28E+08	952
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	PLCH1-AS1	chr3	+	1.55E+08	1.55E+08	1308
ENSG00000(	0	0	1.319414	0	4.60216	0	-0.82615	0.54181	NA	RPL9P5	chr14	+	59030864	59031334	471
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	POM121L7	chr22	-	21477050	21482352	2404
ENSG00000(	0	0	0	10.48706	5.522592	0.821965	-3.2008	0.012052	0.027506	RP11-2A4.:	chr3	+	1.37E+08	1.37E+08	1288
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CADM2-AS:	chr3	-	86041333	86077157	2656
ENSG00000(	84.93494	120.4288	104.2337	47.94084	37.73771	32.8786	1.361	1.19E-05	4.39E-05	GATS	chr7	-	99798276	99869837	3522
ENSG00000(	5.17896	9.634302	7.916483	6.74168	11.96562	12.32947	-0.41626	0.57159	0.69037	MYLK-AS1	chr3	+	1.23E+08	1.23E+08	760
ENSG00000(	1.035792	3.612863	6.597069	0	0	0	2.9294	0.026217	0.055261	RPL32P34	chr19	+	5277745	5278144	400
ENSG00000(	0	3.612863	0	0	5.522592	2.465895	-0.72568	0.57697	0.69526	CTB-118N6	chr5	+	1.16E+08	1.16E+08	369
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	RP11-109N	chr14	-	73430353	73430716	364
ENSG00000(	18.64425	14.45145	13.19414	0	9.20432	7.397684	1.3581	0.088767	0.15893	HOXB-AS2	chr17	+	46634624	46637695	845
ENSG00000(	10.35792	14.45145	7.916483	13.48336	7.363456	11.50751	0.012024	0.98583	0.99155	AC004951.	chr7	-	44024597	44029806	786
ENSG00000(	5.17896	6.021439	7.916483	3.745378	0.920432	2.465895	1.187	0.22092	0.33273	RP11-168J:	chr3	+	52407668	52408898	1231
ENSG00000(	24.85901	55.39724	38.263	29.21395	23.93123	59.18147	0.069228	0.87871	0.92419	RP11-325F	chr7	-	1.05E+08	1.05E+08	736
ENSG00000(	0	0	0	0	2.761296	3.28786	-1.6293	0.2296	0.34285	SETP11	chr3	+	1.51E+08	1.51E+08	690
ENSG00000(	0	0	0	0.749076	0.920432	3.28786	-1.4827	0.27425	NA	RP11-451B	chr3	-	87780552	87842779	766
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP13-480C	chr3	+	49795916	49796089	174
ENSG00000(	1.035792	4.817151	3.958241	0.749076	4.60216	4.93179	-0.0587	0.9564	0.97423	RP11-19G2	chr17	-	35497536	35498349	814
ENSG00000(	0	0	0	0	4.60216	6.575719	-2.478	0.063558	0.11941	MTND1P16	chr3	+	1.07E+08	1.07E+08	898
ENSG00000(	3.107376	1.204288	3.958241	0	2.761296	0.821965	0.8729	0.4793	0.60834	RP11-477J:	chr9	-	1.24E+08	1.24E+08	838
ENSG00000(	0	1.204288	3.958241	0.749076	1.840864	0	0.58798	0.6582	0.7629	RP11-449H	chr5	+	1.46E+08	1.46E+08	321
ENSG00000(	0	0	2.638828	1.498151	0	0.821965	0.061979	0.96354	NA	C2orf61	chr2	-	47314130	47382517	1621
ENSG00000(	0	0	1.319414	0	0	3.28786	-0.58083	0.66501	NA	RUVBL1-AS	chr3	+	1.28E+08	1.28E+08	588
ENSG00000(	0	0	2.638828	0	0	0.821965	0.55859	0.66971	NA	HMGN1P7	chr3	-	93707478	93707790	313
ENSG00000(	2.071584	0	0	2.996302	0	0	-0.22919	0.86516	NA	RP11-302B	chr12	-	49297201	49297596	396
ENSG00000(	0	0	0	2.996302	0.920432	0	-1.1048	0.40628	NA	RPSAP41	chr6	+	74000126	74000985	860
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-543D	chr3	+	1.7E+08	1.7E+08	469
ENSG00000(	0	0	0	2.996302	1.840864	0	-1.3549	0.31496	NA	RP11-52L1	chr3	-	1.07E+08	1.07E+08	276
ENSG00000(	5.17896	4.817151	3.958241	2.996302	2.761296	0.821965	0.89362	0.38918	0.51982	RP4-728D4	chr1	-	36035414	36043330	852
ENSG00000(	2.071584	1.204288	0	0	1.840864	7.397684	-0.98117	0.43896	0.56863	MTND1P3	chr7	-	1.42E+08	1.42E+08	952

ENSG00000(	15.53688	3.612863	7.916483	2.996302	0	9.041614	1.0024	0.28949	0.41321	GUSBP4	chr6	-	58246051	58256569	672
ENSG00000(	14.50109	19.2686	1.319414	6.74168	10.12475	9.041614	0.41256	0.59172	0.708	PSMD6-AS2	chr3	+	63989698	63997824	2456
ENSG00000(	127.4024	99.95588	133.2608	81.64923	77.31629	79.7306	0.58922	0.021426	0.046136	RP11-295P	chr10	+	13652047	13710299	1446
ENSG00000(	2.071584	1.204288	3.958241	2.247227	2.761296	0.821965	0.22897	0.84497	0.90101	RP4-803A2	chr1	+	33452553	33453834	863
ENSG00000(	176.0846	217.9761	230.8974	466.6741	275.2092	363.3085	-0.82177	0.000113	0.000366	NME1	chr17	+	49230897	49239789	1645
ENSG00000(	8.286335	13.24716	15.83297	0	0	0	4.8715	2.39E-05	8.45E-05	PDZRN3-AS	chr3	+	73672719	73674658	494
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	PTGER4P3	chr9	-	68371626	68371877	252
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AP006309.	chr3	-	38144620	38164574	964
ENSG00000(	0	3.612863	1.319414	0	0	1.64393	0.83286	0.53817	0.66199	RP11-665C	chr14	-	55749014	55749361	348
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RPL17P46	chr18	+	48349947	48350490	544
ENSG00000(	31.07376	44.55865	17.15238	25.46857	20.2495	14.79537	0.59674	0.23193	0.34547	TNFSF12	chr17	+	7452208	7464925	1768
ENSG00000(	31.07376	26.49433	15.83297	5.992604	17.48821	13.9734	0.94143	0.10238	0.17876	CDRT4	chr17	-	15339332	15406922	2495
ENSG00000(	0	0	5.277655	0.749076	2.761296	0	0.33594	0.80148	0.87079	RP11-65N1	chr9	+	1.28E+08	1.28E+08	550
ENSG00000(	13.46529	9.634302	10.55531	8.239831	2.761296	4.93179	0.97471	0.20357	0.31172	APOBEC3G	chr22	+	39436924	39483748	2775
ENSG00000(	0	0	1.319414	0.749076	1.840864	0	-0.44914	0.73845	NA	RP4-800G7	chr7	-	1.49E+08	1.49E+08	181
ENSG00000(	4.143168	0	0	3.745378	0	0	0.084793	0.95006	0.96996	TLR9	chr3	-	52255096	52273183	4129
ENSG00000(	1.035792	7.225726	2.638828	0	0	0	2.8774	0.029551	0.061343	RP11-373E	chr3	-	1.7E+08	1.7E+08	263
ENSG00000(	14.50109	16.86003	15.83297	9.737982	4.60216	7.397684	1.0363	0.11766	0.20063	AC009120.	chr16	-	74346507	74347288	473
ENSG00000(	0	2.408575	0	1.498151	2.761296	0	-0.44382	0.74261	0.82838	FAM21EP	chr10	-	51807962	51823136	985
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-496B	chr3	-	1.8E+08	1.8E+08	563
ENSG00000(	184.371	174.6217	131.9414	66.66772	58.90765	101.9236	1.0995	5.06E-05	0.000172	WBP1	chr2	+	74685456	74688018	2047
ENSG00000(	67.32647	69.84869	35.62417	127.3428	78.23672	113.4312	-0.86734	0.007266	0.017436	MRPS17	chr7	+	56019512	56024192	1843
ENSG00000(	0	0	0	2.996302	0	1.64393	-1.3112	0.33001	NA	AC002310.	chr16	+	30583571	30595181	1488
ENSG00000(	0	0	1.319414	1.498151	0	0	-0.08979	0.94423	NA	RPL21P39	chr3	-	1.46E+08	1.46E+08	483
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-755B	chr3	+	57614537	57640645	364
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-379B	chr3	-	1.26E+08	1.26E+08	259
ENSG00000(	12.4295	20.47289	14.51355	0	1.840864	0	3.9707	4.60E-05	0.000157	RP11-309L	chr7	+	1.29E+08	1.29E+08	431
ENSG00000(	1.035792	4.817151	0	0.749076	2.761296	3.28786	-0.14714	0.90405	0.94069	SUGT1P3	chr13	-	41482295	41495910	1051
ENSG00000(	6.214751	4.817151	17.15238	5.992604	5.522592	3.28786	0.81983	0.32172	0.44899	RP11-446H	chr3	-	1.07E+08	1.07E+08	866
ENSG00000(	2.071584	4.817151	0	0	0	0	2.0839	0.12453	0.21	RPS4XP22	chr19	-	9793970	9794749	780
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RNF7P1	chr3	-	57505396	57505737	342
ENSG00000(	0	0	0	0	2.761296	3.28786	-1.6293	0.2296	0.34285	RP11-767L	chr3	+	1.2E+08	1.2E+08	1129
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RPL23AP72	chr16	-	47184043	47184477	435
ENSG00000(	97.36444	67.44011	88.40072	140.0771	172.1208	178.3664	-0.9425	0.000154	0.000489	GET4	chr7	+	916189	936073	4356
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	GAPDHP27	chr1	-	1.2E+08	1.2E+08	1020
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	IGSF11-AS1	chr3	+	1.19E+08	1.19E+08	1604
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RPS27P25	chr12	+	1.21E+08	1.21E+08	484
ENSG00000(	9.322127	15.65574	18.47179	2.247227	3.681728	0.821965	2.4128	0.003403	0.008717	RP11-175I1	chr10	-	46349533	46411606	798
ENSG00000(	67.32647	45.76293	47.4989	95.88167	80.99802	126.5826	-0.90065	0.003777	0.009591	C1orf226	chr1	+	1.62E+08	1.62E+08	4118
ENSG00000(	31.07376	10.83859	18.47179	2.247227	0	1.64393	3.4684	3.78E-05	0.00013	ZNF736P9Y	chrY	-	7936937	7938764	1345
ENSG00000(	1548.509	1521.015	1319.414	2289.924	1753.423	1736.812	-0.39611	0.004374	0.01096	ADSL	chr22	+	40742507	40764823	2525
ENSG00000(	9.322127	0	3.958241	2.996302	9.20432	6.575719	-0.3994	0.68229	0.78264	RP11-34P1	chr1	-	139790	140339	323
ENSG00000(	1.035792	1.204288	0	0	3.681728	1.64393	-0.71243	0.59265	0.70878	PRKAG2-AS	chr7	+	1.52E+08	1.52E+08	1055
ENSG00000(	10.35792	2.408575	9.235896	5.243529	0	4.93179	0.92912	0.34163	0.47049	RPL39P36	chr19	+	53916443	53916598	156

ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	SNRPGP3	chr7	+	1.29E+08	1.29E+08	227
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	AC015691.	chr11	-	5593552	5646126	535
ENSG00000(	0	0	0	0	4.60216	1.64393	-1.6592	0.22125	0.33301	RP11-71N1	chr3	+	1.48E+08	1.48E+08	2569
ENSG00000(	14.50109	4.817151	10.55531	1.498151	11.04518	2.465895	0.90424	0.29476	0.41908	PRDX3P4	chr3	+	64160077	64160823	747
ENSG00000(	5.17896	0	1.319414	0	0	0	1.9904	0.14228	0.23373	AP001625.	chr21	+	43916118	43918313	1603
ENSG00000(	4.143168	0	0	2.247227	2.761296	4.93179	-0.8633	0.47846	0.60751	RP11-803B	chr3	-	75495920	75540353	943
ENSG00000(	0	1.204288	0	8.239831	4.60216	1.64393	-2.4042	0.052463	0.10127	RP11-163E	chr7	+	1.02E+08	1.02E+08	602
ENSG00000(	0	0	2.638828	1.498151	0	1.64393	-0.15775	0.90739	NA	RPL31P60	chr19	+	33454405	33454771	367
ENSG00000(	0	0	0	0	9.20432	2.465895	-2.5149	0.059646	0.11313	FCF1P3	chr3	+	1.07E+08	1.07E+08	590
ENSG00000(	1.035792	2.408575	2.638828	1.498151	0	4.93179	-0.07256	0.95265	0.97177	CTD-2015H	chr5	+	79796151	79797219	752
ENSG00000(	2.071584	1.204288	0	0.749076	0	2.465895	0.026614	0.98418	0.99091	RP11-293A	chr4	-	26861428	26862221	482
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-200A	chr3	+	1.34E+08	1.34E+08	294
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP6-206I17	chr1	+	1.44E+08	1.44E+08	1685
ENSG00000(	4.143168	1.204288	1.319414	0	0	0	2.1615	0.11037	0.19002	SLC9A9-AS:	chr3	+	1.43E+08	1.43E+08	518
ENSG00000(	4.143168	0	0	2.247227	0	0	0.43986	0.74578	0.83076	RP11-90P5	chr8	+	37980792	37982169	621
ENSG00000(	1.035792	0	1.319414	0	0.920432	0.821965	0.21466	0.87415	NA	TEX35	chr1	+	1.78E+08	1.79E+08	2452
ENSG00000(	70.43385	84.30014	85.7619	112.3613	99.40666	157.8173	-0.61727	0.024621	0.052253	RP11-393B	chr3	+	1.83E+08	1.83E+08	1490
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	OR9A3P	chr7	+	1.42E+08	1.42E+08	878
ENSG00000(	10.35792	9.634302	13.19414	2.247227	4.60216	3.28786	1.5493	0.055804	0.10686	RP11-274H	chr3	-	1.46E+08	1.46E+08	709
ENSG00000(	1.035792	1.204288	2.638828	2.996302	1.840864	3.28786	-0.5702	0.62647	0.73774	RP11-587D	chr11	+	27603227	27603602	376
ENSG00000(	6.214751	20.47289	13.19414	11.98521	8.283888	8.219649	0.44037	0.51976	0.64576	AMY2B	chr1	+	1.04E+08	1.04E+08	4716
ENSG00000(	6.214751	4.817151	2.638828	0	0	0	3.2951	0.010503	0.024303	RP11-451G	chr3	-	1.55E+08	1.55E+08	873
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	DDX50P2	chr3	-	1.54E+08	1.54E+08	2193
ENSG00000(	4.143168	2.408575	6.597069	5.243529	4.60216	4.109825	-0.08196	0.93047	0.95822	RP1-93H18	chr6	+	1.17E+08	1.17E+08	1596
ENSG00000(	1.035792	0	0	0	0	2.465895	-0.37334	0.77636	NA	RPL23AP1(	chr14	-	96922913	96923378	466
ENSG00000(	41.43168	45.76293	13.19414	44.19546	31.29469	39.45432	-0.18292	0.68821	0.78696	LY6G5B	chr6	+	31637944	31641553	2654
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-349J!	chr6	+	1.35E+08	1.35E+08	288
ENSG00000(	1.035792	3.612863	5.277655	4.494453	3.681728	1.64393	-0.00648	0.99512	0.9969	RP11-572N	chr3	+	1.13E+08	1.13E+08	764
ENSG00000(	0	2.408575	0	2.996302	0.920432	0	-0.37932	0.77941	0.85472	RP11-225N	chr3	-	1.83E+08	1.83E+08	1877
ENSG00000(	1.035792	1.204288	1.319414	7.490755	6.443024	6.575719	-2.0533	0.04976	0.096705	PSMB9	chr6	+	32811913	32827362	2676
ENSG00000(	0	4.817151	0	0	0	0.821965	1.1172	0.40901	NA	RPL9P30	chr17	+	28182777	28183350	574
ENSG00000(	0	3.612863	0	5.243529	11.04518	4.109825	-1.9536	0.077567	0.14157	RP11-657C	chr3	-	1.35E+08	1.35E+08	827
ENSG00000(	11.39371	10.83859	3.958241	19.47596	10.12475	14.79537	-0.7015	0.30179	0.42683	RP11-254B	chr12	-	68946775	68947662	888
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-88H1	chr3	+	1.46E+08	1.46E+08	569
ENSG00000(	0	0	0	0	5.522592	0	-1.3606	0.30939	NA	RP11-85G2	chr14	-	93689944	93690485	542
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-641C	chr3	+	60602555	60603812	1258
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-61I13	chr6	-	39865116	39867847	436
ENSG00000(	4.143168	0	7.916483	7.490755	9.20432	4.93179	-0.73247	0.43755	0.56717	ETF1P2	chr7	+	1.51E+08	1.51E+08	1586
ENSG00000(	5.17896	10.83859	10.55531	16.47966	14.72691	9.041614	-0.57023	0.40327	0.53429	RP11-103G	chr3	+	1.5E+08	1.5E+08	621
ENSG00000(	0	4.817151	2.638828	0	3.681728	2.465895	0.19648	0.8738	0.92068	RP4-753P9	chrX	+	1.29E+08	1.29E+08	326
ENSG00000(	3.107376	2.408575	0	2.247227	5.522592	3.28786	-0.7446	0.51184	0.63892	RP11-745A	chr15	+	60682570	60682881	312
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RPS7P7	chr4	+	42473827	42474397	571
ENSG00000(	2.071584	1.204288	5.277655	2.247227	2.761296	0.821965	0.41407	0.71915	0.81074	MAGI1-AS1	chr3	+	65879491	65910972	591
ENSG00000(	2638.162	2413.393	2890.836	482.4047	1054.815	789.0863	1.7633	5.22E-19	5.06E-18	PCDHGC3	chr5	+	1.41E+08	1.41E+08	4711

ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	ARHGEF3-A	chr3	+	56974068	56994882	489
ENSG00000(	0	1.204288	0	10.48706	4.60216	4.93179	-2.8789	0.014917	0.03333	SMKR1	chr7	+	1.29E+08	1.29E+08	1035
ENSG00000(	1.035792	3.612863	3.958241	1.498151	1.840864	4.109825	0.15021	0.89296	0.93378	RP11-379F	chr3	+	1.58E+08	1.59E+08	1087
ENSG00000(	0	3.612863	2.638828	0	2.761296	0	0.71299	0.59193	0.7081	RP11-204K	chr14	-	68805445	68806258	801
ENSG00000(	0	0	2.638828	0.749076	0.920432	2.465895	-0.40037	0.76517	0.84498	RP11-758P	chr7	+	1E+08	1E+08	303
ENSG00000(	1.035792	0	2.638828	8.988907	4.60216	4.93179	-1.8711	0.08581	0.15461	RP11-430C	chr1	+	2.05E+08	2.05E+08	2219
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	UGT1A5	chr2	+	2.35E+08	2.35E+08	2345
ENSG00000(	154.333	195.0946	149.0938	429.2203	254.0392	314.8126	-0.99671	6.91E-06	2.61E-05	ZNF542	chr19	+	56879468	56891197	3440
ENSG00000(	264.1269	331.1791	269.1604	299.6302	258.6414	304.127	0.002004	0.99103	0.99471	COX19	chr7	-	938415	1015235	3666
ENSG00000(	0	0	0	469.6704	358.048	442.2171	-9.1826	9.57E-23	1.08E-21	RP11-314N	chr3	+	78316090	78343881	576
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	GAPDHP33	chr1	-	1.2E+08	1.2E+08	1013
ENSG00000(	0	0	1.319414	0.749076	0.920432	0	-0.15244	0.90808	NA	B4GALT4-A	chr3	+	1.19E+08	1.19E+08	544
ENSG00000(	4.143168	0	0	0	8.283888	1.64393	-0.7957	0.53391	0.65841	MAGI1-IT1	chr3	-	65858490	65940233	2567
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RPL12P37	chr17	+	78950254	78950748	495
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	TCAM1P	chr17	+	61926652	61941739	3317
ENSG00000(	0	0	0	0	5.522592	17.26126	-1.4231	0.26707	0.38717	RP11-574H	chr6	+	1.23E+08	1.23E+08	586
ENSG00000(	10.35792	12.04288	15.83297	14.98151	10.12475	12.32947	0.018366	0.97665	0.98648	GHRLOS	chr3	+	10327438	10334601	1176
ENSG00000(	16.57267	22.88147	19.79121	44.94453	17.48821	23.01502	-0.51826	0.31494	0.44162	RP11-499P	chr10	-	18802044	18834580	1028
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-298C	chr3	+	1.68E+08	1.68E+08	661
ENSG00000(	0	0	3.958241	0	0	3.28786	0.12119	0.92879	0.95719	CTA-286B1	chr22	+	35796135	35806001	557
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RPL36AP4(	chr11	-	25610021	25610389	369
ENSG00000(	1.035792	0	1.319414	0	0	1.64393	0.22525	0.86714	NA	ACAD11	chr3	-	1.32E+08	1.32E+08	4142
ENSG00000(	0	1.204288	1.319414	5.243529	0	2.465895	-1.0596	0.41363	0.54407	RP11-1072	chr17	-	42797128	42797965	838
ENSG00000(	1.035792	2.408575	1.319414	0	0	0.821965	1.2918	0.33994	NA	RP11-841C	chr12	+	19661838	19662179	342
ENSG00000(	3.107376	10.83859	17.15238	5.243529	5.522592	23.01502	-0.12427	0.87354	0.92056	RP11-331F	chr16	+	75259972	75262093	1252
ENSG00000(	2006.329	2112.321	1612.324	1083.163	993.1461	1830.516	0.55012	0.004015	0.010141	RPS2P5	chr12	+	1.19E+08	1.19E+08	931
ENSG00000(	329.3818	339.6091	288.9516	426.224	312.9469	329.6079	-0.15783	0.37653	0.50713	PPIL3	chr2	-	2.02E+08	2.02E+08	1370
ENSG00000(	5.17896	0	2.638828	0	0	0	2.2696	0.093866	0.16642	AC017002.	chr2	+	1.12E+08	1.12E+08	757
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-774I5	chr3	-	1.62E+08	1.62E+08	483
ENSG00000(	224.7668	187.8689	216.3839	157.3059	212.6198	202.2034	0.13866	0.49764	0.62603	RPL23AP7	chr2	-	1.14E+08	1.14E+08	2078
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RPL36AP45	chr15	-	75478992	75479309	318
ENSG00000(	5.17896	3.612863	2.638828	0.749076	2.761296	0.821965	1.11	0.32577	0.45346	AP000304.	chr21	-	34931848	34950669	528
ENSG00000(	17.60846	19.2686	17.15238	11.98521	3.681728	9.863579	1.0049	0.11706	0.19984	RPL13P5	chr12	+	6982553	6993905	1438
ENSG00000(	5.17896	6.021439	3.958241	2.996302	0.920432	4.109825	0.76045	0.44782	0.57756	SEC62-AS1	chr3	-	1.7E+08	1.7E+08	346
ENSG00000(	7.250543	0	1.319414	0.749076	1.840864	1.64393	0.75154	0.54002	0.66339	RP11-36C2	chr5	+	33162285	33162913	629
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RPL9P3	chr14	+	35731668	35732242	575
ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	RP11-768G	chr3	-	1.17E+08	1.17E+08	803
ENSG00000(	0	13.24716	1.319414	1.498151	0	1.64393	1.5643	0.19839	0.30567	RP11-231D	chr8	-	42199285	42200152	868
ENSG00000(	6.214751	6.021439	5.277655	11.23613	2.761296	25.48091	-1.0601	0.18716	0.29187	RP1-228P1	chr12	-	48448596	48449374	779
ENSG00000(	6.214751	3.612863	10.55531	2.996302	5.522592	0.821965	0.96775	0.3099	0.43609	AC012358.	chr2	+	55535628	55573185	1110
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-142L	chr3	+	81661941	81662223	283
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-460N	chr3	+	70048728	70064469	2044
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	MTATP8P1	chr1	+	568915	569121	207
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTD-2218K	chr5	+	82073616	82074405	790

ENSG00000(	1.035792	3.612863	2.638828	0.749076	2.761296	0.821965	0.55098	0.64844	0.75494	CTD-2013N	chr19	+	16523495	16524387	893
ENSG00000(	0	6.021439	0	0	0.920432	0	1.3099	0.33429	0.46228	LINC00636	chr3	+	1.08E+08	1.08E+08	1264
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RPS26P34	chr8	+	82539504	82539852	349
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	LIMS1	chr2	+	1.11E+08	1.11E+08	2466
ENSG00000(	10.35792	27.69862	17.15238	5.243529	8.283888	8.219649	1.2599	0.055595	0.10653	LRRFIP1P1	chr3	-	1.79E+08	1.79E+08	2246
ENSG00000(	1.035792	1.204288	0	0.749076	1.840864	2.465895	-0.70485	0.59204	0.70819	RPS12P27	chr16	+	68243345	68243681	337
ENSG00000(	0	3.612863	0	0.749076	0.920432	0	0.5439	0.68847	NA	RP11-95I19	chr5	-	61871778	61872098	321
ENSG00000(	4.143168	0	5.277655	0	2.761296	0	1.1716	0.36399	0.49381	RP11-864J2	chr12	+	1.08E+08	1.08E+08	535
ENSG00000(	75.61281	63.82725	67.2901	41.19916	64.43024	59.18147	0.32803	0.30778	0.43352	FOXO3B	chr17	-	18574259	18576186	1928
ENSG00000(	3.107376	7.225726	1.319414	5.992604	11.04518	15.61733	-1.3144	0.12122	0.20559	RP4-584D1	chr7	-	1.5E+08	1.5E+08	577
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-567P	chr3	+	1.2E+08	1.2E+08	288
ENSG00000(	2.071584	1.204288	2.638828	0	0	0.821965	1.5471	0.2493	0.36656	RPL39P26	chr11	-	13707046	13707203	158
ENSG00000(	9.322127	3.612863	7.916483	0	3.681728	9.041614	0.61186	0.53161	0.65629	RPS19P3	chr14	-	35037895	35038335	441
ENSG00000(	25.8948	39.74149	17.15238	8.239831	0	0	2.3201	0.059576	0.11302	CTD-2021J2	chr3	+	98699902	98701940	962
ENSG00000(	2.071584	3.612863	1.319414	8.988907	6.443024	6.575719	-1.4083	0.13948	0.23005	SETP14	chr3	+	1.56E+08	1.56E+08	873
ENSG00000(	0	0	0	5.243529	1.840864	0.821965	-2.1141	0.11577	0.198	RP11-185E	chr3	+	1.71E+08	1.71E+08	229
ENSG00000(	22.78742	8.430014	13.19414	0	0.920432	4.109825	2.7499	0.002185	0.005782	CDKN2B-AS	chr9	+	21994777	22121096	3835
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP5-1101C	chr7	+	1.22E+08	1.22E+08	743
ENSG00000(	0	0	5.277655	0	2.761296	0	0.49564	0.71429	0.8071	CTC-788C1	chr8	-	94969566	94969919	354
ENSG00000(	3.107376	4.817151	7.916483	2.247227	0	0	2.0458	0.080272	0.14578	UOX	chr1	-	84831111	84863514	899
ENSG00000(	9.322127	14.45145	7.916483	8.239831	12.88605	4.93179	0.26738	0.71103	0.80472	RPL7AP10	chr19	-	21332451	21333241	791
ENSG00000(	53.86118	28.90291	36.94359	31.46117	35.89685	36.98842	0.20122	0.61792	0.7303	RP11-247I1	chr22	-	31832963	31835893	597
ENSG00000(	4.143168	0	2.638828	0	0	0.821965	1.6227	0.22806	0.34132	RPL21P123	chr17	-	28043297	28043703	407
ENSG00000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	TM4SF1-AS	chr3	+	1.49E+08	1.49E+08	754
ENSG00000(	1.035792	3.612863	1.319414	6.74168	6.443024	7.397684	-1.5049	0.12893	0.21583	THOC7-AS1	chr3	+	63846321	63847495	673
ENSG00000(	6.214751	2.408575	2.638828	8.988907	0.920432	0	0.13855	0.90207	0.93926	RP1-184J9.	chr1	-	23346640	23414551	666
ENSG00000(	22.78742	6.021439	10.55531	2179.81	2454.792	2215.195	-7.3127	4.36E-160	7.82E-158	L1TD1	chr1	+	62660503	62678000	3849
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-3P17	chr3	+	1.61E+08	1.61E+08	2845
ENSG00000(	2.071584	1.204288	1.319414	1.498151	6.443024	0	-0.53838	0.66285	0.76691	RP11-775D	chr7	+	1.3E+08	1.3E+08	575
ENSG00000(	3.107376	1.204288	2.638828	0	0.920432	0	1.7118	0.19765	0.30475	RP11-20L2	chr7	-	1.27E+08	1.27E+08	637
ENSG00000(	121.1877	102.3645	122.7055	8.239831	9.20432	3.28786	3.9706	5.04E-22	5.54E-21	AQP1	chr7	+	30893010	30965131	2752
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-403P	chr8	-	1.11E+08	1.11E+08	889
ENSG00000(	1.035792	0	0	1.498151	0	0	-0.08447	0.94679	NA	RP11-247I1	chr22	+	31850237	31860190	615
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	KCNAB1-AS	chr3	-	1.56E+08	1.56E+08	538
ENSG00000(	1.035792	2.408575	0	5.992604	8.283888	7.397684	-2.1188	0.04489	0.08844	AD000092.	chr19	+	13004947	13005694	748
ENSG00000(	1.035792	1.204288	2.638828	0	0	7.397684	-0.40928	0.74906	0.83322	RP11-206L	chr1	-	694412	700305	295
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-521J9	chr3	-	1.24E+08	1.24E+08	712
ENSG00000(	0	0	0	1.498151	4.60216	0	-1.6319	0.22883	0.34221	RP11-1348	chr16	-	28825301	28825994	694
ENSG00000(	0	2.408575	0	0.749076	0	2.465895	-0.218	0.87233	NA	C1QTNF9	chr13	+	24881304	24896673	1854
ENSG00000(	0	7.225726	0	0	0.920432	0	1.5108	0.26454	0.38438	RP11-174C	chr3	+	1.2E+08	1.2E+08	813
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	LSP1P2	chr3	+	75444339	75444471	133
ENSG00000(	0	7.225726	7.916483	1.498151	4.60216	5.753754	0.27998	0.78604	0.85955	MME-AS1	chr3	-	1.55E+08	1.55E+08	457
ENSG00000(	0	1.204288	1.319414	1.498151	5.522592	1.64393	-1.2304	0.32663	0.45436	KRT8P36	chr3	-	1.38E+08	1.38E+08	1440
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC006539.	chr19	-	20190627	20191348	501

ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-366N	chr4	-	1.66E+08	1.66E+08	480
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	MYL6P4	chr7	+	1.42E+08	1.42E+08	453
ENSG00000(	211.3015	234.8361	208.4674	205.2467	176.7229	219.4646	0.12037	0.53187	0.65642	ISY1	chr3	-	1.29E+08	1.29E+08	3842
ENSG00000(	120.1519	125.2459	131.9414	54.68252	76.39586	60.00344	0.97534	0.000238	0.000734	PNMA2	chr8	-	26362202	26371608	4965
ENSG00000(	4.143168	0	1.319414	0.749076	0.920432	4.93179	-0.17365	0.88867	0.93096	RP11-102N	chr3	-	1.36E+08	1.36E+08	730
ENSG00000(	2.071584	0	1.319414	0	0	0.821965	0.88094	0.51378	NA	RPS2P39	chr11	-	1.09E+08	1.09E+08	668
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-64C1	chr3	+	55330228	55334766	1602
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-244K	chr6	+	1.5E+08	1.5E+08	440
ENSG00000(	6.214751	1.204288	0	0	1.840864	0	1.2224	0.35807	0.48758	LRRD1	chr7	-	91741473	91808845	3511
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	CTD-2301A	chr5	+	1.77E+08	1.77E+08	476
ENSG00000(	47.64643	65.03154	38.263	40.45008	42.33987	63.2913	0.047896	0.89654	0.93585	RP5-890O3	chr1	-	1252961	1254069	386
ENSG00000(	0	0	0	0.749076	6.443024	0	-1.8192	0.17996	0.28279	RP11-69M1	chr12	-	8147366	8147680	315
ENSG00000(	2.071584	8.430014	5.277655	2.996302	2.761296	5.753754	0.37829	0.69241	0.79016	RP11-465L	chr20	+	44650415	44656438	400
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	KRBOX1	chr3	+	42850938	43097363	2566
ENSG00000(	1.035792	3.612863	0	1.498151	0	0	0.83258	0.53888	0.66258	RP11-553D	chr3	+	1.13E+08	1.13E+08	1053
ENSG00000(	4.143168	0	0	0	0	2.465895	0.38924	0.7742	0.85182	RP11-588D	chr3	+	78808124	78808524	401
ENSG00000(	93.22127	124.0416	100.2754	79.40201	67.19154	61.64737	0.59947	0.029435	0.061139	RP11-155G	chr7	+	1.28E+08	1.28E+08	662
ENSG00000(	0	0	1.319414	1.498151	0	0.821965	-0.38347	0.77483	NA	AC098831.	chr2	-	2.04E+08	2.04E+08	336
ENSG00000(	506.5022	494.9623	451.2395	5.992604	24.85166	21.37109	4.7784	5.42E-66	2.17E-64	PCDHGC5	chr5	+	1.41E+08	1.41E+08	4641
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	PLCXD2-AS	chr3	-	1.11E+08	1.11E+08	491
ENSG00000(	0	1.204288	1.319414	0.749076	0	0	0.61214	0.64459	NA	C21orf91-C	chr21	-	19135632	19164840	717
ENSG00000(	295.2007	309.5019	215.0644	2.247227	22.09037	23.83698	3.7533	5.01E-07	2.15E-06	ARHGEF25	chr12	+	58003963	58013162	2552
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-343P	chr5	+	18049659	18049981	323
ENSG00000(	0	2.408575	2.638828	0	1.840864	0	0.79984	0.55362	0.67452	AC073934.	chr7	-	1.27E+08	1.27E+08	495
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-100G	chr9	+	94872857	94873150	294
ENSG00000(	4.143168	1.204288	1.319414	0.749076	0	4.93179	0.172	0.88937	0.93132	UBA52P8	chr16	-	48368382	48368765	384
ENSG00000(	0	0	0	1.498151	2.761296	0	-1.199	0.3707	NA	MTND2P14	chr3	+	1.07E+08	1.07E+08	351
ENSG00000(	8.286335	9.634302	13.19414	2.247227	6.443024	2.465895	1.3373	0.10611	0.18414	CTD-3236F	chr11	-	17159523	17159812	290
ENSG00000(	1.035792	0	7.916483	0.749076	1.840864	4.109825	0.29198	0.80639	0.87431	RP11-550F	chr3	+	76483169	76484579	1411
ENSG00000(	1.035792	4.817151	3.958241	0	0	0	2.7313	0.039906	0.079846	RP11-963H	chr17	-	10648870	10649860	476
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RPL21P4	chr17	+	41231319	41231797	479
ENSG00000(	657.7279	632.2511	571.3062	1312.38	1105.439	1133.49	-0.92915	4.24E-12	2.78E-11	TMEM189	chr20	-	48697663	48770335	2916
ENSG00000(	232.0174	225.2018	188.6762	256.9329	213.5402	259.7409	-0.17518	0.35877	0.48843	RDH14	chr2	-	18735989	18741946	1587
ENSG00000(	1.035792	0	1.319414	10.48706	5.522592	3.28786	-2.3208	0.039303	0.078794	AC093627.	chr7	+	149597	155465	5008
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RPL19P14	chr8	+	99794283	99794856	574
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	KRTAP4-7	chr17	+	39240459	39241396	938
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	RPS29P22	chr17	-	26443265	26443432	168
ENSG00000(	25.8948	6.021439	30.34652	26.96672	25.7721	20.54912	-0.22594	0.68321	0.78323	RP11-392A	chr3	-	1.56E+08	1.57E+08	3306
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-174C	chr3	+	1.2E+08	1.2E+08	1227
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP13-635I2	chr3	-	1.43E+08	1.43E+08	441
ENSG00000(	2.071584	1.204288	0	2.247227	9.20432	2.465895	-1.5246	0.18919	0.29425	NDUFB2-AS	chr7	-	1.4E+08	1.4E+08	1648
ENSG00000(	3.107376	2.408575	9.235896	1.498151	13.80648	4.93179	-0.3942	0.67566	0.77742	PLCXD2	chr3	+	1.11E+08	1.12E+08	2063
ENSG00000(	0	4.817151	1.319414	0	0	0	1.8904	0.16312	0.26107	RP11-572C	chr3	-	1.12E+08	1.12E+08	2022
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-119D	chr3	-	1.1E+08	1.1E+08	801

ENSG00000(	12.4295	3.612863	14.51355	5.992604	9.20432	6.575719	0.45062	0.55416	0.67501	RP11-48B1	chr17	+	3568514	3568996	483
ENSG00000(	1.035792	1.204288	0	1.498151	0.920432	0	-0.04875	0.97134	NA	AP000356.	chr22	+	25047814	25048364	551
ENSG00000(	7.250543	1.204288	2.638828	11.98521	4.60216	5.753754	-0.85733	0.35441	0.48417	RPL15P2	chr14	-	95267186	95267800	615
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-659E	chr8	+	63925627	63927240	550
ENSG00000(	5.17896	6.021439	10.55531	3.745378	5.522592	3.28786	0.69764	0.42152	0.55215	LSAMP-AS1	chr3	+	1.16E+08	1.16E+08	553
ENSG00000(	2.071584	0	0	1.498151	8.283888	3.28786	-1.7942	0.14282	0.23442	RPS20P31	chr12	+	1.21E+08	1.21E+08	332
ENSG00000(	1.035792	0	3.958241	0	0	0	1.6134	0.2311	NA	PLGLA	chr2	+	1.07E+08	1.07E+08	3025
ENSG00000(	3.107376	4.817151	0	0	0	0	2.297	0.089789	0.16048	RP11-372E	chr3	-	1.43E+08	1.43E+08	633
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-91A1	chr3	-	89637036	89637720	685
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RPL4P1	chr14	+	22218553	22219830	1278
ENSG00000(	25.8948	19.2686	11.87472	23.22134	30.37426	47.67397	-0.78631	0.11464	0.19636	RPL23AP64	chr11	-	1.19E+08	1.19E+08	435
ENSG00000(	1.035792	12.04288	1.319414	11.23613	0	1.64393	0.11044	0.92066	0.95182	MIF	chr22	+	24236191	24237414	939
ENSG00000(	0	2.408575	0	0	0.920432	1.64393	-0.04249	0.975	NA	CTD-2024I	chr5	+	1.41E+08	1.41E+08	208
ENSG00000(	206.1226	248.0833	196.5927	3.745378	0	0	6.9059	1.62E-31	2.58E-30	HOXA11-AS	chr7	+	27224137	27228912	1723
ENSG00000(	1.035792	3.612863	0	0	0	0	1.5346	0.25314	NA	RPL23AP67	chr12	+	1.34E+08	1.34E+08	474
ENSG00000(	1.035792	2.408575	1.319414	0	0	0	1.6865	0.21314	NA	RP11-142A	chr4	-	1.46E+08	1.46E+08	423
ENSG00000(	2.071584	1.204288	2.638828	3.745378	1.840864	2.465895	-0.35012	0.75993	0.84133	RP11-80H5	chr10	-	91454052	91457685	667
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-22C1	chr8	+	95700456	95700838	383
ENSG00000(	1.035792	0	1.319414	2.247227	1.840864	0	-0.4528	0.73609	0.82343	SEPT7P6	chr7	+	1.52E+08	1.52E+08	1143
ENSG00000(	0	0	0	0	3.681728	4.93179	-2.1075	0.1187	0.20199	RP11-494N	chr11	+	7805244	7805954	711
ENSG00000(	0	0	0	1.498151	0	2.465895	-1.1271	0.39798	NA	RP11-713C	chr4	+	1.89E+08	1.89E+08	357
ENSG00000(	60.07593	51.78437	69.92893	10.48706	13.80648	20.54912	1.9712	2.83E-06	1.12E-05	RP11-244H	chr1	-	35439957	35450914	3163
ENSG00000(	157.4404	131.2674	174.1626	134.8336	187.7681	227.6843	-0.24699	0.30191	0.42697	TPM3P9	chr19	+	53935237	53947923	2920
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CTD-2036J	chr8	-	22247378	22248168	483
ENSG00000(	5.17896	0	0	0	6.443024	2.465895	-0.48869	0.70112	0.79688	RPL29P24	chr12	-	1.21E+08	1.21E+08	453
ENSG00000(	2.071584	0	0	1.498151	0	0	0.18632	0.88758	NA	RP11-689J	chr14	+	21867084	21867441	358
ENSG00000(	26.93059	10.83859	23.74945	29.21395	16.56778	40.27628	-0.46537	0.37401	0.50452	GVQW1	chr9	+	32566787	32568619	1833
ENSG00000(	4.143168	0	0	1.498151	0.920432	1.64393	0.043155	0.97386	0.9848	RP11-173D	chr14	-	35613227	35613686	460
ENSG00000(	0	2.408575	0	2.996302	0.920432	4.93179	-1.25	0.32682	0.45454	AC004985.	chr7	-	44001189	44012924	1170
ENSG00000(	108.7581	121.6331	75.20659	112.3613	131.6218	121.6508	-0.25155	0.32996	0.45781	NSUN6	chr10	-	18834490	18940551	2201
ENSG00000(	0	2.408575	0	6.74168	0	4.109825	-1.4276	0.26505	0.38497	AC090602.	chr15	-	25154076	25154972	894
ENSG00000(	1.035792	0	0	0	3.681728	1.64393	-1.1227	0.40737	0.53818	RPL17P40	chr16	-	16188049	16189066	413
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	RP4-714D9	chr1	-	1.01E+08	1.01E+08	384
ENSG00000(	6.214751	6.021439	1.319414	2.247227	0	0.821965	1.5942	0.17018	0.27041	RP11-488C	chr14	-	77352720	77353093	374
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RPL17P44	chr18	+	60082911	60083460	550
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP11-657G	chr3	-	82855666	82857172	1507
ENSG00000(	3.107376	0	3.958241	0	0.920432	0	1.631	0.22429	0.33681	PRICKLE2-A	chr3	+	64089146	64091732	496
ENSG00000(	0	0	0	2.247227	1.840864	0.821965	-1.4859	0.2733	NA	CEACAMP1	chr19	-	43715943	43752798	1721
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	HLA-DOB	chr6	-	32780540	32784825	1514
ENSG00000(	3.107376	6.021439	14.51355	4.494453	2.761296	5.753754	0.73813	0.40141	0.53262	RP11-129B	chr3	+	64053640	64088807	6505
ENSG00000(	8.286335	6.021439	9.235896	6.74168	2.761296	9.041614	0.30194	0.71032	0.80419	RPL29P14	chr5	-	1.49E+08	1.49E+08	428
ENSG00000(	3.107376	0	5.277655	0.749076	6.443024	10.68554	-0.88601	0.40541	0.53638	HMGN1P8	chr3	-	1.67E+08	1.67E+08	288
ENSG00000(	121.1877	138.4931	164.9267	191.7633	120.5766	171.7907	-0.19376	0.42425	0.55477	YAE1D1	chr7	+	39605975	39649919	968
ENSG00000(	3.107376	2.408575	3.958241	0	2.761296	0	1.2522	0.31734	0.44424	RPL22P19	chr12	-	1.25E+08	1.25E+08	441

ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-6F2.6	chr3	+	1.57E+08	1.57E+08	791
ENSG00000(	1.035792	0	0	5.992604	1.840864	0	-1.5628	0.24323	0.35918	RP11-308D	chrX	+	1.36E+08	1.36E+08	1121
ENSG00000(	6.214751	8.430014	10.55531	0	0	0	4.2688	0.000382	0.001144	RP11-454C	chr3	+	1.51E+08	1.51E+08	580
ENSG00000(	10.35792	12.04288	9.235896	5.992604	4.60216	4.109825	1.0052	0.19112	0.29668	ARHGAP31	chr3	-	1.19E+08	1.19E+08	624
ENSG00000(	3.107376	0	5.277655	1.498151	0	0.821965	1.1973	0.35016	0.47987	RP11-3K24	chr17	-	58322649	58323008	360
ENSG00000(	4.143168	6.021439	6.597069	2.996302	1.840864	4.109825	0.76256	0.42588	0.55622	ADAMTS9-A	chr3	+	64547014	64573878	1727
ENSG00000(	9.322127	25.29004	17.15238	7.490755	2.761296	3.28786	1.7608	0.015912	0.035332	RP11-398A	chr3	-	72084451	72291716	2506
ENSG00000(	22.78742	22.88147	18.47179	0.749076	0	0	4.986	6.66E-07	2.81E-06	RP11-10O2	chr3	+	1.63E+08	1.63E+08	1834
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP4-752I6.	chr1	+	27783709	27786093	428
ENSG00000(	3.107376	6.021439	7.916483	19.47596	6.443024	11.50751	-1.0568	0.17021	0.27045	RP11-147I3	chr11	+	74587331	74631067	723
ENSG00000(	0	2.408575	1.319414	0	0.920432	0	0.92035	0.49653	NA	CTB-2L9.1	chr5	-	1.34E+08	1.34E+08	355
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	RP11-54O7	chr1	+	849551	850351	443
ENSG00000(	10.35792	12.04288	9.235896	0.749076	0.920432	2.465895	2.5262	0.006523	0.015786	AC093734.	chr7	-	1583450	1585885	2224
ENSG00000(	0	0	2.638828	0	1.840864	0.821965	-0.01672	0.99017	NA	RPL21P122	chr17	-	11901670	11924825	531
ENSG00000(	0	1.204288	0	282.4015	280.7318	277.8241	-8.0654	1.02E-22	1.15E-21	TDGF1	chr3	+	46616045	46668033	2513
ENSG00000(	0	3.612863	0	0.749076	0	0	0.87856	0.51086	NA	CTC-209L1(	chr5	+	1.54E+08	1.54E+08	464
ENSG00000(	0	0	0	2.247227	0.920432	0.821965	-1.2297	0.36205	NA	IQCJ-SCHIP	chr3	-	1.59E+08	1.59E+08	508
ENSG00000(	0	2.408575	1.319414	0.749076	0	0	0.98048	0.46819	NA	RP11-768G	chr3	-	1.17E+08	1.17E+08	489
ENSG00000(	15.53688	2.408575	9.235896	1.498151	5.522592	0.821965	1.5613	0.10093	0.17679	RP11-446H	chr3	-	1.07E+08	1.07E+08	1368
ENSG00000(	2.071584	1.204288	0	0.749076	0	0	0.87851	0.5141	NA	RP11-572N	chr3	-	1.13E+08	1.13E+08	1253
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	RP11-292E	chr3	+	1.53E+08	1.53E+08	634
ENSG00000(	1.035792	0	5.277655	0	0	1.64393	1.0768	0.42266	0.55313	RP5-916O1	chr11	-	36018776	36019225	450
ENSG00000(	2.071584	3.612863	0	0	0	0.821965	1.4184	0.29471	0.41906	KRTAP5-8	chr11	+	71249071	71250253	1183
ENSG00000(	4.143168	6.021439	3.958241	0	0	0	3.3516	0.008907	0.020944	AP001052.	chr21	+	45141573	45152146	342
ENSG00000(	0	0	1.319414	1.498151	0	0	-0.08979	0.94423	NA	KRTAP4-16	chr17	-	39257754	39258461	708
ENSG00000(	0	0	3.958241	0	0.920432	0	0.88424	0.51108	NA	AC006378.	chr7	-	93594722	93597702	314
ENSG00000(	617.332	711.734	558.112	985.7834	721.6187	859.7753	-0.44294	0.004496	0.011243	CRCP	chr7	+	65579591	65619555	3139
ENSG00000(	5.17896	16.86003	11.87472	10.48706	16.56778	29.59074	-0.70444	0.27562	0.39711	AC093620.	chr7	+	5459458	5460398	583
ENSG00000(	17.60846	25.29004	21.11062	7.490755	1.840864	6.575719	1.8593	0.005112	0.012643	RP11-379B	chr3	+	1.26E+08	1.26E+08	1086
ENSG00000(	85.97073	96.34302	62.01245	23.22134	28.53339	32.05663	1.5226	1.30E-05	4.75E-05	RP11-379B	chr3	-	1.26E+08	1.26E+08	1996
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	PPATP1	chr3	-	87100342	87101888	1547
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-674E	chr3	+	1.55E+08	1.55E+08	601
ENSG00000(	8.286335	9.634302	3.958241	2.996302	6.443024	9.041614	0.22959	0.78292	0.85707	WWTR1-AS	chr3	+	1.49E+08	1.49E+08	1700
ENSG00000(	6.214751	9.634302	18.47179	28.46487	20.2495	27.12484	-1.112	0.053097	0.10235	RP11-81N1	chr3	+	67705121	67998137	2226
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	SETP6	chr3	-	81661389	81661956	568
ENSG00000(	0	2.408575	1.319414	1.498151	0	0	0.61999	0.64768	NA	CDRT1	chr17	-	15468798	15522826	2571
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-331K	chr3	+	86531093	86546146	1321
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-451G	chr3	+	1.55E+08	1.55E+08	905
ENSG00000(	89.0781	116.8159	64.65128	145.3207	150.0304	113.4312	-0.58641	0.030716	0.063447	RPL36A	chrX	+	1.01E+08	1.01E+08	2240
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	RP11-379B	chr3	-	1.26E+08	1.26E+08	205
ENSG00000(	0	0	0	0.749076	3.681728	4.93179	-2.3524	0.077187	0.14092	RP11-392P	chr12	+	13003916	13004674	759
ENSG00000(	1.035792	0	7.916483	0	0	0	2.4101	0.074732	0.13721	RP11-1042	chr14	-	61068794	61069310	517
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	SYNPR-AS1	chr3	-	63409272	63535727	558
ENSG00000(	45.57484	40.94578	39.58241	54.68252	78.23672	51.78379	-0.53575	0.12432	0.20973	PDXP	chr22	+	38054734	38062941	2010

ENSG00000(	5.17896	12.04288	7.916483	0.749076	1.840864	2.465895	1.9751	0.039407	0.078956	RPL36AP4:	chr15	-	90231168	90231474	307
ENSG00000(	4.143168	1.204288	3.958241	0	0	0	2.6664	0.045428	0.089328	CT64	chr3	-	1.63E+08	1.63E+08	1519
ENSG00000(	9.322127	3.612863	6.597069	7.490755	7.363456	16.4393	-0.61143	0.42936	0.55953	RPP21	chr6	+	30312908	30314661	1492
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	HNF1A-AS1	chr12	-	1.21E+08	1.21E+08	2455
ENSG00000(	239.2679	326.362	281.0351	50.93714	25.7721	41.09825	2.8066	3.44E-27	4.65E-26	CD302	chr2	-	1.61E+08	1.61E+08	3839
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-764I5	chr3	+	1.41E+08	1.41E+08	362
ENSG00000(	30.03797	31.31148	21.11062	11.98521	23.0108	25.48091	0.44063	0.37668	0.50731	EGFL8	chr6	+	32132360	32136058	2441
ENSG00000(	2.071584	0	3.958241	0	0	0	1.8862	0.16413	0.26236	KRT8P13	chr3	+	1.7E+08	1.7E+08	1010
ENSG00000(	0	3.612863	1.319414	8.239831	1.840864	2.465895	-1.048	0.36367	0.49341	RP11-512H	chrX	-	1.31E+08	1.31E+08	511
ENSG00000(	0	6.021439	0	1.498151	0	0	1.0093	0.45643	0.58618	EEF1A1P25	chr3	+	1.39E+08	1.39E+08	1267
ENSG00000(	1.035792	1.204288	3.958241	0	0.920432	0	1.5421	0.24996	0.36731	TDGF1P6	chr3	+	1.36E+08	1.36E+08	448
ENSG00000(	0	6.021439	0	0	0.920432	0	1.3099	0.33429	0.46228	RP4-555L1.	chr7	+	1.51E+08	1.51E+08	564
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	PLSCR5-AS:	chr3	+	1.46E+08	1.46E+08	450
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	RP11-461C	chr5	+	1.38E+08	1.38E+08	618
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP11-579C	chr17	+	56975137	56977053	383
ENSG00000(	134.6529	173.4174	166.2461	176.7818	172.1208	264.6727	-0.37132	0.10879	0.18789	ATP5J2	chr7	-	99046098	99063954	774
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-336K	chr1	-	1.56E+08	1.56E+08	420
ENSG00000(	11.39371	14.45145	21.11062	24.71949	34.05598	47.67397	-1.1493	0.021533	0.046338	PTPRG-AS1	chr3	-	62247498	62355005	2661
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC159540.	chr2	+	98086678	98100408	859
ENSG00000(	0	1.204288	0	43.44638	57.06678	46.852	-5.7164	6.42E-10	3.57E-09	ARHGAP8	chr22	+	45098355	45258665	2905
ENSG00000(	11.39371	32.51577	21.11062	1.498151	8.283888	13.9734	1.353	0.052437	0.10123	AF011889.	chrX	-	1.49E+08	1.49E+08	1044
ENSG00000(	6.214751	8.430014	11.87472	5.992604	3.681728	3.28786	0.91122	0.27087	0.39154	RP11-274B	chr7	-	1.28E+08	1.28E+08	132
ENSG00000(	0	1.204288	1.319414	1.498151	2.761296	0.821965	-0.64646	0.62197	0.73405	RP11-85G2	chr14	+	93710356	93710669	314
ENSG00000(	19.68005	22.88147	21.11062	26.21764	16.56778	45.20807	-0.4543	0.36674	0.49677	PSMC1P1	chr3	+	68684856	68686175	1320
ENSG00000(	2.071584	1.204288	0	0	3.681728	0	-0.06447	0.96194	0.97801	RPS15AP24	chr8	-	29974900	29975295	396
ENSG00000(	2.071584	0	2.638828	3.745378	0	0	0.17919	0.89327	0.93398	AC098820.	chr2	-	2.17E+08	2.17E+08	976
ENSG00000(	3.107376	0	3.958241	0.749076	5.522592	0	0.13246	0.91567	0.94854	CA15P1	chr22	-	19019077	19022077	905
ENSG00000(	10.35792	2.408575	3.958241	7.490755	8.283888	4.109825	-0.201	0.81809	0.88235	RP1-130H1	chr22	-	30770930	30773862	1443
ENSG00000(	0	1.204288	0	0.749076	0	0	0.1572	0.90001	NA	AGGF1P3	chr3	-	75702712	75703924	1213
ENSG00000(	0	4.817151	1.319414	0	0	0	1.8904	0.16312	0.26107	CBX5P1	chr3	-	88144558	88145118	561
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-624D	chr3	+	72821690	72822622	933
ENSG00000(	1.035792	1.204288	3.958241	0	0	0	2.0343	0.13352	0.22221	RP11-6F2.5	chr3	+	1.57E+08	1.57E+08	1497
ENSG00000(	0	0	2.638828	0	0	2.465895	0.027772	0.98358	NA	RP11-767L	chr3	+	1.2E+08	1.2E+08	348
ENSG00000(	6.214751	12.04288	6.597069	6.74168	6.443024	6.575719	0.29833	0.70194	0.79743	RP11-4K3_	chr1	+	27651820	27652287	468
ENSG00000(	50.7538	31.31148	40.90183	26.96672	11.96562	21.37109	0.99201	0.030299	0.062715	GUSBP2	chr6	-	26839263	26924333	1457
ENSG00000(	2219.702	2089.439	2053.008	2584.311	2214.559	2912.222	-0.27683	0.027677	0.05795	ARPC4	chr3	+	9834179	9855035	2582
ENSG00000(	16.57267	10.83859	14.51355	9.737982	5.522592	7.397684	0.82404	0.2232	0.33537	RP11-490G	chr12	-	95861173	95861637	465
ENSG00000(	4.143168	0	5.277655	0	0	0.821965	2.0321	0.12391	0.20916	ZBTB20-AS:	chr3	+	1.14E+08	1.14E+08	1687
ENSG00000(	16.57267	14.45145	14.51355	8.239831	11.96562	7.397684	0.68734	0.27997	0.40221	CORT	chr1	+	10509776	10511959	1130
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-372E	chr3	+	1.43E+08	1.43E+08	912
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	RP11-520D	chr3	-	81295730	81346496	1014
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-326J:	chr3	+	1.15E+08	1.15E+08	562
ENSG00000(	0	0	0	2.996302	1.840864	3.28786	-2.1887	0.10174	0.17796	CTD-2007H	chr5	+	98290098	98290676	579
ENSG00000(	3.107376	4.817151	0	0	7.363456	4.93179	-0.46289	0.68864	0.78734	RP11-34P1	chr1	+	160446	161525	457

ENSG00000(	1.035792	0	2.638828	0	0.920432	0	0.90832	0.50205	NA	RP13-585F	chr4	+	19815372	19815854	483
ENSG00000(	0	6.021439	6.597069	0	2.761296	4.93179	0.53676	0.64258	0.75004	RP11-413E	chr3	+	75707685	75708165	481
ENSG00000(	1.035792	2.408575	1.319414	0	3.681728	0	0.24536	0.85262	0.90604	UBQLN4P1	chr3	-	1.49E+08	1.49E+08	1801
ENSG00000(	13.46529	7.225726	9.235896	18.72689	40.49901	15.61733	-1.2376	0.04116	0.082069	RP11-381E	chr3	-	1.08E+08	1.08E+08	509
ENSG00000(	1.035792	0	0	0	0	2.465895	-0.37334	0.77636	NA	UGT1A1	chr2	+	2.35E+08	2.35E+08	3389
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-71H9	chr3	-	1.64E+08	1.64E+08	576
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	RP11-59H7	chr15	-	59341598	59342584	467
ENSG00000(	0	1.204288	1.319414	2.247227	0	0	0.055815	0.96714	NA	RPS23P6	chr16	+	12175094	12175759	431
ENSG00000(	0	1.204288	2.638828	0	0	0	1.2853	0.33195	NA	INMT	chr7	+	30737601	30797218	2559
ENSG00000(	0	0	6.597069	0	0	0	1.83	0.17508	0.27674	RP11-214C	chr4	-	1.29E+08	1.29E+08	599
ENSG00000(	0	1.204288	0	0	0	1.64393	-0.12916	0.91993	NA	PPP1R2P6	chr7	+	1.4E+08	1.4E+08	588
ENSG00000(	0	0	0	2.247227	4.60216	2.465895	-2.3811	0.072509	0.13365	RP11-732A	chr11	-	6707122	6707600	479
ENSG00000(	14.50109	12.04288	18.47179	0.749076	0	0	4.4642	2.21E-05	7.86E-05	RP11-80H8	chr3	+	1.43E+08	1.43E+08	529
ENSG00000(	0	6.021439	1.319414	1.498151	0	0	1.2946	0.33207	0.46016	RPL31P49	chr12	+	1.11E+08	1.11E+08	375
ENSG00000(	7.250543	13.24716	34.30476	5.992604	8.283888	11.50751	1.002	0.14348	0.23527	ADAMTS9-A	chr3	+	64670585	64997143	3691
ENSG00000(	3507.191	3323.834	3053.123	3809.049	2923.292	2978.801	0.025373	0.84425	0.90064	ARPC1A	chr7	+	98923521	98985787	1702
ENSG00000(	26.93059	8.430014	26.38828	18.72689	42.33987	29.59074	-0.52483	0.32244	0.4497	TMEFF1	chr9	+	1.03E+08	1.03E+08	2611
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP4-735C1	chr1	+	1.1E+08	1.1E+08	808
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-113A	chr3	-	1.58E+08	1.58E+08	613
ENSG00000(	2.071584	1.204288	0	70.4131	84.67974	83.84042	-5.5437	3.40E-14	2.55E-13	RP11-38P2	chr3	+	1.53E+08	1.53E+08	2050
ENSG00000(	1.035792	3.612863	0	0.749076	4.60216	0	-0.11451	0.92982	0.95783	FABP5P3	chr7	+	1.52E+08	1.52E+08	1027
ENSG00000(	6.214751	0	6.597069	2.996302	4.60216	4.109825	0.11207	0.91322	0.94688	ZNF90P1	chr3	+	1.01E+08	1.01E+08	1951
ENSG00000(	9.322127	15.65574	14.51355	1.498151	4.60216	7.397684	1.4131	0.068717	0.12773	RPL7AP30	chr4	-	1.14E+08	1.14E+08	796
ENSG00000(	0	0	0	0	3.681728	4.109825	-1.9686	0.14605	0.23869	RP5-964N1	chrX	-	1.13E+08	1.13E+08	497
ENSG00000(	47.64643	80.68728	84.44248	10.48706	28.53339	13.9734	1.9637	5.89E-06	2.25E-05	RPSAP52	chr12	-	66151800	66220777	1144
ENSG00000(	9.322127	6.021439	7.916483	17.97781	16.56778	25.48091	-1.2855	0.040638	0.081186	AC002467.	chr7	-	1.07E+08	1.07E+08	657
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-159A	chr12	+	69816436	69816775	340
ENSG00000(	23.82321	26.49433	26.38828	2.996302	8.283888	9.863579	1.7717	0.003408	0.008729	AF011889.	chrX	-	1.49E+08	1.49E+08	1120
ENSG00000(	2.071584	1.204288	1.319414	0	1.840864	0.821965	0.51109	0.69769	0.79429	RP11-555N	chr3	+	1.57E+08	1.57E+08	320
ENSG00000(	0	1.204288	0	0.749076	2.761296	3.28786	-1.436	0.27993	0.40221	AC092620.	chr2	+	1.39E+08	1.39E+08	534
ENSG00000(	5.17896	0	2.638828	4.494453	0	8.219649	-0.5286	0.64656	0.7533	RP11-91P2	chr11	-	77579768	77580241	474
ENSG00000(	1.035792	6.021439	0	2.247227	0	0.821965	0.76067	0.55723	0.67773	RP11-342N	chr1	-	43302599	43312033	627
ENSG00000(	0	0	0	1.498151	3.681728	0	-1.4292	0.2903	NA	MTND4P16	chr3	-	1.07E+08	1.07E+08	1367
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	COX6B1P2	chr17	+	46791092	46791321	230
ENSG00000(	4.143168	0	0	0.749076	0	1.64393	0.43985	0.74507	0.83029	RP11-1000	chr15	-	32948285	32965266	461
ENSG00000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	RP11-637A	chr12	+	69078375	69080088	679
ENSG00000(	0	0	0	2.996302	1.840864	2.465895	-2.0363	0.13003	0.21728	RP11-277J2	chr12	+	8013033	8013360	328
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	RPL21P54	chr5	+	34883162	34883625	464
ENSG00000(	79.75598	103.5687	105.5531	111.6123	69.95283	83.01846	0.11834	0.67622	0.77792	ATP5O	chr21	-	35275757	35288284	2839
ENSG00000(	283.807	390.1892	324.5758	188.767	153.7121	203.8473	0.86272	1.12E-05	4.11E-05	PLEKHO2	chr15	+	65134088	65160206	3720
ENSG00000(	3.107376	1.204288	1.319414	3.745378	0.920432	0	0.18308	0.88486	0.92812	RP1-20N2.4	chr6	+	1.44E+08	1.44E+08	853
ENSG00000(	179.192	207.1375	196.5927	452.4416	374.6158	337.8276	-0.99641	6.22E-08	2.91E-07	C8orf58	chr8	+	22457114	22461663	2021
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-147K	chr4	+	89084731	89085119	389
ENSG00000(	1.035792	3.612863	0	23.22134	18.40864	11.50751	-3.0685	0.000446	0.001321	KALP	chrY	+	15863536	16027704	1816

ENSG00000(	33.14534	52.98866	21.11062	24.71949	31.29469	41.92021	0.13148	0.76889	0.84793	RP11-34P1	chr1	-	141474	173862	4860
ENSG00000(	0	2.408575	1.319414	0	0	0	1.2548	0.34239	NA	TOMM22P(	chr3	-	1.62E+08	1.62E+08	409
ENSG00000(	297.2723	356.4692	325.8952	735.5922	699.5283	701.1361	-1.1231	1.25E-14	9.64E-14	PISD	chr22	-	32014477	32058418	2669
ENSG00000(	1.035792	0	3.958241	0	0.920432	0.821965	0.85957	0.52209	0.64757	RP11-85I2:	chr3	+	67346724	67356783	2084
ENSG00000(	2.071584	1.204288	5.277655	0	8.283888	4.109825	-0.41801	0.70887	0.80322	RP11-242C	chrX	+	30716324	30740049	562
ENSG00000(	6.214751	4.817151	5.277655	0.749076	4.60216	0.821965	1.1756	0.25824	0.37694	RP11-435F	chr3	+	1.14E+08	1.14E+08	734
ENSG00000(	4.143168	0	0	0	4.60216	0	-0.05342	0.96844	0.98169	RPL13P4	chr15	+	75680608	75681169	562
ENSG00000(	5.17896	8.430014	9.235896	2.247227	1.840864	0.821965	1.8671	0.054947	0.10553	CTB-46E9.1	chr5	-	1.49E+08	1.49E+08	355
ENSG00000(	1.035792	0	0	2.996302	0	0	-0.53136	0.68956	NA	RP11-292E	chr3	+	1.53E+08	1.53E+08	382
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP5-1073F	chr17	+	57989558	57989727	170
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	RFTN1P1	chrY	-	7581026	7644748	996
ENSG00000(	0	0	0	0	0	4.93179	-1.2404	0.35057	NA	RP11-425I:	chr4	-	1.41E+08	1.41E+08	622
ENSG00000(	3.107376	0	0	0	0.920432	1.64393	0.16717	0.90192	NA	RP5-1154E	chr7	-	1.42E+08	1.42E+08	745
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-755B	chr3	+	57678932	57682323	2919
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	HOGA1	chr10	+	99344080	99372559	2581
ENSG00000(	1.035792	0	0	1.498151	6.443024	0.821965	-1.7608	0.18038	0.28334	RPL32P26	chr12	+	63052603	63053005	403
ENSG00000(	489.9296	492.5537	451.2395	991.776	925.9546	1014.305	-1.0292	4.66E-15	3.69E-14	PWP2	chr21	+	45527171	45551063	4564
ENSG00000(	0	1.204288	1.319414	0	1.840864	2.465895	-0.45422	0.73462	0.82247	RP1-149A1	chr22	+	32779773	32781618	444
ENSG00000(	8.286335	9.634302	2.638828	0	0	0	3.9243	0.001525	0.004143	CTC-340A1	chr5	+	1.64E+08	1.65E+08	1618
ENSG00000(	12.4295	6.021439	9.235896	84.64554	63.50981	71.51095	-2.8897	1.45E-10	8.50E-10	C2orf15	chr2	+	99757948	99939204	2569
ENSG00000(	1372.424	1269.319	1245.527	1095.898	1223.254	1151.573	0.16411	0.16785	0.2673	PI4KA	chr22	-	21061979	21213705	6752
ENSG00000(	6.214751	2.408575	0	0	0.920432	0	1.8876	0.15515	0.25086	TCEB1P19	chr1	+	89294785	89295102	318
ENSG00000(	0	3.612863	0	5.243529	11.96562	4.109825	-2.0106	0.067769	0.12628	AKAP2	chr9	+	1.13E+08	1.13E+08	6866
ENSG00000(	0	3.612863	1.319414	0	4.60216	0.821965	-0.08373	0.94852	0.96902	AF224669.	chr4	+	1.04E+08	1.04E+08	463
ENSG00000(	5.17896	1.204288	1.319414	2.996302	1.840864	0	0.49159	0.68758	0.78648	RP11-407N	chr14	+	39625946	39627056	740
ENSG00000(	9.322127	9.634302	1.319414	5.992604	7.363456	5.753754	0.092022	0.91423	0.94763	WWTR1-IT:	chr3	-	1.49E+08	1.49E+08	451
ENSG00000(	0	1.204288	7.916483	0	0	0	2.4336	0.07182	0.13268	RP6-109B7	chr22	+	46449585	46453090	877
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP11-95I1!	chr5	-	61857686	61858043	358
ENSG00000(	0	0	0	1.498151	1.840864	0.821965	-1.2806	0.34348	NA	RP11-287A	chr9	+	1.08E+08	1.08E+08	576
ENSG00000(	81.82756	92.73015	76.526	88.39091	82.83888	99.45776	-0.10747	0.68919	0.78771	USP27X	chrX	+	49644470	49647166	2697
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-268G	chrX	-	27177022	27194415	594
ENSG00000(	31.07376	19.2686	21.11062	17.97781	20.2495	6.575719	0.65031	0.24879	0.36593	HYPK	chr15	+	44088340	44095241	4777
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-1396	chr4	-	9555234	9555605	372
ENSG00000(	0	9.634302	0	4.494453	0	0	0.67242	0.60844	0.72255	RP11-190C	chr3	-	1.19E+08	1.19E+08	625
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	MARK2P6	chr3	-	1.29E+08	1.29E+08	897
ENSG00000(	236.1606	267.3519	170.2044	95.13259	98.48622	164.393	0.90528	0.000445	0.001317	RPL7AP6	chr14	-	70352057	70352869	813
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP11-738B	chr7	-	1.29E+08	1.29E+08	305
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP1-90G24	chr22	+	32601102	32665653	876
ENSG00000(	4.143168	2.408575	1.319414	2.996302	0.920432	0	0.71016	0.56446	0.68398	RPL7AP31	chr4	+	57222301	57223098	798
ENSG00000(	7.250543	6.021439	5.277655	1.498151	1.840864	11.50751	0.27966	0.76516	0.84498	RPS20P33	chr14	+	1.06E+08	1.06E+08	354
ENSG00000(	326.2744	325.1577	224.3003	361.0544	250.3575	339.4715	-0.11723	0.5645	0.684	AC069513.	chr3	+	1.95E+08	1.95E+08	4208
ENSG00000(	3.107376	0	0	0	0.920432	0	0.70943	0.5938	NA	RPL36AP41	chr12	-	64265519	64265824	306
ENSG00000(	1.035792	0	0	0	2.761296	3.28786	-1.2678	0.34807	0.47773	AC090602.	chr15	-	25156021	25156272	252
ENSG00000(	6.214751	25.29004	5.277655	0	0.920432	1.64393	3.187	0.001524	0.004141	FOXP1-IT1	chr3	-	71619406	71623608	3539

ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RPL9P32	chr19	-	30447276	30447895	620
ENSG00000(	1.035792	6.021439	14.51355	0.749076	6.443024	3.28786	0.87606	0.37535	0.50594	AMACR	chr5	-	33986283	34008220	4153
ENSG00000(	6.214751	4.817151	5.277655	9.737982	11.96562	8.219649	-0.79102	0.30745	0.43321	MTFP1	chr22	+	30821518	30825045	1375
ENSG00000(	845.2062	832.1628	783.7318	2349.101	1619.04	1862.573	-1.2409	2.04E-17	1.83E-16	SNHG3	chr1	+	28832492	28837404	2614
ENSG00000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	RPL5P13	chr4	-	1.43E+08	1.43E+08	709
ENSG00000(	0	0	0	0.749076	0.920432	0.821965	-0.73223	0.57364	NA	RP11-734K	chr2	+	9243569	9245243	547
ENSG00000(	7.250543	2.408575	10.55531	2.247227	7.363456	5.753754	0.3526	0.69152	0.78954	RP13-463N	chr10	-	5636954	5638081	697
ENSG00000(	0	0	5.277655	0	0.920432	0	1.1592	0.39256	0.52329	RP4-778K6	chr7	+	1.05E+08	1.05E+08	546
ENSG00000(	0	0	0	1.498151	1.840864	0.821965	-1.2806	0.34348	NA	RP11-299L	chr14	-	81799305	81799705	401
ENSG00000(	6.214751	2.408575	2.638828	2.247227	3.681728	1.64393	0.48356	0.64868	0.7551	ARHGDIG	chr16	+	318726	333003	1272
ENSG00000(	1.035792	1.204288	1.319414	0	0.920432	0	0.95183	0.48289	NA	RP11-142L	chr3	-	81811857	81813907	376
ENSG00000(	11.39371	32.51577	17.15238	29.96302	27.61296	19.72716	-0.33346	0.5239	0.6491	RP11-568K	chr1	-	1.78E+08	1.78E+08	2921
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-588L	chr4	+	40493750	40494041	292
ENSG00000(	14.50109	10.83859	5.277655	2.996302	9.20432	9.041614	0.49975	0.51716	0.64348	CTD-2235C	chr5	+	74670288	74670634	347
ENSG00000(	2.071584	1.204288	0	0	1.840864	0.821965	0.19367	0.88581	0.92875	RP11-71H1	chr3	-	1.24E+08	1.24E+08	337
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	HOXB-AS4	chr17	+	46706037	46712294	566
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC006445.	chr4	-	13649321	13650024	405
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	MTND3P6	chr3	-	1.07E+08	1.07E+08	339
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	TCP10L	chr21	-	33948862	33957843	984
ENSG00000(	0	0	0	12.73428	10.12475	1.64393	-3.787	0.001955	0.005216	PSG2	chr19	-	43568363	43587197	1538
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RPS3AP14	chr3	+	1.26E+08	1.26E+08	780
ENSG00000(	15.53688	21.67718	22.43003	9.737982	9.20432	18.90519	0.61877	0.28727	0.41083	PVRL3-AS1	chr3	-	1.11E+08	1.11E+08	792
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	ATP5G1P3	chr3	-	1.39E+08	1.39E+08	410
ENSG00000(	865.922	959.8173	1080.6	323.6006	270.607	258.097	1.7617	1.30E-30	2.01E-29	ARFGAP3	chr22	-	43192508	43254112	2857
ENSG00000(	0	2.408575	1.319414	1.498151	2.761296	8.219649	-1.315	0.26379	0.38363	BGLAP	chr1	+	1.56E+08	1.56E+08	931
ENSG00000(	0	0	0	2.996302	3.681728	0.821965	-2.0473	0.12821	0.21482	RP11-511P	chr7	+	1.5E+08	1.5E+08	2043
ENSG00000(	139.8319	151.7403	105.5531	197.7559	195.1316	175.0785	-0.50973	0.020651	0.044615	C22orf39	chr22	-	19338891	19435755	2979
ENSG00000(	55.93276	55.39724	34.30476	68.91495	65.35067	78.90863	-0.53537	0.105	0.18257	RP11-62J1.	chr7	+	1.28E+08	1.28E+08	1030
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	RP11-100N	chr4	+	47708389	47709004	616
ENSG00000(	2795.602	2799.969	3749.774	14601.73	20627.8	15129.91	-2.4226	4.20E-57	1.37E-55	PEG10	chr7	+	94285637	94299007	6618
ENSG00000(	0	4.817151	1.319414	0	0.920432	0	1.4368	0.28779	0.41144	RP11-368I2	chr3	+	1.69E+08	1.69E+08	710
ENSG00000(	23.82321	14.45145	14.51355	25.46857	14.72691	18.90519	-0.15245	0.77967	0.85491	AC108488.	chr2	-	3579403	3584463	914
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RPL6P8	chr3	+	1.6E+08	1.6E+08	843
ENSG00000(	25.8948	44.55865	40.90183	33.7084	33.13555	36.16646	0.10323	0.79895	0.8689	RP11-464F	chr10	-	75434053	75490272	3810
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-197K	chr3	+	1.14E+08	1.14E+08	622
ENSG00000(	6.214751	2.408575	6.597069	5.992604	9.20432	18.08323	-1.0156	0.20752	0.31682	CTB-161A2	chr7	+	99933748	99938951	683
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	RP11-522B	chr15	+	96991384	96991723	340
ENSG00000(	52.82539	51.78437	43.54065	32.21025	36.81728	37.81039	0.46681	0.19975	0.30742	RP11-234A	chr3	-	1.01E+08	1.01E+08	459
ENSG00000(	0	0	0	1.498151	3.681728	0	-1.4292	0.2903	NA	RPS26P52	chr16	-	14016189	14016536	348
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-572C	chr3	-	1.12E+08	1.12E+08	159
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-428G	chr12	+	32101268	32101761	494
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-810D	chr4	+	99330441	99330914	474
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-117F	chr3	+	1.39E+08	1.39E+08	390
ENSG00000(	8.286335	6.021439	6.597069	2.996302	0	1.64393	1.7676	0.083596	0.15102	RPS12P31	chr19	+	33126984	33127381	398

ENSG00000(	3.107376	0	0	1.498151	0	0.821965	0.22369	0.86904	NA	RP11-59H1	chr12	-	12993738	12994013	276
ENSG00000(	7.250543	10.83859	9.235896	0.749076	0.920432	4.109825	1.9211	0.04083	0.081526	TFP1	chr3	+	1.33E+08	1.33E+08	1573
ENSG00000(	15.53688	6.021439	19.79121	7.490755	6.443024	13.9734	0.52352	0.44961	0.57944	BMS1P4	chr10	-	75475601	75490227	1716
ENSG00000(	3.107376	6.021439	2.638828	9.737982	11.04518	11.50751	-1.3089	0.10769	0.18643	NPPA-AS1	chr1	+	11901074	11908136	1032
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-403I:	chr1	+	1.49E+08	1.49E+08	2544
ENSG00000(	8.286335	1.204288	6.597069	0	10.12475	0	0.53652	0.63771	0.74611	RP11-809C	chr10	+	709498	712562	550
ENSG00000(	1337.207	1369.275	1204.625	1095.148	1087.03	1263.36	0.18281	0.14425	0.23632	EIF6	chr20	-	33866714	33872788	1289
ENSG00000(	3.107376	2.408575	0	2.247227	1.840864	1.64393	-0.0222	0.98554	0.99136	RP11-498P	chr9	-	99957633	99959969	474
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	TBC1D3H	chr17	-	34581086	34808061	3389
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RBMY1E	chrY	-	24026223	24064214	1921
ENSG00000(	0	0	2.638828	0	0	0.821965	0.55859	0.66971	NA	RP11-427D	chr3	+	1.42E+08	1.42E+08	859
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP4-631H1	chr1	-	53346888	53347402	380
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-67L3	chr1	+	55352548	55353674	575
ENSG00000(	0	0	2.638828	1.498151	0	0	0.308	0.81734	NA	RP11-267J:	chr12	+	12308196	12308706	511
ENSG00000(	10.35792	1.204288	10.55531	0	0	0	3.9799	0.001349	0.003708	CTD-2377D	chr17	+	46810453	46811250	532
ENSG00000(	2.071584	0	0	0	0.920432	0.821965	0.13309	0.92108	NA	DBIL5P2	chr2	-	63344986	63346677	1692
ENSG00000(	105.6508	79.48299	79.16483	128.841	157.3939	164.393	-0.75708	0.002433	0.006383	PCDHGC4	chr5	+	1.41E+08	1.41E+08	4623
ENSG00000(	1.035792	0	3.958241	0	2.761296	1.64393	0.11352	0.93056	0.95822	RP11-19G2	chr17	+	35519530	35520053	524
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CTD-2349P	chr17	+	29157919	29158336	418
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-320N	chr12	-	4218827	4227298	555
ENSG00000(	3.107376	3.612863	1.319414	2.996302	2.761296	4.93179	-0.32562	0.75881	0.84057	RPL7AP11	chr3	+	1.21E+08	1.21E+08	799
ENSG00000(	1.035792	0	2.638828	2.996302	0.920432	2.465895	-0.56336	0.6552	0.76041	RBBP4P2	chr3	-	93794756	93796019	1264
ENSG00000(	9.322127	6.021439	6.597069	23.97042	20.2495	22.19305	-1.5024	0.014404	0.032322	AC093627.	chr7	-	135853	149466	662
ENSG00000(	1.035792	1.204288	3.958241	2.996302	0.920432	3.28786	-0.18786	0.87274	0.92018	CTD-2161E	chr5	-	86180048	86180698	651
ENSG00000(	900.1032	833.3671	752.0659	1402.269	1217.732	1426.109	-0.70057	8.76E-08	4.04E-07	MRPL20	chr1	-	1337288	1342693	1693
ENSG00000(	7.250543	4.817151	1.319414	0.749076	1.840864	0.821965	1.5464	0.17231	0.27335	RP11-270N	chr14	-	76304500	76305457	958
ENSG00000(	121.1877	164.9874	134.5802	124.3465	161.0756	179.1884	-0.14201	0.54817	0.66983	C15orf38	chr15	-	90443159	90456188	2670
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP3-477O4	chr20	-	34108569	34117481	2087
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	NDUFB4P1	chr3	+	67564364	67564744	381
ENSG00000(	85.97073	56.60152	77.84541	31.46117	45.10117	25.48091	1.098	0.002181	0.005773	RP11-413E	chr3	+	75721542	75728454	2126
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-159H	chr11	+	27505397	27505675	279
ENSG00000(	1.035792	0	3.958241	0	0.920432	3.28786	0.1455	0.91153	0.94567	RP11-299J:	chr3	-	1.22E+08	1.22E+08	131
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP11-290K	chr3	-	1.58E+08	1.58E+08	716
ENSG00000(	165.7267	148.1274	200.5509	110.1141	108.611	92.88204	0.7161	0.001906	0.005097	AC007620.	chr3	+	1.79E+08	1.79E+08	1697
ENSG00000(	8.286335	1.204288	9.235896	14.23244	12.88605	6.575719	-0.76731	0.33321	0.46133	AC010729.	chr2	+	5836352	5847791	763
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	SERPINB10	chr18	+	61564408	61603345	2122
ENSG00000(	0	3.612863	6.597069	0	0	0	2.6451	0.04889	0.095178	POU5F1P6	chr3	-	1.28E+08	1.28E+08	990
ENSG00000(	7.250543	7.225726	9.235896	0.749076	11.04518	10.68554	0.075985	0.92882	0.95719	AP001432.	chr21	+	38593720	38610045	520
ENSG00000(	4.143168	0	1.319414	2.247227	2.761296	1.64393	-0.18215	0.881	0.92557	RP11-316N	chr1	-	1.51E+08	1.51E+08	582
ENSG00000(	0	0	0	3.745378	0.920432	0	-1.3029	0.33256	NA	DCAF13P1	chr7	+	1.06E+08	1.06E+08	1330
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-435B	chr1	+	1.43E+08	1.43E+08	2609
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RPL21P11	chr14	-	90833041	90833523	483
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	HLA-DMB	chr6	-	32902406	32908847	4569
ENSG00000(	0	0	0	12.73428	5.522592	2.465895	-3.5616	0.004	0.010112	AC012501.	chr2	-	1.54E+08	1.54E+08	1281

ENSG0000(	0	0	1.319414	1.498151	1.840864	0	-0.6531	0.62966	NA	RP11-469J4	chr3	+	1.7E+08	1.7E+08	664
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-379K	chr3	+	1.7E+08	1.7E+08	708
ENSG0000(	300.3797	309.5019	344.367	119.103	231.9489	216.9987	0.74538	0.001191	0.003299	RP11-274B	chr7	+	1.28E+08	1.28E+08	1894
ENSG0000(	0	8.430014	2.638828	1.498151	0	0	1.7948	0.165	0.26351	RP5-921G1	chr7	+	1.24E+08	1.24E+08	4310
ENSG0000(	4.143168	3.612863	0	1.498151	0.920432	3.28786	0.33858	0.77696	0.85319	RP11-648L	chr8	-	59025748	59026181	434
ENSG0000(	4.143168	0	2.638828	6.74168	9.20432	4.93179	-1.336	0.18168	0.2849	MBL1P	chr10	+	81664654	81710092	1424
ENSG0000(	0	6.021439	10.55531	0.749076	10.12475	6.575719	-0.07075	0.9443	0.96669	CTD-2339N	chr5	-	72174695	72175012	318
ENSG0000(	0	0	7.916483	7.490755	15.64734	6.575719	-1.6365	0.10178	0.178	RPS3AP34	chr8	-	12427859	12428639	781
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-398A	chr3	+	72136039	72136876	838
ENSG0000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	OR5BH1P	chrX	-	1.31E+08	1.31E+08	919
ENSG0000(	191.6215	185.4603	199.2315	129.5901	92.0432	102.7456	0.81975	0.000247	0.00076	DECR2	chr16	+	451826	462487	2062
ENSG0000(	14.50109	6.021439	1.319414	14.23244	29.45382	21.37109	-1.4277	0.038723	0.07781	CTC-359D2	chr19	-	12252621	12254137	1517
ENSG0000(	8.286335	1.204288	3.958241	2.996302	8.283888	5.753754	-0.27024	0.7743	0.85187	GNG10	chr9	+	1.14E+08	1.14E+08	1491
ENSG0000(	27.96638	22.88147	25.06886	26.96672	32.21512	32.8786	-0.26685	0.54408	0.66633	RP11-18H7	chr3	+	1.2E+08	1.2E+08	982
ENSG0000(	1.035792	0	3.958241	0	0	0	1.6134	0.2311	NA	AC009228.	chr2	+	24437250	24444385	432
ENSG0000(	19.68005	12.04288	42.22124	51.68621	60.74851	59.18147	-1.1948	0.006281	0.015256	USP6NL-IT1	chr10	-	11605186	11615495	2491
ENSG0000(	0	0	1.319414	0.749076	6.443024	0	-1.3497	0.31531	0.44191	RP11-342N	chr15	+	67524784	67525175	392
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-358L	chr10	-	46048560	46090046	559
ENSG0000(	0	2.408575	0	0	1.840864	1.64393	-0.27261	0.84063	NA	RP11-271C	chr3	-	1.13E+08	1.13E+08	303
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-196G	chr1	-	1.5E+08	1.5E+08	459
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-232N	chr3	+	1.47E+08	1.47E+08	1829
ENSG0000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	ANKRD20A	chr1	-	1.43E+08	1.43E+08	2393
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTB-46B19	chr5	-	1.38E+08	1.38E+08	518
ENSG0000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-1191	chr4	-	646639	649434	1388
ENSG0000(	42.46747	48.17151	58.05421	35.20655	43.2603	46.03004	0.24924	0.4879	0.61709	AC004893.	chr7	+	98610788	98645863	3398
ENSG0000(	8.286335	9.634302	3.958241	13.48336	20.2495	6.575719	-0.79972	0.2718	0.39245	CNTF	chr11	+	58390146	58393198	1886
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	CCT4P1	chr7	-	1.41E+08	1.41E+08	1558
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTD-2015H	chr5	-	79794353	79794790	438
ENSG0000(	24.85901	25.29004	21.11062	25.46857	23.0108	6.575719	0.35697	0.52161	0.64721	CCDC169	chr13	-	36801182	36871977	1632
ENSG0000(	552.0771	494.9623	613.5274	124.3465	191.4499	175.0785	1.7529	1.49E-20	1.55E-19	RGAG4	chrX	-	71346958	71351758	4359
ENSG0000(	2.071584	1.204288	1.319414	4.494453	2.761296	0	-0.46189	0.70848	0.80296	RP11-562A	chr15	+	50758935	50759293	359
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-20B7	chr3	+	73857752	73952017	782
ENSG0000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	RP11-30K9	chr15	+	59161858	59162333	476
ENSG0000(	3.107376	0	5.277655	2.996302	0.920432	0	0.73775	0.55751	0.67797	RP3-511B2	chr20	+	39825331	39825797	467
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-716C	chr6	+	11487459	11515943	686
ENSG0000(	18.64425	14.45145	14.51355	85.39461	67.19154	85.48435	-2.2662	6.54E-09	3.34E-08	RP11-280F	chr3	-	1.07E+08	1.07E+08	2718
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC105749.	chr3	-	36810216	36825658	571
ENSG0000(	10.35792	10.83859	17.15238	143.8225	185.0068	154.5294	-3.6079	5.77E-24	6.87E-23	ZNF702P	chr19	-	53471504	53541151	2990
ENSG0000(	1.035792	3.612863	2.638828	0	0	0	2.2878	0.090046	0.16086	RP11-451G	chr3	+	1.55E+08	1.55E+08	444
ENSG0000(	0	0	3.958241	11.23613	5.522592	9.041614	-2.2489	0.032633	0.066877	RP11-651P	chr3	+	1.5E+08	1.5E+08	680
ENSG0000(	14.50109	0	5.277655	0.749076	2.761296	2.465895	1.4087	0.1903	0.29565	GLYCTK-AS1	chr3	-	52322596	52333083	697
ENSG0000(	20.71584	15.65574	7.916483	4.494453	11.04518	18.08323	0.38486	0.57109	0.69012	RP11-506N	chr7	-	99712837	99724762	572
ENSG0000(	1242.95	1241.621	1030.462	849.4517	723.4595	841.6921	0.54052	6.57E-05	0.000219	AP5Z1	chr7	+	4815253	4833943	5660
ENSG0000(	0	2.408575	0	6.74168	3.681728	0.821965	-1.53	0.22003	0.33169	SOX2-OT	chr3	+	1.81E+08	1.82E+08	3576

ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	MRPL42P6	chr3	-	1.51E+08	1.51E+08	371
ENSG00000(	0	0	2.638828	1.498151	0.920432	0	0.039324	0.97687	NA	RPS26P21	chr3	+	1.19E+08	1.19E+08	348
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	RP11-52L1	chr3	-	1.07E+08	1.07E+08	781
ENSG00000(	1.035792	2.408575	3.958241	2.247227	0.920432	3.28786	0.12932	0.91103	0.94536	ZNF709	chr19	-	12571998	12624668	4910
ENSG00000(	22.78742	19.2686	21.11062	11.23613	18.40864	23.01502	0.25709	0.62946	0.7397	RP11-285F	chr1	-	2.26E+08	2.26E+08	348
ENSG00000(	1.035792	2.408575	0	0	0	1.64393	0.52159	0.70059	NA	STRC	chr15	-	43891596	44010458	5680
ENSG00000(	0	0	2.638828	5.243529	0	0	-0.54684	0.68643	0.78551	CTB-104F4.	chr7	-	91321323	91510004	380
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-190P	chr3	+	1.15E+08	1.15E+08	533
ENSG00000(	8.286335	1.204288	3.958241	0	0	0	3.2237	0.013079	0.0296	RP11-489G	chr4	-	1.74E+08	1.74E+08	893
ENSG00000(	0	0	0	2.247227	0	0.821965	-0.85594	0.51054	NA	RP11-436N	chr14	-	1E+08	1E+08	814
ENSG00000(	2.071584	3.612863	3.958241	5.243529	0.920432	1.64393	0.21968	0.84138	0.89856	RP11-309L	chr7	-	1.28E+08	1.29E+08	559
ENSG00000(	0	0	1.319414	0	3.681728	2.465895	-1.2105	0.36916	0.49955	RP11-454C	chr3	-	1.51E+08	1.52E+08	628
ENSG00000(	1.035792	0	0	0	0.920432	0.821965	-0.16752	0.89839	NA	RP11-666A	chr17	-	74426499	74427206	708
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-402L	chr4	-	96566103	96566444	342
ENSG00000(	9.322127	12.04288	21.11062	19.47596	32.21512	22.19305	-0.774	0.16114	0.25864	ERVW-1	chr7	-	92097694	92107300	3352
ENSG00000(	3.107376	2.408575	5.277655	0	0.920432	3.28786	1.0148	0.38867	0.5193	RP11-507E	chr14	-	76062148	76062549	402
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-803B	chr3	-	75444555	75444687	133
ENSG00000(	0	2.408575	0	2.247227	0.920432	0	-0.20772	0.87831	NA	RP11-662B	chr8	+	28667620	28667935	316
ENSG00000(	8.286335	18.06432	25.06886	5.992604	0	4.109825	2.0811	0.009775	0.02278	FTH1P23	chr3	+	72978195	72978744	550
ENSG00000(	0	1.204288	0	0	1.840864	0	-0.18234	0.88799	NA	AC068522.	chr8	-	59500979	59501323	345
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RPS15AP18	chr5	-	1.79E+08	1.79E+08	392
ENSG00000(	1.035792	0	0	0.749076	2.761296	1.64393	-1.1603	0.38948	0.52002	RP11-1110	chr12	-	29811309	29811731	423
ENSG00000(	4.143168	1.204288	9.235896	4.494453	2.761296	0	0.78695	0.47248	0.60157	FTH1P4	chr3	-	1.28E+08	1.28E+08	553
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-504P	chr1	+	2.24E+08	2.24E+08	343
ENSG00000(	0	2.408575	2.638828	4.494453	3.681728	1.64393	-0.74649	0.52373	0.64899	AC005062.	chr7	-	19958604	20180076	804
ENSG00000(	1.035792	0	3.958241	0	0	1.64393	0.84154	0.53385	0.65836	RP5-1070G	chr7	+	1.51E+08	1.51E+08	216
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-766N	chr12	-	65261736	65262479	744
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	UBA52P3	chr14	+	58607997	58608378	382
ENSG00000(	4.143168	0	1.319414	0	1.840864	0	0.89572	0.50629	0.63393	RPS11P6	chr12	+	64616117	64790845	1366
ENSG00000(	0	1.204288	2.638828	0	1.840864	0	0.54056	0.69028	NA	RPL31P58	chr17	+	27129462	27129840	379
ENSG00000(	5.17896	1.204288	2.638828	3.745378	0.920432	0.821965	0.54143	0.64048	0.74827	GK-AS1	chrX	-	30718115	30742291	651
ENSG00000(	8.286335	3.612863	3.958241	6.74168	0.920432	8.219649	-0.00034	0.99971	0.99974	EIF4EBP3	chr5	+	1.4E+08	1.4E+08	691
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	IGKV3-7	chr2	-	89277987	89278600	445
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	ABCC13	chr21	+	15608527	15735075	4080
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	ARHGEF26-	chr3	-	1.54E+08	1.54E+08	2598
ENSG00000(	1.035792	1.204288	0	1.498151	0	1.64393	-0.25796	0.84879	NA	RP11-613N	chr12	+	77054185	77054664	480
ENSG00000(	4.143168	2.408575	1.319414	4.494453	1.840864	2.465895	-0.12029	0.91285	0.94661	RP11-204J	chr3	-	62246540	62248415	352
ENSG00000(	4.143168	2.408575	1.319414	0	0	0	2.42	0.071961	0.13287	LINC00870	chr3	+	72200408	72223483	2693
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-779P	chr3	-	99226031	99245957	465
ENSG00000(	0	1.204288	0	0	2.761296	0.821965	-0.69224	0.6093	NA	RP11-1084	chr15	-	34378112	34378515	404
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RPL3P10	chr8	-	39015057	39016220	1164
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RPS3P7	chr16	+	78859178	78859903	726
ENSG00000(	12.4295	18.06432	21.11062	17.22874	24.85166	13.15144	-0.09724	0.86127	0.91189	AC000120.	chr7	-	91829328	91836171	1589
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	RP11-564C	chr3	-	1.59E+08	1.59E+08	878

ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP11-377D	chr12	-	13174194	13174540	347
ENSG00000(	0	0	0	4.494453	1.840864	0	-1.6936	0.21189	0.32187	PSG11	chr19	-	43511808	43530664	1942
ENSG00000(	0	0	0	122.0993	116.8949	69.86702	-7.3722	2.45E-13	1.75E-12	PSG4	chr19	-	43696854	43711451	2294
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-757G	chr12	+	12491710	12492188	479
ENSG00000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	RP11-115N	chr7	+	90940683	91144724	681
ENSG00000(	558.2918	608.1653	457.8366	713.1199	683.881	859.7753	-0.47195	0.00255	0.006667	MRPL33	chr2	+	27994584	28210954	729
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-538P	chr3	-	1.58E+08	1.58E+08	1640
ENSG00000(	0	2.408575	2.638828	0.749076	2.761296	2.465895	-0.18372	0.88241	0.92658	RP11-342N	chr1	-	43300352	43312093	514
ENSG00000(	3.107376	8.430014	1.319414	9.737982	8.283888	6.575719	-0.82249	0.34804	0.47772	RP11-46A1	chr1	-	1.81E+08	1.81E+08	2424
ENSG00000(	544.8265	516.6394	667.6234	237.4569	683.881	485.7813	0.2901	0.4978	0.62617	MICAL3	chr22	-	18270415	18507325	9445
ENSG00000(	1.035792	3.612863	7.916483	6.74168	4.60216	0	0.099208	0.9269	0.95607	RP11-58H1	chr4	+	1.44E+08	1.44E+08	1261
ENSG00000(	10.35792	6.021439	3.958241	5.243529	13.80648	8.219649	-0.36103	0.64747	0.75399	RP11-550I2	chr3	+	1.57E+08	1.57E+08	567
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC110769.	chr2	+	1.15E+08	1.15E+08	815
ENSG00000(	3.107376	1.204288	0	2.996302	0.920432	0.821965	-0.07543	0.9531	0.97205	RP11-734J2	chr8	+	34731677	34732151	475
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CCDC39-AS	chr3	+	1.8E+08	1.8E+08	283
ENSG00000(	84.93494	74.66584	68.60952	57.67882	51.54419	95.34793	0.15685	0.62567	0.73701	RP11-408P	chr4	+	66439177	66440046	870
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	AC006159.	chr7	-	1.16E+08	1.16E+08	692
ENSG00000(	13.46529	3.612863	10.55531	5.992604	2.761296	4.93179	0.9024	0.28056	0.40284	RP5-1157N	chr3	+	52273274	52275113	1101
ENSG00000(	0	1.204288	0	14.98151	16.56778	5.753754	-3.7532	0.000582	0.001694	RP11-7F17	chr14	+	77435026	77435488	463
ENSG00000(	1.035792	7.225726	6.597069	10.48706	1.840864	6.575719	-0.32495	0.72892	0.81842	RP11-286H	chr7	-	1.29E+08	1.29E+08	535
ENSG00000(	33.14534	24.08575	39.58241	18.72689	51.54419	27.12484	-0.00226	0.99615	0.99759	PCDHAC2	chr5	+	1.4E+08	1.4E+08	5970
ENSG00000(	0	1.204288	2.638828	0	0	0	1.2853	0.33195	NA	CTD-2583A	chr19	-	58464526	58465127	602
ENSG00000(	1.035792	8.430014	13.19414	10.48706	5.522592	16.4393	-0.4921	0.54261	0.66519	AC073130.	chr7	-	1.16E+08	1.16E+08	842
ENSG00000(	185.4068	158.966	142.4967	49.43899	60.74851	35.34449	1.7299	3.56E-10	2.02E-09	STON1	chr2	+	48756522	48826025	5802
ENSG00000(	0	1.204288	1.319414	0.749076	4.60216	0	-0.64569	0.62788	0.73868	RPS6P16	chr11	-	1.12E+08	1.12E+08	655
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	PGBD3	chr10	-	50723151	50747086	3411
ENSG00000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	RP11-1149	chr8	+	23064431	23064882	452
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-166N	chr3	+	1.51E+08	1.51E+08	565
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-384F	chr3	-	1.18E+08	1.18E+08	787
ENSG00000(	396.7083	395.0064	406.3794	128.0919	105.8497	112.6092	1.7789	6.94E-23	7.88E-22	PRAF2	chrX	-	48928813	48931730	1336
ENSG00000(	0	0	0	2.996302	2.761296	0.821965	-1.8697	0.16674	0.26571	RP11-477G	chr4	+	1.13E+08	1.13E+08	313
ENSG00000(	10.35792	0	3.958241	0	0	0	3.1822	0.015622	0.03472	VSIG8	chr1	-	1.6E+08	1.6E+08	1818
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RPL31P61	chr19	+	37392644	37393019	376
ENSG00000(	275.5206	307.0934	270.4798	191.0143	258.6414	194.8057	0.40495	0.03446	0.070187	RP11-274B	chr7	+	1.28E+08	1.28E+08	1150
ENSG00000(	7.250543	9.634302	0	2.996302	11.04518	0.821965	0.17348	0.86556	0.91516	CTC-428G2	chr5	-	1.15E+08	1.15E+08	796
ENSG00000(	1.035792	4.817151	0	0	0	0.821965	1.43	0.29086	0.41492	RP11-538P	chr3	+	1.58E+08	1.58E+08	374
ENSG00000(	888.7095	955.0002	897.2014	1217.997	1033.645	1087.46	-0.28484	0.02386	0.050822	C7orf73	chr7	+	1.35E+08	1.35E+08	2004
ENSG00000(	0	0	1.319414	7.490755	4.60216	3.28786	-2.4895	0.041174	0.082089	RP11-167H	chr3	-	1.5E+08	1.5E+08	1967
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC092573.	chr2	-	1.74E+08	1.74E+08	243
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	PTPRVP	chr1	+	2.02E+08	2.02E+08	5067
ENSG00000(	371.8493	378.1463	390.5465	222.4754	256.8005	266.3166	0.61159	0.000221	0.000687	KCTD7	chr7	+	66093868	66276446	4873
ENSG00000(	0	0	1.319414	0	0	3.28786	-0.58083	0.66501	NA	RP11-667N	chr11	-	1.14E+08	1.14E+08	171
ENSG00000(	197.8363	181.8474	134.5802	145.3207	164.7573	187.408	0.051952	0.81657	0.88106	EFNA4	chr1	+	1.55E+08	1.55E+08	1263
ENSG00000(	1.035792	6.021439	2.638828	2.247227	5.522592	2.465895	-0.06413	0.95184	0.97123	MCCC1-AS1	chr3	+	1.83E+08	1.83E+08	765

ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CTD-2110K	chr5	+	82497048	82497960	584
ENSG0000(	2.071584	2.408575	3.958241	1.498151	0.920432	0	1.2367	0.3207	0.44793	AC012442.	chr2	+	1.13E+08	1.13E+08	425
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-454H	chr3	-	1.01E+08	1.01E+08	402
ENSG0000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP11-330L	chr15	+	64885178	64885525	348
ENSG0000(	6.214751	2.408575	14.51355	5.243529	3.681728	7.397684	0.43186	0.6161	0.72901	RPL35AP32	chr15	-	66738793	66739115	323
ENSG0000(	1.035792	0	2.638828	5.243529	0	0	-0.32143	0.80979	0.87669	TICAM2	chr5	-	1.15E+08	1.15E+08	3509
ENSG0000(	5.17896	3.612863	9.235896	0.749076	1.840864	1.64393	1.7139	0.099865	0.17529	RP11-274H	chr3	+	1.46E+08	1.46E+08	555
ENSG0000(	6.214751	4.817151	0	0	0	0	2.803	0.03585	0.072671	AC009518.	chr7	+	1.32E+08	1.32E+08	559
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-555K	chr4	-	1.53E+08	1.53E+08	777
ENSG0000(	11.39371	14.45145	17.15238	14.98151	18.40864	18.90519	-0.27444	0.62908	0.73943	RP11-413E	chr3	-	75673837	75674304	468
ENSG0000(	2.071584	0	0	0	1.840864	2.465895	-0.5292	0.69572	0.79272	RP5-837J1.	chr17	+	33403756	33404026	271
ENSG0000(	21.75163	28.90291	13.19414	6.74168	5.522592	4.93179	1.7784	0.005825	0.014238	RPL5P30	chr11	+	1.18E+08	1.18E+08	891
ENSG0000(	7.250543	9.634302	1.319414	1.498151	0.920432	2.465895	1.5508	0.13836	0.22861	RP11-148K	chr7	-	1.51E+08	1.51E+08	511
ENSG0000(	36.25272	45.76293	54.09597	42.69731	50.62376	50.96182	-0.08709	0.80713	0.87475	PALM2	chr9	+	1.12E+08	1.13E+08	9292
ENSG0000(	493.0369	388.9849	343.0476	358.0581	251.2779	360.8426	0.33547	0.08435	0.15226	C4orf48	chr4	+	2043689	2045697	477
ENSG0000(	534.4686	532.2952	573.945	347.5711	344.2416	383.0357	0.60773	3.25E-05	0.000113	NBPF15	chr1	+	1.49E+08	1.49E+08	4707
ENSG0000(	0	2.408575	3.958241	0	0.920432	0.821965	1.1203	0.3977	0.5287	RP4-545L1	chr20	+	1146924	1160596	326
ENSG0000(	129.474	146.9231	93.67838	58.42789	56.14635	36.16646	1.2816	2.13E-05	7.59E-05	NAT6	chr3	-	50333833	50336852	1820
ENSG0000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AOX2P	chr2	+	2.02E+08	2.02E+08	3179
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-217E	chr3	+	1.54E+08	1.54E+08	703
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-521D	chr2	-	9897625	9910470	1947
ENSG0000(	3.107376	3.612863	0	0	0	0.821965	1.6197	0.22885	0.34222	UBA52P5	chr8	+	1.24E+08	1.24E+08	211
ENSG0000(	1.035792	0	0	0	0.920432	2.465895	-0.67443	0.61786	NA	RP11-775J2	chr3	-	1.25E+08	1.25E+08	713
ENSG0000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RPL32P33	chr17	+	70623370	70623763	394
ENSG0000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-627K	chr12	-	31404926	31405531	606
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-639F	chr3	-	1.55E+08	1.55E+08	840
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	IGLVIVOR2	chr22	+	32772669	32773122	330
ENSG0000(	2.071584	3.612863	5.277655	0	4.60216	4.109825	0.26487	0.81054	0.87711	RP11-293G	chr1	+	2.36E+08	2.36E+08	337
ENSG0000(	2.071584	1.204288	0	0	0.920432	0	0.824	0.54141	NA	HNRNPKP4	chr3	+	96068398	96069783	1386
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-483E	chr3	-	1.5E+08	1.5E+08	335
ENSG0000(	83.89914	113.203	84.44248	86.14369	71.7937	115.0751	0.041842	0.88333	0.92688	AC004967.	chr7	-	97598317	97601566	447
ENSG0000(	0	1.204288	2.638828	0	0	0	1.2853	0.33195	NA	AC009950.	chr2	+	2.31E+08	2.31E+08	580
ENSG0000(	3.107376	2.408575	1.319414	35.95563	30.37426	27.94681	-3.4636	1.14E-06	4.71E-06	UPK3B	chr7	+	76139745	76648340	1608
ENSG0000(	0	0	0	4.494453	0	0	-1.1446	0.38559	NA	RP11-2I17.	chr15	+	72426982	72427777	796
ENSG0000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-889D	chr3	+	55212200	55223242	474
ENSG0000(	6.214751	4.817151	17.15238	5.243529	7.363456	3.28786	0.73441	0.37206	0.50265	C6orf183	chr6	+	1.09E+08	1.1E+08	2469
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RPL17P22	chr5	+	55432806	55433358	553
ENSG0000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-152P	chr8	-	1.07E+08	1.07E+08	486
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RPL35AP26	chr11	-	1.26E+08	1.26E+08	321
ENSG0000(	5.17896	3.612863	1.319414	0	1.840864	4.109825	0.59695	0.60764	0.72182	RPS2P44	chr16	-	48611435	48612280	846
ENSG0000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-649A	chr3	-	1.47E+08	1.47E+08	570
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AC003989.	chr7	+	1.11E+08	1.11E+08	169
ENSG0000(	0	0	1.319414	0	1.840864	0.821965	-0.46629	0.72905	NA	AP000322.	chr21	-	35791013	35796264	1050
ENSG0000(	0	1.204288	2.638828	2.247227	0.920432	3.28786	-0.54313	0.66612	0.76965	RP11-18I14	chr10	+	1.04E+08	1.04E+08	723

ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP11-6F2.4	chr3	-	1.57E+08	1.57E+08	2018
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-281P	chr3	+	1.04E+08	1.04E+08	567
ENSG00000(	0	0	1.319414	1.498151	0	0.821965	-0.38347	0.77483	NA	AC019221.	chr2	+	2.34E+08	2.34E+08	623
ENSG00000(	211.3015	268.5562	230.8974	124.3465	90.20234	113.4312	1.1043	4.03E-07	1.74E-06	IL10RB	chr21	+	34638663	34669539	1991
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-215P	chr5	+	1.34E+08	1.34E+08	498
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	CFB	chr6	+	31895475	31919861	3874
ENSG00000(	0	1.204288	0	0	3.681728	0.821965	-0.89986	0.50718	NA	MTND5P16	chr3	+	1.07E+08	1.07E+08	1703
ENSG00000(	5.17896	0	2.638828	0	0	2.465895	1.037	0.42986	0.55987	RP11-4K3_	chr1	+	27637731	27638329	282
ENSG00000(	38.3243	60.21439	51.45714	29.21395	34.05598	30.4127	0.66338	0.081988	0.14848	ZNF487	chr10	+	43932282	43991517	2745
ENSG00000(	1.035792	2.408575	2.638828	0	0	0	2.0265	0.13497	0.22409	RP11-21K2	chr12	-	1866397	1867177	781
ENSG00000(	84.93494	71.05298	64.65128	198.505	126.0992	145.4878	-1.0785	5.68E-05	0.000191	WDR92	chr2	-	68350068	68384692	2626
ENSG00000(	0	1.204288	0	0.749076	0	0	0.1572	0.90001	NA	RP11-379F	chr3	+	1.58E+08	1.58E+08	323
ENSG00000(	22.78742	9.634302	11.87472	23.22134	48.7829	17.26126	-0.94684	0.094025	0.16664	NME1-NME	chr17	+	49242796	49249108	866
ENSG00000(	227.8742	236.0404	139.8579	266.6709	221.8241	180.0103	-0.14337	0.53995	0.66334	RP11-274B	chr7	+	1.28E+08	1.28E+08	754
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RPL37P23	chr19	+	52646296	52646589	294
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RP11-432B	chr3	+	1.6E+08	1.6E+08	331
ENSG00000(	2.071584	1.204288	0	1.498151	8.283888	3.28786	-1.4444	0.21783	0.32919	MUSTN1	chr3	-	52847298	52869745	5640
ENSG00000(	5.17896	3.612863	2.638828	3.745378	2.761296	0	0.64017	0.56701	0.68622	RP11-463C	chr16	+	86559063	86559858	796
ENSG00000(	1.035792	0	3.958241	0	0	0.821965	1.2459	0.35843	NA	RP11-574K	chr10	-	75570442	75571556	545
ENSG00000(	207.1584	202.3203	215.0644	1019.492	1165.267	948.5475	-2.3198	1.16E-53	3.46E-52	RP11-446H	chr3	+	1.07E+08	1.07E+08	2737
ENSG00000(	5.17896	9.634302	0	0.749076	5.522592	11.50751	-0.2065	0.83902	0.89715	PLA2G4B	chr15	+	42129973	42140345	3035
ENSG00000(	1.035792	2.408575	0	3.745378	0	0	-0.07475	0.95581	0.97381	LEFTY1	chr1	-	2.26E+08	2.26E+08	1626
ENSG00000(	0	6.021439	5.277655	10.48706	2.761296	4.93179	-0.60252	0.54731	0.66903	WDR65	chr1	+	43637820	43720029	4244
ENSG00000(	1.035792	0	0	2.996302	0	0	-0.53136	0.68956	NA	CACNA2D3	chr3	-	54908632	54935282	2078
ENSG00000(	163.6551	162.5788	166.2461	445.7	255.8801	268.7825	-0.97365	1.93E-05	6.90E-05	61E3.4	chr16	+	22490442	22547842	5708
ENSG00000(	1.035792	0	1.319414	2.247227	0	0	0.018495	0.9891	NA	RP11-472I2	chr11	+	43740226	43740696	471
ENSG00000(	10.35792	6.021439	7.916483	11.98521	0.920432	8.219649	0.17104	0.83945	0.89727	TTC4	chr1	+	55181495	55208330	2395
ENSG00000(	0	2.408575	1.319414	2.247227	0	0	0.35636	0.79265	0.86445	RP1-136J1!	chrX	-	1.09E+08	1.09E+08	464
ENSG00000(	88.04231	66.23582	77.84541	0	2.761296	2.465895	5.2084	4.87E-17	4.27E-16	RPLP0P2	chr11	+	61382508	61406921	3525
ENSG00000(	0	2.408575	0	0.749076	0	0	0.55104	0.6711	NA	EEF1A1P10	chr7	-	1.44E+08	1.44E+08	1390
ENSG00000(	55.93276	42.15007	35.62417	7.490755	9.20432	8.219649	2.3494	1.93E-06	7.74E-06	HLA-L	chr6	+	30227361	30260791	4587
ENSG00000(	0	0	3.958241	12.73428	3.681728	8.219649	-2.1682	0.04328	0.085727	RP11-125K	chr9	+	4860454	4885917	1878
ENSG00000(	5.17896	2.408575	1.319414	0	3.681728	0.821965	0.74568	0.53876	0.66251	ST13P15	chr3	-	1.43E+08	1.43E+08	1107
ENSG00000(	11.39371	16.86003	19.79121	1.498151	0	0	4.0471	3.48E-05	0.000121	HOTTIP	chr7	+	27238194	27246878	4511
ENSG00000(	0	2.408575	0	0	1.840864	0	0.16879	0.89944	NA	CTD-3131K	chr19	-	17700404	17700880	477
ENSG00000(	1.035792	0	0	2.247227	1.840864	0.821965	-1.1159	0.40841	0.53916	AC007390.	chr2	+	37440610	37443336	367
ENSG00000(	3.107376	4.817151	2.638828	0	1.840864	1.64393	1.2046	0.30881	0.43487	JMJD7	chr15	+	42120283	42129779	1416
ENSG00000(	0	0	0	0	1.840864	2.465895	-1.2108	0.36631	NA	CTD-2026G	chr3	+	75570954	75571163	210
ENSG00000(	1.035792	9.634302	3.958241	0	1.840864	0	2.1435	0.078544	0.14308	RP11-572N	chr3	-	1.13E+08	1.13E+08	2502
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-390K	chr11	-	47212732	47213093	362
ENSG00000(	2.071584	8.430014	5.277655	0	0	7.397684	0.83506	0.46372	0.59299	CTC-484P3	chr5	-	94161666	94162399	734
ENSG00000(	11.39371	16.86003	19.79121	16.47966	11.04518	19.72716	0.0113	0.98445	0.99094	APOBEC3D	chr22	+	39410368	39429256	2503
ENSG00000(	7.250543	4.817151	2.638828	6.74168	4.60216	0.821965	0.23868	0.80799	0.87541	RP11-434C	chr14	-	35209542	35210039	498
ENSG00000(	5.17896	0	1.319414	0	0	0	1.9904	0.14228	0.23373	CTB-33G10	chr19	-	50222755	50223338	584

ENSG00000(	7.250543	7.225726	1.319414	26.21764	37.73771	64.11326	-2.8261	3.35E-06	1.31E-05	WDR86-AS:	chr7	+	1.51E+08	1.51E+08	751
ENSG00000(	22.78742	16.86003	22.43003	10.48706	11.96562	4.93179	1.1221	0.063994	0.12011	AC108058.	chr2	+	1.06E+08	1.06E+08	781
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	WDR52-AS:	chr3	+	1.13E+08	1.13E+08	686
ENSG00000(	1.035792	4.817151	5.277655	4.494453	7.363456	10.68554	-0.90406	0.32177	0.44901	OR2A7	chr7	-	1.44E+08	1.44E+08	1116
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	BMS1P7	chr10	-	49256241	49268060	1318
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	RP1-63G5.!	chr22	-	37735624	37823505	1970
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-600F	chr14	-	1.04E+08	1.04E+08	884
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	TUBA4B	chr2	+	2.2E+08	2.2E+08	1380
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	PRKRIRP2	chr3	+	86061711	86064270	2267
ENSG00000(	0	0	3.958241	2.247227	1.840864	2.465895	-0.51792	0.68516	0.78455	TIPARP-AS1	chr3	-	1.56E+08	1.56E+08	735
ENSG00000(	569.6855	552.7681	573.945	567.0502	503.4763	542.4968	0.071819	0.60224	0.7174	MRPS6	chr21	+	35445524	35515334	3934
ENSG00000(	456.7842	488.9408	451.2395	534.0909	366.3319	419.2021	0.080157	0.63589	0.74475	ZNF512	chr2	+	27805897	27858041	3422
ENSG00000(	2.071584	0	1.319414	1.498151	0	0	0.5543	0.68269	NA	RP11-167H	chr3	+	1.5E+08	1.5E+08	557
ENSG00000(	5.17896	3.612863	2.638828	0	0	1.64393	1.9245	0.12095	0.20519	RP11-439C	chr3	-	1.55E+08	1.55E+08	521
ENSG00000(	0	1.204288	0	2.247227	3.681728	5.753754	-2.1327	0.091402	0.16289	GSTA1	chr6	-	52656462	52668708	1019
ENSG00000(	6.214751	9.634302	5.277655	5.243529	7.363456	5.753754	0.1866	0.81894	0.88301	RP11-552M	chr1	-	1.12E+08	1.12E+08	723
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP5-839B4	chr20	+	9966736	10023864	1036
ENSG00000(	8.286335	0	0	0	0	0	2.1807	0.10792	0.18669	RP11-439C	chr3	-	1.55E+08	1.55E+08	351
ENSG00000(	7.250543	1.204288	2.638828	4.494453	1.840864	3.28786	0.17736	0.8658	0.91536	PPIEL	chr1	-	39997510	40024379	813
ENSG00000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	RP11-473P	chr3	-	1.79E+08	1.79E+08	707
ENSG00000(	20.71584	7.225726	2.638828	2.247227	0	2.465895	2.2521	0.022757	0.048645	RGAG1	chrX	+	1.1E+08	1.1E+08	5426
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-347C	chr8	+	95903467	95904335	558
ENSG00000(	1.035792	0	3.958241	4.494453	2.761296	6.575719	-1.1726	0.29522	0.41958	ENO1P3	chr3	-	1.25E+08	1.25E+08	1224
ENSG00000(	4.143168	3.612863	10.55531	5.992604	2.761296	15.61733	-0.38225	0.6574	0.76224	ACY1	chr3	+	52009066	52023213	1836
ENSG00000(	298.3081	405.845	333.8117	295.1358	313.8673	302.4831	0.18586	0.28368	0.40661	NFS1	chr20	-	34220262	34287281	3012
ENSG00000(	0	0	1.319414	0.749076	0	7.397684	-1.4992	0.26207	0.38146	RP11-227J!	chr3	+	1.6E+08	1.6E+08	806
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RPL35P6	chr8	-	18632057	18632428	372
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	MT1HL1	chr1	-	2.37E+08	2.37E+08	256
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-622L	chr3	+	1.45E+08	1.45E+08	878
ENSG00000(	215.4447	214.3632	246.7304	253.1875	214.4607	221.9305	-0.0301	0.87165	0.91935	FAM86DP	chr3	-	75470703	75484261	2425
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-306G	chr7	+	1.3E+08	1.3E+08	832
ENSG00000(	7093.103	7290.758	6329.228	6090.733	4592.956	4869.32	0.41233	0.001189	0.003293	DDOST	chr1	-	20978270	20988000	2079
ENSG00000(	10.35792	8.430014	19.79121	11.23613	10.12475	12.32947	0.17301	0.79076	0.86306	RP1-90J20.	chr6	+	2988201	2991401	2804
ENSG00000(	37.28851	50.58008	36.94359	133.3354	102.168	125.7606	-1.517	3.70E-07	1.61E-06	TMEM199	chr17	+	26684604	26708716	3148
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP11-266K	chr12	-	8352195	8371507	509
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RPL13AP2	chr14	-	47669778	47670307	530
ENSG00000(	3.107376	1.204288	9.235896	2.996302	2.761296	0.821965	0.82395	0.44462	0.57419	LINC00539	chr13	+	21872278	21878694	347
ENSG00000(	3.107376	8.430014	5.277655	3.745378	0.920432	4.109825	0.77518	0.43044	0.56031	AC007566.	chr7	+	92086878	92120924	643
ENSG00000(	2.071584	3.612863	1.319414	0	5.522592	0	0.25471	0.84031	0.89775	RPS2P41	chr12	-	1.12E+08	1.12E+08	603
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-389C	chr5	+	71677621	71678220	600
ENSG00000(	0	0	2.638828	3.745378	0	0	-0.27361	0.84016	0.89774	AC024704.	chr2	-	1.15E+08	1.15E+08	416
ENSG00000(	0	3.612863	2.638828	0	0	0.821965	1.5079	0.26427	0.38417	RP11-221E	chr3	-	1.29E+08	1.29E+08	841
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	GSTA2	chr6	-	52614897	52628367	1303
ENSG00000(	6.214751	0	0	0	3.681728	4.109825	-0.18889	0.8819	0.9263	CTD-2284C	chr5	+	37085158	37085954	797

ENSG00000(	0	0	3.958241	2.996302	0	0	0.17782	0.89571	0.93537	RPS20P35	chr17	+	37011567	37011923	357
ENSG00000(	0	0	0	2.247227	5.522592	0	-1.9602	0.14787	0.24097	RPS4XP17	chr17	-	560034	560787	754
ENSG00000(	3.107376	0	2.638828	1.498151	0	0.821965	0.79132	0.5486	0.67019	RP11-468H	chr8	-	17007810	17008397	588
ENSG00000(	4.143168	1.204288	0	6.74168	5.522592	6.575719	-1.4379	0.16869	0.26847	PDCL3P4	chr3	+	1.01E+08	1.01E+08	720
ENSG00000(	19.68005	28.90291	9.235896	8.239831	25.7721	30.4127	-0.13809	0.81654	0.88106	ATP1B3-AS	chr3	-	1.42E+08	1.42E+08	376
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-85M	chr3	+	1.65E+08	1.65E+08	1075
ENSG00000(	2.071584	0	2.638828	0	0	0.821965	1.2046	0.37464	NA	RPSAP51	chr12	+	8895024	8895668	645
ENSG00000(	1.035792	2.408575	1.319414	0	0	2.465895	0.55563	0.6771	0.77848	RPS12P20	chr11	+	72419231	72419610	380
ENSG00000(	0	8.430014	0	0	0	1.64393	1.3144	0.32739	0.45507	RP11-99J1(	chr1	-	2.31E+08	2.31E+08	850
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-757F	chr3	-	1.12E+08	1.12E+08	519
ENSG00000(	0	1.204288	0	0	0	1.64393	-0.12916	0.91993	NA	RP11-373L	chr3	+	88206039	88217879	433
ENSG00000(	0	0	1.319414	0	1.840864	1.64393	-0.68367	0.61391	NA	RP11-148K	chr7	-	1.51E+08	1.51E+08	1230
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	CYP4F34P	chr13	-	19315870	19316858	481
ENSG00000(	0	0	0	4.494453	7.363456	0.821965	-2.7896	0.032305	0.066303	RP11-1070	chr8	-	54799568	54799804	237
ENSG00000(	5.17896	4.817151	7.916483	26.21764	41.41944	25.48091	-2.2615	0.000172	0.000544	FLNB-AS1	chr3	-	58148274	58156363	3709
ENSG00000(	134.6529	144.5145	76.526	83.89646	107.6905	150.4196	0.060674	0.83771	0.89628	P2RY11	chr19	+	10222214	10226048	1943
ENSG00000(	4.143168	1.204288	2.638828	0	0	0	2.437	0.069832	0.1295	RP4-733B9	chr7	+	7217583	7217955	373
ENSG00000(	3.107376	2.408575	1.319414	2.247227	2.761296	5.753754	-0.51052	0.63855	0.74678	PBX2P1	chr3	+	1.43E+08	1.43E+08	2181
ENSG00000(	5.17896	0	0	0	0	4.93179	0.057437	0.96585	0.98015	RP11-315C	chr6	+	1.11E+08	1.11E+08	315
ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	RP11-314A	chr17	+	4607525	4608824	472
ENSG00000(	424.6747	352.8563	278.3963	310.8664	343.3211	392.0773	0.016628	0.92924	0.95736	TMEM141	chr9	+	1.4E+08	1.4E+08	839
ENSG00000(	11.39371	4.817151	10.55531	11.23613	14.72691	10.68554	-0.41601	0.5462	0.66826	RP4-545C2	chr7	+	1.44E+08	1.44E+08	856
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	FOXP1-AS1	chr3	+	71338920	71355004	700
ENSG00000(	0	2.408575	0	0.749076	0.920432	0	0.23282	0.86283	NA	KB-1554H1	chr8	+	95365151	95365881	731
ENSG00000(	4.143168	1.204288	1.319414	0	0	0.821965	1.6901	0.20594	0.31477	GS1-259H1	chr7	+	99195689	99208436	1314
ENSG00000(	2.071584	4.817151	1.319414	0	10.12475	3.28786	-0.53994	0.62931	0.73963	RPL26P35	chr18	-	74546385	74546844	460
ENSG00000(	197.8363	157.7617	141.1773	11.98521	20.2495	15.61733	3.3428	4.62E-25	5.72E-24	IFITM10	chr11	-	1753640	1771821	3807
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-120B	chr5	+	1.08E+08	1.08E+08	359
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	RP11-441N	chr3	-	1.59E+08	1.59E+08	685
ENSG00000(	5.17896	16.86003	0	0	0	9.863579	0.50147	0.70943	0.80364	PKD1P1	chr16	+	16404198	16428047	6805
ENSG00000(	1.035792	2.408575	2.638828	0	9.20432	4.93179	-0.93999	0.40738	0.53818	SIAH2-AS1	chr3	+	1.5E+08	1.5E+08	441
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-244C	chr11	+	44650907	44651224	318
ENSG00000(	2.071584	2.408575	5.277655	2.996302	4.60216	0.821965	0.16431	0.87972	0.92479	RP11-529G	chr3	-	1.53E+08	1.53E+08	323
ENSG00000(	3.107376	12.04288	3.958241	11.23613	17.48821	17.26126	-1.1723	0.10578	0.18366	DBNDD2	chr20	+	44034697	44039250	1537
ENSG00000(	0	2.408575	0	8.239831	0	10.68554	-2.1236	0.078762	0.14341	ECEL1P2	chr2	-	2.33E+08	2.33E+08	1295
ENSG00000(	0	0	3.958241	0.749076	0	0	0.94769	0.48013	NA	RP11-564P	chr3	-	81416141	81417172	1032
ENSG00000(	2.071584	0	0	2.247227	9.20432	0.821965	-1.6874	0.1762	0.27816	ITGB5-AS1	chr3	+	1.25E+08	1.25E+08	460
ENSG00000(	46.61064	28.90291	23.74945	39.701	25.7721	47.67397	-0.17752	0.6825	0.78278	C7orf13	chr7	-	1.56E+08	1.56E+08	2292
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RP11-707F	chr7	+	1.42E+08	1.42E+08	481
ENSG00000(	0	2.408575	3.958241	268.9181	270.607	221.9305	-6.6301	6.96E-30	1.06E-28	RP11-475N	chr3	+	1.28E+08	1.28E+08	1578
ENSG00000(	16.57267	22.88147	22.43003	0	0	1.64393	4.4039	2.35E-06	9.37E-06	CTD-2314B	chr14	-	19854098	19925348	4264
ENSG00000(	36.25272	51.78437	55.41538	53.18436	37.73771	60.8254	-0.08816	0.8083	0.87558	RP11-425L	chr11	-	46450163	46450700	498
ENSG00000(	0	0	1.319414	0.749076	0.920432	0	-0.15244	0.90808	NA	RP11-383G	chr3	-	1.42E+08	1.42E+08	765
ENSG00000(	3.107376	4.817151	3.958241	4.494453	2.761296	4.93179	-0.03925	0.96778	0.98106	RP11-119K	chr10	+	96337196	96370995	645

ENSG00000(	0	1.204288	9.235896	3.745378	6.443024	0	0.010412	0.99294	0.99552	RP11-531F	chr3	-	1.83E+08	1.83E+08	543
ENSG00000(	0	9.634302	0	11.23613	5.522592	16.4393	-1.5185	0.11942	0.20292	HCG16	chr6	+	28954577	28956313	317
ENSG00000(	0	0	1.319414	0	4.60216	0	-0.82615	0.54181	NA	RP11-202A	chr3	-	1.34E+08	1.34E+08	823
ENSG00000(	16.57267	10.83859	7.916483	5.243529	8.283888	4.93179	0.87689	0.2342	0.34824	RPL7P23p	chr5	+	76878198	76879010	813
ENSG00000(	0	3.612863	1.319414	0.749076	3.681728	0	0.10125	0.9383	0.96256	PFN1P8	chr1	-	1.46E+08	1.46E+08	543
ENSG00000(	5.17896	1.204288	0	0	0	1.64393	1.1196	0.40386	0.53493	RPS2P45	chr16	+	69067578	69069945	2057
ENSG00000(	0	9.634302	1.319414	0	1.840864	0	1.6469	0.20463	0.31312	RP11-24C3	chr3	-	48481762	48488060	885
ENSG00000(	0	0	1.319414	0	0.920432	0.821965	-0.17431	0.89516	NA	RP11-592B	chr10	-	51253146	51371338	980
ENSG00000(	262.0554	337.2006	224.3003	154.3096	160.1552	286.8658	0.45025	0.069452	0.12886	RP11-466H	chr11	-	16996240	16996560	321
ENSG00000(	1104.154	1042.913	1250.804	626.2272	798.935	571.2656	0.76542	4.43E-07	1.91E-06	ETV5	chr3	-	1.86E+08	1.86E+08	4111
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	KRTAP5-7	chr11	+	71238313	71239210	898
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-463H	chr4	-	55842326	55842538	213
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	PGBD4P7	chr1	-	95138474	95139717	612
ENSG00000(	22.78742	27.69862	25.06886	14.23244	17.48821	24.65895	0.40755	0.41336	0.54384	RP4-655L2	chrX	+	1.2E+08	1.2E+08	632
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-359H	chr3	+	1.2E+08	1.2E+08	339
ENSG00000(	0	0	2.638828	0.749076	0.920432	0	0.28247	0.83431	NA	RPL34P21	chr11	-	1.3E+08	1.3E+08	287
ENSG00000(	20.71584	20.47289	17.15238	0.749076	1.840864	2.465895	3.2029	5.04E-05	0.000171	RP11-1398	chr4	-	1575789	1581980	579
ENSG00000(	879.3873	844.2057	916.9926	1759.578	1850.989	1549.404	-0.96457	6.31E-15	4.96E-14	RBM12	chr20	-	34236847	34252878	6662
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-201E	chr3	+	99316908	99342664	2305
ENSG00000(	0	0	0	2.996302	3.681728	3.28786	-2.4933	0.058396	0.11114	RP11-206M	chr3	+	1.49E+08	1.49E+08	551
ENSG00000(	1.035792	0	6.597069	11.23613	9.20432	8.219649	-1.6699	0.079364	0.14436	ERVFRD-1	chr6	-	11102722	11111965	3198
ENSG00000(	35.21692	16.86003	22.43003	28.46487	52.46462	32.05663	-0.56932	0.21823	0.32961	RP4-798C1	chr7	-	1.44E+08	1.44E+08	1268
ENSG00000(	13.46529	8.430014	23.74945	0.749076	4.60216	0	2.7372	0.002201	0.005822	AC005154.	chr7	-	30562759	30564151	1393
ENSG00000(	10.35792	8.430014	6.597069	3.745378	18.40864	4.93179	-0.06571	0.93384	0.96025	LILRA6	chr19	-	54720737	54746649	2238
ENSG00000(	1825.065	1683.594	1306.22	575.29	428.0009	441.3952	1.7301	4.99E-27	6.68E-26	SCARF2	chr22	-	20778874	20792146	3460
ENSG00000(	8.286335	2.408575	1.319414	1.498151	2.761296	0	1.151	0.32457	0.45206	RWDD4P1	chr7	+	1.05E+08	1.05E+08	565
ENSG00000(	855.5641	844.2057	608.2498	408.2462	476.7838	527.7015	0.70733	2.38E-05	8.44E-05	APOBEC3C	chr22	+	39410088	39414931	1309
ENSG00000(	0	0	1.319414	1.498151	0	0	-0.08979	0.94423	NA	GS1-124K5	chr7	-	65947788	65955095	151
ENSG00000(	17.60846	25.29004	14.51355	11.98521	14.72691	13.15144	0.50593	0.3715	0.50206	CTD-2013N	chr3	+	69063092	69105773	962
ENSG00000(	3.107376	6.021439	2.638828	1.498151	1.840864	7.397684	0.10883	0.91591	0.94865	KRT18P34	chr3	-	1.57E+08	1.57E+08	1270
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP1-181J2	chr11	+	32779814	32780160	347
ENSG00000(	0	0	0	0.749076	2.761296	0	-0.97685	0.45852	NA	RP11-167H	chr3	+	1.5E+08	1.5E+08	525
ENSG00000(	0	4.817151	3.958241	0	3.681728	10.68554	-0.55917	0.62457	0.73612	RP11-128A	chr7	+	1.29E+08	1.29E+08	1639
ENSG00000(	23.82321	21.67718	23.74945	0.749076	1.840864	3.28786	3.268	1.20E-05	4.39E-05	RP4-800G7	chr7	+	1.49E+08	1.49E+08	2804
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-14D2	chr3	+	64430907	64440508	565
ENSG00000(	34.18113	56.60152	31.66593	33.7084	10.12475	27.12484	0.75222	0.11675	0.19937	AC096772.	chr2	-	2.09E+08	2.09E+08	1262
ENSG00000(	1.035792	0	0	1.498151	0	0.821965	-0.37092	0.78098	NA	RP11-515B	chr12	-	14509776	14518437	358
ENSG00000(	8.286335	7.225726	6.597069	3.745378	2.761296	1.64393	1.2489	0.17194	0.27295	RP11-548C	chr3	-	1.39E+08	1.39E+08	3538
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RPL21P12(	chr17	+	21407884	21408385	502
ENSG00000(	251.6974	175.826	332.4923	14.98151	37.73771	24.65895	3.265	6.38E-25	7.85E-24	WNT5A-AS1	chr3	+	55521727	55522336	500
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	RAD21L1	chr20	+	1206700	1277065	1808
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	RP11-713H	chr17	+	8464548	8464894	347
ENSG00000(	5.17896	8.430014	0	2.247227	8.283888	4.109825	-0.06824	0.94592	0.96733	CCDC13	chr3	-	42734155	42814745	2943
ENSG00000(	10.35792	6.021439	13.19414	10.48706	2.761296	9.863579	0.31216	0.68372	0.78358	ASPRV1	chr2	-	70187226	70189397	2172

ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	OR2AE1	chr7	-	99473610	99474680	1071
ENSG00000(	33.14534	30.10719	23.74945	35.20655	36.81728	26.30288	-0.16641	0.69729	0.79394	CTA-211A9	chr22	+	27068730	27176170	1006
ENSG00000(	145.0109	140.9017	104.2337	146.8188	138.0648	152.0635	-0.15895	0.48905	0.61818	RP3-449O1	chr22	-	38731767	38794934	974
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-241J	chr5	-	80151326	80151662	337
ENSG00000(	6.214751	0	0	29.21395	9.20432	9.041614	-2.4602	0.00789	0.018786	CTD-2377D	chr17	+	46782565	46784708	1436
ENSG00000(	1.035792	0	1.319414	0	3.681728	2.465895	-0.83662	0.52591	0.65083	RP11-103G	chr3	-	1.5E+08	1.5E+08	476
ENSG00000(	0	0	0	1.498151	1.840864	0	-0.93652	0.47589	NA	RPS3AP15	chr3	-	75591300	75592080	781
ENSG00000(	2.071584	8.430014	0	0	0.920432	0.821965	1.7228	0.17644	0.27844	AC108676.	chr3	-	1.94E+08	1.94E+08	2962
ENSG00000(	4.143168	4.817151	2.638828	0	0.920432	0	2.4158	0.05605	0.10727	AL109761.	chr21	+	19165805	19183162	422
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-219E	chr3	-	95373267	95402037	2595
ENSG00000(	0	0	0	0.749076	6.443024	0	-1.8192	0.17996	0.28279	FCGR2C	chr1	+	1.62E+08	1.62E+08	1632
ENSG00000(	42.46747	63.82725	59.37362	33.7084	50.62376	35.34449	0.4608	0.20744	0.31674	UBE2V1	chr20	-	48697661	48732496	2536
ENSG00000(	0	2.408575	2.638828	0.749076	3.681728	0	0.11833	0.92766	0.95653	RP11-600F	chr14	-	1.04E+08	1.04E+08	643
ENSG00000(	2.071584	1.204288	0	14.98151	10.12475	7.397684	-2.7047	0.006234	0.01515	CTAGE8	chr7	-	1.44E+08	1.44E+08	2588
ENSG00000(	398.7799	361.2863	369.4359	158.804	160.1552	172.6126	1.1961	4.12E-12	2.70E-11	PTCHD4	chr6	-	47845764	48036425	3232
ENSG00000(	1.035792	2.408575	5.277655	0	9.20432	1.64393	-0.24045	0.83422	0.89384	RP11-378J	chr1	+	2.23E+08	2.23E+08	1302
ENSG00000(	1.035792	2.408575	1.319414	0	0	0	1.6865	0.21314	NA	RP11-803B	chr3	-	75433210	75440961	369
ENSG00000(	1.035792	6.021439	0	2.247227	10.12475	11.50751	-1.4477	0.15611	0.25219	RP5-894A1	chr7	-	1.41E+08	1.41E+08	770
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-874G	chr12	-	28717611	28718074	464
ENSG00000(	70.43385	81.89156	62.01245	54.68252	29.45382	64.93523	0.51104	0.14553	0.23809	RP11-20O2	chr1	+	1.1E+08	1.1E+08	612
ENSG00000(	3.107376	0	0	2.247227	2.761296	0.821965	-0.53955	0.6792	0.78006	RP11-179A	chr3	-	1.1E+08	1.1E+08	869
ENSG00000(	10.35792	8.430014	6.597069	2.247227	1.840864	1.64393	1.8554	0.044923	0.08846	ASLP1	chr22	-	23991400	23995521	637
ENSG00000(	2.071584	1.204288	0	0	1.840864	1.64393	-0.02642	0.98424	0.99091	RP13-1056	chr3	+	49812718	49813047	330
ENSG00000(	16.57267	21.67718	17.15238	2.996302	3.681728	7.397684	1.8396	0.007587	0.018132	C4A	chr6	+	31949801	31970458	5460
ENSG00000(	3.107376	1.204288	6.597069	2.247227	0	0	1.5333	0.21867	0.33016	RP11-506N	chr10	+	81420645	81436856	941
ENSG00000(	0	0	2.638828	5.992604	0	0	-0.66508	0.62265	0.73452	RP11-8P13	chr12	+	33016052	33016367	316
ENSG00000(	1167.337	1398.178	1319.414	882.411	763.9586	806.3476	0.66082	3.48E-07	1.52E-06	N4BP2L2	chr13	-	33006554	33112970	5317
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	RP11-1042	chr14	-	61038742	61039029	288
ENSG00000(	4.143168	4.817151	2.638828	0	1.840864	0	1.8844	0.12732	0.21373	RP11-45A1	chr9	-	1.19E+08	1.19E+08	728
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-65D1	chr8	+	1.27E+08	1.27E+08	1422
ENSG00000(	110.8297	173.4174	147.7743	164.0475	132.5422	166.0369	-0.10275	0.66441	0.76835	GABPB1-AS	chr15	+	50647156	50659636	2310
ENSG00000(	0	3.612863	1.319414	5.992604	10.12475	17.26126	-2.358	0.01453	0.032558	CTB-36O1.7	chr5	-	1.34E+08	1.34E+08	747
ENSG00000(	7.250543	0	10.55531	0	4.60216	0.821965	1.3334	0.2446	0.36085	RP11-613D	chr11	-	43930842	43942494	1906
ENSG00000(	27.96638	34.92434	43.54065	24.71949	30.37426	29.59074	0.31763	0.451	0.58063	RP11-529F	chr3	+	1.29E+08	1.29E+08	517
ENSG00000(	8.286335	3.612863	17.15238	15.73059	21.16994	16.4393	-0.83303	0.20322	0.31124	RP11-1379	chr5	-	1.79E+08	1.79E+08	1966
ENSG00000(	1.035792	4.817151	3.958241	2.996302	1.840864	4.93179	-0.01205	0.99093	0.99468	RP11-1000	chr15	+	32905934	32907312	732
ENSG00000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	RP11-613D	chr11	-	43965337	43968756	2045
ENSG00000(	11.39371	8.430014	18.47179	3.745378	12.88605	3.28786	0.87312	0.24969	0.36697	LIFR-AS1	chr5	+	38556888	38671318	3803
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	CTD-3064M	chr8	-	1.42E+08	1.42E+08	1380
ENSG00000(	1.035792	7.225726	0	3.745378	3.681728	0	0.11149	0.92709	0.95611	RP11-181C	chr12	-	98879322	98897633	1825
ENSG00000(	2.071584	1.204288	3.958241	1.498151	2.761296	2.465895	0.076844	0.94656	0.96771	RP11-875C	chr8	-	22842109	22876848	1945
ENSG00000(	0	1.204288	1.319414	0	1.840864	5.753754	-1.0214	0.43286	0.56272	RP11-303E	chr16	+	81110924	81112466	1088
ENSG00000(	192.6573	189.0732	200.5509	158.804	161.0756	147.9537	0.3138	0.11312	0.19409	LINC00847	chr5	+	1.8E+08	1.8E+08	1871
ENSG00000(	5.17896	7.225726	6.597069	2.996302	0	0	2.0306	0.068477	0.12734	RP11-12A1	chr4	+	57975928	58071676	1389

ENSG00000	0	0	7.916483	0	0.920432	0	1.6015	0.23603	0.35043	RP11-320N	chr8	-	96079036	96085410	2632
ENSG00000	5.17896	4.817151	3.958241	2.996302	7.363456	5.753754	-0.16958	0.85183	0.90549	A2M-AS1	chr12	+	9217773	9220651	2187
ENSG00000	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	SMARCA5-A	chr4	-	1.44E+08	1.44E+08	945
ENSG00000	6.214751	10.83859	6.597069	11.98521	5.522592	16.4393	-0.48709	0.50688	0.6345	CTB-131B5	chr5	-	1.39E+08	1.39E+08	2769
ENSG00000	9.322127	16.86003	3.958241	0	0.920432	8.219649	1.4588	0.13589	0.22519	ARAP1-AS2	chr11	+	72411519	72416652	1824
ENSG00000	34.18113	42.15007	36.94359	32.21025	43.2603	41.09825	-0.03931	0.91875	0.95073	RP11-383J2	chr8	-	1.25E+08	1.25E+08	5654
ENSG00000	12.4295	8.430014	7.916483	14.23244	7.363456	9.041614	-0.08262	0.90642	0.94228	RP11-867G	chr11	-	66037303	66045996	2792
ENSG00000	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	LINC00861	chr8	-	1.27E+08	1.27E+08	5330
ENSG00000	8.286335	8.430014	15.83297	5.992604	5.522592	4.93179	0.89137	0.24038	0.35565	EEF1A1P4	chr12	-	19609178	19610582	1405
ENSG00000	6.214751	18.06432	5.277655	16.47966	7.363456	11.50751	-0.24585	0.73239	0.82109	RP11-10K1	chr4	-	1.74E+08	1.74E+08	2036
ENSG00000	5.17896	2.408575	5.277655	8.239831	14.72691	4.109825	-0.94464	0.27154	0.39231	RP11-305N	chr11	+	1.19E+08	1.19E+08	2486
ENSG00000	14.50109	21.67718	17.15238	7.490755	13.80648	21.37109	0.30664	0.60706	0.72142	CTB-157D1	chr5	-	1.54E+08	1.54E+08	1039
ENSG00000	1.035792	3.612863	2.638828	10.48706	2.761296	6.575719	-1.2341	0.21318	0.32348	CTD-2547L	chr8	+	17942377	17953903	1052
ENSG00000	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	RP11-286E	chr4	-	1.09E+08	1.09E+08	2810
ENSG00000	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-165P	chr12	-	27542722	27599558	804
ENSG00000	11.39371	31.31148	21.11062	8.988907	8.283888	8.219649	1.2442	0.043739	0.086521	CTC-241N9	chr5	+	1.79E+08	1.79E+08	1454
ENSG00000	2.071584	0	1.319414	0	2.761296	2.465895	-0.37306	0.77619	0.85302	RP11-15B1	chr4	+	1.01E+08	1.01E+08	769
ENSG00000	0	1.204288	0	0	0.920432	0.821965	-0.17164	0.89643	NA	RP11-367J2	chr4	-	7102967	7105112	2146
ENSG00000	0	0	2.638828	0.749076	1.840864	0	4.10E-05	0.99998	NA	RP11-387D	chr15	+	91203465	91208198	1295
ENSG00000	5.17896	4.817151	2.638828	1.498151	13.80648	8.219649	-0.75945	0.40751	0.5383	RP11-677M	chr11	+	1.25E+08	1.25E+08	2886
ENSG00000	24.85901	21.67718	31.66593	11.98521	41.41944	23.83698	0.023386	0.9639	0.97911	RP11-540A	chr11	-	9776317	9781080	2311
ENSG00000	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	LINC00461	chr5	-	87803363	87986858	3558
ENSG00000	12355.96	16161.54	13017.34	669.6735	1841.784	1751.607	3.1963	3.19E-13	2.26E-12	NEAT1	chr11	+	65190245	65213011	22743
ENSG00000	0	12.04288	3.958241	0.749076	2.761296	1.64393	1.2744	0.25734	0.37592	RP11-219B	chr15	+	60771377	60922836	869
ENSG00000	15.53688	19.2686	18.47179	17.22874	46.0216	30.4127	-0.7803	0.12816	0.21482	RP11-712B	chr11	+	94883703	94967268	1926
ENSG00000	89.0781	34.92434	67.2901	56.18067	51.54419	52.60575	0.25403	0.48337	0.61261	CTD-2037K	chr5	-	77638189	77656331	1479
ENSG00000	3.107376	0	0	0	3.681728	0	-0.09374	0.94492	0.96694	RP11-367J2	chr4	-	7096298	7105107	1500
ENSG00000	11.39371	9.634302	14.51355	33.7084	49.70333	20.54912	-1.4869	0.005429	0.013351	AP001258.	chr11	-	58897606	58910488	2110
ENSG00000	30.03797	20.47289	46.17948	14.98151	15.64734	27.94681	0.6929	0.16488	0.26336	BDNF-AS	chr11	+	27528385	27719721	2324
ENSG00000	7.250543	3.612863	5.277655	12.73428	11.96562	5.753754	-0.82165	0.29959	0.42453	DACT3-AS1	chr19	+	47163621	47180704	1304
ENSG00000	11.39371	15.65574	11.87472	21.72319	39.57858	22.19305	-1.0523	0.051023	0.098825	DDX11-AS1	chr12	-	31173697	31226781	2031
ENSG00000	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-277P	chr12	+	10516368	10551105	2830
ENSG00000	11.39371	13.24716	10.55531	0	0	0	4.7969	3.37E-05	0.000117	RP11-620J2	chr12	-	58263618	58290265	3507
ENSG00000	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-184E	chr5	+	25190791	25306281	937
ENSG00000	6.214751	2.408575	6.597069	0.749076	4.60216	6.575719	0.30553	0.75598	0.83858	RP5-940J5.	chr12	+	6652670	6654097	560
ENSG00000	135.6887	139.6974	159.6491	68.16587	87.44104	71.51095	0.93114	0.000173	0.000545	ZNF585B	chr19	-	37672481	37709055	6210
ENSG00000	4.143168	6.021439	3.958241	5.243529	13.80648	3.28786	-0.5729	0.51594	0.64256	AF146191.	chr4	-	1.91E+08	1.91E+08	979
ENSG00000	190.5857	190.2775	196.5927	98.1289	127.0196	99.45776	0.8282	0.000157	0.000497	CRNDE	chr16	-	54952775	54963101	735
ENSG00000	9.322127	13.24716	29.0271	0.749076	3.681728	0.821965	2.9498	0.000518	0.001519	NADKD1-AS	chr5	+	36221157	36222004	720
ENSG00000	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-34F1	chr15	-	68126648	68131217	1986
ENSG00000	9.322127	0	7.916483	2.247227	10.12475	4.109825	0.069753	0.94296	0.9656	RP11-367J2	chr4	-	7032281	7047958	4300
ENSG00000	2.071584	2.408575	2.638828	0	0.920432	2.465895	0.74598	0.55093	0.67209	RP11-279F	chr15	+	69755365	69863775	1358
ENSG00000	63.18331	52.98866	65.97069	1.498151	0	0	5.9839	1.64E-13	1.19E-12	RP11-175K	chr5	+	1.59E+08	1.59E+08	2664
ENSG00000	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-179A	chr11	-	81590893	82429124	1397

ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CEBPA	chr19	-	33790840	33793470	2631
ENSG00000(	113.9371	105.9773	81.80365	80.15108	58.90765	80.55256	0.4539	0.10718	0.18573	CTD-2339L	chr15	-	40978922	40987305	1151
ENSG00000(	0	0	5.277655	2.996302	7.363456	7.397684	-1.4089	0.20597	0.31479	GS1-24F4.2	chr8	+	6693076	6742798	1110
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-158I9	chr11	-	1.19E+08	1.19E+08	1646
ENSG00000(	1.035792	4.817151	0	2.247227	0	0	0.77564	0.5628	0.68256	CTD-3203P	chr16	+	27279526	27301813	2594
ENSG00000(	7.250543	24.08575	3.958241	2.247227	1.840864	0	2.62	0.007023	0.016908	RP11-796E	chr12	+	92539349	92583436	5699
ENSG00000(	928.0695	958.613	766.5794	638.9614	694.0057	830.1846	0.29472	0.048452	0.094428	SNHG6	chr8	-	67833919	67838633	648
ENSG00000(	2.071584	0	2.638828	0	0	0	1.5584	0.24658	NA	RP11-630D	chr4	+	76901943	76927095	1685
ENSG00000(	191.6215	163.7831	188.6762	181.2763	161.996	143.8439	0.15819	0.44749	0.57723	CTC-228N2	chr5	-	1.27E+08	1.27E+08	2977
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-18H2	chr4	+	1.53E+08	1.53E+08	1592
ENSG00000(	97.36444	34.92434	73.88717	77.15478	100.3271	70.68898	-0.2567	0.46318	0.5925	RP11-33B1	chr4	+	1.2E+08	1.2E+08	2376
ENSG00000(	6.214751	15.65574	21.11062	21.72319	14.72691	35.34449	-0.72193	0.21997	0.33166	KB-1208A1	chr8	+	99053954	99056349	1989
ENSG00000(	3.107376	1.204288	0	8.988907	11.96562	18.08323	-2.6639	0.004138	0.010427	RP11-30K9	chr15	-	59060271	59063173	1396
ENSG00000(	18.64425	30.10719	63.33186	45.69361	66.2711	47.67397	-0.50862	0.23851	0.35341	RP11-113K	chr11	+	82783108	82817761	860
ENSG00000(	3.107376	10.83859	1.319414	7.490755	0	0.821965	0.67061	0.54695	0.6688	NUDT16P	chr3	+	1.31E+08	1.31E+08	2208
ENSG00000(	117.0445	90.32158	96.31721	128.841	84.67974	143.8439	-0.23239	0.39263	0.52336	RP11-115C	chr8	-	6261072	6264663	2413
ENSG00000(	59.04014	63.82725	54.09597	85.39461	62.58938	73.97684	-0.32424	0.28882	0.41244	RP11-696N	chr4	+	1E+08	1E+08	4825
ENSG00000(	0	0	0	3.745378	0	1.64393	-1.4934	0.26982	NA	AC006445.	chr4	-	13547699	13549425	1263
ENSG00000(	7.250543	8.430014	10.55531	3.745378	9.20432	1.64393	0.76312	0.36684	0.49687	CTC-774J1.	chr11	-	1.16E+08	1.16E+08	3322
ENSG00000(	13.46529	19.2686	14.51355	14.23244	22.09037	24.65895	-0.35114	0.522	0.64756	RP11-875C	chr8	+	22925742	22941132	2636
ENSG00000(	1.035792	1.204288	6.597069	7.490755	22.09037	32.8786	-2.5731	0.001575	0.00427	RP11-346I	chr8	-	67331824	67341212	4366
ENSG00000(	60.07593	36.12863	36.94359	84.64554	56.14635	84.66239	-0.74107	0.033431	0.06831	RP11-705C	chr11	+	77850817	77886369	1789
ENSG00000(	35.21692	50.58008	43.54065	4.494453	12.88605	12.32947	2.057	5.04E-05	0.000171	RP11-29H2	chr1	-	1.56E+08	1.56E+08	2505
ENSG00000(	0	0	0	0	0.920432	3.28786	-1.1769	0.37857	NA	RP11-260E	chr5	+	16616035	16630078	1674
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-17A1	chr11	+	22850926	22966939	2029
ENSG00000(	3.107376	3.612863	1.319414	11.98521	6.443024	7.397684	-1.4548	0.11002	0.18962	RP11-382A	chr8	-	1.28E+08	1.28E+08	1420
ENSG00000(	15.53688	12.04288	6.597069	0	11.96562	5.753754	0.86057	0.32269	0.45	RP11-613D	chr11	-	43851259	43902276	2190
ENSG00000(	26.93059	32.51577	55.41538	45.69361	32.21512	38.63235	-0.03278	0.93651	0.96168	KB-431C1.4	chr8	+	1.03E+08	1.03E+08	2048
ENSG00000(	12.4295	15.65574	21.11062	96.63075	72.71413	71.51095	-2.2574	1.15E-08	5.76E-08	SBF2-AS1	chr11	+	9779839	9832866	2709
ENSG00000(	2.071584	3.612863	6.597069	9.737982	10.12475	9.863579	-1.1633	0.16032	0.25764	RP11-685N	chr11	+	10830844	10844478	2335
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	RP11-325L	chr5	+	1.37E+08	1.37E+08	1253
ENSG00000(	0	1.204288	1.319414	0	3.681728	3.28786	-0.93214	0.47548	0.60463	RP11-77I22	chr12	+	30908008	30933673	1552
ENSG00000(	65.25489	51.78437	50.13772	30.7121	31.29469	50.13986	0.56814	0.12486	0.21048	PRR7-AS1	chr5	-	1.77E+08	1.77E+08	741
ENSG00000(	14.50109	21.67718	10.55531	11.23613	11.04518	16.4393	0.25882	0.6699	0.77272	EXTL3-AS1	chr8	-	28553718	28558981	3688
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP5-1186N	chr6	+	28555155	28559524	2874
ENSG00000(	5.17896	4.817151	5.277655	0	1.840864	1.64393	1.6901	0.12829	0.21493	RP11-13A1	chr12	-	89404458	89413456	2941
ENSG00000(	13.46529	6.021439	10.55531	3.745378	3.681728	0.821965	1.6457	0.060929	0.11511	RP11-382J1	chr8	+	71520812	71575514	3716
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP11-10L7	chr4	+	89206094	89252573	1654
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	RP11-461C	chr16	-	56126899	56225006	2678
ENSG00000(	7.250543	0	0	2.247227	0	2.465895	0.41664	0.74758	0.83221	RP11-386I8	chr12	-	1.34E+08	1.34E+08	1151
ENSG00000(	0	2.408575	0	0	4.60216	0	-0.46148	0.73374	0.82196	CTD-2024I7	chr5	+	1.41E+08	1.41E+08	2480
ENSG00000(	3.107376	3.612863	5.277655	0	0	0	3.0852	0.01784	0.039172	RP11-16M8	chr8	-	57408805	57472382	2366
ENSG00000(	2.071584	2.408575	1.319414	0	0	0	1.9715	0.14607	NA	RP13-578N	chr4	+	1.45E+08	1.45E+08	566
ENSG00000(	156.4046	136.0845	135.8996	75.65663	118.7357	165.2149	0.25295	0.36238	0.49203	RP11-894P	chr14	-	1.04E+08	1.04E+08	1404

ENSG00000(	8.286335	9.634302	3.958241	33.7084	30.37426	32.8786	-2.0356	0.000333	0.001007	RP11-57A1	chr16	-	28296206	28303385	2481
ENSG00000(	15.53688	12.04288	14.51355	11.23613	11.04518	9.863579	0.36855	0.55538	0.67608	AF131216.	chr8	-	11173374	11182938	5850
ENSG00000(	5.17896	1.204288	1.319414	0.749076	5.522592	13.15144	-1.0631	0.30922	0.43534	RP11-736K	chr11	+	86666661	86712001	1223
ENSG00000(	1.035792	0	0	0.749076	3.681728	4.93179	-1.8612	0.1534	0.24867	RP11-539L	chr4	-	6689175	6692246	1821
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-159H	chr8	+	70746346	70767206	828
ENSG00000(	0	1.204288	2.638828	0	2.761296	0	0.25736	0.84918	0.90393	RP11-7F17	chr14	+	77507407	77535846	2924
ENSG00000(	15.53688	14.45145	10.55531	30.7121	14.72691	14.79537	-0.54358	0.35177	0.48154	RP11-10L1	chr4	+	1.04E+08	1.04E+08	883
ENSG00000(	18.64425	25.29004	18.47179	14.23244	10.12475	19.72716	0.47568	0.38862	0.5193	AC093162.	chr2	+	85542164	85543652	704
ENSG00000(	15.53688	16.86003	22.43003	21.72319	26.69253	27.94681	-0.466	0.34863	0.4783	RP11-1149	chr8	+	23081984	23088439	1970
ENSG00000(	33.14534	27.69862	40.90183	2.247227	11.04518	0.821965	2.7037	4.05E-05	0.000139	RP11-1277	chr5	-	1.77E+08	1.77E+08	853
ENSG00000(	0	3.612863	10.55531	0	2.761296	1.64393	1.2478	0.29298	0.4173	CACNA1C-A	chr12	-	2785167	2800366	2191
ENSG00000(	2.071584	0	1.319414	2.247227	0	1.64393	-0.12066	0.92771	0.95653	RP11-1094	chr17	-	48127713	48133103	2533
ENSG00000(	5.17896	8.430014	10.55531	11.98521	4.60216	4.109825	0.18304	0.82041	0.88415	LINC00535	chr8	-	94225531	94712661	1914
ENSG00000(	200.9436	228.8147	224.3003	112.3613	119.6562	78.08667	1.0691	2.64E-06	1.05E-05	RP11-877E	chr12	-	26092262	26112698	2610
ENSG00000(	1085.51	980.2902	816.7171	894.3962	998.6687	1301.992	-0.14683	0.36401	0.49381	H2AFJ	chr12	+	14927270	14930936	3665
ENSG00000(	15.53688	12.04288	0	4.494453	2.761296	6.575719	0.87355	0.34204	0.47095	CTD-2514K	chr17	-	72206119	72209481	2501
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CTD-2382E	chr15	+	42264961	42291292	2499
ENSG00000(	13.46529	18.06432	26.38828	1.498151	5.522592	3.28786	2.3097	0.001526	0.004145	CTC-463N1	chr5	-	98105322	98109173	2034
ENSG00000(	3.107376	1.204288	0	0	0	0	1.4526	0.27741	NA	AC004051.	chr4	+	1.1E+08	1.1E+08	1951
ENSG00000(	10.35792	6.021439	6.597069	15.73059	9.20432	18.90519	-0.86174	0.20921	0.31883	RP11-61A1	chr16	+	66785655	66788643	2894
ENSG00000(	9.322127	2.408575	13.19414	4.494453	0	3.28786	1.3965	0.15347	0.24876	RP11-68L1	chr8	+	91658669	91668826	3473
ENSG00000(	3.107376	8.430014	11.87472	5.992604	0.920432	4.93179	0.8301	0.3614	0.49107	RP11-544A	chr9	-	1.34E+08	1.34E+08	3084
ENSG00000(	241.3395	179.4389	311.3817	31.46117	48.7829	37.81039	2.6113	1.82E-21	1.96E-20	STARD4-AS	chr5	+	1.11E+08	1.11E+08	5525
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-325N	chr15	+	40213243	40218081	4811
ENSG00000(	4.143168	13.24716	5.277655	2.996302	0	4.93179	1.2603	0.20119	0.30879	DNM1P35	chr15	-	76020011	76030964	3188
ENSG00000(	10.35792	14.45145	17.15238	21.72319	25.7721	32.8786	-0.9094	0.084224	0.15206	AP000487.	chr11	-	70218352	70244594	2602
ENSG00000(	11.39371	7.225726	10.55531	22.47227	24.85166	16.4393	-1.067	0.071995	0.13291	CTD-2258A	chr16	+	66442427	66446038	2147
ENSG00000(	94.25706	126.4502	104.2337	53.93344	66.2711	75.62077	0.72311	0.009928	0.023109	UBAP1L	chr15	-	65385338	65407535	7377
ENSG00000(	7.250543	8.430014	3.958241	2.247227	3.681728	1.64393	1.1886	0.21258	0.32269	RP1-179N1	chr6	-	36114475	36164982	1230
ENSG00000(	21.75163	31.31148	15.83297	35.20655	24.85166	48.49593	-0.63544	0.1739	0.27542	SOCS2-AS1	chr12	-	93936239	93965544	3325
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-700H	chr17	-	49012350	49022074	2054
ENSG00000(	230.9816	185.4603	222.9809	1355.078	1123.847	1390.765	-2.5883	1.51E-63	5.71E-62	PGAM5	chr12	+	1.33E+08	1.33E+08	2742
ENSG00000(	114.9729	155.3531	116.1084	29.21395	41.41944	44.38611	1.7308	6.74E-09	3.44E-08	RP11-318N	chr8	-	1.04E+08	1.04E+08	1353
ENSG00000(	68.36227	55.39724	60.69303	158.804	153.7121	178.3664	-1.3972	2.68E-08	1.30E-07	SNHG10	chr14	-	95998634	96001209	1531
ENSG00000(	234.089	295.0505	178.1209	23.97042	37.73771	29.59074	2.9314	1.82E-25	2.30E-24	MIR210HG	chr11	-	565660	568457	1965
ENSG00000(	2.071584	8.430014	2.638828	8.988907	5.522592	8.219649	-0.70427	0.42518	0.55556	CTD-2260A	chr5	-	96149731	96271513	2245
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	RP11-588G	chr12	-	70107413	70132348	2538
ENSG00000(	132.5814	160.1703	134.5802	189.5161	117.8153	138.0901	-0.06287	0.79545	0.86649	RP11-11N9	chr8	+	32853696	32902373	737
ENSG00000(	53.86118	49.3758	68.60952	31.46117	38.65814	33.70056	0.7138	0.046332	0.09084	RP11-727A	chr11	-	82895533	82904836	2295
ENSG00000(	2.071584	3.612863	2.638828	0	1.840864	4.109825	0.36416	0.7583	0.8402	CSTF3-AS1	chr11	+	33183203	33213144	2031
ENSG00000(	2.071584	10.83859	5.277655	0.749076	0	1.64393	2.2281	0.047759	0.093255	RP11-434C	chr12	+	11700964	11743303	3673
ENSG00000(	3.107376	0	5.277655	2.996302	0.920432	8.219649	-0.43011	0.69881	0.79519	RP11-373N	chr5	-	1.48E+08	1.48E+08	2033
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-13G1	chr12	-	1.09E+08	1.09E+08	2984
ENSG00000(	101.5076	110.7945	73.88717	188.767	132.5422	161.9271	-0.74762	0.003114	0.008021	RP11-296I	chr16	-	70190243	70207351	2242

ENSG00000(	10.35792	18.06432	9.235896	44.19546	53.38506	52.60575	-1.9345	3.07E-05	0.000107	RP11-10O1	chr15	+	74753606	74773643	1612
ENSG00000(	41.43168	50.58008	32.98534	59.92604	84.67974	74.79881	-0.79378	0.018972	0.041383	CTD-2003C	chr11	+	10879806	10928349	1071
ENSG00000(	0	4.817151	0	9.737982	9.20432	12.32947	-2.2638	0.022556	0.048277	RP11-902B	chr14	-	61764882	61789536	4499
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	CTC-441N1	chr5	-	1.21E+08	1.21E+08	731
ENSG00000(	2.071584	0	0	5.992604	1.840864	0.821965	-1.2932	0.31505	0.44164	RP11-273G	chr8	-	1.44E+08	1.44E+08	1781
ENSG00000(	0	1.204288	2.638828	0.749076	0	0.821965	0.65583	0.62812	NA	RP11-510N	chr16	+	71496181	71499844	2793
ENSG00000(	1.035792	6.021439	1.319414	0.749076	0.920432	2.465895	0.74026	0.53835	0.66217	RP11-266N	chr5	+	58335588	58359330	729
ENSG00000(	2.071584	0	0	0.749076	0.920432	2.465895	-0.52545	0.69619	0.79304	RP11-637A	chr12	-	69068151	69081535	1733
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	CTD-2235C	chr5	-	74615980	74632739	527
ENSG00000(	23.82321	31.31148	29.0271	15.73059	21.16994	27.94681	0.36363	0.44473	0.57426	RP11-486C	chr12	-	1.24E+08	1.24E+08	1950
ENSG00000(	18.64425	28.90291	26.38828	29.96302	26.69253	20.54912	-0.0668	0.88716	0.92967	DNAJC3-AS	chr13	-	96325089	96329179	2908
ENSG00000(	0	2.408575	0	3.745378	7.363456	1.64393	-1.699	0.16368	0.26186	CTD-2340E	chr5	+	1.02E+08	1.02E+08	391
ENSG00000(	1.035792	0	0	5.243529	0	2.465895	-1.558	0.24439	0.36059	RP11-629G	chr11	-	1.13E+08	1.13E+08	1934
ENSG00000(	9.322127	9.634302	7.916483	0	0.920432	7.397684	1.4348	0.14109	0.23226	CARS-AS1	chr11	+	3050624	3062490	2664
ENSG00000(	3.107376	12.04288	9.235896	5.243529	15.64734	11.50751	-0.3798	0.61738	0.72983	RP11-392P	chr12	+	13080660	13137579	1746
ENSG00000(	2722.061	2919.193	3119.094	2195.54	2098.585	2280.131	0.41301	0.000177	0.000558	OIP5-AS1	chr15	+	41576188	41601901	8829
ENSG00000(	34.18113	34.92434	32.98534	48.68991	66.2711	80.55256	-0.91821	0.011117	0.025581	CTC-281B1	chr5	-	80499915	80597379	2463
ENSG00000(	21.75163	31.31148	19.79121	21.72319	11.96562	20.54912	0.4041	0.4334	0.56314	SPTY2D1-A	chr11	+	18621334	18631802	1454
ENSG00000(	508.5738	441.9736	405.06	388.7702	324.9125	456.1905	0.2124	0.21907	0.33064	TWF2	chr3	-	52262626	52273177	1619
ENSG00000(	6.214751	3.612863	3.958241	0.749076	1.840864	0.821965	1.5967	0.15089	0.24523	AC006296.	chr4	-	14911585	15003669	1806
ENSG00000(	100.4718	87.913	112.1502	309.3682	357.1276	292.6195	-1.6655	4.16E-16	3.51E-15	MARS2	chr2	+	1.99E+08	1.99E+08	3027
ENSG00000(	1.035792	3.612863	3.958241	2.996302	1.840864	10.68554	-0.7193	0.48614	0.61526	MTND4P12	chr5	-	1.34E+08	1.34E+08	1377
ENSG00000(	1.035792	4.817151	3.958241	3.745378	4.60216	6.575719	-0.52441	0.59581	0.71157	LRP4-AS1	chr11	+	46867963	46895947	1504
ENSG00000(	56.96855	51.78437	71.24834	14.98151	35.89685	36.16646	1.0297	0.011129	0.025606	RP11-1277	chr5	+	1.77E+08	1.77E+08	1751
ENSG00000(	16.57267	4.817151	5.277655	7.490755	4.60216	10.68554	0.21895	0.78209	0.85651	RP11-323F	chr4	+	4543858	4639631	724
ENSG00000(	2.071584	3.612863	0	0	0	1.64393	0.99881	0.45786	0.58749	RP11-932C	chr15	-	30909201	30917976	970
ENSG00000(	16.57267	20.47289	11.87472	26.21764	11.96562	15.61733	-0.13419	0.81513	0.87993	CTD-2574D	chr16	+	29938157	29940254	1762
ENSG00000(	45.57484	62.62296	79.16483	108.616	106.7701	104.3895	-0.77114	0.007742	0.018466	USP51	chrX	-	55511049	55515635	4407
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-447H	chr5	-	43231914	43233275	1362
ENSG00000(	9.322127	10.83859	7.916483	0.749076	10.12475	4.93179	0.75602	0.37548	0.50601	RP11-32B5	chr15	-	21941147	21968151	2161
ENSG00000(	0	0	0	4.494453	0	1.64393	-1.6577	0.22164	0.3333	PCED1B-AS	chr12	-	47599681	47610239	2494
ENSG00000(	0	2.408575	0	0	1.840864	0	0.16879	0.89944	NA	RP11-67M1	chr4	+	90757559	90763129	2646
ENSG00000(	29.00217	16.86003	31.66593	26.96672	9.20432	22.19305	0.38437	0.47144	0.60042	CTD-2366F	chr5	+	52405672	52410956	3137
ENSG00000(	230.9816	254.1047	319.2981	42.69731	75.47542	106.0335	1.8256	4.60E-11	2.79E-10	NR2F2-AS1	chr15	-	96670598	96870590	1930
ENSG00000(	82.86335	68.6444	91.03955	47.19176	68.11197	51.78379	0.53379	0.083397	0.15069	TMEM161B	chr5	+	87564712	87732502	1101
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	CCAT1	chr8	-	1.28E+08	1.28E+08	2131
ENSG00000(	14.50109	8.430014	14.51355	14.23244	11.04518	14.79537	-0.09374	0.8806	0.92529	RP5-940J5.	chr12	+	6687788	6693905	2196
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	SPCS2P3	chr5	+	816461	817116	656
ENSG00000(	1.035792	4.817151	1.319414	4.494453	1.840864	3.28786	-0.3449	0.7562	0.83879	CTD-2001C	chr5	-	99785458	99870966	1569
ENSG00000(	53.86118	90.32158	73.88717	363.3016	351.605	388.7894	-2.3318	1.34E-26	1.77E-25	RP11-421F	chr12	+	27124519	27132515	2549
ENSG00000(	0	0	7.916483	0	1.840864	0	1.1723	0.38334	0.51398	HMGN1P1	chr5	-	70833479	70833673	195
ENSG00000(	0	0	1.319414	0.749076	0	1.64393	-0.40261	0.76414	NA	RP3-510L9	chr6	+	11173685	11259332	704
ENSG00000(	2.071584	7.225726	2.638828	6.74168	2.761296	4.93179	-0.24459	0.80081	0.87027	RP11-967K	chr12	-	28316231	28343299	739
ENSG00000(	44.53905	33.72006	17.15238	15.73059	19.32907	15.61733	0.89217	0.075905	0.13903	SEC24B-AS	chr4	-	1.1E+08	1.1E+08	1433

ENSG00000(	4.143168	1.204288	0	0	0	4.93179	0.08707	0.94741	0.96827	RP11-543C	chr14	+	1E+08	1E+08	1039
ENSG00000(	41.43168	21.67718	34.30476	36.7047	19.32907	17.26126	0.39426	0.41191	0.54262	RP11-358N	chr15	+	57592563	57599959	2530
ENSG00000(	175.0488	174.6217	142.4967	227.719	221.8241	196.4496	-0.38786	0.053652	0.1033	RP11-18C2	chr12	-	1.21E+08	1.21E+08	1901
ENSG00000(	7.250543	9.634302	3.958241	0	11.96562	21.37109	-0.58326	0.518	0.64423	AC005329.	chr19	-	1392169	1396466	3571
ENSG00000(	16.57267	12.04288	23.74945	5.992604	1.840864	6.575719	1.7048	0.016649	0.036807	FAM13A-AS	chr4	+	89630940	89651254	3210
ENSG00000(	2.071584	3.612863	6.597069	0.749076	12.88605	6.575719	-0.6132	0.52791	0.65261	CTD-2383N	chr11	-	1.01E+08	1.01E+08	1865
ENSG00000(	65.25489	46.96722	67.2901	39.701	41.41944	50.96182	0.4358	0.20402	0.31228	CTD-2653N	chr5	-	36864527	36876759	2589
ENSG00000(	100.4718	113.203	67.2901	156.5568	110.4518	124.1167	-0.47066	0.082488	0.14932	RP11-453E	chr4	+	68566998	68946670	3352
ENSG00000(	0	0	0	9.737982	12.88605	2.465895	-3.8453	0.001521	0.004134	RP11-422N	chr8	+	1.11E+08	1.11E+08	3075
ENSG00000(	4.143168	0	1.319414	0.749076	7.363456	4.93179	-0.92677	0.41935	0.55005	ATPBD4-AS	chr15	+	35838396	36151202	1477
ENSG00000(	56.96855	50.58008	46.17948	23.22134	28.53339	18.90519	1.1029	0.005343	0.013158	RP11-159F	chr5	-	43575425	43603332	1040
ENSG00000(	0	0	1.319414	1.498151	0	2.465895	-0.80883	0.55106	NA	BCKDHA	chr19	+	41856758	41930910	2103
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	INSL3	chr19	-	17927321	17932383	899
ENSG00000(	16.57267	6.021439	23.74945	1.498151	18.40864	6.575719	0.74875	0.33144	0.45936	RP11-709A	chr12	-	27699983	27705706	2639
ENSG00000(	121.1877	87.913	134.5802	13.48336	109.5314	69.86702	0.77142	0.28491	0.40797	CTC-338M1	chr5	+	1.81E+08	1.81E+08	549
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTD-2218K	chr5	+	82120703	82121003	301
ENSG00000(	0	3.612863	1.319414	5.243529	2.761296	0.821965	-0.62845	0.60257	0.71764	RP11-78C3	chr5	-	82215195	82216938	745
ENSG00000(	5.17896	1.204288	5.277655	0.749076	0.920432	0	1.9708	0.10768	0.18642	RP11-752D	chr4	+	53811816	53824254	2517
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-301A	chr5	-	40967607	40967865	259
ENSG00000(	24.85901	18.06432	17.15238	20.22504	24.85166	22.19305	-0.14892	0.76598	0.84553	SMURF2P1	chr17	+	28927814	28942998	570
ENSG00000(	184.371	219.1804	174.1626	126.5938	138.9852	131.5144	0.53876	0.01049	0.024277	RRN3P1	chr16	-	21807951	21831731	2608
ENSG00000(	10.35792	1.204288	10.55531	0	0	0	3.9799	0.001349	0.003708	CTB-73N10	chr5	+	1.45E+08	1.45E+08	654
ENSG00000(	0	0	0	2.247227	0	4.93179	-1.8667	0.16863	0.26839	CTD-2012J	chr5	+	1598242	1598362	121
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	CTC-235G5	chr5	-	75377771	75380011	691
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	ADH1C	chr4	-	1E+08	1E+08	1740
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP1-167G2	chr5	-	16373470	16440190	2120
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	RP11-650J	chr4	-	1.14E+08	1.14E+08	1176
ENSG00000(	0	0	1.319414	0	2.761296	0	-0.44505	0.73801	NA	WI2-89927	chr4	-	2609597	2609873	277
ENSG00000(	0	0	1.319414	0	5.522592	0	-0.99212	0.46461	0.59373	HSPA8P11	chr8	+	30094898	30098513	1898
ENSG00000(	10.35792	6.021439	2.638828	15.73059	9.20432	9.041614	-0.74753	0.32852	0.45624	RP11-499E	chr4	-	1.03E+08	1.03E+08	673
ENSG00000(	2.071584	13.24716	10.55531	0	1.840864	0	2.9835	0.007244	0.017392	RP11-148L	chr4	-	1.75E+08	1.75E+08	1328
ENSG00000(	59.04014	73.46155	72.56776	44.19546	37.73771	57.53754	0.54334	0.10066	0.17642	CTC-428G2	chr5	-	1.15E+08	1.15E+08	2231
ENSG00000(	4.143168	0	1.319414	0.749076	0.920432	0.821965	0.73295	0.57494	0.69339	GAPDHP60	chr4	+	88128244	88129238	995
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTD-2049C	chr5	+	62597350	62597883	300
ENSG00000(	7.250543	4.817151	2.638828	22.47227	17.48821	19.72716	-1.8592	0.006681	0.01613	RP11-184N	chr4	-	1.29E+08	1.29E+08	1623
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	ATG10-AS1	chr5	-	81368874	81369521	648
ENSG00000(	0	1.204288	1.319414	0.749076	0	0	0.61214	0.64459	NA	RP11-476C	chr4	+	88087996	88088886	891
ENSG00000(	0	0	2.638828	0	0	1.64393	0.26729	0.84149	NA	RP11-115A	chr4	+	1.11E+08	1.11E+08	571
ENSG00000(	12.4295	6.021439	13.19414	0.749076	0	0.821965	3.4355	0.000956	0.002688	RP4-671G1	chr1	+	1.13E+08	1.13E+08	1459
ENSG00000(	3.107376	3.612863	3.958241	0	0	0	2.9061	0.027122	0.056934	RP11-455B	chr5	+	97217124	97258399	705
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-739P	chr4	+	1.85E+08	1.85E+08	622
ENSG00000(	0	0	0	3.745378	0.920432	0	-1.3029	0.33256	NA	TRPC7-AS1	chr5	+	1.36E+08	1.36E+08	460
ENSG00000(	63.18331	90.32158	68.60952	20.22504	40.49901	41.92021	1.0978	0.002938	0.007603	CICP16	chr4	-	1.2E+08	1.2E+08	2813
ENSG00000(	0	3.612863	5.277655	4.494453	0	2.465895	0.22932	0.84879	0.90373	RP11-722N	chr4	-	36498159	36643522	788

ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-648N	chr5	-	37505790	37506959	1170
ENSG0000(	0	4.817151	2.638828	0	0	0	2.1804	0.10782	0.18657	STX18-IT1	chr4	-	4477848	4483427	542
ENSG0000(	0	1.204288	0	0	6.443024	2.465895	-1.6514	0.21334	0.32365	CTB-174D1	chr5	+	1.68E+08	1.68E+08	1489
ENSG0000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-83C7	chr4	+	38368535	38387380	500
ENSG0000(	0	1.204288	6.597069	0	0.920432	1.64393	1.0195	0.43202	0.56187	SLIT2-IT1	chr4	+	20393812	20396479	601
ENSG0000(	0	2.408575	1.319414	0	0.920432	0	0.92035	0.49653	NA	KRT8P4	chr8	-	90424850	90427300	1454
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTD-2108C	chr5	-	38429994	38430262	269
ENSG0000(	1.035792	6.021439	2.638828	0	0	1.64393	1.6689	0.19134	0.29698	RP11-159F	chr5	+	43515376	43525412	512
ENSG0000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-556I1	chr4	-	1.06E+08	1.06E+08	575
ENSG0000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	RP11-93K2	chr3	-	1.3E+08	1.3E+08	713
ENSG0000(	4.143168	9.634302	10.55531	4.494453	0	0.821965	1.7822	0.078166	0.14251	AC092597.	chr4	-	47558748	47562276	601
ENSG0000(	7.250543	12.04288	6.597069	9.737982	8.283888	6.575719	0.066152	0.92914	0.95732	OCIAD1-AS	chr4	-	48854025	48862220	265
ENSG0000(	0	2.408575	1.319414	1.498151	2.761296	0	-0.12372	0.92546	0.95485	RP11-834C	chr12	+	54452038	54516018	3942
ENSG0000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-402C	chr4	+	1.83E+08	1.83E+08	286
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTC-499J9.	chr5	-	1.11E+08	1.11E+08	565
ENSG0000(	137.7603	125.2459	71.24834	167.0438	96.64536	118.3629	-0.18811	0.52092	0.64664	CTC-338M1	chr5	+	1.81E+08	1.81E+08	807
ENSG0000(	14.50109	22.88147	3.958241	19.47596	13.80648	9.863579	-0.05279	0.9365	0.96168	RP11-463N	chr17	-	46952222	46986345	738
ENSG0000(	8.286335	9.634302	1.319414	8.988907	18.40864	14.79537	-1.0175	0.17368	0.27514	RP11-33B1	chr4	-	1.2E+08	1.2E+08	356
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-473D	chr4	-	42563474	42564442	969
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-158J1	chr5	-	63253720	63276870	219
ENSG0000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	CTD-2194F	chr5	+	64505748	64506775	737
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	TNXA	chr6	-	31976391	31980249	2038
ENSG0000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	CTD-2308B	chr5	-	1.24E+08	1.24E+08	797
ENSG0000(	3.107376	2.408575	0	0	0	0	1.7825	0.18787	NA	RP11-74M1	chr4	-	11742572	11771092	657
ENSG0000(	2.071584	10.83859	14.51355	10.48706	11.04518	10.68554	-0.23249	0.75481	0.83784	CTC-454M9	chr5	+	88179145	88762215	1754
ENSG0000(	8.286335	12.04288	14.51355	0	11.04518	0	1.4231	0.14715	0.24022	RP11-713N	chr8	+	1.22E+08	1.22E+08	1973
ENSG0000(	9.322127	4.817151	6.597069	17.22874	16.56778	10.68554	-1.015	0.14188	0.2334	RP11-213H	chr5	-	90598846	90610219	2672
ENSG0000(	39.36009	19.2686	18.47179	0	0	0	5.9269	5.08E-08	2.40E-07	RP11-366N	chr4	+	1.66E+08	1.66E+08	2602
ENSG0000(	476.4643	398.6192	387.9077	861.4369	642.4615	708.5338	-0.80503	5.38E-07	2.30E-06	CDK11B	chr1	-	1570603	1590473	2384
ENSG0000(	78.72018	54.19295	52.77655	15.73059	16.56778	29.59074	1.552	0.000153	0.000487	WHAMMP2	chr15	+	28982729	29002537	2962
ENSG0000(	0	0	0	0	0.920432	4.109825	-1.3831	0.30514	NA	RP11-102N	chr4	+	1.42E+08	1.42E+08	402
ENSG0000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-293A	chr4	-	26875183	26875971	743
ENSG0000(	1.035792	8.430014	9.235896	0	0.920432	0.821965	2.5626	0.02679	0.056318	RP11-292D	chr4	+	1.48E+08	1.48E+08	518
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTC-470E21	chr5	-	1.12E+08	1.12E+08	211
ENSG0000(	4.143168	1.204288	1.319414	0	0.920432	0	1.6534	0.21531	0.32601	RP11-557J1	chr4	-	1.47E+08	1.47E+08	745
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTC-327F1(	chr5	-	1.47E+08	1.47E+08	793
ENSG0000(	1.035792	3.612863	2.638828	7.490755	10.12475	6.575719	-1.5025	0.10856	0.18758	CTB-129O4	chr5	+	1.8E+08	1.8E+08	393
ENSG0000(	12.4295	21.67718	11.87472	0	0	0	5.185	4.51E-06	1.74E-05	CTC-347C2	chr5	-	71869947	71956496	594
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-501N	chr3	+	1.43E+08	1.43E+08	684
ENSG0000(	9.322127	1.204288	1.319414	14.23244	11.96562	16.4393	-1.6182	0.047002	0.091985	RP11-177B	chr4	-	53586248	53586998	751
ENSG0000(	39.36009	19.2686	23.74945	38.20285	86.52061	66.57916	-1.1712	0.00558	0.013698	PCDHAC1	chr5	+	1.4E+08	1.4E+08	5299
ENSG0000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP11-313E	chr4	+	1.78E+08	1.78E+08	332
ENSG0000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	FOSL1P1	chr4	+	1.29E+08	1.29E+08	816
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	LINC00498	chr4	-	1.39E+08	1.39E+08	455

ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-576N	chr4	+	84168332	84169359	1028
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	PRR5-ARHG	chr22	+	45098113	45258586	2043
ENSG00000(	0	0	0	19.47596	34.05598	38.63235	-5.7713	6.98E-08	3.26E-07	KB-1269D1	chr22	+	23734958	23736026	629
ENSG00000(	5.17896	1.204288	5.277655	5.243529	3.681728	4.93179	-0.21245	0.82688	0.8884	GAPDHP61	chr15	-	64820866	64821870	1005
ENSG00000(	8.286335	18.06432	3.958241	0	1.840864	1.64393	2.6252	0.008654	0.020416	RP11-1191	chr4	-	716064	717823	569
ENSG00000(	1.035792	4.817151	0	0	3.681728	0.821965	0.26272	0.83922	0.89724	RP11-235P	chr8	-	15546423	15547071	649
ENSG00000(	46.61064	52.98866	92.35896	44.19546	39.57858	35.34449	0.66731	0.069354	0.12875	RP11-597D	chr4	+	1.59E+08	1.59E+08	2917
ENSG00000(	0	0	0	3.745378	1.840864	3.28786	-2.3167	0.081577	0.1478	RP11-269F	chr4	-	1.13E+08	1.13E+08	300
ENSG00000(	0	0	0	5.243529	3.681728	2.465895	-2.689	0.039185	0.078612	CTD-2536I1	chr15	-	95819690	95870358	1384
ENSG00000(	5.17896	8.430014	3.958241	9.737982	63.50981	22.19305	-2.2588	0.001133	0.003149	CTB-118N6	chr5	+	1.16E+08	1.16E+08	862
ENSG00000(	22.78742	10.83859	19.79121	11.98521	5.522592	13.15144	0.75058	0.23336	0.34712	PCDHGB8P	chr5	+	1.41E+08	1.41E+08	2367
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-324H	chr4	+	26113487	26115461	1647
ENSG00000(	0	0	0	26.96672	11.04518	9.041614	-4.801	2.32E-05	8.22E-05	AC004510.	chr19	-	15947287	15947865	579
ENSG00000(	2.071584	1.204288	10.55531	0	1.840864	0	2.0466	0.096869	0.17086	AL139147.	chr1	-	67131547	67142710	1156
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-93K2	chr3	+	1.3E+08	1.3E+08	406
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	CTD-2207A	chr5	+	38148582	38153817	2573
ENSG00000(	3.107376	0	5.277655	0.749076	0	0.821965	1.5077	0.24549	0.36192	RP11-517B	chr3	+	1.31E+08	1.31E+08	575
ENSG00000(	0	0	1.319414	1.498151	1.840864	0	-0.6531	0.62966	NA	DDX11L9	chr15	-	1.03E+08	1.03E+08	1653
ENSG00000(	17.60846	25.29004	15.83297	13.48336	21.16994	11.50751	0.33805	0.54484	0.66705	BACH1-IT1	chr21	+	30723955	30734215	821
ENSG00000(	2.071584	9.634302	3.958241	1.498151	2.761296	10.68554	0.052087	0.95729	0.97479	RP11-848G	chr5	+	68902926	68919876	1073
ENSG00000(	27.96638	30.10719	31.66593	0	0	0	6.1634	7.96E-09	4.02E-08	RP11-807H	chr4	+	66567920	66571271	385
ENSG00000(	1.035792	0	3.958241	0	0.920432	0	1.2088	0.37284	NA	POU5F2	chr5	-	93075976	93077309	1334
ENSG00000(	0	0	0	8.239831	3.681728	2.465895	-3.0283	0.017918	0.039318	PCP4L1	chr1	+	1.61E+08	1.61E+08	1424
ENSG00000(	117.0445	118.0202	75.20659	46.44268	32.21512	47.67397	1.2775	5.81E-05	0.000196	ABHD14A	chr3	+	52005442	52015212	1064
ENSG00000(	3.107376	6.021439	2.638828	1.498151	3.681728	10.68554	-0.36199	0.71255	0.80567	CTD-2007H	chr5	+	98264875	98330717	478
ENSG00000(	1.035792	0	1.319414	1.498151	0.920432	0	-0.02384	0.98598	NA	RP11-125C	chr4	-	1.28E+08	1.28E+08	645
ENSG00000(	5.17896	0	0	4.494453	0.920432	0	-0.02553	0.98452	0.99098	LNX1-AS2	chr4	+	54459123	54470214	628
ENSG00000(	6.214751	1.204288	3.958241	0	5.522592	2.465895	0.42145	0.70779	0.8024	RP5-1000K	chrX	+	77166238	77220387	2363
ENSG00000(	70.43385	55.39724	55.41538	60.67512	40.49901	36.98842	0.38421	0.27169	0.39243	RP11-521C	chr15	+	40331512	40359491	2317
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-174F	chr4	-	1.51E+08	1.51E+08	998
ENSG00000(	0	0	0	0	9.20432	0	-2.0051	0.13944	0.23001	SBF1P1	chr8	-	56362069	56367699	5631
ENSG00000(	1885.141	2074.988	2034.536	3435.26	2278.069	2853.04	-0.51412	0.00036	0.001081	MTATP6P1	chr1	+	569076	569756	681
ENSG00000(	0	1.204288	0	2.996302	0	0	-0.51443	0.69981	NA	RP11-517B	chr3	+	1.31E+08	1.31E+08	733
ENSG00000(	4.143168	0	1.319414	0	0.920432	0	1.3284	0.32679	0.45453	CTD-2201E	chr5	+	9363387	9422593	391
ENSG00000(	0	2.408575	1.319414	26.21764	10.12475	11.50751	-3.1877	0.000619	0.001794	RP11-10A1	chr8	+	9046521	9060364	699
ENSG00000(	4.143168	7.225726	2.638828	23.97042	24.85166	28.76877	-2.3104	0.000388	0.001161	RP11-247C	chr15	-	74418256	74421619	2924
ENSG00000(	4.143168	2.408575	1.319414	5.992604	11.96562	13.15144	-1.7098	0.053615	0.10325	CTB-47B11	chr5	-	1.57E+08	1.57E+08	1932
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	MTND4P8	chr4	-	1.56E+08	1.56E+08	1362
ENSG00000(	1.035792	8.430014	1.319414	5.243529	0.920432	9.041614	-0.41651	0.68971	0.78814	RP11-159F	chr5	+	43511160	43521913	572
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-61G2	chr5	-	89454156	89585888	561
ENSG00000(	4.143168	2.408575	3.958241	3.745378	10.12475	0.821965	-0.38959	0.70164	0.79732	RP11-390G	chr3	+	1.26E+08	1.26E+08	528
ENSG00000(	6.214751	8.430014	1.319414	20.22504	17.48821	25.48091	-1.8301	0.007641	0.01825	RP11-215P	chr5	+	1.34E+08	1.34E+08	520
ENSG00000(	0	2.408575	2.638828	0.749076	5.522592	1.64393	-0.47504	0.6969	0.79358	RP11-478C	chr4	-	331886	332372	487
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	TECRP2	chr4	-	1.25E+08	1.25E+08	928

ENSG00000(	0	4.817151	1.319414	0	0	0	1.8904	0.16312	0.26107	CTC-362D1	chr5	-	1.46E+08	1.46E+08	1220
ENSG00000(	0	0	0	1.498151	0.920432	1.64393	-1.2565	0.35231	NA	CTC-512J1	chr5	-	79646840	79647775	936
ENSG00000(	6.214751	0	2.638828	0	0	0	2.4522	0.069405	0.12882	EGFLAM-AS	chr5	-	38399916	38403515	539
ENSG00000(	4.143168	0	2.638828	0	8.283888	0	-0.17446	0.89099	0.93235	RP11-834C	chr12	+	54556923	54562379	403
ENSG00000(	2.071584	2.408575	7.916483	0	0.920432	0	2.4664	0.050853	0.098528	RP11-241F	chr4	-	49488943	49491571	670
ENSG00000(	2.071584	2.408575	2.638828	0	0	0	2.2753	0.091747	0.16332	RP11-90P5	chr8	-	38059217	38061756	791
ENSG00000(	0	0	3.958241	0	0.920432	0	0.88424	0.51108	NA	CTD-2516K	chr5	-	56613816	56615847	2032
ENSG00000(	12.4295	18.06432	10.55531	23.97042	59.82808	52.60575	-1.6652	0.000917	0.002585	GDNF-AS1	chr5	+	37840540	37875901	2913
ENSG00000(	2.071584	7.225726	1.319414	0.749076	4.60216	8.219649	-0.28488	0.78531	0.85883	TMEM110-I	chr3	-	52867137	52931578	5280
ENSG00000(	54.89697	66.23582	64.65128	39.701	34.97642	34.52253	0.75051	0.028442	0.059318	DSTNP2	chr12	+	6993846	6994950	1105
ENSG00000(	9.322127	14.45145	13.19414	1.498151	1.840864	4.109825	2.0616	0.013378	0.030227	RP11-844P	chr5	-	1.76E+08	1.76E+08	3632
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	RP11-302J	chr8	+	1.02E+08	1.02E+08	1948
ENSG00000(	50.7538	77.07441	54.09597	26.96672	18.40864	33.70056	1.171	0.002711	0.007059	RP3-412A9	chr22	+	31497862	31500743	2608
ENSG00000(	0	0	0	25.46857	17.48821	12.32947	-5.06	5.12E-06	1.96E-05	CTD-2306M	chr5	-	25404842	25446034	638
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-206P	chr4	+	25506619	25508297	1679
ENSG00000(	0	6.021439	0	2.996302	0	0	0.54323	0.68699	0.78601	HSPA8P4	chr5	+	1.29E+08	1.29E+08	1920
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-366M	chr4	-	1.66E+08	1.66E+08	1416
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CTC-573M9	chr5	+	1.28E+08	1.28E+08	462
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-1267	chr4	-	69570318	69578216	750
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-768F	chr12	-	1.2E+08	1.2E+08	695
ENSG00000(	6.214751	4.817151	15.83297	2.996302	9.20432	2.465895	0.77808	0.36514	0.49491	HMGA1P2	chr4	+	73964539	73964862	324
ENSG00000(	0	2.408575	5.277655	3.745378	0.920432	4.109825	-0.17659	0.87866	0.92418	RP11-485M	chr5	+	1.32E+08	1.32E+08	247
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP11-255I1	chr4	+	1.13E+08	1.13E+08	610
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	RP11-263I1	chr3	-	1.29E+08	1.29E+08	474
ENSG00000(	0	0	1.319414	2.247227	20.2495	8.219649	-3.3844	0.002985	0.007713	CTC-504A5	chr5	+	1.17E+08	1.17E+08	617
ENSG00000(	4.143168	1.204288	11.87472	5.992604	0.920432	4.109825	0.51555	0.60552	0.72022	CTC-498J12	chr5	-	68408939	68432221	946
ENSG00000(	1.035792	2.408575	2.638828	1.498151	0	0	1.1666	0.37957	0.51029	RP11-56D1	chr9	-	1.3E+08	1.3E+08	759
ENSG00000(	0	4.817151	1.319414	0	1.840864	1.64393	0.52689	0.6854	0.78467	OXCT1-AS1	chr5	+	41870132	41871059	499
ENSG00000(	3.107376	2.408575	3.958241	0.749076	4.60216	1.64393	0.35773	0.74777	0.83239	CTD-2313N	chr11	-	71505409	71524905	2165
ENSG00000(	0	0	0	2.247227	5.522592	7.397684	-3.1062	0.014563	0.032619	CTC-419K1	chr5	-	73665201	73832801	568
ENSG00000(	6.214751	12.04288	2.638828	0	2.761296	2.465895	1.6593	0.11086	0.19074	CTD-2044J	chr5	-	6686438	6707824	3364
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-548L	chr4	-	34122516	34271369	546
ENSG00000(	10.35792	16.86003	10.55531	4.494453	8.283888	4.93179	1.0152	0.16313	0.26107	HAS2-AS1	chr8	+	1.23E+08	1.23E+08	1656
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP11-84A1	chr4	-	62937470	63031272	606
ENSG00000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	RP11-18D7	chr4	-	1.84E+08	1.84E+08	444
ENSG00000(	3.107376	0	2.638828	0	0	3.28786	0.48527	0.71491	0.80763	AC011406.	chr5	-	1.49E+08	1.49E+08	370
ENSG00000(	5.17896	10.83859	10.55531	0	0	0	4.3411	0.000288	0.000879	RP11-341G	chr4	+	14113592	14141676	1984
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTD-2316B	chr5	-	87008952	87029086	592
ENSG00000(	2.071584	0	2.638828	0	0	0	1.5584	0.24658	NA	AC006023.	chr7	+	40191212	40193750	1480
ENSG00000(	6.214751	10.83859	1.319414	11.98521	6.443024	13.9734	-0.73355	0.35915	0.48869	CCDC153	chr11	-	1.19E+08	1.19E+08	1701
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-766F	chr4	-	1.01E+08	1.01E+08	10086
ENSG00000(	11.39371	1.204288	7.916483	1.498151	2.761296	1.64393	1.5107	0.13469	0.22378	RP11-1079	chr17	+	47438527	47447360	601
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-377G	chr4	-	81104434	81111323	566
ENSG00000(	3.107376	0	0	0	0	0.821965	0.7418	0.57612	NA	AC063976.	chr5	-	1.32E+08	1.32E+08	463

ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AK3P4	chr5	+	1.15E+08	1.15E+08	583
ENSG00000(	3.107376	0	0	0	0.920432	0	0.70943	0.5938	NA	NPHP3-AS1	chr3	+	1.32E+08	1.33E+08	2972
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	CTC-236F1.	chr5	-	55753622	55777773	656
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-531A	chr5	-	5395491	5396070	580
ENSG00000(	2.071584	2.408575	7.916483	0	0	0	3.095	0.017733	0.038965	AC090103.	chr8	-	25798739	25801385	2645
ENSG00000(	7.250543	1.204288	3.958241	14.98151	12.88605	17.26126	-1.676	0.029208	0.060743	CTD-2260A	chr5	+	96120481	96121703	993
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	R3HDM2P1	chr4	+	1.34E+08	1.34E+08	1960
ENSG00000(	0	0	1.319414	5.992604	4.60216	8.219649	-2.7789	0.019083	0.041602	RP11-328K	chr4	+	1.04E+08	1.04E+08	527
ENSG00000(	15.53688	9.634302	18.47179	1.498151	10.12475	0	1.7132	0.048378	0.094292	ACTN3	chr11	+	66313866	66330800	3084
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	MTND5P9	chr4	-	1.56E+08	1.56E+08	1755
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-42A4	chr4	-	85292546	85301342	702
ENSG00000(	2.071584	0	2.638828	0	0	0	1.5584	0.24658	NA	RP11-114J	chr5	-	1.25E+08	1.26E+08	547
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTC-276P9	chr5	+	1.34E+08	1.34E+08	532
ENSG00000(	0	2.408575	0	4.494453	0	0	-0.46297	0.73291	0.8214	CTD-2215E	chr5	-	96523794	96537584	193
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-31K2	chr8	-	96998336	97005331	941
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	WI2-2373I	chr7	+	331310	334388	530
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-665C	chr4	-	1.82E+08	1.82E+08	207
ENSG00000(	11.39371	1.204288	0	3.745378	2.761296	0.821965	0.62295	0.58522	0.70271	RP11-231L	chr3	+	1.41E+08	1.41E+08	393
ENSG00000(	1.035792	0	3.958241	9.737982	8.283888	12.32947	-2.2389	0.020612	0.044546	RP11-798N	chr4	-	1.74E+08	1.74E+08	521
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	RP11-53O1	chr5	+	44753051	44765846	591
ENSG00000(	0	0	0	6.74168	2.761296	1.64393	-2.6344	0.04454	0.087838	RP11-632F	chr4	+	40788127	40788727	601
ENSG00000(	1.035792	0	2.638828	1.498151	1.840864	1.64393	-0.30218	0.81389	0.87912	HIGD1AP1	chr4	+	1.11E+08	1.11E+08	282
ENSG00000(	18.64425	7.225726	11.87472	2.247227	6.443024	5.753754	1.2798	0.098114	0.17259	RP11-666A	chr3	-	1.26E+08	1.26E+08	427
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CTD-2165H	chr5	+	14620129	14621422	1294
ENSG00000(	1.035792	0	3.958241	5.992604	6.443024	0	-0.97813	0.41516	0.54568	CTD-2248H	chr5	-	80538149	80538418	270
ENSG00000(	0	2.408575	0	0	1.840864	1.64393	-0.27261	0.84063	NA	RP11-173E	chr4	+	1.39E+08	1.39E+08	1238
ENSG00000(	0	0	0	2.996302	1.840864	6.575719	-2.6739	0.04084	0.081526	RP11-664D	chr8	-	69215703	69243726	1600
ENSG00000(	12.4295	0	10.55531	0	0	2.465895	2.3945	0.039851	0.079776	RP11-362F	chr4	-	1.42E+08	1.42E+08	2839
ENSG00000(	0	0	1.319414	0	1.840864	0.821965	-0.46629	0.72905	NA	RP11-18D7	chr4	-	1.84E+08	1.84E+08	518
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	ZNF807	chr19	-	35033367	35036300	1707
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTB-179I1.	chr4	-	78271523	78272388	866
ENSG00000(	21.75163	3.612863	2.638828	71.91125	61.66894	68.22309	-2.6846	3.78E-07	1.64E-06	RP5-955M1	chr20	-	49620194	49624577	3722
ENSG00000(	66.29068	55.39724	35.62417	94.38352	69.95283	69.04505	-0.55416	0.095347	0.16859	AL357673.	chr1	-	54635333	54637997	2665
ENSG00000(	4.143168	9.634302	6.597069	0	5.522592	2.465895	1.1456	0.25548	0.37375	RP11-357G	chr4	+	3314239	3314785	324
ENSG00000(	2.071584	4.817151	2.638828	0	0	0	2.7135	0.041136	0.082035	RP11-357G	chr4	-	3325704	3326489	786
ENSG00000(	7.250543	10.83859	14.51355	1.498151	2.761296	0	2.5213	0.007643	0.018253	RP11-100L	chr8	-	93711970	93891730	4282
ENSG00000(	4.143168	0	6.597069	5.243529	4.60216	2.465895	-0.16758	0.87299	0.92028	RP11-83A2	chr4	-	1.4E+08	1.4E+08	997
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC121336.	chr12	-	40223927	40229562	436
ENSG00000(	20.71584	8.430014	22.43003	21.72319	19.32907	26.30288	-0.36986	0.49571	0.62441	USP46-AS1	chr4	+	53525573	53527835	1048
ENSG00000(	3.107376	7.225726	6.597069	8.239831	0.920432	2.465895	0.43572	0.65418	0.75978	RP11-138I	chr4	-	1.38E+08	1.38E+08	1668
ENSG00000(	0	2.408575	1.319414	0	0.920432	0.821965	0.58326	0.66656	NA	SERBP1P6	chr5	-	42465502	42468970	932
ENSG00000(	42.46747	60.21439	60.69303	29.96302	34.97642	8.219649	1.1242	0.015275	0.034036	HHIP-AS1	chr4	-	1.46E+08	1.46E+08	1094
ENSG00000(	0	0	2.638828	14.98151	24.85166	18.90519	-3.8674	4.00E-05	0.000138	CTD-2135J	chr8	+	10586824	10628902	821
ENSG00000(	2.071584	6.021439	5.277655	0	0	0.821965	2.6299	0.035349	0.071767	CTD-2288C	chr5	-	51971027	52083860	593

ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	AC008834.	chr5	-	97421964	97496897	651
ENSG00000(	53.86118	92.73015	120.0667	65.16957	145.4283	86.30632	-0.15479	0.6539	0.75961	FMN1	chr15	-	33057747	33486897	12355
ENSG00000(	0	0	0	4.494453	0	0	-1.1446	0.38559	NA	MTND2P33	chr4	-	1.56E+08	1.56E+08	1031
ENSG00000(	5.17896	8.430014	0	5.992604	8.283888	1.64393	-0.17506	0.86125	0.91189	HMGB1P21	chr5	-	77940088	77940668	581
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	NUP210P3	chr3	-	1.29E+08	1.29E+08	388
ENSG00000(	0	4.817151	2.638828	0	0.920432	0.821965	1.3033	0.32006	0.44721	ATP5J2-PT(	chr7	-	99017372	99063787	2491
ENSG00000(	4.143168	10.83859	3.958241	2.996302	20.2495	32.8786	-1.422	0.068522	0.12741	MTND5P11	chr5	-	1.34E+08	1.34E+08	1812
ENSG00000(	3.107376	9.634302	5.277655	8.988907	0	4.93179	0.29489	0.76456	0.84451	CTD-2083E	chr5	-	269973	271631	522
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	RP11-777B	chr4	-	78879154	78879934	781
ENSG00000(	2.071584	2.408575	9.235896	0.749076	0	0	2.6595	0.034241	0.069814	CTD-2334D	chr5	+	1.2E+08	1.2E+08	1114
ENSG00000(	4.143168	0	0	0	0.920432	0	0.95689	0.47805	NA	RP11-72K1	chr5	-	97013251	97014385	1135
ENSG00000(	35.21692	32.51577	55.41538	46.44268	52.46462	47.67397	-0.25218	0.49654	0.62512	RP11-319G	chr3	+	1.39E+08	1.39E+08	602
ENSG00000(	0	1.204288	1.319414	2.247227	1.840864	0.821965	-0.61909	0.6373	0.74586	RP11-36B1	chr4	-	37589709	37590497	534
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-661C	chr5	+	946430	956635	559
ENSG00000(	0	1.204288	0	2.247227	0	0	-0.3239	0.80512	NA	HMGB1P44	chr4	+	78885094	78885665	572
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CTD-2287N	chr5	-	4012822	4013763	559
ENSG00000(	0	3.612863	3.958241	2.247227	4.60216	2.465895	-0.24723	0.82738	0.88874	RP11-94H1	chr8	-	29672520	29712059	1867
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTB-174D1	chr5	+	1.68E+08	1.68E+08	365
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-241J:	chr5	-	80042158	80042638	481
ENSG00000(	3.107376	1.204288	0	0	2.761296	0.821965	0.19477	0.88316	0.92688	CTD-2256P	chr5	+	10248437	10250027	688
ENSG00000(	2.071584	4.817151	0	0	0	0	2.0839	0.12453	0.21	CTD-2113L	chr5	-	35678586	35827120	540
ENSG00000(	4.143168	6.021439	0	3.745378	21.16994	3.28786	-1.2241	0.20691	0.31605	KRT8P46	chr4	-	1.04E+08	1.04E+08	1426
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-445C	chr5	-	4452043	4866334	721
ENSG00000(	0	0	0	1.498151	1.840864	0	-0.93652	0.47589	NA	LAMTOR3P	chr5	-	1.18E+08	1.18E+08	232
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	RP11-815N	chr4	+	1.6E+08	1.6E+08	717
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-73G1	chr4	+	1.53E+08	1.53E+08	488
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-259C	chr5	+	1933977	1959290	718
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-766N	chr12	-	65314625	65376304	447
ENSG00000(	3.107376	6.021439	7.916483	0	9.20432	17.26126	-0.54941	0.56148	0.6815	RP11-1334	chr5	+	1.77E+08	1.77E+08	434
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	RP11-742B	chr4	-	88489187	88655108	821
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	RP11-510N	chr1	+	2.02E+08	2.02E+08	987
ENSG00000(	1.035792	0	0	0	1.840864	2.465895	-0.90898	0.50286	NA	RP11-731D	chr4	+	1.52E+08	1.52E+08	486
ENSG00000(	0	0	0	0.749076	0.920432	0.821965	-0.73223	0.57364	NA	HMGN2P4	chr5	-	75537849	75538229	381
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-58B2	chr5	+	1.02E+08	1.02E+08	527
ENSG00000(	0	0	1.319414	1.498151	0	0.821965	-0.38347	0.77483	NA	RP11-539G	chr4	-	39715462	39716071	287
ENSG00000(	2.071584	2.408575	2.638828	0	0.920432	3.28786	0.53585	0.66513	0.76874	SNORA58	chr3	-	1.31E+08	1.31E+08	137
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	CTNNAP1	chr5	-	1.15E+08	1.15E+08	2728
ENSG00000(	1.035792	2.408575	1.319414	0	1.840864	0.821965	0.53814	0.68205	0.78248	RP5-951N9	chr12	-	1489226	1500668	2088
ENSG00000(	7.250543	6.021439	9.235896	13.48336	19.32907	13.15144	-0.96393	0.14999	0.24403	AC005609.	chr5	-	1.4E+08	1.4E+08	2884
ENSG00000(	53.86118	62.62296	51.45714	0	20.2495	13.15144	1.9059	0.06883	0.12788	CTB-113P1	chr5	+	1.51E+08	1.51E+08	1973
ENSG00000(	37.28851	68.6444	48.81831	99.62705	89.2819	86.30632	-0.8248	0.008804	0.020726	CTD-2015H	chr5	-	79778112	79783882	1151
ENSG00000(	44.53905	50.58008	54.09597	27.7158	53.38506	46.03004	0.22958	0.54121	0.66411	RP11-330N	chr9	-	99660348	99711867	548
ENSG00000(	0	1.204288	0	0.749076	1.840864	3.28786	-1.2679	0.34386	0.47307	COX6B1P5	chr4	+	2235978	2236226	249
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	TBCAP3	chr4	-	99830688	99830999	312

ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	MAST4-IT1	chr5	+	65958159	65958816	658
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	KRT18P25	chr4	+	40021860	40023137	1278
ENSG00000(	1.035792	3.612863	0	0	0	1.64393	0.7866	0.56136	0.68149	CTC-287O8	chr5	-	1.09E+08	1.09E+08	565
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-461C	chr5	+	53616774	53710955	735
ENSG00000(	8.286335	0	1.319414	0	0	0	2.5459	0.059133	0.11229	RP11-478C	chr4	+	2326194	2326809	616
ENSG00000(	1.035792	4.817151	0	1.498151	4.60216	3.28786	-0.50272	0.66798	0.7712	RP11-376C	chr4	-	1.78E+08	1.78E+08	753
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	AC051649.	chr11	+	1885407	1887897	330
ENSG00000(	45.57484	68.6444	47.4989	29.21395	40.49901	68.22309	0.22502	0.56517	0.68462	C1orf213	chr1	+	23695490	23698332	2547
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	CTD-2325A	chr5	-	42892421	42892919	499
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP1-7G5.6	chr12	+	1.1E+08	1.1E+08	728
ENSG00000(	4.143168	2.408575	0	0	1.840864	2.465895	0.43146	0.73467	0.82247	RP11-290F	chr4	-	1.85E+08	1.85E+08	2040
ENSG00000(	1.035792	3.612863	3.958241	0	2.761296	2.465895	0.53262	0.65571	0.76072	RP11-39E3	chr3	-	1.31E+08	1.31E+08	572
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTD-2066L	chr5	+	33009100	33025830	599
ENSG00000(	2.071584	2.408575	1.319414	2.996302	2.761296	0	0.011231	0.99272	0.99538	RP11-43D2	chr5	+	1.24E+08	1.24E+08	832
ENSG00000(	198.872	214.3632	207.148	489.1463	555.9409	549.8945	-1.3577	3.05E-17	2.70E-16	HAUS5	chr19	+	36103646	36116251	4462
ENSG00000(	0	0	0	5.992604	0.920432	0.821965	-2.0618	0.12611	0.21212	CTD-2194D	chr5	+	1884080	1884763	425
ENSG00000(	1.035792	2.408575	0	0	3.681728	0.821965	-0.21393	0.87189	0.91953	MTND6P4	chr5	+	1.34E+08	1.34E+08	522
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-227F	chr4	+	41752362	41759358	561
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	RP11-381N	chr4	+	1.24E+08	1.24E+08	539
ENSG00000(	7.250543	4.817151	13.19414	4.494453	4.60216	9.863579	0.36496	0.65116	0.7573	SUDS3P1	chr5	+	1.77E+08	1.77E+08	966
ENSG00000(	0	2.408575	2.638828	0	0	0.821965	1.2658	0.35072	NA	CTB-35F21.	chr5	-	1.39E+08	1.39E+08	412
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-701P	chr4	-	1.86E+08	1.86E+08	751
ENSG00000(	1.035792	2.408575	3.958241	3.745378	0	0.821965	0.46262	0.70765	0.80236	PRDX2P3	chr5	+	1.79E+08	1.79E+08	586
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTD-2290P	chr5	+	32522864	32523971	1108
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	AC006445.	chr4	-	13633444	13634223	472
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CTC-472C2	chr5	-	1.16E+08	1.16E+08	553
ENSG00000(	155.3688	134.8802	241.4527	53.18436	99.40666	80.55256	1.1777	4.90E-05	0.000167	PCDHA11	chr5	+	1.4E+08	1.4E+08	5257
ENSG00000(	0	0	0	1.498151	1.840864	1.64393	-1.5124	0.26495	NA	CTB-118N6	chr5	+	1.16E+08	1.16E+08	482
ENSG00000(	4.143168	4.817151	1.319414	0	0.920432	0	2.2285	0.083145	0.15032	CTC-484P3	chr5	+	94124494	94129304	1940
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	MTND4P29	chr2	+	2.02E+08	2.02E+08	1372
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTC-506B8	chr5	-	96076783	96078402	565
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP11-556C	chr8	+	8011830	8074438	999
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CTB-36O1.3	chr5	-	1.34E+08	1.34E+08	135
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	HSPD1P5	chr4	+	1.46E+08	1.46E+08	1720
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CTD-2139B	chr5	-	17369334	17375686	285
ENSG00000(	5.17896	3.612863	3.958241	6.74168	6.443024	2.465895	-0.25033	0.78819	0.86142	RP11-360F	chr4	-	39114297	39128438	946
ENSG00000(	1.035792	4.817151	7.916483	0	0	1.64393	2.1238	0.083278	0.15055	ATP1B1P1	chr4	+	42031226	42032140	915
ENSG00000(	0	0	0	0	1.840864	3.28786	-1.4188	0.29365	NA	AC022558.	chr15	+	83684154	83684448	132
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-227F	chr4	-	41690875	41694814	435
ENSG00000(	3.107376	0	0	0	1.840864	0.821965	0.14551	0.91456	NA	ATP5L2	chr22	-	43035809	43036607	799
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTC-342P1	chr5	-	1.44E+08	1.44E+08	1115
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-452J	chr4	+	16180562	16184743	414
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-83M	chr5	+	66932210	66934770	2561
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC195454.	chr4	+	40318502	40332436	957

ENSG00000(	1.035792	12.04288	11.87472	23.22134	6.443024	18.90519	-0.90482	0.23023	0.3436	TMEM150C	chr4	-	83405743	83483510	1990
ENSG00000(	4.143168	2.408575	3.958241	0	0	1.64393	1.8087	0.14924	0.24295	RP11-548H	chr4	-	1.2E+08	1.2E+08	3505
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-557J:	chr4	-	1.47E+08	1.47E+08	1877
ENSG00000(	4.143168	2.408575	6.597069	2.247227	1.840864	3.28786	0.67936	0.51057	0.6379	AC010226.	chr5	+	1.15E+08	1.15E+08	765
ENSG00000(	2.071584	18.06432	13.19414	1.498151	5.522592	0	1.9202	0.047695	0.093154	RP11-665G	chr4	-	15006566	15429538	630
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	PGAM1P9	chr11	-	92099662	92100416	755
ENSG00000(	15.53688	9.634302	25.06886	8.239831	3.681728	5.753754	1.3837	0.047256	0.092419	RP11-468H	chr8	+	16988690	17007298	2292
ENSG00000(	9.322127	3.612863	9.235896	0.749076	1.840864	4.109825	1.4721	0.12855	0.21529	EEF1A1P9	chr4	+	1.06E+08	1.06E+08	1383
ENSG00000(	0	0	0	5.243529	4.60216	0.821965	-2.5476	0.053447	0.10297	RP5-916L7	chr12	-	1.26E+08	1.26E+08	4972
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-756P	chr4	+	1.9E+08	1.9E+08	437
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC084854.	chr15	-	66108640	66109819	879
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-319J:	chr3	+	98501032	98502037	1006
ENSG00000(	0	0	0	0	0.920432	4.109825	-1.3831	0.30514	NA	RP11-688H	chr4	-	77430437	77430872	436
ENSG00000(	8.286335	6.021439	10.55531	2.996302	6.443024	0	1.2097	0.20161	0.30921	CTD-2210P	chr5	-	43587020	43588325	994
ENSG00000(	0	0	2.638828	0	0.920432	0	0.55591	0.6721	NA	CTC-575I1(	chr5	-	73073864	73082316	556
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-241G	chr5	-	68773299	68798293	326
ENSG00000(	8.286335	3.612863	1.319414	0.749076	4.60216	0	1.0317	0.36954	0.49992	FTH1P24	chr4	+	1.4E+08	1.4E+08	462
ENSG00000(	4.143168	8.430014	7.916483	2.996302	11.96562	3.28786	0.1539	0.85903	0.91042	RP11-26P1	chr4	+	1.15E+08	1.15E+08	441
ENSG00000(	0	0	0	9.737982	6.443024	4.109825	-3.5684	0.003692	0.009395	RP11-267A	chr5	+	1.74E+08	1.74E+08	844
ENSG00000(	12.4295	7.225726	18.47179	6.74168	9.20432	8.219649	0.61006	0.37986	0.5105	RP11-438E	chr4	+	79892902	80229952	973
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	RP11-153N	chr4	+	1.55E+08	1.55E+08	521
ENSG00000(	0	0	0	22.47227	12.88605	19.72716	-5.0629	4.86E-06	1.87E-05	OR5H5P	chr3	+	97916055	97916982	928
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	CTD-2194D	chr5	+	1887446	1900607	1635
ENSG00000(	9.322127	7.225726	6.597069	0	13.80648	2.465895	0.45529	0.6354	0.7444	RP11-26J3.	chr8	-	80681607	80783994	2126
ENSG00000(	0	0	2.638828	0	0	1.64393	0.26729	0.84149	NA	RP11-317N	chr4	+	54525375	54603323	1616
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CTD-2275D	chr5	+	73618311	73624122	724
ENSG00000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	RP3-468B3	chr6	-	33835283	33864691	3151
ENSG00000(	42.46747	21.67718	34.30476	21.72319	29.45382	20.54912	0.45103	0.32525	0.45279	UGDH-AS1	chr4	+	39529639	39596327	2787
ENSG00000(	236.1606	245.6747	226.9392	313.1136	230.108	330.4299	-0.30155	0.11614	0.19851	NPM1P27	chr5	-	93018544	93019373	830
ENSG00000(	3.107376	0	0	0	1.840864	0	0.36193	0.78835	NA	RP11-432N	chr5	+	17604866	17605486	621
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP13-297E	chrX	+	1746639	1755356	510
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-374A	chr5	-	21323982	21341484	5454
ENSG00000(	13.46529	2.408575	10.55531	0	0.920432	0.821965	3.0977	0.004387	0.01099	CTB-78O21	chr5	-	1.45E+08	1.45E+08	876
ENSG00000(	5.17896	10.83859	15.83297	0	0	2.465895	2.991	0.003719	0.009454	RP11-434D	chr5	+	66675206	67101066	1556
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-508N	chr5	+	1.24E+08	1.24E+08	451
ENSG00000(	0	0	0	0.749076	1.840864	0	-0.68825	0.58858	NA	RP11-1136	chr8	-	1.29E+08	1.29E+08	3301
ENSG00000(	43.50326	49.3758	32.98534	17.97781	16.56778	15.61733	1.2923	0.00345	0.008825	RP11-219G	chr4	+	1.89E+08	1.9E+08	2435
ENSG00000(	1.035792	3.612863	0	0	3.681728	1.64393	-0.11195	0.93107	0.95857	RP1-27K12	chr6	+	53367983	53371717	547
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-1018	chr17	-	49389970	49412526	1723
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-503N	chr4	+	2428248	2452087	927
ENSG00000(	122.2234	131.2674	138.5384	41.19916	60.74851	54.24968	1.3176	1.53E-06	6.20E-06	RP11-697N	chr8	-	76135639	76236976	1164
ENSG00000(	2.071584	2.408575	1.319414	0	0	0	1.9715	0.14607	NA	RP11-1C1.4	chr5	-	10493639	10502840	2130
ENSG00000(	11.39371	2.408575	1.319414	1.498151	2.761296	0	1.4315	0.20922	0.31883	RP11-893F	chr17	+	48286333	48291820	839
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	CTC-563A5	chr5	+	1.79E+08	1.79E+08	569

ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-25H1	chr4	+	66864564	67015730	754
ENSG00000(	2.071584	0	5.277655	0	0.920432	0	1.6646	0.21441	0.32488	RP11-438D	chr3	-	1.41E+08	1.41E+08	422
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC005741.	chr5	+	1.3E+08	1.3E+08	432
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-497K	chr4	+	1.63E+08	1.63E+08	1105
ENSG00000(	2.071584	1.204288	0	14.98151	23.0108	19.72716	-3.5222	7.34E-05	0.000244	RP11-346A	chr5	-	1.29E+08	1.29E+08	786
ENSG00000(	3.107376	0	2.638828	0	0	0	1.8293	0.17689	NA	CTC-448D2	chr5	-	1.18E+08	1.18E+08	497
ENSG00000(	4.143168	3.612863	1.319414	0	0	0	2.6368	0.048148	0.09393	RP11-503N	chr4	+	2451700	2464668	1398
ENSG00000(	125.3308	111.9988	106.8725	95.88167	196.052	169.3248	-0.41306	0.13151	0.21931	CTD-2231H	chr5	+	92266	139978	705
ENSG00000(	16.57267	32.51577	18.47179	32.21025	20.2495	18.90519	-0.08277	0.8709	0.91882	NAIP	chr5	-	70264310	70320941	6124
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-94C2	chr17	-	48580773	48585689	349
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP13-497K	chr4	+	23781213	23784183	442
ENSG00000(	17.60846	6.021439	9.235896	3.745378	21.16994	4.109825	0.1853	0.81364	0.87897	RP11-298J	chr10	+	1.27E+08	1.27E+08	555
ENSG00000(	307.6302	287.8248	306.104	171.5383	169.3595	170.1467	0.81546	4.35E-06	1.68E-05	ZNF286B	chr17	-	18561742	18585575	5328
ENSG00000(	2.071584	3.612863	1.319414	2.996302	0	0	0.77812	0.54656	0.66857	RP11-93L9	chr4	+	1.25E+08	1.25E+08	5262
ENSG00000(	9.322127	14.45145	6.597069	5.243529	3.681728	2.465895	1.2658	0.12422	0.20958	RBMXP4	chr4	-	1.1E+08	1.1E+08	1134
ENSG00000(	127.4024	105.9773	118.7472	107.8669	94.8045	129.0485	0.085409	0.72928	0.81855	ZNF324B	chr19	+	58962971	58969200	3770
ENSG00000(	26.93059	30.10719	15.83297	6.74168	17.48821	9.041614	1.0927	0.060812	0.11496	CTD-2587N	chr5	-	1.09E+08	1.09E+08	5471
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	SPATS1	chr6	+	44310397	44344904	1354
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	AC091969.	chr5	-	1.52E+08	1.53E+08	2193
ENSG00000(	0	4.817151	0	0	0.920432	0.821965	0.77746	0.56586	0.68521	RBBP4P1	chr5	-	14797234	14798509	1276
ENSG00000(	1.035792	0	2.638828	0	1.840864	0	0.50894	0.70757	NA	RP11-97O1	chr15	-	89128802	89148341	1835
ENSG00000(	5.17896	9.634302	11.87472	3.745378	7.363456	3.28786	0.79893	0.33256	0.4606	RP11-159F	chr5	+	43484061	43509458	482
ENSG00000(	3.107376	0	5.277655	9.737982	13.80648	11.50751	-1.8242	0.037673	0.075954	ANKRD20A	chr21	+	15436646	15441408	492
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTB-161M1	chr5	-	1.18E+08	1.18E+08	812
ENSG00000(	7.250543	9.634302	5.277655	0	1.840864	0	2.8182	0.01151	0.02638	RP11-340B	chr4	+	1.67E+08	1.67E+08	2163
ENSG00000(	3.107376	2.408575	3.958241	0	6.443024	0.821965	0.30787	0.79185	0.86401	AC006160.	chr4	-	17589090	17616194	750
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-404I7	chr4	-	1.34E+08	1.34E+08	462
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTD-2201E	chr5	+	42917516	42918086	571
ENSG00000(	4.143168	4.817151	3.958241	2.247227	3.681728	0	0.89816	0.41477	0.54526	CTB-35F21.	chr5	+	1.39E+08	1.39E+08	568
ENSG00000(	1.035792	0	2.638828	0.749076	0.920432	0.821965	0.32125	0.80985	0.87669	RP11-148B	chr4	-	1.14E+08	1.14E+08	640
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-83C7	chr4	-	38422283	38524801	2059
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-692C	chr5	-	2787565	2788663	1099
ENSG00000(	0	3.612863	1.319414	0	0	0	1.6005	0.2346	NA	CTC-558O1	chr5	+	94314855	94316597	527
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-438N	chr12	-	1.14E+08	1.14E+08	2088
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	RP11-116C	chr5	-	24578403	24578670	268
ENSG00000(	7.250543	3.612863	3.958241	9.737982	11.04518	11.50751	-1.0054	0.19796	0.30517	SERBP1P5	chr4	-	79102020	79103200	1181
ENSG00000(	0	2.408575	2.638828	0.749076	0	0	1.296	0.33942	NA	RP11-234C	chr4	+	1.62E+08	1.62E+08	2840
ENSG00000(	10.35792	9.634302	6.597069	3.745378	11.04518	13.9734	-0.09225	0.90187	0.93908	CTD-2203K	chr5	-	33424131	33440725	537
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	CTD-2195N	chr5	+	1.27E+08	1.27E+08	297
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	RP11-478P	chr5	-	57186154	57194989	4069
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTC-537E7.	chr5	+	67819705	67825834	587
ENSG00000(	110.8297	124.0416	75.20659	32.95932	79.15715	81.37453	0.6761	0.050777	0.098412	RP11-440L	chr4	-	756175	775637	618
ENSG00000(	3.107376	9.634302	6.597069	0	2.761296	9.041614	0.59349	0.55539	0.67608	CTB-46B19	chr5	+	1.38E+08	1.38E+08	1067
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-168E	chr4	-	95664951	95678684	511

ENSG00000(	2.071584	0	0	3.745378	2.761296	9.863579	-2.109	0.074213	0.13635	RP11-98D1	chr1	-	1.52E+08	1.52E+08	382
ENSG00000(	0	6.021439	1.319414	0	0	0	2.1383	0.11496	0.19679	RP11-286E	chr4	-	1.09E+08	1.09E+08	3147
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTC-218H9	chr5	+	1.44E+08	1.44E+08	469
ENSG00000(	4.143168	8.430014	14.51355	2.247227	8.283888	4.109825	0.79157	0.35021	0.47991	RP11-635L	chr4	-	1.7E+08	1.7E+08	552
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTC-441N1	chr5	-	1.21E+08	1.21E+08	428
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-703G	chr4	+	1.05E+08	1.05E+08	812
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	HMGN1P1:	chr5	-	1.11E+08	1.11E+08	138
ENSG00000(	1.035792	0	0	3.745378	0	0	-0.7218	0.59124	NA	RP11-321E	chr5	-	17511942	17512347	406
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	CTD-2544H	chr5	-	1.22E+08	1.22E+08	583
ENSG00000(	7.250543	3.612863	1.319414	0	0	1.64393	1.9895	0.10905	0.18821	RP11-610J:	chr4	-	1.7E+08	1.7E+08	448
ENSG00000(	2.071584	2.408575	6.597069	0	0	1.64393	1.8528	0.13905	0.2295	IFNAR2	chr21	+	34619079	34656082	1363
ENSG00000(	1.035792	1.204288	2.638828	14.98151	9.20432	27.94681	-3.0234	0.000546	0.001593	RP11-496H	chr3	+	1.97E+08	1.97E+08	1497
ENSG00000(	3.107376	8.430014	5.277655	4.494453	3.681728	1.64393	0.65413	0.49533	0.62403	RP3-340I3.	chr12	-	1609691	1616484	2417
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-281P	chr4	+	11627338	11815582	747
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	OR52V1P	chr11	-	5548507	5549404	898
ENSG00000(	8.286335	1.204288	1.319414	0	0	0	2.8572	0.031277	0.064469	RP11-710F	chr4	-	1.07E+08	1.07E+08	3526
ENSG00000(	2.071584	0	0	13.48336	11.96562	13.9734	-3.3665	0.000827	0.00235	CTC-329D1	chr5	-	1.4E+08	1.4E+08	549
ENSG00000(	0	0	0	0	4.60216	0.821965	-1.4643	0.27877	NA	HOXC-AS5	chr12	-	54329112	54333427	1408
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-436H	chr5	+	1.24E+08	1.24E+08	607
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTC-349C3	chr5	-	1.35E+08	1.35E+08	2162
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	MRPS33P2	chr4	-	38008405	38008726	322
ENSG00000(	0	2.408575	1.319414	0.749076	0	0	0.98048	0.46819	NA	RP11-310P	chr5	-	602735	612325	591
ENSG00000(	0	1.204288	7.916483	9.737982	11.04518	18.08323	-1.8778	0.035846	0.072671	CTC-325J2:	chr5	-	79926132	79927409	549
ENSG00000(	12.4295	3.612863	6.597069	5.243529	31.29469	18.90519	-1.1684	0.11038	0.19002	TNRC18P1	chr4	-	1.42E+08	1.42E+08	3650
ENSG00000(	2.071584	0	0	0.749076	0	0	0.47431	0.71145	NA	CTD-2227C	chr5	-	82308104	82308928	825
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-432N	chr5	+	17632197	17632792	596
ENSG00000(	262.0554	304.6848	258.6051	8.239831	20.2495	23.01502	3.9713	1.07E-40	2.25E-39	MIR143HG	chr5	+	1.49E+08	1.49E+08	8398
ENSG00000(	244.4469	215.5675	271.7992	174.5346	208.0176	207.9571	0.30832	0.10969	0.18908	NOP14-AS1	chr4	+	2936626	2963465	3860
ENSG00000(	0	0	0	4.494453	11.04518	4.93179	-3.5685	0.003711	0.009437	RP11-619J:	chr4	-	30777879	30795592	180
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-279C	chr4	+	1.86E+08	1.86E+08	394
ENSG00000(	18.64425	16.86003	18.47179	8.988907	5.522592	10.68554	1.0319	0.097578	0.17188	RP11-423H	chr5	+	1.77E+08	1.77E+08	613
ENSG00000(	10.35792	4.817151	11.87472	8.239831	1.840864	9.863579	0.38555	0.63491	0.74398	RP11-360F	chr4	+	39135533	39137228	455
ENSG00000(	1.035792	0	1.319414	1.498151	2.761296	1.64393	-0.84788	0.51292	0.63984	RP11-1336	chr4	+	1.52E+08	1.52E+08	2209
ENSG00000(	0	0	2.638828	0	1.840864	0.821965	-0.01672	0.99017	NA	THEGL	chr4	+	57396775	57469673	1650
ENSG00000(	0	0	0	4.494453	0	0	-1.1446	0.38559	NA	RP11-378A	chr8	-	2447076	2480453	1705
ENSG00000(	0	1.204288	0	4.494453	1.840864	1.64393	-1.6444	0.21006	0.31976	RP11-598F	chr12	-	246577	258335	4913
ENSG00000(	16.57267	45.76293	35.62417	9.737982	2.761296	5.753754	2.2676	0.000216	0.00067	SRD5A3-AS	chr4	-	56230138	56262009	1617
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-1026	chr5	+	1.77E+08	1.77E+08	504
ENSG00000(	2.071584	2.408575	9.235896	3.745378	3.681728	9.041614	-0.24747	0.7939	0.86525	ZNF564	chr19	-	12636184	12662356	2935
ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	CTD-2236F	chr5	-	75902433	75904795	1588
ENSG00000(	6.214751	14.45145	3.958241	3.745378	3.681728	0.821965	1.3623	0.14417	0.23624	FER1L5	chr2	+	97308474	97370624	6477
ENSG00000(	1.035792	3.612863	2.638828	0	0	2.465895	0.99812	0.44116	0.57098	RP3-486L4	chr6	+	88360648	88362932	562
ENSG00000(	1.035792	0	0	2.247227	0	1.64393	-0.82311	0.54382	NA	RP11-83M:	chr5	-	66988640	66989028	389
ENSG00000(	39.36009	32.51577	63.33186	1.498151	3.681728	2.465895	3.922	4.57E-10	2.57E-09	CTD-2127H	chr5	-	38736157	38845931	837

ENSG00000(	4.143168	1.204288	0	1.498151	0	2.465895	0.28998	0.82347	0.88612	RP11-673E	chr4	-	1.45E+08	1.45E+08	540
ENSG00000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	RP11-60A8	chr5	+	72509774	72590761	941
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-254I2	chr5	-	95549050	95550779	652
ENSG00000(	32.10955	26.49433	38.263	4.494453	0	5.753754	3.0018	5.00E-06	1.92E-05	ECSCR	chr5	-	1.39E+08	1.39E+08	450
ENSG00000(	3.107376	6.021439	0	3.745378	5.522592	4.93179	-0.51001	0.62271	0.73456	RP11-415I1	chr12	-	64017568	64189498	275
ENSG00000(	4.143168	2.408575	1.319414	0	0	0	2.42	0.071961	0.13287	RP11-466G	chr4	+	89448311	89449321	657
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTD-2278B	chr5	-	96672562	96672744	183
ENSG00000(	2.071584	0	0	2.247227	0.920432	1.64393	-0.67686	0.61225	0.72568	RP11-1286	chr4	+	9080749	9143334	933
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CTD-2193P	chr5	-	80409204	80410671	555
ENSG00000(	0	2.408575	1.319414	0	4.60216	0	-0.17031	0.89897	0.93731	RP11-447H	chr5	+	43206811	43207913	1103
ENSG00000(	2.071584	2.408575	3.958241	0	0	0.821965	2	0.12681	0.21305	CTD-2143L	chr5	-	9629558	9903938	1847
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	SCARNA22	chr4	+	1976363	1976487	125
ENSG00000(	3.107376	3.612863	3.958241	0	0	4.93179	0.80719	0.50335	0.6313	EAF1-AS1	chr3	-	15477678	15485576	950
ENSG00000(	4.143168	0	0	0	0.920432	0	0.95689	0.47805	NA	RP11-346J2	chr5	+	99737145	99744603	563
ENSG00000(	181.2636	181.8474	195.2732	653.943	579.8722	663.3257	-1.7601	2.00E-28	2.87E-27	RP11-20D1	chr12	+	8940853	8948385	1972
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTC-428G2	chr5	+	1.15E+08	1.15E+08	370
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	HSD3BP3	chr1	+	1.2E+08	1.2E+08	994
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	CTD-2199C	chr5	+	10137250	10138477	943
ENSG00000(	0	4.817151	0	26.21764	45.10117	22.19305	-3.8461	1.80E-06	7.26E-06	RP11-269F	chr4	-	1.13E+08	1.13E+08	583
ENSG00000(	2.071584	1.204288	0	1.498151	5.522592	3.28786	-1.1637	0.33274	0.46076	RP11-311D	chr4	+	1.07E+08	1.07E+08	744
ENSG00000(	1.035792	4.817151	0	2.247227	11.04518	8.219649	-1.5202	0.14614	0.23883	CTD-2201I1	chr5	-	79348197	79379477	2705
ENSG00000(	2.071584	2.408575	9.235896	0	3.681728	0.821965	1.2387	0.28204	0.4047	VCAN-AS1	chr5	-	82827171	82877139	453
ENSG00000(	0	8.430014	0	0	0	0	2.183	0.10757	0.18626	CTD-2325B	chr4	-	1.25E+08	1.25E+08	430
ENSG00000(	1.035792	1.204288	0	0	1.840864	0.821965	-0.10652	0.9374	NA	AC011330.	chr15	-	43955852	43976537	3235
ENSG00000(	8.286335	12.04288	17.15238	17.97781	21.16994	15.61733	-0.53041	0.36805	0.49825	RP11-77P1	chr3	+	1.3E+08	1.3E+08	1608
ENSG00000(	2.071584	0	9.235896	0	3.681728	1.64393	0.79149	0.51267	0.63966	CTD-2653M	chr5	+	36885308	36886599	1292
ENSG00000(	6.214751	8.430014	5.277655	0	0	0	3.9028	0.001564	0.004241	AC145676.	chr7	-	227554	229557	2004
ENSG00000(	11.39371	9.634302	14.51355	92.88537	69.0324	62.46933	-2.5981	1.33E-09	7.19E-09	HS3ST5	chr6	-	1.14E+08	1.15E+08	3901
ENSG00000(	14.50109	12.04288	29.0271	11.98521	17.48821	13.9734	0.33253	0.56832	0.68742	EEF1A1P19	chr5	-	43495175	43496556	1382
ENSG00000(	0	0	0	0.749076	1.840864	1.64393	-1.2986	0.33698	NA	CTD-2503C	chr5	-	74213551	74319753	846
ENSG00000(	305.5586	320.3405	298.1875	269.6672	254.9597	275.3582	0.20698	0.21186	0.32187	PVT1	chr8	+	1.29E+08	1.29E+08	1699
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	MTRNR2L5	chr10	+	57358750	57360488	1739
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	LGALS16	chr19	+	40146534	40151287	654
ENSG00000(	9.322127	4.817151	18.47179	23.97042	26.69253	21.37109	-1.0984	0.063528	0.11936	RP11-177C	chr4	+	37869913	37871599	1058
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-39K2	chr9	-	5131979	5164251	443
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-115J1	chr11	+	28724162	29085368	806
ENSG00000(	2.071584	0	9.235896	11.98521	5.522592	5.753754	-0.91487	0.34258	0.4716	RP11-63E5	chr8	-	255306	281026	880
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-481C	chr17	+	49119885	49162832	332
ENSG00000(	2.071584	0	2.638828	0	0	0	1.5584	0.24658	NA	CTC-563A5	chr5	-	1.79E+08	1.79E+08	676
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP11-665I2	chr4	+	31508288	31560443	426
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-447H	chr5	-	43225608	43225915	308
ENSG00000(	0	0	0	0	5.522592	0.821965	-1.658	0.22147	0.33315	ALG1L11P	chr8	+	12036206	12040228	450
ENSG00000(	0	0	0	2.247227	0.920432	0.821965	-1.2297	0.36205	NA	RP11-586D	chr4	+	6202460	6240044	2547
ENSG00000(	30.03797	15.65574	32.98534	20.97412	24.85166	20.54912	0.23864	0.62476	0.73627	CTD-2541M	chr8	-	6475996	6565730	2147

ENSG0000(	0	1.204288	0	1.498151	0.920432	2.465895	-1.0724	0.42642	0.55667	CTD-2175A	chr5	-	52228249	52286108	595
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP5-1029K	chr17	-	47583019	47651426	1221
ENSG0000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	TRIM51CP	chr11	+	48967246	48973447	1357
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-122C	chr5	-	38710469	38720375	800
ENSG0000(	2.071584	0	0	0.749076	0	4.109825	-0.63913	0.63613	0.74488	RP4-671G1	chr1	-	1.13E+08	1.13E+08	646
ENSG0000(	1282.31	1322.308	1225.735	1099.643	911.2277	1037.32	0.32832	0.008684	0.020476	PDCD6	chr5	+	271736	353971	3763
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTD-2280E	chr5	-	1.22E+08	1.22E+08	563
ENSG0000(	0	1.204288	1.319414	2.247227	2.761296	0	-0.60198	0.65099	0.75715	LINC00536	chr8	-	1.17E+08	1.17E+08	2692
ENSG0000(	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	CTC-329H1	chr5	+	1.08E+08	1.08E+08	948
ENSG0000(	3.107376	0	1.319414	1.498151	0	1.64393	0.30205	0.81979	0.88374	GOLGA8K	chr15	-	32684983	32695396	1894
ENSG0000(	14.50109	12.04288	14.51355	8.239831	10.12475	20.54912	0.073895	0.90726	0.94286	RAC1P2	chr4	-	46725793	46726625	833
ENSG0000(	4.143168	12.04288	3.958241	0	0	0	3.8836	0.001756	0.004724	RP11-454P	chr5	+	17684693	17955966	781
ENSG0000(	0	0	0	0.749076	3.681728	3.28786	-2.0813	0.12163	0.20618	AC142293.	chr4	-	75418301	75514664	732
ENSG0000(	1.035792	15.65574	3.958241	7.490755	8.283888	11.50751	-0.36636	0.66547	0.76904	XBP1P1	chr5	+	1.12E+08	1.12E+08	652
ENSG0000(	1.035792	0	6.597069	0	0	0	2.1847	0.10719	0.18573	CCDC79	chr16	-	66788879	66835523	2541
ENSG0000(	1.035792	0	3.958241	0	0.920432	0.821965	0.85957	0.52209	0.64757	CDC42P4	chr4	+	1.1E+08	1.1E+08	563
ENSG0000(	0	0	0	2.996302	0.920432	5.753754	-2.4092	0.069626	0.12915	CHCHD2P7	chr4	-	88707072	88707523	452
ENSG0000(	0	0	0	5.992604	0	0.821965	-1.772	0.19153	0.29714	OR5H3P	chr3	+	97926267	97927185	919
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-580P	chr4	-	74202950	74203488	539
ENSG0000(	5.17896	0	0	2.996302	0	0	0.43033	0.75031	0.8343	RP11-155G	chr5	-	96785062	96785445	384
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTC-529L1	chr5	-	92011663	92023961	730
ENSG0000(	2.071584	0	2.638828	0	1.840864	0	0.7447	0.58184	0.69955	YWHAQP6	chr3	-	1.41E+08	1.41E+08	304
ENSG0000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RPS4XP20	chr19	-	34513561	34514332	772
ENSG0000(	227.8742	236.0404	211.1062	149.8151	138.0648	97.81383	0.80217	0.000264	0.00081	TMEM158	chr3	-	45265958	45267770	1813
ENSG0000(	0	0	0	16.47966	11.04518	8.219649	-4.4275	0.000126	0.000404	RP11-91K8	chr3	-	1.33E+08	1.33E+08	894
ENSG0000(	2.071584	2.408575	0	0	1.840864	0.821965	0.46891	0.72503	0.81553	RP11-359P	chr5	+	1.22E+08	1.22E+08	561
ENSG0000(	0	0	3.958241	0	3.681728	0	0.050432	0.97032	0.98261	CTD-2201E	chr5	-	9519965	9523290	543
ENSG0000(	0	0	0	3.745378	0	0.821965	-1.2809	0.34031	NA	RP11-814P	chr15	+	35047285	35105124	2727
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	HMGB1P3	chr2	+	2.31E+08	2.31E+08	616
ENSG0000(	2.071584	0	0	0	1.840864	4.109825	-0.83184	0.53481	0.65917	RP11-124N	chr3	+	1.26E+08	1.26E+08	444
ENSG0000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	CTC-339F2.	chr5	-	1.16E+08	1.16E+08	206
ENSG0000(	1.035792	2.408575	0	0.749076	4.60216	0	-0.37507	0.77577	0.85283	RP11-811I	chr5	+	58313	59030	718
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTC-359M8	chr5	-	1.46E+08	1.46E+08	582
ENSG0000(	3.107376	2.408575	2.638828	2.996302	2.761296	1.64393	0.11263	0.91885	0.95073	RP11-563E	chr4	+	1.64E+08	1.64E+08	777
ENSG0000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	RP11-584P	chr4	+	68311985	68312292	308
ENSG0000(	1.035792	1.204288	2.638828	0	9.20432	2.465895	-0.92659	0.43634	0.56592	RP11-114N	chr8	-	59337147	59339244	1779
ENSG0000(	2.071584	4.817151	6.597069	3.745378	14.72691	1.64393	-0.49646	0.60129	0.71656	SLC7A11-A	chr4	+	1.39E+08	1.39E+08	4654
ENSG0000(	0	2.408575	2.638828	0	0	1.64393	0.85739	0.5258	0.65076	RP11-17E2	chr4	+	21950638	22331953	1874
ENSG0000(	30.03797	24.08575	38.263	5.243529	2.761296	12.32947	2.0608	0.000601	0.001744	CTD-2003C	chr11	-	10906432	10920869	557
ENSG0000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-91J3.	chr4	+	1.88E+08	1.88E+08	498
ENSG0000(	5.17896	0	2.638828	0	0	2.465895	1.037	0.42986	0.55987	CBX3P3	chr5	-	1.12E+08	1.12E+08	532
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-148B	chr4	-	1.14E+08	1.14E+08	740
ENSG0000(	1.035792	2.408575	1.319414	0	0	1.64393	0.85879	0.52286	0.64815	RP11-348J	chr5	+	91378414	91815133	2957
ENSG0000(	4.143168	0	0	0.749076	0	0	1.0202	0.44849	NA	MTND4P9	chr4	-	25719704	25721367	1346

ENSG00000(	0	4.817151	0	2.996302	3.681728	0	-0.3045	0.81474	0.87963	CTD-2195N	chr5	+	6582249	6588612	3036
ENSG00000(	1.035792	0	1.319414	0	0	2.465895	-0.03351	0.98027	NA	RP11-541P	chr5	-	1.62E+08	1.63E+08	630
ENSG00000(	78.72018	91.52587	50.13772	81.64923	84.67974	147.9537	-0.50106	0.12076	0.20491	YJEFN3	chr19	+	19639704	19648393	2769
ENSG00000(	1.035792	0	0	0.749076	0	1.64393	-0.39004	0.77029	NA	RP11-576C	chr9	-	1.15E+08	1.15E+08	260
ENSG00000(	0	3.612863	0	2.996302	0	0.821965	-0.05832	0.96545	0.97997	CTB-131B5	chr5	+	1.4E+08	1.4E+08	3025
ENSG00000(	0	0	0	5.243529	2.761296	1.64393	-2.429	0.06661	0.12437	CTD-2060C	chr5	+	74094819	74095925	1107
ENSG00000(	0	0	0	4.494453	1.840864	0	-1.6936	0.21189	0.32187	CTC-529P8	chr5	+	1.48E+08	1.48E+08	3091
ENSG00000(	4.143168	4.817151	2.638828	9.737982	5.522592	1.64393	-0.4638	0.62852	0.73907	RP11-677N	chr11	+	1.25E+08	1.25E+08	1493
ENSG00000(	3.107376	0	0	5.992604	5.522592	2.465895	-1.5498	0.18838	0.2933	RP11-584P	chr4	-	68283023	68333969	1991
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-141P	chr4	-	33012570	33013368	799
ENSG00000(	1.035792	1.204288	0	19.47596	14.72691	12.32947	-3.594	0.000214	0.000667	CTD-2116N	chr5	-	64782271	64782875	365
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP13-401N	chr20	-	25816621	25817468	222
ENSG00000(	114.9729	104.773	112.1502	29.96302	22.09037	35.34449	1.8944	1.44E-09	7.79E-09	DNAH10OS	chr12	-	1.24E+08	1.24E+08	5040
ENSG00000(	1.035792	0	0	0	0	2.465895	-0.37334	0.77636	NA	RP4-639F2	chr1	-	95449106	95492759	159
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	NREP-AS1	chr5	+	1.11E+08	1.11E+08	610
ENSG00000(	2.071584	6.021439	5.277655	0	1.840864	1.64393	1.493	0.19297	0.2988	RP11-1252	chr5	+	1.77E+08	1.77E+08	547
ENSG00000(	4.143168	3.612863	7.916483	0	0	0	3.5029	0.005806	0.014197	RP11-314N	chr4	+	1.32E+08	1.32E+08	523
ENSG00000(	3.107376	0	0	28.46487	14.72691	37.81039	-3.9941	4.05E-06	1.57E-05	RP11-380D	chr4	-	1.12E+08	1.12E+08	493
ENSG00000(	8.286335	8.430014	2.638828	0	1.840864	0.821965	2.2812	0.038529	0.077461	ANKRD33B	chr5	-	10627372	10628337	522
ENSG00000(	4.143168	10.83859	3.958241	0	0	0	3.7936	0.002362	0.006218	CACNA1G-A	chr17	-	48633568	48639469	1433
ENSG00000(	1.035792	4.817151	0	1.498151	0	0.821965	0.79986	0.54518	0.66736	AC107982.	chr17	+	18739020	18745677	1300
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	CTB-95B16	chr5	+	1.63E+08	1.63E+08	207
ENSG00000(	8.286335	8.430014	6.597069	2.996302	8.283888	2.465895	0.69227	0.42016	0.55093	RP11-417F	chr2	-	46795395	46807377	1519
ENSG00000(	8.286335	8.430014	19.79121	74.15848	60.74851	47.67397	-2.2751	1.03E-06	4.28E-06	PCDHA10	chr5	+	1.4E+08	1.4E+08	5254
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP13-884E	chr4	-	1.39E+08	1.39E+08	396
ENSG00000(	6.214751	7.225726	6.597069	0.749076	0	3.28786	1.8631	0.077003	0.14065	RP11-265F	chr3	-	1.31E+08	1.31E+08	671
ENSG00000(	6.214751	1.204288	0	1.498151	0.920432	0	1.0446	0.42186	0.55236	RP11-616K	chr15	+	44646889	44647890	1002
ENSG00000(	3.107376	6.021439	2.638828	89.13999	75.47542	101.1017	-4.312	5.42E-16	4.53E-15	RP11-130F	chr4	+	1.78E+08	1.79E+08	2161
ENSG00000(	46.61064	28.90291	36.94359	31.46117	38.65814	30.4127	0.16459	0.6845	0.78423	RP11-359B	chr12	-	1084464	1099207	2042
ENSG00000(	16.57267	3.612863	9.235896	0	0	0	4.4703	0.000183	0.000575	HOXC-AS2	chr12	-	54387594	54390569	2090
ENSG00000(	26.93059	16.86003	29.0271	4.494453	27.61296	4.109825	0.95887	0.15131	0.24579	RP11-848G	chr5	+	68927790	68932312	4437
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	CTD-2517C	chr5	-	34860888	34861611	425
ENSG00000(	0	0	0	0.749076	1.840864	1.64393	-1.2986	0.33698	NA	KRT8P31	chr5	-	60039390	60040797	1408
ENSG00000(	8.286335	22.88147	34.30476	0.749076	11.96562	3.28786	1.8723	0.014527	0.032555	CTD-2353F	chr5	-	36666316	36725297	681
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	CTC-498M1	chr5	-	87705664	87794514	761
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-381K	chr5	-	1.37E+08	1.37E+08	1148
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	CSNK1A1P3	chr5	+	98169086	98169415	330
ENSG00000(	0	4.817151	6.597069	2.247227	0.920432	0.821965	1.0981	0.35432	0.4841	RP11-476C	chr4	-	88140676	88161466	1924
ENSG00000(	0	0	0	4.494453	4.60216	1.64393	-2.5881	0.048654	0.094766	CTC-321K1	chr5	+	1.35E+08	1.35E+08	634
ENSG00000(	1.035792	0	2.638828	0	0.920432	7.397684	-0.78832	0.53865	0.66245	RASA2-IT1	chr3	+	1.41E+08	1.41E+08	612
ENSG00000(	0	0	5.277655	0	0.920432	0	1.1592	0.39256	0.52329	MYLK-AS2	chr3	+	1.23E+08	1.23E+08	754
ENSG00000(	53.86118	37.33292	59.37362	39.701	20.2495	27.12484	0.76412	0.061118	0.11541	EEF1A1P13	chr5	-	14652047	14653438	1389
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-300N	chr4	+	58020743	58022618	560
ENSG00000(	2.071584	0	0	0.749076	0	0	0.47431	0.71145	NA	RP11-371F	chr4	-	1.4E+08	1.4E+08	421

ENSG00000(	0	10.83859	0	0	0	0	2.5435	0.060316	0.11416	HMGN1P1!	chr5	-	1.15E+08	1.15E+08	295
ENSG00000(	5.17896	1.204288	3.958241	0	0	0	2.8275	0.032683	0.066962	RP11-143A	chr5	+	8839844	8881637	2702
ENSG00000(	4.143168	1.204288	2.638828	0	9.20432	1.64393	-0.31428	0.78529	0.85883	RP11-436H	chr5	+	1.24E+08	1.24E+08	563
ENSG00000(	0	1.204288	1.319414	32.21025	31.29469	33.70056	-4.6283	1.03E-07	4.70E-07	RP11-143E	chr12	-	1.31E+08	1.31E+08	4159
ENSG00000(	0	0	1.319414	1.498151	0	2.465895	-0.80883	0.55106	NA	RP13-488H	chr4	-	78785662	78785958	297
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	CIR1P2	chr4	-	1.16E+08	1.16E+08	1342
ENSG00000(	12.4295	18.06432	13.19414	1.498151	23.0108	8.219649	0.39634	0.59461	0.71058	RP11-692D	chr4	+	74124926	74183670	685
ENSG00000(	5.17896	0	1.319414	0	0.920432	0.821965	1.1637	0.3798	0.5105	CTC-338M1	chr5	+	1.81E+08	1.81E+08	392
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RP11-397D	chr4	+	1.15E+08	1.15E+08	155
ENSG00000(	0	0	0	4.494453	5.522592	7.397684	-3.3425	0.007355	0.017626	RP11-855C	chr11	+	61355966	61375022	2349
ENSG00000(	5.17896	1.204288	2.638828	0	0	1.64393	1.5976	0.21337	0.32365	CTD-2024P	chr5	-	34656517	34657355	407
ENSG00000(	1.035792	1.204288	0	8.239831	2.761296	3.28786	-1.9388	0.099973	0.17544	CTD-2154I:	chr5	-	95036953	95067999	809
ENSG00000(	7.250543	7.225726	9.235896	6.74168	17.48821	10.68554	-0.51179	0.47681	0.6061	RP11-9G1.:	chr4	-	1.34E+08	1.34E+08	2820
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	CTB-49A3.4	chr5	+	1.33E+08	1.33E+08	389
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	SEPHS1P5	chr5	+	14960341	14961502	1162
ENSG00000(	0	2.408575	1.319414	0	0	0	1.2548	0.34239	NA	CTD-2350J:	chr5	-	15602298	15607457	362
ENSG00000(	358.384	415.4793	358.8805	92.13629	163.8369	188.23	1.3436	6.06E-09	3.11E-08	PKD1P6	chr16	-	15219099	15248421	4769
ENSG00000(	0	0	0	0	2.761296	1.64393	-1.2339	0.35779	NA	RP11-267A	chr5	+	1.74E+08	1.74E+08	659
ENSG00000(	1.035792	3.612863	1.319414	7.490755	4.60216	2.465895	-1.0478	0.32566	0.45334	CTC-431G1	chr5	-	79070171	79112013	460
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-460I:	chr4	+	1021466	1022760	272
ENSG00000(	0	0	0	1.498151	0	2.465895	-1.1271	0.39798	NA	RP11-325L	chr5	+	1.37E+08	1.37E+08	646
ENSG00000(	0	0	6.597069	0	2.761296	0.821965	0.53155	0.68792	0.78671	AC007050.	chr22	-	20941783	20946505	1123
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-789C	chr4	+	1.71E+08	1.71E+08	469
ENSG00000(	0	2.408575	0	2.247227	5.522592	1.64393	-1.3219	0.29522	0.41958	RP11-122A	chr8	+	1.1E+08	1.1E+08	1643
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	PSMC1P5	chr5	+	1.07E+08	1.07E+08	177
ENSG00000(	12.4295	7.225726	17.15238	2.247227	6.443024	5.753754	1.2368	0.11014	0.1898	RP11-305C	chr12	+	65675437	65680508	3457
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP5-875H1	chr17	-	48178068	48179284	430
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-94C2	chr17	-	48614655	48616115	717
ENSG00000(	2.071584	3.612863	0	0	2.761296	0	0.6365	0.63353	0.74324	CTC-820M8	chr8	-	1.22E+08	1.22E+08	1814
ENSG00000(	2.071584	0	2.638828	1.498151	2.761296	6.575719	-0.90414	0.4386	0.56822	RP11-434I:	chr8	-	74209946	74268696	3261
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	MRPS31P4	chr13	+	53191693	53211581	919
ENSG00000(	36.25272	45.76293	43.54065	11.98521	11.04518	23.83698	1.3741	0.003406	0.008722	RP11-356J!	chr11	+	1.12E+08	1.12E+08	2749
ENSG00000(	31.07376	48.17151	38.263	298.8811	293.6178	274.5363	-2.8666	2.17E-31	3.46E-30	KIAA1456	chr8	+	12803151	12889012	9587
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTC-498M1	chr5	+	87678765	87679077	313
ENSG00000(	92.18548	101.1602	131.9414	239.7042	248.5166	244.9455	-1.1708	4.91E-08	2.32E-07	ZNF718	chr4	+	124386	157779	3214
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-5P22	chr5	-	65803372	65807432	661
ENSG00000(	423.6389	396.2107	361.5194	278.6561	289.0156	321.3883	0.41021	0.01156	0.026486	SMIM20	chr4	+	25863452	25931435	935
ENSG00000(	29.00217	24.08575	6.597069	6.74168	2.761296	3.28786	2.0399	0.005318	0.013107	CTA-963H5	chr22	-	31049864	31050801	612
ENSG00000(	21.75163	20.47289	23.74945	13.48336	30.37426	18.90519	0.075972	0.88324	0.92688	CTD-2269F	chr5	+	83680245	83786583	792
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTB-51E13.	chr4	-	1.24E+08	1.24E+08	170
ENSG00000(	1.035792	0	1.319414	0	0.920432	0	0.55201	0.67753	NA	MRPL22P1	chr4	-	57186885	57187500	616
ENSG00000(	0	0	2.638828	1.498151	0	0.821965	0.061979	0.96354	NA	IGBP1P4	chr4	-	83322731	83323609	879
ENSG00000(	19.68005	6.021439	7.916483	0.749076	8.283888	4.93179	1.1543	0.1756	0.27738	RP11-284N	chr4	-	1.44E+08	1.44E+08	759
ENSG00000(	3.107376	6.021439	6.597069	0	3.681728	0.821965	1.4429	0.19265	0.29849	RP11-173N	chr4	+	1.87E+08	1.87E+08	864

ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	CTC-210G5	chr5	-	1.22E+08	1.22E+08	1424
ENSG00000(	0	2.408575	0	0	0	1.64393	0.21935	0.86915	NA	KDELC1P1	chr5	+	1.27E+08	1.27E+08	1509
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTC-422A1	chr5	+	78525727	78526411	359
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-1E3.1	chr5	+	96840400	97006750	724
ENSG00000(	168.8341	178.2346	246.7304	304.8737	354.3663	381.3917	-0.80877	4.25E-05	0.000146	RP11-46C2	chr5	+	27472399	27496508	1610
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-785F	chr4	+	1.38E+08	1.38E+08	1576
ENSG00000(	5.17896	0	1.319414	0	0	0.821965	1.5609	0.24758	0.36438	RP11-647P	chr4	+	1.22E+08	1.22E+08	621
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-780N	chr4	-	1.45E+08	1.45E+08	1171
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	AC005740.	chr5	-	1.41E+08	1.41E+08	419
ENSG00000(	0	0	0	0	0	4.93179	-1.2404	0.35057	NA	RP11-466P	chr5	-	75581367	75607287	756
ENSG00000(	0	2.408575	0	0	2.761296	0	-0.08034	0.95255	NA	RP11-731D	chr4	-	1.52E+08	1.52E+08	163
ENSG00000(	0	0	1.319414	0.749076	0	3.28786	-0.81202	0.54946	NA	RP11-159K	chr5	+	1.12E+08	1.12E+08	615
ENSG00000(	18.64425	27.69862	11.87472	11.98521	5.522592	4.93179	1.2813	0.05084	0.098517	CTD-2213F	chr14	+	31889492	31922089	1213
ENSG00000(	2.071584	0	0	14.23244	4.60216	13.15144	-3.0454	0.004043	0.010205	LINC00617	chr14	+	96342729	96391908	3197
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RP11-22A3	chr4	-	12860725	12866585	2694
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	RP11-219C	chr4	+	1.66E+08	1.66E+08	1407
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTD-2005D	chr4	+	69650336	69653192	714
ENSG00000(	0	0	0	0.749076	7.363456	0	-1.9761	0.14479	0.23707	RP11-119J	chr5	+	1.35E+08	1.35E+08	377
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-23P1	chr15	-	42117297	42120134	585
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	UNC93B4	chr4	-	4145185	4152148	747
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	CTD-2197I	chr5	-	1.08E+08	1.08E+08	398
ENSG00000(	3.107376	4.817151	3.958241	0.749076	1.840864	3.28786	0.81459	0.45272	0.58249	UBE2CP3	chr4	+	57938849	57939298	450
ENSG00000(	5.17896	1.204288	0	8.988907	11.96562	6.575719	-1.736	0.071776	0.13261	RP11-432N	chr5	-	17625660	17626068	409
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-338H	chr11	+	95215570	95230717	570
ENSG00000(	56.96855	69.84869	48.81831	20.97412	20.2495	48.49593	0.94565	0.022893	0.048905	RP11-1391	chr11	-	856880	859795	2061
ENSG00000(	14.50109	6.021439	23.74945	0	0	0	5.0876	8.92E-06	3.33E-05	RP11-1057	chr8	-	1.3E+08	1.3E+08	1163
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-15B1	chr4	-	1.01E+08	1.01E+08	741
ENSG00000(	31.07376	43.35436	18.47179	23.97042	29.45382	29.59074	0.16354	0.72013	0.81165	AC090587.	chr11	+	3837982	3843130	2843
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP13-539F	chr4	+	1.46E+08	1.46E+08	2807
ENSG00000(	4.143168	16.86003	3.958241	0	0	0	4.189	0.0006	0.001743	CTB-99A3.1	chr5	+	1.46E+08	1.46E+08	691
ENSG00000(	6.214751	6.021439	2.638828	6.74168	6.443024	9.041614	-0.50543	0.55002	0.67142	RP11-714G	chr4	+	1.86E+08	1.86E+08	587
ENSG00000(	0	2.408575	5.277655	3.745378	3.681728	1.64393	-0.20913	0.85467	0.9076	KLHL2P1	chr4	+	1.2E+08	1.2E+08	521
ENSG00000(	0	0	0	10.48706	6.443024	9.041614	-3.9567	0.000904	0.002552	AACSP1	chr5	-	1.78E+08	1.78E+08	2822
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-83M1	chr5	-	66995257	67198428	589
ENSG00000(	5.17896	0	0	0.749076	0	0	1.2383	0.36072	NA	RP11-834C	chr12	-	54478916	54519776	719
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-13L2	chr3	-	1.4E+08	1.4E+08	2693
ENSG00000(	0	0	2.638828	0	0.920432	0	0.55591	0.6721	NA	RP11-47F1	chr5	-	1.08E+08	1.08E+08	282
ENSG00000(	3.107376	1.204288	1.319414	0.749076	9.20432	3.28786	-0.9359	0.40225	0.53346	AC128709.	chr3	-	1.97E+08	1.97E+08	1715
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	CCT5P1	chr5	+	1.15E+08	1.15E+08	1618
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CTD-2275D	chr5	-	73623820	73630591	502
ENSG00000(	9.322127	27.69862	21.11062	0	0.920432	0	4.7758	3.08E-06	1.21E-05	HOXC-AS1	chr12	-	54392806	54393794	548
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-648N	chr5	+	37377151	37378073	323
ENSG00000(	10.35792	8.430014	7.916483	12.73428	8.283888	6.575719	-0.04364	0.95193	0.97123	RP11-631N	chr5	+	60670939	60671682	744
ENSG00000(	0	0	0	3.745378	1.840864	2.465895	-2.1746	0.10423	0.18143	GMPSP1	chr4	+	8176148	8176726	579

ENSG00000(	1.035792	1.204288	1.319414	0	3.681728	0	-0.01311	0.99218	0.99518	DUTP7	chr4	-	52731216	52731701	486
ENSG00000(	3.107376	3.612863	0	4.494453	5.522592	1.64393	-0.60498	0.58615	0.70351	WBP1LP2	chr7	+	1.07E+08	1.07E+08	946
ENSG00000(	0	1.204288	0	0.749076	0.920432	0	-0.14992	0.90929	NA	RP11-312A	chr4	-	1.59E+08	1.59E+08	890
ENSG00000(	355.2766	327.5663	275.7575	346.0729	323.0716	369.0622	-0.11268	0.50577	0.63344	CHCHD10	chr22	-	24108021	24110630	1171
ENSG00000(	0	6.021439	6.597069	7.490755	3.681728	8.219649	-0.55455	0.56555	0.68491	PPM1AP1	chr8	-	15663658	15664792	1135
ENSG00000(	15.53688	4.817151	7.916483	4.494453	1.840864	16.4393	0.28407	0.73423	0.82224	FAM218A	chr4	+	1.66E+08	1.66E+08	2174
ENSG00000(	0	2.408575	0	2.996302	2.761296	0	-0.72953	0.58549	0.70297	CTD-2324F	chr5	-	6310554	6339997	2419
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	INTS6P1	chr5	-	39719086	39721615	2530
ENSG00000(	1.035792	6.021439	1.319414	0	0.920432	0	1.9135	0.14625	0.23897	RP11-640N	chr11	-	1.21E+08	1.21E+08	6314
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-119H	chr4	-	1.14E+08	1.14E+08	1352
ENSG00000(	9.322127	1.204288	2.638828	2.996302	0	4.109825	0.70144	0.52917	0.65392	CDK3	chr17	+	73996987	74002080	1582
ENSG00000(	9.322127	7.225726	2.638828	0	1.840864	0	2.5881	0.024729	0.052459	RP11-757G	chr11	+	68638132	68642010	3252
ENSG00000(	138.7961	140.9017	112.1502	38.20285	34.05598	46.852	1.6986	2.79E-09	1.47E-08	GPR162	chr12	+	6930711	6936586	2768
ENSG00000(	0	0	0	2.996302	0	1.64393	-1.3112	0.33001	NA	RP11-380D	chr4	-	1.11E+08	1.11E+08	1447
ENSG00000(	4.143168	0	1.319414	2.996302	0	6.575719	-0.56507	0.64411	0.75127	RP11-680H	chr11	+	93971316	94012372	570
ENSG00000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	AC004066.	chr4	-	1.06E+08	1.06E+08	572
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-756P	chr4	+	1.9E+08	1.9E+08	336
ENSG00000(	0	0	1.319414	0	3.681728	6.575719	-1.8024	0.1693	0.26923	ABHD17AP	chr1	-	2.15E+08	2.15E+08	1137
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	RP11-92A5	chr4	-	1.56E+08	1.56E+08	1568
ENSG00000(	19.68005	12.04288	23.74945	13.48336	34.05598	15.61733	-0.17267	0.75907	0.84082	KRT8P33	chr5	-	1.23E+08	1.23E+08	1423
ENSG00000(	6.214751	3.612863	2.638828	0	2.761296	0.821965	1.392	0.23145	0.34491	RP11-302F	chr4	+	25771888	25775199	483
ENSG00000(	0	0	0	2.247227	1.840864	1.64393	-1.6991	0.21004	NA	CTC-493L2	chr5	+	86042635	86045589	2094
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-8L2.1	chr4	-	84717589	85214565	2795
ENSG00000(	8.286335	4.817151	13.19414	0	0	3.28786	2.4147	0.022038	0.04731	RP11-47I22	chr14	-	62023031	62037371	5103
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	RP11-254I2	chr5	+	95385819	95551223	704
ENSG00000(	0	0	0	0.749076	3.681728	2.465895	-1.924	0.15425	0.24976	CCDC34P1	chr4	+	1.13E+08	1.13E+08	517
ENSG00000(	2.071584	6.021439	2.638828	1.498151	4.60216	6.575719	-0.19881	0.84446	0.90071	RP11-397D	chr9	+	37432084	37433878	370
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-215P	chr5	-	1.34E+08	1.34E+08	669
ENSG00000(	38.3243	69.84869	47.4989	71.16218	61.66894	68.22309	-0.36813	0.27286	0.39366	ATP6V1E2	chr2	-	46717889	46769696	2334
ENSG00000(	0	0	1.319414	0	1.840864	0.821965	-0.46629	0.72905	NA	RP11-333E	chr4	-	39974748	39975062	315
ENSG00000(	17.60846	14.45145	18.47179	1.498151	6.443024	0.821965	2.3214	0.003253	0.008358	NTAN1P2	chr8	-	87493983	87495231	940
ENSG00000(	236.1606	287.8248	191.315	178.28	172.1208	178.3664	0.43448	0.034021	0.069402	GLI4	chr8	+	1.44E+08	1.44E+08	2333
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC006499.	chr4	-	10261069	10261762	694
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP4-669L1	chr1	+	326096	328112	1239
ENSG00000(	4.143168	6.021439	5.277655	0	0	1.64393	2.3419	0.048175	0.093973	CTD-2297D	chr5	-	5132893	5140167	889
ENSG00000(	5.17896	1.204288	17.15238	0	1.840864	0	2.7941	0.01493	0.033354	RP11-301H	chr4	-	1.46E+08	1.46E+08	1090
ENSG00000(	1.035792	2.408575	1.319414	0.749076	0	0	1.3221	0.32896	NA	CTD-2233C	chr5	-	33519721	33522335	917
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP11-325I2	chr5	-	1363697	1380182	1616
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	LINC00604	chr5	+	40260759	40267759	499
ENSG00000(	34.18113	22.88147	63.33186	125.8447	173.0412	134.8022	-1.8308	3.33E-08	1.60E-07	IQCJ-SCHIP	chr3	+	1.59E+08	1.6E+08	2633
ENSG00000(	5.17896	2.408575	1.319414	0	0.920432	2.465895	1.0102	0.41037	0.5411	RP11-39E3	chr3	-	1.31E+08	1.31E+08	340
ENSG00000(	0	0	0	1.498151	3.681728	0	-1.4292	0.2903	NA	RP11-440I	chr4	-	1.75E+08	1.75E+08	2202
ENSG00000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	AC064853.	chr2	-	2.28E+08	2.29E+08	1139
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	ROPN1L-AS	chr5	-	10441402	10441904	189

ENSG00000(	6.214751	3.612863	3.958241	0.749076	1.840864	1.64393	1.3731	0.20667	0.31574	RP11-517I:	chr5	-	1.26E+08	1.26E+08	747
ENSG00000(	11.39371	7.225726	19.79121	11.23613	1.840864	12.32947	0.53031	0.47939	0.60841	RP11-933H	chr3	-	1.31E+08	1.31E+08	2189
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-158C	chr4	+	1.55E+08	1.55E+08	1022
ENSG00000(	3.107376	4.817151	3.958241	0.749076	1.840864	0.821965	1.3952	0.22007	0.33172	RP11-738E	chr4	-	57896939	57931769	1033
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	RP11-136I:	chr4	+	10412620	10413268	329
ENSG00000(	2.071584	0	2.638828	0	0	0	1.5584	0.24658	NA	AC007078.	chr7	-	76103904	76108173	453
ENSG00000(	2.071584	2.408575	3.958241	5.992604	0.920432	6.575719	-0.57242	0.58328	0.70082	RP11-455F	chr16	+	30107751	30115437	1650
ENSG00000(	7.250543	0	0	0	0	0	1.994	0.1408	0.23194	CTD-2215L	chr5	+	9001886	9046052	805
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-91J3.	chr4	+	1.88E+08	1.88E+08	536
ENSG00000(	2.071584	0	0	1.498151	0	0	0.18632	0.88758	NA	RP11-317B	chr4	+	2141400	2142785	581
ENSG00000(	0	0	0	0	11.04518	4.93179	-2.9862	0.022305	0.047809	RP11-93M:	chr4	-	30886065	30886804	740
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-756P	chr4	-	1.9E+08	1.9E+08	1991
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	RP11-122C	chr5	+	38783682	38792856	565
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	RP11-341G	chr4	+	13656803	13978699	2228
ENSG00000(	12.4295	15.65574	13.19414	0	3.681728	3.28786	2.3029	0.006964	0.01678	CTD-3224K	chr5	-	1.39E+08	1.39E+08	577
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	MEGT1	chr6	+	31674681	31685695	1266
ENSG00000(	23.82321	16.86003	23.74945	0.749076	0	0	4.9883	6.68E-07	2.82E-06	CTD-2228K	chr5	+	418818	419224	407
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-530I:	chr4	+	55919227	55958701	455
ENSG00000(	2.071584	1.204288	0	0	0	1.64393	0.48832	0.71876	NA	PABPC1P7	chr4	+	1.04E+08	1.04E+08	1513
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-834C	chr12	-	54470622	54475687	564
ENSG00000(	0	1.204288	1.319414	0.749076	0	0	0.61214	0.64459	NA	ST3GAL1P1	chr4	-	68582093	68583106	1014
ENSG00000(	17.60846	16.86003	2.638828	0	0	0	4.7942	4.55E-05	0.000155	RP11-1E6.1	chr4	+	43342892	43347617	653
ENSG00000(	0	0	7.916483	5.992604	16.56778	13.9734	-1.9225	0.045645	0.089701	RP11-138B	chr4	-	1.88E+08	1.88E+08	2114
ENSG00000(	13.46529	12.04288	10.55531	14.23244	25.7721	22.19305	-0.74025	0.19836	0.30565	RP11-864I4	chr11	+	62304784	62309490	264
ENSG00000(	2.071584	3.612863	1.319414	0.749076	4.60216	4.109825	-0.32701	0.77052	0.84912	RP11-458I7	chr1	+	1.5E+08	1.5E+08	484
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	HNRNPKP5	chr5	-	14877776	14878028	253
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-463J:	chr4	+	1.91E+08	1.91E+08	592
ENSG00000(	0	0	1.319414	0	7.363456	0	-1.2778	0.34511	0.47447	RP11-83M:	chr5	-	66985861	66986265	405
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-6L6.2	chr4	+	1.47E+08	1.47E+08	397
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-576N	chr4	+	84158456	84158597	142
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTB-161M1	chr5	+	1.18E+08	1.18E+08	483
ENSG00000(	11.39371	6.021439	23.74945	11.98521	22.09037	18.08323	-0.32889	0.59887	0.71426	LINC00491	chr5	-	1.02E+08	1.02E+08	944
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	KB-1042C1	chr8	-	1.04E+08	1.04E+08	429
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-497H	chr5	+	69758071	69775042	1073
ENSG00000(	0	0	0	5.243529	2.761296	2.465895	-2.5608	0.051308	0.09931	CTD-2074D	chr5	-	24352418	24353552	487
ENSG00000(	6.214751	8.430014	3.958241	0	0	0	3.7875	0.002359	0.006209	CTD-2066L	chr5	-	32925745	33298016	619
ENSG00000(	2.071584	1.204288	0	0	0.920432	0	0.824	0.54141	NA	RP11-392B	chr4	+	1.41E+08	1.41E+08	657
ENSG00000(	0	3.612863	0	0	0	1.64393	0.50971	0.70603	NA	AP000892.	chr11	-	1.17E+08	1.17E+08	488
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-161D	chr4	+	1.75E+08	1.75E+08	511
ENSG00000(	38.3243	40.94578	44.86007	56.18067	64.43024	53.42772	-0.48102	0.15983	0.25705	SEPP1	chr5	-	42799982	42887494	4175
ENSG00000(	21.75163	7.225726	14.51355	16.47966	11.04518	29.59074	-0.36622	0.55026	0.67158	TPM3P6	chr19	+	53982604	53983345	742
ENSG00000(	2.071584	3.612863	5.277655	0	6.443024	10.68554	-0.53293	0.60857	0.72266	RP11-404E	chr1	+	1.52E+08	1.52E+08	535
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-710F	chr4	-	1.07E+08	1.07E+08	483
ENSG00000(	29.00217	16.86003	15.83297	75.65663	71.7937	66.57916	-1.7412	7.57E-06	2.85E-05	RP11-834C	chr12	+	54519882	54526627	1369

ENSG00000(	1.035792	1.204288	0	2.247227	0	1.64393	-0.44193	0.74269	0.82838	RP11-39C1	chr4	+	1.65E+08	1.65E+08	2057
ENSG00000(	66.29068	71.05298	83.12307	2.247227	0	0	5.8943	1.21E-15	9.87E-15	RP11-230G	chr12	-	65860600	66036152	1072
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	RP11-451H	chr5	-	1.8E+08	1.8E+08	459
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-225B	chr7	+	32827946	32828054	109
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP11-711G	chr5	-	7707915	7749879	522
ENSG00000(	3.107376	0	0	2.247227	1.840864	0	-0.19799	0.88309	0.92688	RP1-313L4	chr1	-	1.68E+08	1.68E+08	266
ENSG00000(	8.286335	8.430014	25.06886	14.98151	5.522592	9.041614	0.44257	0.52824	0.65296	RP11-974F	chr5	+	69274357	69293569	3763
ENSG00000(	12.4295	9.634302	2.638828	3.745378	1.840864	1.64393	1.5251	0.10399	0.18112	CTD-2152N	chr5	-	32103551	32122047	834
ENSG00000(	6.214751	10.83859	3.958241	1.498151	1.840864	0.821965	1.9432	0.055123	0.10582	RP5-1063N	chr12	-	3405368	3409390	2303
ENSG00000(	9.322127	2.408575	3.958241	0	0	0	3.4928	0.00616	0.014989	RP11-12K2	chr4	-	64334419	64359996	448
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-432N	chr5	+	17634569	17635162	594
ENSG00000(	2.071584	3.612863	3.958241	2.996302	3.681728	6.575719	-0.39348	0.69373	0.79116	RP11-540D	chr1	+	1.55E+08	1.55E+08	928
ENSG00000(	724.0185	744.2498	670.2622	179.0291	164.7573	206.3132	1.9516	1.90E-35	3.44E-34	CTD-2001E	chr5	+	9546312	9550721	1799
ENSG00000(	2.071584	8.430014	3.958241	2.247227	3.681728	4.93179	0.34587	0.72388	0.8146	RP11-46H1	chr12	+	1.33E+08	1.33E+08	1118
ENSG00000(	0	0	0	0	3.681728	1.64393	-1.4596	0.2805	NA	ALG1L12P	chr8	+	12278541	12282509	434
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-723C	chr3	+	1.29E+08	1.29E+08	329
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	PRODH2	chr19	-	36290890	36304201	1956
ENSG00000(	31.07376	36.12863	40.90183	23.97042	23.93123	23.83698	0.57294	0.17788	0.28024	ZBED3-AS1	chr5	+	76382565	76462734	1987
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-447B	chr5	+	9854489	9890049	499
ENSG00000(	0	2.408575	1.319414	0	0.920432	0	0.92035	0.49653	NA	RP11-91H1	chr5	-	1.75E+08	1.75E+08	568
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-11N5	chr4	+	1.88E+08	1.88E+08	188
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	CTD-2232E	chr5	-	88762354	88765856	253
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	LSM3P4	chr4	+	1.43E+08	1.43E+08	309
ENSG00000(	1.035792	2.408575	1.319414	4.494453	12.88605	12.32947	-2.2366	0.020394	0.044129	RP11-501C	chr17	-	47072628	47074854	428
ENSG00000(	3.107376	4.817151	7.916483	0	0	0	3.5156	0.0056	0.013744	CTC-806A2	chr5	-	1.45E+08	1.45E+08	530
ENSG00000(	44.53905	59.0101	89.72014	0	0	0	7.1745	2.68E-12	1.78E-11	RP11-807H	chr4	+	66535679	66563747	1177
ENSG00000(	9.322127	12.04288	7.916483	2.996302	15.64734	4.109825	0.34634	0.66217	0.76644	CTD-2083E	chr5	-	288948	290436	1203
ENSG00000(	2.071584	3.612863	3.958241	0	0	0	2.7354	0.039239	0.078686	RNF138P1	chr5	-	54825984	54826529	546
ENSG00000(	0	1.204288	0	1.498151	0	4.109825	-1.1514	0.39461	0.52549	RP11-269F	chr4	+	1.13E+08	1.13E+08	481
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTD-2265D	chr5	-	42466995	42468402	1408
ENSG00000(	3.107376	2.408575	3.958241	1.498151	3.681728	4.93179	-0.07458	0.94325	0.96582	RP11-453N	chr8	-	68045789	68048146	2358
ENSG00000(	0	8.430014	2.638828	0	2.761296	0.821965	1.1528	0.35209	0.48182	METTL21EP	chr13	+	1.04E+08	1.04E+08	2312
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTC-459M5	chr5	+	1.12E+08	1.12E+08	457
ENSG00000(	1.035792	1.204288	0	1.498151	0	2.465895	-0.4555	0.73498	0.82274	CTD-2046J	chr5	+	35081325	35082094	456
ENSG00000(	0	7.225726	10.55531	15.73059	19.32907	23.83698	-1.6203	0.028959	0.060273	RP11-229C	chr5	-	74343544	74348668	534
ENSG00000(	0	1.204288	2.638828	0.749076	1.840864	4.109825	-0.57194	0.6498	0.75611	CTD-2281N	chr5	-	1.18E+08	1.18E+08	2803
ENSG00000(	1.035792	0	2.638828	5.992604	7.363456	3.28786	-1.7212	0.1207	0.20482	RP11-1365	chr4	-	195198	198798	950
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-588L	chr4	+	40428136	40429602	862
ENSG00000(	1.035792	1.204288	2.638828	2.996302	1.840864	7.397684	-1.0507	0.34899	0.47864	RNPS1P1	chr4	+	11373599	11374516	918
ENSG00000(	99.43602	81.89156	87.08131	147.5679	278.8909	309.8808	-1.4375	1.31E-07	5.96E-07	RP11-253E	chr12	+	3150603	3154116	3514
ENSG00000(	0	0	2.638828	2.247227	0	2.465895	-0.50041	0.70994	0.80395	CTC-338M1	chr5	+	1.81E+08	1.81E+08	738
ENSG00000(	46.61064	46.96722	30.34652	14.98151	8.283888	17.26126	1.5563	0.001156	0.003212	RP1-80B9.2	chr6	+	2245982	2413825	8217
ENSG00000(	0	4.817151	0	0	2.761296	0.821965	0.25674	0.84796	0.90301	RP11-632F	chr4	+	40814796	40828168	477
ENSG00000(	11.39371	4.817151	13.19414	1.498151	3.681728	5.753754	1.2731	0.13674	0.2264	RP11-843P	chr5	+	1.76E+08	1.76E+08	504

ENSG00000(	1.035792	0	2.638828	3.745378	0.920432	0.821965	-0.40309	0.75376	0.83714	AC097467.	chr4	+	1.56E+08	1.56E+08	840
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-1084	chr5	+	33970968	33972733	1145
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP4-785G1	chr20	-	32822646	32868979	478
ENSG00000(	2.071584	13.24716	2.638828	2.247227	1.840864	0	1.6727	0.13034	0.21772	RP11-497H	chr5	+	69825198	69826377	1180
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	RP11-297P	chr4	-	1.04E+08	1.04E+08	830
ENSG00000(	1.035792	1.204288	6.597069	0	0	0	2.5314	0.059212	0.1124	KB-1639H6	chr8	+	1.04E+08	1.04E+08	556
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	LNX1-AS1	chr4	+	54362567	54415745	550
ENSG00000(	2.071584	0	0	0	0.920432	0.821965	0.13309	0.92108	NA	GAPDHP66	chr18	-	3977649	3978615	967
ENSG00000(	8.286335	0	0	4.494453	0.920432	3.28786	-0.03086	0.9795	0.98804	RP11-71E1	chr3	+	1.26E+08	1.26E+08	501
ENSG00000(	1.035792	1.204288	0	1.498151	2.761296	2.465895	-1.0161	0.42819	0.55842	RP11-679C	chr4	+	1.21E+08	1.21E+08	2339
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP11-180A	chr4	+	9678932	9679558	627
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-810P	chr4	-	1.28E+08	1.28E+08	648
ENSG00000(	5.17896	2.408575	1.319414	0	1.840864	0	1.5254	0.23444	0.34856	RP11-1079	chr17	+	47452742	47457456	245
ENSG00000(	4.143168	10.83859	9.235896	7.490755	23.0108	9.863579	-0.68238	0.34772	0.4774	RP11-33B1	chr4	+	1.2E+08	1.2E+08	573
ENSG00000(	0	2.408575	1.319414	1.498151	0	0	0.61999	0.64768	NA	RP11-79E3	chr4	-	33777969	34041515	2404
ENSG00000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	RP11-248N	chr4	-	1.75E+08	1.75E+08	1144
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	LINC00492	chr5	+	1.02E+08	1.02E+08	593
ENSG00000(	76.6486	43.35436	68.60952	28.46487	35.89685	61.64737	0.57268	0.13807	0.2282	GLUD1P3	chr10	+	75490320	75497069	896
ENSG00000(	0	0	0	2.996302	2.761296	0	-1.5727	0.24592	NA	CTD-2023N	chr5	+	56690887	56829251	897
ENSG00000(	1.035792	0	0	0	9.20432	0	-1.599	0.23549	0.34987	RP11-423H	chr5	+	1.77E+08	1.77E+08	568
ENSG00000(	1.035792	6.021439	0	0	1.840864	0.821965	0.90913	0.4857	0.6148	RP11-402J(	chr4	+	1.13E+08	1.13E+08	411
ENSG00000(	6.214751	1.204288	6.597069	0	0	0.821965	2.6778	0.032114	0.06597	RP11-364L	chr4	+	1.44E+08	1.44E+08	624
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	CKS1BP5	chr5	+	1.44E+08	1.44E+08	273
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-94C2	chr17	-	48640564	48641144	156
ENSG00000(	1.035792	0	1.319414	0	0	0.821965	0.54471	0.68089	NA	RP11-357D	chr5	-	66759637	66771420	685
ENSG00000(	0	2.408575	1.319414	0	3.681728	0	0.015586	0.99078	0.99468	RP11-656G	chr8	-	73114986	73163800	3048
ENSG00000(	1.035792	1.204288	1.319414	0	1.840864	0	0.52252	0.69958	NA	RP11-529H	chr4	-	1.54E+08	1.54E+08	769
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-19O2	chr5	+	16129287	16141711	708
ENSG00000(	0	3.612863	7.916483	0.749076	11.04518	11.50751	-0.8627	0.39524	0.52627	AC141928.	chr4	-	3760475	3765117	4525
ENSG00000(	36.25272	62.62296	35.62417	35.20655	34.05598	55.07165	0.10943	0.78334	0.85731	RP11-752G	chr15	+	83419316	83425958	790
ENSG00000(	7.250543	4.817151	0	0	2.761296	0	1.4826	0.23901	0.35399	AC073635.	chr7	-	76875657	76887440	570
ENSG00000(	4.143168	1.204288	3.958241	0	0.920432	0	2.0879	0.10796	0.18672	MICE	chr6	-	29709508	29716746	1157
ENSG00000(	0	1.204288	0	1.498151	0	1.64393	-0.60583	0.65413	NA	RP11-404J2	chr4	-	1.8E+08	1.8E+08	539
ENSG00000(	6.214751	6.021439	5.277655	8.988907	21.16994	9.041614	-1.0564	0.15627	0.25228	RP11-1379	chr5	+	1.79E+08	1.79E+08	485
ENSG00000(	4.143168	2.408575	0	1.498151	5.522592	5.753754	-0.727	0.51092	0.63813	AC008592.	chr5	-	95170128	95170750	418
ENSG00000(	0	0	0	0.749076	2.761296	0.821965	-1.3133	0.33155	NA	CTD-2193P	chr5	-	80293002	80293866	536
ENSG00000(	186.4425	199.9118	224.3003	1.498151	0.920432	1.64393	6.8121	6.62E-31	1.04E-29	RP11-152P	chr8	-	1.07E+08	1.07E+08	801
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	ORAOV1P1	chr4	-	1.87E+08	1.87E+08	395
ENSG00000(	1.035792	1.204288	0	1.498151	0.920432	0	-0.04875	0.97134	NA	RP13-494C	chr4	-	25866503	25871172	762
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-6L6.7	chr4	+	1.47E+08	1.47E+08	732
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-402L	chr3	-	1.33E+08	1.33E+08	2427
ENSG00000(	3.107376	0	1.319414	2.247227	0	0	0.52296	0.69882	0.79519	GAPDHP62	chr8	-	1.02E+08	1.02E+08	990
ENSG00000(	3.107376	1.204288	0	2.247227	0	0	0.50489	0.70888	0.80322	SLC25A30-	chr13	+	45992297	45994506	701
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP11-80G7	chr5	-	1.63E+08	1.63E+08	800

ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	HIGD1AP1:	chr4	-	79570108	79570396	289
ENSG00000(	192.6573	274.5776	196.5927	441.9546	319.3899	355.0888	-0.74786	0.000192	0.000599	THAP9-AS1	chr4	-	83814639	83822113	2585
ENSG00000(	3.107376	1.204288	3.958241	1.498151	0	5.753754	0.1344	0.90893	0.94397	RP11-549J:	chr5	-	93196375	93199531	3157
ENSG00000(	0	1.204288	0	0	0	1.64393	-0.12916	0.91993	NA	CTC-367F4.	chr5	-	1.45E+08	1.45E+08	493
ENSG00000(	7.250543	19.2686	9.235896	11.98521	9.20432	4.93179	0.41237	0.56528	0.68469	RP11-582J:	chr8	-	22398358	22402918	4076
ENSG00000(	2.071584	1.204288	1.319414	3.745378	5.522592	3.28786	-1.1277	0.30736	0.43312	AC006157.	chrY	+	2722771	2800041	454
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CTD-2275D	chr5	+	73617456	73635977	550
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	CTC-321K1	chr5	-	1.35E+08	1.35E+08	2141
ENSG00000(	1.035792	13.24716	0	2.247227	0.920432	0.821965	1.3546	0.25182	0.36946	ZNF969P	chr4	+	1.11E+08	1.11E+08	2341
ENSG00000(	10.35792	18.06432	5.277655	11.98521	0	13.15144	0.36948	0.66276	0.76688	RP11-168A	chr5	+	79315432	79315743	312
ENSG00000(	0	1.204288	0	2.247227	0.920432	2.465895	-1.2325	0.35797	0.4875	CTD-2215E	chr5	-	96559075	96563661	414
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	ANKRD20A	chr4	-	49504162	49508039	1330
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTD-2218G	chr5	-	32888096	32888251	156
ENSG00000(	0	2.408575	1.319414	0.749076	0.920432	0.821965	0.33249	0.80324	0.87237	BMS1P6	chr10	+	48187416	48199256	1331
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-434D	chr5	-	1.26E+08	1.26E+08	914
ENSG00000(	5.17896	0	0	1.498151	0.920432	0	0.63395	0.63748	0.74595	NUDT19P5	chr4	+	1.59E+08	1.59E+08	569
ENSG00000(	0	0	0	1.498151	0.920432	4.109825	-1.8535	0.1707	0.27109	HTT-AS1	chr4	-	3065198	3076241	515
ENSG00000(	5.17896	7.225726	1.319414	0	0.920432	4.109825	1.1235	0.32454	0.45206	RP11-526F	chr5	+	1.12E+08	1.12E+08	711
ENSG00000(	2.071584	1.204288	1.319414	0.749076	0.920432	4.109825	-0.22656	0.85474	0.90762	BMS1P2	chr10	-	47228366	47241942	1858
ENSG00000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	RP11-713M	chr4	+	1.08E+08	1.08E+08	557
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-893F	chr17	+	48292055	48292781	455
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-414H	chr5	-	90522292	90522888	597
ENSG00000(	7.250543	6.021439	7.916483	155.8077	99.40666	111.7872	-4.005	9.75E-20	9.75E-19	RP11-115D	chr4	+	90472507	90647654	1816
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTBP2P4	chr5	+	97912045	97912964	920
ENSG00000(	0	6.021439	1.319414	0	0	0	2.1383	0.11496	0.19679	FCF1P8	chr4	-	56217979	56218575	597
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-280G	chr8	-	62671653	62678528	2750
ENSG00000(	5.17896	0	0	0	0.920432	0.821965	0.87011	0.51979	0.64576	WWC2-AS1	chr4	-	1.84E+08	1.84E+08	404
ENSG00000(	1.035792	0	0	1.498151	8.283888	2.465895	-2.2008	0.083388	0.15069	RP11-734I:	chr4	+	31999019	32157028	734
ENSG00000(	7.250543	7.225726	5.277655	1.498151	3.681728	1.64393	1.3226	0.16962	0.26964	CTD-2035E	chr5	+	43018531	43024349	472
ENSG00000(	109.7939	90.32158	80.48424	79.40201	115.054	83.01846	0.023109	0.9338	0.96025	RP11-37B2	chr8	-	90621638	90769955	3802
ENSG00000(	2.071584	0	3.958241	0	0	0	1.8862	0.16413	0.26236	RP11-701P	chr4	+	1.86E+08	1.86E+08	617
ENSG00000(	27.96638	21.67718	22.43003	2.247227	8.283888	2.465895	2.3376	0.000504	0.001482	RP11-53O1	chr5	-	44745002	44808879	775
ENSG00000(	30.03797	26.49433	3.958241	4.494453	7.363456	6.575719	1.6006	0.025376	0.053681	RP11-849H	chr11	+	71725337	71731956	4233
ENSG00000(	19.68005	14.45145	25.06886	0.749076	0	1.64393	3.9793	7.34E-06	2.76E-05	CTD-2532K	chr5	+	1.74E+08	1.74E+08	287
ENSG00000(	6.214751	6.021439	5.277655	0	0.920432	0	3.0248	0.011499	0.026361	RP11-478C	chr4	+	2297311	2320816	563
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	HOXC-AS3	chr12	-	54375293	54379303	2816
ENSG00000(	7.250543	16.86003	7.916483	5.243529	10.12475	3.28786	0.71646	0.35675	0.48624	RP11-384K	chr4	+	1.2E+08	1.2E+08	186
ENSG00000(	0	0	0	1.498151	0.920432	1.64393	-1.2565	0.35231	NA	RP11-399D	chr4	-	35949843	36075457	1969
ENSG00000(	1.035792	16.86003	13.19414	10.48706	8.283888	16.4393	-0.18072	0.81297	0.87865	RP11-540C	chr15	+	41199009	41201540	589
ENSG00000(	0	0	0	0.749076	0	5.753754	-1.7034	0.2092	0.31883	HULC	chr6	+	8652370	8654079	556
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-215A	chr4	-	1.87E+08	1.87E+08	1512
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	OR7E163P	chr4	-	3891083	3891976	894
ENSG00000(	1.035792	0	1.319414	0.749076	0	0.821965	0.26466	0.84506	NA	RP11-327C	chr4	+	1.7E+08	1.7E+08	637
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	UCHL1-AS1	chr4	-	41222091	41258744	592

ENSG00000(	2.071584	3.612863	5.277655	2.996302	2.761296	3.28786	0.21569	0.83449	0.89396	RP11-45L9	chr4	-	1.07E+08	1.07E+08	481
ENSG00000(	18.64425	20.47289	25.06886	2.996302	0	0	3.8047	9.57E-06	3.56E-05	RP11-893F	chr17	-	48358938	48365216	750
ENSG00000(	0	1.204288	0	0	1.840864	0.821965	-0.461	0.73167	NA	RP11-689P	chr4	-	8455137	8456669	664
ENSG00000(	0	0	0	1.498151	2.761296	5.753754	-2.4738	0.061229	0.11559	CTC-459M5	chr5	+	1.12E+08	1.12E+08	588
ENSG00000(	12.4295	14.45145	1.319414	51.68621	51.54419	73.15488	-2.5198	8.26E-07	3.45E-06	RP11-478C	chr4	-	262771	263320	550
ENSG00000(	1.035792	4.817151	0	0	0.920432	0	1.3927	0.30336	0.42851	LINC00589	chr8	-	29531438	29605625	1404
ENSG00000(	117.0445	78.2787	116.1084	104.8706	98.48622	123.2947	-0.06801	0.79585	0.86672	ZNF674	chrX	-	46357162	46404892	4073
ENSG00000(	10.35792	31.31148	31.66593	6.74168	1.840864	0.821965	2.6805	0.00033	0.000997	RP1-68D18	chr11	+	35234097	35235554	704
ENSG00000(	114.9729	116.8159	167.5656	44.19546	104.0088	60.00344	0.93077	0.003387	0.008679	RP11-54F2	chr5	-	10652323	10656037	800
ENSG00000(	5.17896	3.612863	0	0	0	0	2.4569	0.068737	0.12775	CTC-278L1.	chr5	-	1.06E+08	1.06E+08	1666
ENSG00000(	0	1.204288	1.319414	0	1.840864	0	0.21033	0.87627	NA	CTD-2187J7	chr5	+	66563850	66566010	509
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-82I1(	chr15	-	98285448	98417780	2036
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	GOLGA5P1	chr5	-	39169312	39170437	980
ENSG00000(	0	4.817151	2.638828	0	0	0	2.1804	0.10782	0.18657	RP11-161D	chr4	-	1.75E+08	1.75E+08	1824
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-1057	chr8	+	1.36E+08	1.36E+08	2096
ENSG00000(	1.035792	0	3.958241	4.494453	0.920432	5.753754	-0.8976	0.44382	0.57349	CTC-325J23	chr5	-	79904442	79918343	440
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-627H	chr4	-	1.56E+08	1.56E+08	1534
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	CNOT10-AS	chr3	-	32772127	32778946	466
ENSG00000(	0	0	0	0	1.840864	4.93179	-1.7714	0.19169	0.29733	RP11-469N	chr11	+	1.35E+08	1.35E+08	3684
ENSG00000(	10.35792	10.83859	13.19414	6.74168	10.12475	4.93179	0.61138	0.3923	0.52313	RP11-503N	chr4	-	2506808	2508006	900
ENSG00000(	11.39371	1.204288	3.958241	0	0	0	3.53	0.005776	0.014133	RP11-701P	chr4	-	1.86E+08	1.86E+08	729
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	PSMA2P2	chr8	-	94951592	94955105	686
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	CTD-2207L	chr5	+	52185498	52185786	289
ENSG00000(	55.93276	67.44011	54.09597	54.68252	63.50981	41.09825	0.15536	0.64207	0.74961	ZNF345	chr19	+	37341263	37403931	3527
ENSG00000(	2.071584	4.817151	1.319414	0.749076	1.840864	0	1.1585	0.35539	0.48497	RP11-73G1	chr4	+	1.53E+08	1.53E+08	2652
ENSG00000(	1.035792	0	5.277655	0	8.283888	2.465895	-0.56142	0.64377	0.75103	GTF2F2P1	chr4	+	1.48E+08	1.48E+08	675
ENSG00000(	18.64425	45.76293	21.11062	0	0	0	6.0559	2.21E-08	1.08E-07	CTD-2263F	chr5	-	38461029	38468441	456
ENSG00000(	0	1.204288	0	0	1.840864	0.821965	-0.461	0.73167	NA	RFPL4B	chr6	+	1.13E+08	1.13E+08	1900
ENSG00000(	1.035792	9.634302	1.319414	0	0.920432	2.465895	1.3264	0.27136	0.39211	AC004069.	chr4	-	1.06E+08	1.06E+08	549
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-545H	chr4	-	55306669	55312890	624
ENSG00000(	18.64425	34.92434	13.19414	7.490755	18.40864	16.4393	0.63351	0.28082	0.40315	RP1-5O6.6	chr22	-	38616982	38618939	1063
ENSG00000(	0	0	0	1.498151	2.761296	2.465895	-1.9136	0.15629	0.25228	RP11-231L	chr3	-	1.41E+08	1.41E+08	392
ENSG00000(	1.035792	4.817151	1.319414	5.243529	0	11.50751	-0.97478	0.37741	0.50811	ALG1L7P	chr4	+	3937174	3944248	768
ENSG00000(	0	0	1.319414	0	3.681728	0.821965	-0.89047	0.5116	NA	RP11-436H	chr5	+	1.24E+08	1.24E+08	526
ENSG00000(	1.035792	3.612863	0	0	0	0	1.5346	0.25314	NA	MAGI2-AS1	chr7	+	78569166	78570211	472
ENSG00000(	4.143168	2.408575	0	2.996302	0	0.821965	0.51385	0.68905	0.78762	CTC-436P1	chr5	+	60457897	60527867	796
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	CTD-2066L	chr5	-	33011428	33017713	425
ENSG00000(	13.46529	12.04288	6.597069	6.74168	11.04518	18.90519	-0.16828	0.80619	0.8743	ALG1L2	chr3	+	1.3E+08	1.3E+08	969
ENSG00000(	0	6.021439	1.319414	0	5.522592	2.465895	-0.08309	0.94604	0.96742	RP11-10L1	chr4	+	1.04E+08	1.04E+08	1241
ENSG00000(	0	0	0	5.243529	0	1.64393	-1.8073	0.18279	0.2864	RP11-380P	chr4	-	23724885	23735202	639
ENSG00000(	0	1.204288	6.597069	0	0	0	2.2118	0.10284	0.17949	RP11-81H1	chr12	-	68726668	68845443	904
ENSG00000(	0	0	0	0.749076	1.840864	0	-0.68825	0.58858	NA	CTD-2003D	chr5	+	59926341	59926800	460
ENSG00000(	2.071584	0	1.319414	1.498151	0	0	0.5543	0.68269	NA	NDUFB4P2	chr5	+	58824687	58825077	391
ENSG00000(	0	1.204288	0	2.996302	3.681728	4.109825	-2.0385	0.10878	0.18789	RP11-506H	chr5	+	54529762	54591029	770

ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-706F	chr4	+	1.9E+08	1.9E+08	412
ENSG00000(	1.035792	0	1.319414	1.498151	0	0	0.26794	0.842	NA	CTD-2337A	chr5	+	95297705	95966789	581
ENSG00000(	0	0	0	2.996302	0	0.821965	-1.0802	0.41594	NA	CTC-327F1(	chr5	+	1.47E+08	1.47E+08	593
ENSG00000(	853.4925	763.5184	664.9845	195.5087	212.6198	189.8739	1.9277	4.39E-34	7.65E-33	SHANK3	chr22	+	51112843	51171726	7394
ENSG00000(	2.071584	9.634302	11.87472	17.97781	17.48821	18.90519	-1.1497	0.088787	0.15894	RP11-452H	chr11	-	78135028	78140882	1642
ENSG00000(	3.107376	3.612863	9.235896	2.247227	6.443024	0	0.71728	0.49699	0.62546	CTD-2283N	chr5	+	1.48E+08	1.48E+08	514
ENSG00000(	0	0	0	0.749076	5.522592	4.109825	-2.4974	0.058964	0.11206	RP11-689K	chr4	-	82380633	82965397	539
ENSG00000(	0	0	1.319414	0.749076	0.920432	1.64393	-0.6955	0.60822	NA	RP11-177C	chr4	-	37997115	37997824	710
ENSG00000(	1.035792	1.204288	3.958241	0	0	3.28786	0.56883	0.66301	0.76704	RTN3P1	chr4	+	1.46E+08	1.46E+08	711
ENSG00000(	3.107376	1.204288	0	3.745378	3.681728	1.64393	-0.75613	0.52694	0.65171	RP11-461G	chr5	+	93905245	93906381	1137
ENSG00000(	5.17896	7.225726	21.11062	0	11.04518	9.041614	0.64989	0.46345	0.59277	HSPD1P11	chr5	+	95104703	95106404	1702
ENSG00000(	2.071584	14.45145	2.638828	2.996302	1.840864	2.465895	1.1516	0.25318	0.37101	RP11-697N	chr8	-	48459366	48460488	779
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RAB5CP2	chr5	+	90772199	90772835	637
ENSG00000(	19.68005	20.47289	15.83297	8.239831	13.80648	11.50751	0.71087	0.22542	0.33812	WWC2-AS2	chr4	-	1.84E+08	1.84E+08	2183
ENSG00000(	4.143168	0	7.916483	1.498151	0	0	1.9237	0.13175	0.21966	CTD-2091N	chr5	-	92355369	92404375	625
ENSG00000(	26.93059	21.67718	19.79121	32.21025	66.2711	39.45432	-0.97362	0.027595	0.057814	RP11-129N	chr14	+	41424103	41445082	696
ENSG00000(	5.17896	7.225726	1.319414	5.992604	5.522592	3.28786	-0.08436	0.92872	0.95719	CTD-2516F	chr11	-	7448497	7533746	4433
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	RP11-332J	chr5	+	6766004	6772066	596
ENSG00000(	165.7267	163.7831	155.6908	129.5901	114.1336	98.63579	0.49912	0.026497	0.055796	ZNF550	chr19	-	58046625	58071231	4305
ENSG00000(	2.071584	4.817151	7.916483	0.749076	3.681728	1.64393	1.0483	0.32211	0.44943	CTD-2201E	chr5	+	9511445	9518198	1679
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	LINC00499	chr4	+	1.39E+08	1.39E+08	587
ENSG00000(	1.035792	0	2.638828	4.494453	0.920432	0	-0.36993	0.778	0.85377	RPS23P5	chr5	-	81560976	81561078	103
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP11-484C	chr4	-	15359765	15421656	871
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CTB-35F21.	chr5	-	1.39E+08	1.39E+08	553
ENSG00000(	0	1.204288	2.638828	0.749076	0	0	1.0049	0.45751	NA	YTHDF1P1	chr5	+	96704480	96706125	1646
ENSG00000(	1.035792	1.204288	0	2.996302	0.920432	1.64393	-0.81367	0.5334	0.65798	RP11-276A	chr20	+	825767	838106	1328
ENSG00000(	15.53688	8.430014	14.51355	6.74168	5.522592	15.61733	0.43161	0.53507	0.65925	RP11-163N	chr8	-	61297147	61429354	2444
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	ALDH7A1P	chr5	+	76586093	76587625	1533
ENSG00000(	1.035792	10.83859	0	3.745378	0	4.109825	0.43507	0.71238	0.80558	FAM90A25	chr8	-	12272593	12275599	1391
ENSG00000(	2.071584	1.204288	5.277655	11.98521	11.96562	5.753754	-1.5915	0.074963	0.13757	CTB-109A1	chr5	-	1.57E+08	1.57E+08	1992
ENSG00000(	1.035792	0	0	1.498151	0	0	-0.08447	0.94679	NA	RP11-586D	chr4	+	6204055	6208376	4121
ENSG00000(	1.035792	6.021439	6.597069	1.498151	1.840864	0	1.5294	0.18673	0.2914	RP11-397E	chr4	-	87834419	87835970	1110
ENSG00000(	24.85901	40.94578	11.87472	8.988907	7.363456	13.9734	1.2885	0.031121	0.064211	RP11-843P	chr5	+	1.76E+08	1.76E+08	528
ENSG00000(	2.071584	0	0	2.247227	0.920432	0	-0.28364	0.8344	NA	RP11-140N	chr4	-	1.79E+08	1.79E+08	255
ENSG00000(	4.143168	4.817151	10.55531	17.97781	7.363456	6.575719	-0.66607	0.39584	0.52694	RP11-1348	chr16	+	28814097	28829149	1930
ENSG00000(	7.250543	6.021439	7.916483	3.745378	1.840864	0	1.5864	0.11646	0.19898	RP11-597D	chr4	+	1.59E+08	1.59E+08	3115
ENSG00000(	26.93059	18.06432	14.51355	27.7158	12.88605	10.68554	0.20503	0.72134	0.81267	RP11-420A	chr4	+	1.29E+08	1.29E+08	2012
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	NDUFS5P4	chr4	-	99897951	99898268	318
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-431N	chr4	-	36312812	36394032	541
ENSG00000(	5.17896	0	0	0	0	0	1.5469	0.24589	NA	RTEL1P1	chr4	+	1.13E+08	1.13E+08	3685
ENSG00000(	26.93059	51.78437	32.98534	3.745378	2.761296	4.109825	3.2016	1.45E-07	6.53E-07	RP11-792D	chr4	+	79567057	79603853	2186
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-483A	chr4	+	1.7E+08	1.7E+08	183
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-71E1	chr3	-	1.26E+08	1.26E+08	254
ENSG00000(	0	0	0	23.22134	8.283888	14.79537	-4.7919	2.29E-05	8.14E-05	CTC-459I6.	chr5	-	80243516	80256726	665

ENSG00000(	1.035792	3.612863	2.638828	0	0	0.821965	1.7946	0.17647	0.27846	GS1-124K5	chr7	-	65872275	65874226	301
ENSG00000(	3.107376	8.430014	9.235896	7.490755	2.761296	4.109825	0.44744	0.61081	0.72464	RP11-164P	chr4	+	1.53E+08	1.53E+08	2565
ENSG00000(	0	0	2.638828	0.749076	0	0	0.57076	0.66213	NA	RP11-436H	chr5	-	1.24E+08	1.24E+08	558
ENSG00000(	3.107376	1.204288	1.319414	2.996302	0	5.753754	-0.46242	0.6988	0.79519	RP11-501C	chr17	-	47090299	47091087	271
ENSG00000(	0	0	2.638828	0	0.920432	0.821965	0.26148	0.84655	NA	FKBP4P1	chr4	-	1.19E+08	1.19E+08	1347
ENSG00000(	5.17896	6.021439	7.916483	0	0	0	3.8344	0.001979	0.005277	CTC-250P2	chr5	+	72292747	72293469	723
ENSG00000(	2.071584	6.021439	0	74.90755	52.46462	60.00344	-4.2495	1.01E-11	6.45E-11	RP11-369K	chr8	+	12815896	12819709	1418
ENSG00000(	317.9881	298.6634	273.1187	118.3539	180.4047	177.5444	0.90032	1.54E-05	5.58E-05	RPL32P3	chr3	-	1.29E+08	1.29E+08	2816
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-531A	chr5	-	5396590	5397081	492
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTD-2122P	chr5	-	41585984	41587889	1562
ENSG00000(	2.071584	2.408575	3.958241	3.745378	6.443024	6.575719	-0.84614	0.38601	0.51688	RP5-1065J	chr1	-	1.1E+08	1.1E+08	609
ENSG00000(	6.214751	0	0	4.494453	1.840864	4.109825	-0.52393	0.65894	0.76349	AC068134.	chr2	+	2.33E+08	2.33E+08	788
ENSG00000(	10.35792	15.65574	9.235896	4.494453	0	0.821965	2.3121	0.012495	0.028421	FOXD1	chr5	-	72740654	72744352	2270
ENSG00000(	0	7.225726	0	1.498151	0	1.64393	0.73071	0.57895	0.69729	PPIAP11	chr5	-	81305421	81305913	493
ENSG00000(	8.286335	0	1.319414	4.494453	0.920432	4.109825	0.025556	0.98207	0.98984	RP11-197N	chr12	+	1.24E+08	1.24E+08	2191
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-171N	chr4	+	1.58E+08	1.58E+08	993
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	RP11-155G	chr5	+	96519303	96772921	893
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	CTD-2130F	chr5	+	37948593	37951157	546
ENSG00000(	2.071584	7.225726	6.597069	0	1.840864	0	2.2986	0.05304	0.10227	RP11-46A1	chr1	+	1.81E+08	1.81E+08	537
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	IMPA1P	chr8	-	82517804	82543369	842
ENSG00000(	9.322127	13.24716	18.47179	0	4.60216	0.821965	2.5815	0.004325	0.010849	RP11-724N	chr4	+	99417515	99431086	489
ENSG00000(	0	1.204288	0	0	1.840864	0	-0.18234	0.88799	NA	RP11-478C	chr4	-	330047	330575	529
ENSG00000(	0	0	1.319414	2.247227	0	1.64393	-0.7954	0.55767	NA	TRIM16	chr17	-	15474805	15554967	5514
ENSG00000(	0	0	0	2.996302	0	0.821965	-1.0802	0.41594	NA	RP11-166A	chr5	-	1.22E+08	1.22E+08	1651
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	SNX18P24	chr4	+	49563496	49564166	671
ENSG00000(	3.107376	4.817151	5.277655	1.498151	4.60216	0.821965	0.76738	0.46783	0.59711	RP11-32M2	chr9	-	1.15E+08	1.15E+08	584
ENSG00000(	4.143168	2.408575	2.638828	1.498151	0	4.109825	0.53345	0.64857	0.75506	MTND5P12	chr5	+	93903166	93904614	1449
ENSG00000(	0	1.204288	1.319414	1.498151	0	0	0.30687	0.81977	NA	RP11-215G	chr5	-	10664607	10665225	619
ENSG00000(	7.250543	3.612863	5.277655	8.988907	15.64734	5.753754	-0.81186	0.30953	0.43571	RP11-501C	chr17	+	47114484	47114791	308
ENSG00000(	2.071584	6.021439	10.55531	0	8.283888	5.753754	0.3437	0.73048	0.81959	RP11-118N	chr5	+	1.45E+08	1.45E+08	439
ENSG00000(	53466.54	65860.09	56780.97	3753.618	28180.87	26487	1.4693	0.042168	0.083815	MALAT1	chr11	+	65265233	65273940	8708
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	ALG3P1	chr5	-	5375836	5376949	1114
ENSG00000(	0	0	0	2.996302	0.920432	3.28786	-2.001	0.13762	0.22759	RP11-6N13	chr5	-	1.04E+08	1.05E+08	777
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-536I(	chr3	-	14389951	14394068	2284
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP11-297P	chr4	+	1.04E+08	1.05E+08	825
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-39E3	chr3	-	1.31E+08	1.31E+08	523
ENSG00000(	0	14.45145	5.277655	2.247227	0	0.821965	1.9885	0.085904	0.15473	RP11-539L	chr4	-	6672452	6675557	422
ENSG00000(	7.250543	10.83859	5.277655	14.98151	22.09037	16.4393	-1.1162	0.084907	0.15315	RP11-464F	chr10	-	75432880	75435692	508
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-440I2	chr4	+	1.75E+08	1.75E+08	792
ENSG00000(	2.071584	1.204288	2.638828	0.749076	3.681728	0	0.29916	0.81261	0.87847	TET2-AS1	chr4	-	1.06E+08	1.06E+08	537
ENSG00000(	0	0	0	0.749076	0.920432	1.64393	-1.0185	0.44577	NA	LDHAP1	chr4	-	4895909	4896900	992
ENSG00000(	1.035792	2.408575	1.319414	0	0	0	1.6865	0.21314	NA	MSNP1	chr5	+	25909612	25911343	1732
ENSG00000(	16.57267	25.29004	5.277655	25.46857	31.29469	33.70056	-0.89068	0.10025	0.17584	ABCA11P	chr4	-	419224	467918	2110
ENSG00000(	5.17896	1.204288	6.597069	1.498151	0.920432	1.64393	1.3019	0.24377	0.35975	HADHAP1	chr4	-	1.66E+08	1.66E+08	2284

ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-232L	chr5	-	72427835	72446419	449
ENSG00000(	39.36009	38.53721	23.74945	50.18806	34.97642	30.4127	-0.17777	0.66965	0.77259	RP11-521B	chr14	-	1.06E+08	1.06E+08	2279
ENSG00000(	5.17896	1.204288	1.319414	17.22874	12.88605	16.4393	-2.2851	0.0052	0.012848	RP11-164P	chr4	+	1.53E+08	1.53E+08	304
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	RP11-79P5	chr5	+	72747323	72749220	780
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CTD-2037K	chr5	+	77603327	77603738	412
ENSG00000(	0	2.408575	3.958241	2.996302	0	3.28786	-0.01443	0.99076	0.99468	SETP12	chr4	-	1.22E+08	1.22E+08	805
ENSG00000(	0	0	0	0.749076	0.920432	0.821965	-0.73223	0.57364	NA	RP11-610P	chr4	-	1.52E+08	1.52E+08	358
ENSG00000(	3.107376	1.204288	0	0	0	0	1.4526	0.27741	NA	HSPA8P19	chr3	+	1.32E+08	1.32E+08	1517
ENSG00000(	33.14534	32.51577	25.06886	17.97781	11.04518	26.30288	0.68724	0.16486	0.26336	RP11-774C	chr4	-	8356817	8359103	2287
ENSG00000(	0	0	0	4.494453	0	0	-1.1446	0.38559	NA	RP11-485N	chr5	-	1.32E+08	1.32E+08	678
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	UNC93B7	chr4	+	9495380	9499710	705
ENSG00000(	0	0	0	2.996302	1.840864	4.109825	-2.3265	0.080173	0.14563	RP11-371N	chr5	+	1.13E+08	1.13E+08	570
ENSG00000(	0	0	6.597069	2.247227	1.840864	0	0.41187	0.75376	0.83714	RP11-714L	chr4	+	1.38E+08	1.39E+08	2264
ENSG00000(	25.8948	12.04288	11.87472	17.97781	11.04518	18.08323	0.08449	0.88629	0.92915	RP11-1280	chr5	-	70398725	70424580	2851
ENSG00000(	0	0	0	3.745378	1.840864	2.465895	-2.1746	0.10423	0.18143	EMCN-IT1	chr4	-	1.02E+08	1.02E+08	481
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-20I2(	chr4	-	1093804	1095346	1204
ENSG00000(	0	0	0	5.992604	3.681728	1.64393	-2.6634	0.041739	0.083088	RP11-91J3.	chr4	-	1.88E+08	1.88E+08	1223
ENSG00000(	0	0	0	0	0	4.93179	-1.2404	0.35057	NA	RP11-576N	chr4	-	84298516	84299229	639
ENSG00000(	0	3.612863	1.319414	0	0.920432	0	1.1993	0.37664	NA	RP11-20I2(	chr4	+	1107427	1126765	468
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-192H	chr5	-	25219082	25298721	558
ENSG00000(	4.143168	0	0	0	0.920432	0	0.95689	0.47805	NA	PRB1	chr12	-	11504757	11548500	1173
ENSG00000(	1.035792	4.817151	2.638828	2.996302	0	2.465895	0.44957	0.70565	0.80056	CTD-2154I:	chr5	+	94993766	95020477	725
ENSG00000(	19.68005	45.76293	36.94359	0	0	0	6.3138	3.18E-09	1.67E-08	RP11-326C	chr11	+	318640	325631	1151
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	SUMO2P5	chr5	+	74521249	74521493	245
ENSG00000(	50.7538	26.49433	44.86007	57.67882	82.83888	84.66239	-0.86201	0.015015	0.033521	PCDHA12	chr5	+	1.4E+08	1.4E+08	5233
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-700H	chr17	+	49021465	49026111	789
ENSG00000(	11.39371	12.04288	7.916483	13.48336	3.681728	7.397684	0.31583	0.66968	0.77259	ZNF346-IT1	chr5	+	1.76E+08	1.76E+08	745
ENSG00000(	5.17896	0	0	0	0	3.28786	0.37286	0.78257	0.85688	RP11-844P	chr5	+	1.76E+08	1.76E+08	951
ENSG00000(	27.96638	10.83859	26.38828	38.95193	21.16994	25.48091	-0.38051	0.45465	0.58428	FAM86EP	chr4	-	3943487	3957146	2845
ENSG00000(	9.322127	8.430014	23.74945	16.47966	50.62376	27.94681	-1.1477	0.04718	0.092287	CTC-458I2.	chr5	+	79424184	79439706	664
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	RP11-614F	chr4	+	1.33E+08	1.33E+08	680
ENSG00000(	0	1.204288	0	0	0	1.64393	-0.12916	0.91993	NA	CTC-575N7	chr5	-	1.29E+08	1.29E+08	631
ENSG00000(	5.17896	4.817151	3.958241	1.498151	4.60216	6.575719	0.12806	0.89372	0.93425	RP11-631N	chr5	+	60642953	60643543	591
ENSG00000(	3.107376	6.021439	2.638828	2.247227	8.283888	3.28786	-0.18455	0.85074	0.9049	RP11-181K	chr4	+	1.47E+08	1.47E+08	794
ENSG00000(	8.286335	12.04288	13.19414	23.22134	23.93123	29.59074	-1.153	0.036181	0.073274	RP11-478C	chr4	-	263655	263964	310
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	PTX4	chr16	-	1535887	1538982	1516
ENSG00000(	52.82539	45.76293	54.09597	36.7047	39.57858	35.34449	0.44482	0.21234	0.32243	RP11-158K	chr8	+	1.26E+08	1.26E+08	2355
ENSG00000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	RP11-136C	chr8	+	1.26E+08	1.27E+08	785
ENSG00000(	3.107376	4.817151	3.958241	1.498151	0	1.64393	1.4236	0.22105	0.33288	CTD-2373N	chr8	+	30454431	30455049	407
ENSG00000(	2.071584	4.817151	17.15238	8.239831	5.522592	3.28786	0.41353	0.63769	0.74611	RP11-648L	chr8	-	59004001	59018853	625
ENSG00000(	2.071584	0	0	1.498151	2.761296	0	-0.5204	0.70059	0.7965	CTB-45I8.1	chr5	-	1.54E+08	1.54E+08	982
ENSG00000(	0	0	0	0.749076	0.920432	2.465895	-1.2662	0.34855	NA	RP11-659E	chr8	+	63936931	63937853	667
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP11-527N	chr8	-	37184093	37189502	3692
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	TRAPPC2P2	chr8	-	72361046	72361454	409

ENSG00000(	0	0	0	2.996302	2.761296	7.397684	-2.8941	0.024777	0.052546	CTD-3023L	chr8	+	8418901	8427198	643
ENSG00000(	2.071584	3.612863	1.319414	0.749076	1.840864	4.109825	0.054225	0.96286	0.97847	RP11-360L	chr8	-	41391674	41435887	559
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-509P	chr8	+	85591033	85592077	1045
ENSG00000(	0	2.408575	0	20.22504	22.09037	13.9734	-3.8307	5.45E-05	0.000184	RP11-366K	chr8	+	67104328	67109550	1502
ENSG00000(	7.250543	6.021439	2.638828	0	0	0	3.5319	0.00539	0.01326	CTB-164N1	chr5	+	1.73E+08	1.73E+08	753
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-333A	chr8	-	71383347	71392858	736
ENSG00000(	0	0	0	9.737982	6.443024	9.041614	-3.9135	0.001064	0.002972	RP11-628E	chr8	+	56438745	56446511	865
ENSG00000(	5.17896	9.634302	2.638828	0	0	0	3.663	0.003636	0.00926	CTA-392E5.	chr8	+	86851934	86963312	517
ENSG00000(	14.50109	19.2686	21.11062	9.737982	23.0108	13.9734	0.22484	0.69518	0.79224	PCDHGA12	chr5	+	1.41E+08	1.41E+08	4747
ENSG00000(	107.7224	71.05298	73.88717	3.745378	4.60216	0	4.713	1.74E-17	1.56E-16	RP11-150C	chr8	-	37278859	37411701	1093
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-563N	chr8	+	20207721	20230280	759
ENSG00000(	0	2.408575	1.319414	0	0.920432	2.465895	0.074258	0.95568	0.97381	RP11-585F	chr8	-	152660	152897	164
ENSG00000(	2.071584	0	2.638828	0	0	0	1.5584	0.24658	NA	KIAA0196-A	chr8	+	1.26E+08	1.26E+08	587
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-326L	chr8	+	17561497	17563696	735
ENSG00000(	0	0	0	3.745378	2.761296	3.28786	-2.4687	0.061332	0.11575	RP11-431J:	chr4	+	98041852	98056210	525
ENSG00000(	1.035792	0	3.958241	0.749076	0	0	1.2761	0.34694	NA	CTB-118P1	chr8	+	88986393	89031341	647
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	CTC-209H2	chr5	-	1.73E+08	1.73E+08	496
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	RP11-152C	chr8	-	71016028	71016414	387
ENSG00000(	0	0	0	0.749076	4.60216	11.50751	-3.1847	0.012687	0.028799	RP11-360L	chr8	-	41397900	41402563	884
ENSG00000(	0	1.204288	0	4.494453	0	1.64393	-1.2526	0.35322	0.48286	RP11-267N	chr8	+	95577264	95577943	375
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-1149	chr8	+	27695994	27697899	717
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-100L	chr8	+	93681064	93691822	866
ENSG00000(	1.035792	4.817151	2.638828	2.996302	2.761296	0	0.40827	0.73116	0.82011	RP11-410L	chr8	-	1E+08	1E+08	436
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-863K	chr8	+	37575097	37591274	1228
ENSG00000(	0	2.408575	2.638828	0	0	0	1.6365	0.22501	NA	RP11-13N1	chr8	+	16461764	16522388	458
ENSG00000(	41.43168	38.53721	30.34652	2.996302	0	2.465895	3.9757	7.28E-09	3.70E-08	HOXA-AS4	chr7	+	27208238	27211534	1161
ENSG00000(	0	2.408575	0	0	1.840864	0	0.16879	0.89944	NA	AC084082.	chr8	+	67024902	67027440	954
ENSG00000(	4.143168	0	0	0	0	2.465895	0.38924	0.7742	0.85182	FCGR1C	chr1	+	1.49E+08	1.49E+08	1122
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RP11-351A	chr6	+	1.19E+08	1.19E+08	471
ENSG00000(	2.071584	1.204288	1.319414	0	0	0	1.6469	0.22376	NA	CTD-3239E	chr8	+	93895212	93977873	602
ENSG00000(	21.75163	18.06432	17.15238	14.23244	6.443024	15.61733	0.6135	0.29916	0.42415	RP11-582J:	chr8	-	22471421	22474170	2750
ENSG00000(	29.00217	21.67718	18.47179	45.69361	33.13555	32.05663	-0.65696	0.13836	0.22861	GUSBP3	chr5	-	68790040	69006341	1334
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP5-1009N	chr8	+	30778576	30778851	276
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-1G11	chr8	+	26405185	26405979	795
ENSG00000(	5.17896	8.430014	2.638828	0.749076	11.96562	7.397684	-0.25023	0.78817	0.86142	RP11-809C	chr8	-	1.42E+08	1.42E+08	505
ENSG00000(	0	4.817151	0	0.749076	0	0.821965	0.82903	0.54057	0.66379	RP11-546B	chr5	+	1.71E+08	1.71E+08	1117
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-1149	chr8	+	82066514	82076834	820
ENSG00000(	1.035792	1.204288	2.638828	0	0.920432	0.821965	0.88904	0.50367	0.63148	KLF3P1	chr5	-	1.72E+08	1.72E+08	1022
ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	RP11-103H	chr8	+	1.28E+08	1.28E+08	489
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-409C	chr8	-	67896370	67898422	2053
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	PGAM5P1	chr5	-	1.09E+08	1.09E+08	814
ENSG00000(	11.39371	2.408575	0	0	0	0	3.114	0.018506	0.040465	RP11-383J:	chr8	+	1.25E+08	1.25E+08	553
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	HIGD1AP6	chr8	+	76214531	76214809	279
ENSG00000(	0	0	0	1.498151	0.920432	1.64393	-1.2565	0.35231	NA	LINC00599	chr8	-	9757574	9762876	3334

ENSG00000	0	2.408575	0	0	4.60216	1.64393	-0.79476	0.55163	0.67269	MTND1P36	chr11	-	1.03E+08	1.03E+08	936
ENSG00000	91.14969	92.73015	127.9831	60.67512	69.0324	53.42772	0.75733	0.008259	0.019552	RP11-122A	chr8	-	91970865	91997485	894
ENSG00000	13.46529	8.430014	23.74945	44.19546	34.05598	32.05663	-1.2409	0.013167	0.029774	CTC-534A2	chr5	+	64920592	64926718	1766
ENSG00000	0	0	5.277655	0	0	0	1.5386	0.24869	NA	CTB-11I22.	chr5	+	1.59E+08	1.59E+08	638
ENSG00000	0	0	1.319414	0	0	0	0.45211	0.71784	NA	MTND4P7	chr8	-	13210910	13211039	130
ENSG00000	6.214751	10.83859	3.958241	0	1.840864	0	2.7255	0.015999	0.035501	KB-1507C5	chr8	+	1.04E+08	1.04E+08	533
ENSG00000	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	PCAT2	chr8	-	1.28E+08	1.28E+08	575
ENSG00000	0	0	0	2.247227	2.761296	4.109825	-2.3558	0.075912	0.13903	RP11-128L	chr8	+	1.42E+08	1.42E+08	1064
ENSG00000	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	RP11-1105	chr8	+	19536083	19546445	467
ENSG00000	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-99A1	chr8	+	74743378	74744182	805
ENSG00000	234.089	237.2447	275.7575	125.0956	112.2927	122.4728	1.0453	1.81E-07	8.09E-07	CCDC71L	chr7	-	1.06E+08	1.06E+08	4232
ENSG00000	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-94H1	chr8	+	29779029	29811240	2651
ENSG00000	0	0	0	1.498151	2.761296	0	-1.199	0.3707	NA	RP11-716D	chr8	-	59168330	59184678	1690
ENSG00000	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	KB-1410C5	chr8	+	1.02E+08	1.02E+08	731
ENSG00000	4.143168	9.634302	7.916483	13.48336	14.72691	13.15144	-0.87592	0.20728	0.31652	RP11-282K	chr12	+	19300008	19307593	5391
ENSG00000	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-238K	chr8	-	1.39E+08	1.39E+08	4171
ENSG00000	326.2744	370.9206	420.893	8.239831	2.761296	0.821965	6.3512	4.93E-55	1.52E-53	HOXA10	chr7	-	27210210	27219880	2541
ENSG00000	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	HTR4-IT1	chr5	-	1.48E+08	1.48E+08	1704
ENSG00000	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC008703.	chr5	-	1.59E+08	1.59E+08	2012
ENSG00000	0	0	0	2.247227	7.363456	7.397684	-3.2755	0.009193	0.021557	STAU2-AS1	chr8	+	74332239	74353761	2076
ENSG00000	187.4783	216.7718	191.315	143.8225	197.8929	188.23	0.16921	0.4182	0.54887	TMEM200B	chr1	-	29445940	29450447	2553
ENSG00000	1975.255	1944.925	2246.962	187.2689	424.3192	241.6577	2.8076	5.27E-16	4.41E-15	PCDHGB6	chr5	+	1.41E+08	1.41E+08	4599
ENSG00000	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	RP11-10J2	chr8	-	1.42E+08	1.42E+08	397
ENSG00000	16.57267	26.49433	34.30476	31.46117	24.85166	23.83698	-0.06149	0.89643	0.93579	SERPINE3	chr13	+	51909909	51938871	2293
ENSG00000	2.071584	0	0	59.92604	66.2711	67.40112	-5.6186	4.55E-12	2.98E-11	C1orf210	chr1	-	43747554	43751288	1478
ENSG00000	0	0	0	2.247227	1.840864	0	-1.1573	0.3864	NA	CTB-11I22.	chr5	+	1.59E+08	1.59E+08	573
ENSG00000	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-142A	chr8	+	73108569	73114504	798
ENSG00000	13.46529	10.83859	7.916483	5.992604	2.761296	5.753754	1.0434	0.18071	0.28367	KB-1507C5	chr8	+	1.04E+08	1.04E+08	756
ENSG00000	0	0	0	0	0.920432	4.109825	-1.3831	0.30514	NA	RP11-261C	chr1	-	2.43E+08	2.43E+08	1243
ENSG00000	1.035792	0	0	8.239831	3.681728	2.465895	-2.4494	0.048487	0.09448	RAD21-AS1	chr8	+	1.18E+08	1.18E+08	2010
ENSG00000	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	KB-431C1.3	chr8	-	1.03E+08	1.03E+08	295
ENSG00000	18.64425	32.51577	22.43003	3.745378	8.283888	9.863579	1.6621	0.006487	0.015711	RP11-697N	chr8	-	48423596	48424703	1108
ENSG00000	2.071584	0	0	0	0	0	0.74702	0.55047	NA	CTC-207P7	chr5	-	1.64E+08	1.64E+08	674
ENSG00000	0	2.408575	0	1.498151	0.920432	2.465895	-0.61136	0.64596	0.75302	RP11-497H	chr5	-	69790927	69796730	371
ENSG00000	0	1.204288	1.319414	0	0.920432	0.821965	0.25429	0.85125	NA	RP13-923C	chr8	+	82704058	82727949	478
ENSG00000	7.250543	4.817151	2.638828	0	0.920432	0	2.7533	0.025274	0.053485	RP11-420B	chr8	+	18846789	18858462	545
ENSG00000	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-468C	chr8	+	1.24E+08	1.24E+08	2149
ENSG00000	1.035792	1.204288	5.277655	0.749076	0.920432	1.64393	0.82109	0.50511	0.63283	RP11-730G	chr8	-	75515479	75516479	1001
ENSG00000	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-346L	chr8	-	37483533	37531905	836
ENSG00000	21.75163	15.65574	19.79121	19.47596	13.80648	3.28786	0.6052	0.34398	0.4732	CTD-2026D	chr17	-	45486688	45500892	513
ENSG00000	0	0	0	9.737982	1.840864	4.93179	-3.2215	0.010942	0.025222	MIR4454	chr5	-	1.7E+08	1.7E+08	602
ENSG00000	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	RP11-127H	chr8	+	1.06E+08	1.06E+08	720
ENSG00000	1300.955	1324.716	1971.204	1225.488	1272.037	868.8169	0.44685	0.012288	0.027994	TUG1	chr22	+	31366663	31375381	5673
ENSG00000	6.214751	7.225726	2.638828	0	0	0	3.5468	0.005149	0.01273	CTA-392C1	chr8	+	40227547	40259367	473

ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	KB-1460A1	chr8	+	1.02E+08	1.02E+08	498
ENSG00000(	0	1.204288	0	28.46487	14.72691	31.23467	-4.7516	1.91E-06	7.70E-06	CTB-78F1.2	chr5	+	1.67E+08	1.67E+08	474
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	GS1-251I9.	chr8	+	92028816	92030883	398
ENSG00000(	0	0	0	0	0.920432	5.753754	-1.7332	0.2014	0.30905	RP11-675F	chr8	-	38401170	38410198	379
ENSG00000(	3.107376	6.021439	6.597069	1.498151	3.681728	3.28786	0.75412	0.4435	0.57318	RP11-589F	chr5	+	70046954	70149508	640
ENSG00000(	975.716	963.4302	868.1743	265.1727	210.7789	264.6727	1.9148	2.51E-37	4.81E-36	TRNP1	chr1	+	27320198	27327389	1958
ENSG00000(	0	0	0	3.745378	1.840864	0	-1.5327	0.25777	NA	RP11-1081	chr8	-	54307771	54308506	594
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTB-56J15.	chr5	-	1.56E+08	1.56E+08	110
ENSG00000(	2.071584	0	0	4.494453	18.40864	17.26126	-3.3436	0.001178	0.003265	RP11-44N1	chr8	+	1.24E+08	1.24E+08	758
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-21C1	chr8	-	70087814	70090424	453
ENSG00000(	0	0	2.638828	0	0.920432	0	0.55591	0.6721	NA	RP11-44D1	chr8	-	58802135	58803368	780
ENSG00000(	3.107376	3.612863	1.319414	0	6.443024	2.465895	-0.09128	0.93708	0.96179	RP11-1102	chr8	-	72315675	72504260	1797
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-116B	chr8	+	74502809	74503118	310
ENSG00000(	0	0	0	0	2.761296	1.64393	-1.2339	0.35779	NA	CTD-2547L	chr8	-	17946078	17947196	1119
ENSG00000(	1.035792	2.408575	3.958241	4.494453	7.363456	11.50751	-1.4383	0.13118	0.21882	KB-1254G8	chr8	+	1.04E+08	1.04E+08	770
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-150C	chr8	+	37337607	37338327	169
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-930P	chr8	+	41518509	41523084	1088
ENSG00000(	7.250543	8.430014	5.277655	10.48706	4.60216	9.041614	-0.18778	0.811	0.87744	CTC-756D1	chr8	+	23316114	23342484	630
ENSG00000(	3.107376	0	2.638828	0.749076	0.920432	0	1.0548	0.42833	0.55849	AC006277.	chr19	-	2915144	2926805	776
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	LINC00534	chr8	+	91233716	91581546	812
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	KB-1460A1	chr8	-	1.02E+08	1.02E+08	430
ENSG00000(	1.035792	9.634302	2.638828	0	0	4.93179	1.0401	0.38652	0.51736	AC078852.	chr4	+	1352267	1353249	441
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	RP11-337A	chr9	+	26801731	26805860	371
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AC034243.	chr5	-	1.38E+08	1.38E+08	587
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC012613.	chr5	-	1.49E+08	1.49E+08	4533
ENSG00000(	4.143168	1.204288	0	0	0.920432	0	1.3097	0.33381	0.46191	RP11-231D	chr8	-	42091193	42128715	815
ENSG00000(	1.035792	9.634302	2.638828	1.498151	3.681728	4.109825	0.42409	0.68469	0.78423	RP11-150C	chr8	-	37373928	37374539	510
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-642D	chr8	-	1.07E+08	1.07E+08	649
ENSG00000(	3.107376	0	2.638828	0	1.840864	0	0.94811	0.4804	0.60954	RP11-10A1	chr8	+	9009252	9025646	826
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-103H	chr8	+	1.27E+08	1.28E+08	415
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-14I17	chr8	+	26280109	26281445	508
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-90P5	chr8	+	37979892	37979998	107
ENSG00000(	0	0	0	17.22874	25.7721	9.041614	-4.9526	9.89E-06	3.67E-05	PCAT1	chr8	+	1.28E+08	1.28E+08	1992
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	RP11-473J(	chr8	+	35719641	35828183	578
ENSG00000(	2.071584	2.408575	2.638828	0.749076	3.681728	0.821965	0.33802	0.77634	0.85303	CTD-2594K	chr8	+	1.06E+08	1.06E+08	344
ENSG00000(	2.071584	6.021439	9.235896	0	0	0	3.6315	0.004026	0.010167	RP11-770E	chr8	+	49533025	49536455	289
ENSG00000(	7.250543	9.634302	1.319414	0	0	0	3.6973	0.0034	0.008709	CTD-2363C	chr5	+	1.58E+08	1.58E+08	542
ENSG00000(	2.071584	0	3.958241	0	0.920432	2.465895	0.53221	0.68252	0.78278	SMIM18	chr8	+	30496117	30503581	905
ENSG00000(	2.071584	2.408575	0	2.247227	5.522592	9.041614	-1.4848	0.17381	0.2753	AL139099.	chr14	-	50064193	50065882	1690
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	IGKV2OR22	chr22	-	17402333	17403063	360
ENSG00000(	1.035792	2.408575	0	0	0.920432	0	0.86086	0.52404	NA	HMGB1P19	chr8	+	1.24E+08	1.24E+08	577
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	KB-1517D1	chr8	-	99425110	99426012	587
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-697B	chr8	-	1.27E+08	1.27E+08	636
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-10H3	chr8	+	50081098	50141484	833

ENSG00000(	0	2.408575	0	1.498151	0.920432	1.64393	-0.43801	0.74404	0.8295	RP11-110G	chr8	-	52808517	52808934	283
ENSG00000(	6.214751	9.634302	9.235896	4.494453	6.443024	5.753754	0.53045	0.50546	0.63317	RP11-395I:	chr8	-	25283037	25284096	528
ENSG00000(	18.64425	14.45145	2.638828	23.97042	38.65814	39.45432	-1.4191	0.012581	0.028587	RP11-1C8.4	chr8	-	1.04E+08	1.05E+08	722
ENSG00000(	0	0	0	5.243529	0.920432	6.575719	-2.8132	0.030575	0.063206	RP11-744J:	chr8	-	70337270	70360479	1134
ENSG00000(	11.39371	4.817151	5.277655	6.74168	1.840864	7.397684	0.3797	0.66167	0.76606	CTC-756D1	chr8	-	23340529	23341047	519
ENSG00000(	4.143168	4.817151	5.277655	0	2.761296	5.753754	0.60708	0.56717	0.68635	PCDHGA5	chr5	+	1.41E+08	1.41E+08	4602
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	AC145110.	chr8	+	29605825	29656008	2980
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	CDH12P3	chr5	+	69428506	69428800	295
ENSG00000(	2.071584	0	3.958241	0	0	0	1.8862	0.16413	0.26236	RP11-13N1	chr8	-	16534414	16772553	543
ENSG00000(	3.107376	0	0	0.749076	0	0	0.76338	0.56438	NA	AF121898.	chr8	-	88554214	88767946	1044
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-653B	chr8	-	83426803	83589388	544
ENSG00000(	25.8948	12.04288	34.30476	0	0	0	5.819	1.08E-07	4.94E-07	RP1-170O1	chr7	-	27226192	27233067	556
ENSG00000(	1.035792	0	2.638828	0	0	1.64393	0.56423	0.6775	NA	CTD-3080F	chr8	-	41132634	41134522	255
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-6D1.:	chr8	-	1.26E+08	1.26E+08	412
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	HMGB1P41	chr8	-	81724377	81724816	440
ENSG00000(	2.071584	0	1.319414	0.749076	0	0.821965	0.56841	0.67506	NA	AC106801.	chr5	+	1.57E+08	1.57E+08	1845
ENSG00000(	0	0	0	0	6.443024	1.64393	-1.9973	0.14023	0.23115	RP11-798K	chr5	-	1.79E+08	1.79E+08	290
ENSG00000(	1.035792	0	3.958241	2.996302	0	0	0.39693	0.76739	0.84668	hsa-mir-14	chr5	+	1.6E+08	1.6E+08	2301
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-1112	chr8	-	58943893	58945241	877
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	CTD-2114J:	chr8	+	92169513	92170976	1464
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-152P	chr8	+	1.07E+08	1.07E+08	445
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-347C	chr8	-	95986801	95987081	281
ENSG00000(	0	0	0	8.239831	0	4.109825	-2.6392	0.046733	0.091506	RP11-103H	chr8	+	1.28E+08	1.28E+08	429
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	CTD-2340D	chr8	+	1E+08	1E+08	595
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	RP11-624C	chr8	-	24153327	24769586	741
ENSG00000(	0	1.204288	0	1.498151	0.920432	4.109825	-1.3913	0.29649	0.4209	RP11-1174	chr5	-	70771588	70772143	556
ENSG00000(	1.035792	2.408575	3.958241	0.749076	4.60216	0	0.33982	0.78188	0.85639	PCDHGA7	chr5	+	1.41E+08	1.41E+08	4605
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-402L	chr8	-	1.01E+08	1.01E+08	648
ENSG00000(	44.53905	72.25726	56.73479	26.21764	38.65814	51.78379	0.56119	0.14024	0.23115	FAM86HP	chr3	-	1.3E+08	1.3E+08	959
ENSG00000(	0	0	0	4.494453	2.761296	3.28786	-2.5778	0.049406	0.096073	RP11-317J:	chr8	-	86354080	86377144	591
ENSG00000(	0	3.612863	0	1.498151	0	0	0.55191	0.68269	NA	RP11-115C	chr8	-	6331366	6331809	444
ENSG00000(	45.57484	61.41867	46.17948	13.48336	14.72691	17.26126	1.7081	6.24E-05	0.000209	HOXA-AS2	chr7	+	27147396	27173921	2455
ENSG00000(	1.035792	4.817151	7.916483	0	0.920432	0	2.597	0.038132	0.076786	RP11-586K	chr8	+	89339065	89749363	1469
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	RP11-16E1	chr8	-	64048782	64050643	1406
ENSG00000(	5.17896	1.204288	1.319414	0	0	0	2.3675	0.079089	0.14394	RP11-1080	chr8	-	18942502	19116979	723
ENSG00000(	0	4.817151	1.319414	4.494453	2.761296	3.28786	-0.61514	0.59114	0.70759	CTD-2179L	chr5	-	77337703	77339962	2260
ENSG00000(	3.107376	9.634302	6.597069	11.98521	15.64734	5.753754	-0.72556	0.34749	0.47714	OSGEPL1-A	chr2	+	1.91E+08	1.91E+08	567
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	CTD-2340D	chr8	-	1E+08	1E+08	493
ENSG00000(	1.035792	3.612863	0	0	1.840864	0	0.72975	0.58976	0.70665	RP11-181B	chr8	+	28304781	28313419	443
ENSG00000(	6.214751	1.204288	1.319414	0.749076	1.840864	4.93179	0.18923	0.86829	0.91722	RNF5P1	chr8	-	38458179	38458718	540
ENSG00000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	RP11-351C	chr8	-	1.28E+08	1.28E+08	292
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	GS1-5L10.1	chr8	+	92988136	92989646	410
ENSG00000(	10.35792	12.04288	19.79121	0	3.681728	0	3.0547	0.001271	0.003508	RP11-649G	chr8	-	1.08E+08	1.08E+08	504
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-573J:	chr8	+	64498558	64501966	730

ENSG00000(	0	4.817151	5.277655	0	0	0	2.6348	0.049808	0.096782	KB-1184D1	chr8	-	95109992	95116550	668
ENSG00000(	2.071584	6.021439	0	0	0.920432	0	1.795	0.17829	0.28076	RP11-723D	chr8	+	38657161	38659814	356
ENSG00000(	4.143168	6.021439	5.277655	0	0	0	3.4949	0.005887	0.014376	CTC-265N9	chr5	-	1.7E+08	1.7E+08	1571
ENSG00000(	0	0	0	0	0	5.753754	-1.4203	0.28986	NA	CTD-2320G	chr8	-	75259992	75262285	590
ENSG00000(	9.322127	10.83859	19.79121	8.239831	17.48821	9.041614	0.1858	0.77789	0.85374	SLC10A5	chr8	-	82605842	82608409	2568
ENSG00000(	0	0	5.277655	1.498151	0	0	0.86834	0.52216	0.64762	RP11-557C	chr8	+	1.24E+08	1.24E+08	625
ENSG00000(	3.107376	6.021439	3.958241	1.498151	0	0.821965	1.8258	0.1191	0.20253	RP11-770E	chr8	+	49464127	49611069	2372
ENSG00000(	0	1.204288	2.638828	2.247227	0	0	0.37614	0.78137	0.85605	RP11-875C	chr8	-	22928890	22932001	484
ENSG00000(	0	3.612863	0	0	0	1.64393	0.50971	0.70603	NA	RP11-394C	chr5	-	1.49E+08	1.49E+08	401
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-369K	chr8	+	1.22E+08	1.22E+08	776
ENSG00000(	1.035792	0	0	0	0	1.64393	-0.12526	0.92174	NA	AC144568.	chr8	-	14091	14320	137
ENSG00000(	15.53688	12.04288	11.87472	59.92604	17.48821	51.78379	-1.6425	0.001945	0.005195	EIF5AL1	chr10	+	81272357	81276188	3832
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-513H	chr8	-	1.35E+08	1.35E+08	426
ENSG00000(	0	3.612863	0	0.749076	1.840864	3.28786	-0.45234	0.72785	0.8177	CTC-370J7.	chr5	-	1.57E+08	1.57E+08	204
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-486N	chr8	+	29384829	29387840	642
ENSG00000(	1.035792	8.430014	1.319414	0	4.60216	0	0.88186	0.477	0.60623	KB-1980E6	chr8	+	1.04E+08	1.04E+08	740
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-587H	chr8	-	93577671	93667722	587
ENSG00000(	32.10955	27.69862	21.11062	71.16218	75.47542	76.44274	-1.4281	5.99E-05	0.000201	RP11-531A	chr8	+	73964413	73975296	3549
ENSG00000(	0	0	0	20.22504	10.12475	4.93179	-4.3694	0.000184	0.000579	RP11-981G	chr8	+	10332075	10339484	562
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTD-2270F	chr5	+	1.7E+08	1.7E+08	1215
ENSG00000(	1.035792	0	0	8.239831	14.72691	9.863579	-3.6168	0.001078	0.00301	PRSS51	chr8	-	10340388	10405095	1123
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	SOD1P3	chr8	-	1.27E+08	1.27E+08	454
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	CTC-248O1	chr5	-	1.57E+08	1.57E+08	911
ENSG00000(	0	0	1.319414	0.749076	0	0.821965	-0.12362	0.92519	NA	RP11-600K	chr8	-	69824038	70016425	2367
ENSG00000(	0	4.817151	1.319414	98.87797	64.43024	68.22309	-4.9316	6.15E-14	4.55E-13	CTC-353G1	chr5	-	1.67E+08	1.67E+08	663
ENSG00000(	106.6866	111.9988	126.6637	3.745378	8.283888	8.219649	4.0136	1.89E-22	2.12E-21	ZFHX4-AS1	chr8	-	77403435	77595513	1711
ENSG00000(	5.17896	0	0	4.494453	3.681728	2.465895	-0.72731	0.54171	0.66457	RP11-359E	chr8	+	39972170	39984987	739
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	KB-1615E4	chr8	+	1.01E+08	1.02E+08	558
ENSG00000(	10.35792	12.04288	13.19414	11.98521	34.05598	22.19305	-0.88932	0.13198	0.22001	RP11-30L1	chr8	+	54883791	54886770	2479
ENSG00000(	16.57267	14.45145	17.15238	6.74168	3.681728	10.68554	1.1052	0.10055	0.17627	KB-1732A1	chr8	+	1.04E+08	1.04E+08	2770
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	RP11-806C	chr8	+	17666450	17678377	745
ENSG00000(	0	12.04288	10.55531	2.996302	8.283888	1.64393	0.67722	0.49244	0.62149	TAGLN2P1	chr8	-	1.08E+08	1.08E+08	587
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-981G	chr8	-	10335001	10336885	489
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	KB-1410C5	chr8	-	1.02E+08	1.02E+08	979
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-59O2	chr8	-	86529573	86529741	169
ENSG00000(	12.4295	7.225726	10.55531	9.737982	5.522592	7.397684	0.3796	0.60374	0.71879	CTB-79E8.3	chr5	-	1.72E+08	1.72E+08	192
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CTB-43E15.	chr5	-	1.73E+08	1.73E+08	2361
ENSG00000(	9.322127	4.817151	2.638828	0	1.840864	0	2.3932	0.042161	0.083815	RP11-567J:	chr8	-	49464575	49469001	764
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-380I:	chr8	-	28107580	28196772	887
ENSG00000(	0	0	3.958241	0	1.840864	0	0.51729	0.70257	NA	RP11-177H	chr8	+	10698086	10704011	439
ENSG00000(	2.071584	1.204288	0	1.498151	1.840864	2.465895	-0.52803	0.67836	0.77958	RP11-439C	chr8	+	1919563	1924644	815
ENSG00000(	5.17896	6.021439	3.958241	0	0	1.64393	2.3185	0.051178	0.099099	RP11-1081	chr8	-	9515805	9515948	144
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-1259	chr5	+	1.78E+08	1.78E+08	666
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTD-3118D	chr8	+	87192647	87224465	501

ENSG00000(	12.4295	9.634302	9.235896	0	0	0	4.6171	8.16E-05	0.000269	RP11-567J.	chr8	-	49510018	49533578	559
ENSG00000(	9.322127	8.430014	5.277655	1.498151	3.681728	4.109825	1.159	0.19792	0.30512	RP11-267M	chr8	+	95565950	95581973	1789
ENSG00000(	2.071584	1.204288	1.319414	2.996302	0.920432	0	0.14506	0.91071	0.94514	RP11-758M	chr8	-	75711019	75779174	2810
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-51J9.	chr8	-	30034070	30038404	583
ENSG00000(	127.4024	95.13873	149.0938	65.91865	98.48622	78.90863	0.60704	0.027902	0.05833	ALG11	chr13	+	52586534	52603800	4574
ENSG00000(	5.17896	0	0	0	0	0.821965	1.2091	0.37233	0.50277	RP11-697M	chr8	-	76079939	76088891	490
ENSG00000(	50.7538	55.39724	39.58241	47.19176	25.7721	43.56414	0.31318	0.4144	0.54495	RP13-582C	chr8	-	1.44E+08	1.44E+08	689
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	RP11-281C	chr5	+	1.78E+08	1.78E+08	358
ENSG00000(	1851.996	1810.044	1942.177	1480.173	1573.018	1684.206	0.24197	0.033046	0.067581	ATXN7L3B	chr12	+	74931551	74935223	3673
ENSG00000(	2.071584	2.408575	2.638828	0.749076	0	1.64393	1.0454	0.40986	0.54061	RP11-473C	chr8	+	1.31E+08	1.31E+08	549
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP11-313C	chr8	+	73644280	73664078	1722
ENSG00000(	4213.601	3930.795	5701.187	5276.488	6527.704	4561.083	-0.24054	0.12529	0.21099	PRKDC	chr8	-	48685669	48872743	13508
ENSG00000(	0	0	0	0.749076	1.840864	0.821965	-1.0455	0.43461	NA	RP11-893F	chr17	-	48235694	48238637	547
ENSG00000(	18.64425	20.47289	10.55531	5.243529	6.443024	9.041614	1.1864	0.07503	0.13767	PCDHGA6	chr5	+	1.41E+08	1.41E+08	4605
ENSG00000(	7.250543	9.634302	11.87472	2.247227	5.522592	0	1.643	0.077614	0.14164	LZTS1-AS1	chr8	+	20133284	20147969	892
ENSG00000(	3.107376	2.408575	5.277655	0	0	0	2.9106	0.026951	0.056627	RP11-779C	chr5	+	1.72E+08	1.72E+08	352
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	KB-1460A1	chr8	+	1.02E+08	1.02E+08	473
ENSG00000(	331.4534	351.652	314.0205	322.8516	343.3211	323.8542	0.011156	0.94418	0.9666	GS1-251I9.	chr8	-	92072137	92082417	4275
ENSG00000(	7.250543	3.612863	0	2.996302	0.920432	3.28786	0.47273	0.67532	0.77715	RP11-90P5	chr8	-	38023530	38023636	107
ENSG00000(	4.143168	6.021439	9.235896	1.498151	0	4.109825	1.451	0.16132	0.25887	CTD-2292P	chr8	-	1.44E+08	1.44E+08	5684
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC025442.	chr5	-	65439984	65440623	481
ENSG00000(	25.8948	16.86003	18.47179	0	0.920432	1.64393	4.0129	5.03E-06	1.93E-05	RP11-527N	chr8	-	37262957	37264242	578
ENSG00000(	3.107376	2.408575	1.319414	2.247227	0.920432	1.64393	0.37495	0.75342	0.83689	RP11-35G2	chr8	+	1.09E+08	1.09E+08	447
ENSG00000(	3.107376	2.408575	3.958241	0.749076	0	3.28786	0.89353	0.45552	0.5852	RP11-439C	chr8	-	1920736	1922803	557
ENSG00000(	10.35792	12.04288	21.11062	8.988907	17.48821	8.219649	0.30544	0.63625	0.74499	PCDHGA8	chr5	+	1.41E+08	1.41E+08	4605
ENSG00000(	4.143168	3.612863	7.916483	0	0	0	3.5029	0.005806	0.014197	CTB-33O18	chr5	+	1.73E+08	1.73E+08	455
ENSG00000(	1.035792	0	0	1.498151	0	0	-0.08447	0.94679	NA	HMGB1P23	chr8	+	29076422	29076989	568
ENSG00000(	1.035792	8.430014	2.638828	15.73059	11.96562	4.93179	-1.2762	0.14202	0.23357	TPTE2P1	chr13	-	25498815	25542625	770
ENSG00000(	0	0	0	3.745378	4.60216	2.465895	-2.6105	0.046181	0.090601	RP11-34P1	chr5	+	1.6E+08	1.6E+08	701
ENSG00000(	0	0	0	0	6.443024	3.28786	-2.2725	0.091117	0.16246	KB-1047C1	chr8	+	96216684	96822364	617
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	CTD-3023L	chr8	+	8417404	8419634	579
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	AC100802.	chr8	+	19936816	19975953	1026
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-6N13	chr5	+	1.04E+08	1.04E+08	567
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-386D	chr8	+	87778163	87830786	761
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	ZNF317P1	chr8	+	94658294	94659320	1027
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	CTC-308K2	chr5	+	1.72E+08	1.72E+08	864
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	MTND1P5	chr8	+	1.04E+08	1.04E+08	940
ENSG00000(	514.7886	439.565	597.6944	349.8183	403.1492	339.4715	0.50476	0.002244	0.005925	UTP14C	chr13	+	52598827	52607736	5529
ENSG00000(	0	1.204288	6.597069	0	0	0	2.2118	0.10284	0.17949	AB015752.	chr8	-	91605032	91618293	738
ENSG00000(	40.39588	38.53721	30.34652	0	0	0	6.4348	1.06E-09	5.80E-09	CTA-392C1	chr8	-	40156260	40200921	881
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-93O7	chr5	-	1.24E+08	1.24E+08	285
ENSG00000(	4.143168	15.65574	1.319414	0	0	0	3.8803	0.001969	0.00525	CTD-2363C	chr5	+	1.58E+08	1.58E+08	563
ENSG00000(	10.35792	2.408575	10.55531	8.239831	8.283888	11.50751	-0.24037	0.75443	0.83765	RP11-1415	chr5	-	69515745	69580686	593
ENSG00000(	0	0	0	0	2.761296	3.28786	-1.6293	0.2296	0.34285	RP11-973F	chr8	-	1.24E+08	1.24E+08	571

ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-246K	chr8	+	58405443	58504118	567
ENSG0000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-96A1	chr4	-	1.21E+08	1.21E+08	474
ENSG0000(	2.071584	2.408575	1.319414	3.745378	7.363456	0	-0.69798	0.54827	0.66989	RP11-723D	chr8	-	38702384	38703957	387
ENSG0000(	15.53688	4.817151	7.916483	0.749076	2.761296	2.465895	1.9563	0.035603	0.072221	AC005895.	chr5	-	1.5E+08	1.5E+08	1023
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTD-2168K	chr8	+	24849516	24867292	603
ENSG0000(	3.107376	0	3.958241	3.745378	0	1.64393	0.25705	0.83679	0.89561	RP11-367E	chr8	+	74896728	74897118	391
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-731N	chr8	-	83775014	83870931	814
ENSG0000(	61.11172	48.17151	52.77655	3.745378	11.04518	15.61733	2.3458	1.61E-06	6.54E-06	RP11-177H	chr8	+	23193684	23223638	4374
ENSG0000(	5.17896	1.204288	2.638828	0.749076	0	0	2.1105	0.10667	0.18494	RP11-546K	chr8	+	52874018	52935534	672
ENSG0000(	60.07593	42.15007	75.20659	40.45008	57.06678	62.46933	0.14688	0.6753	0.77715	PCDHGA10	chr5	+	1.41E+08	1.41E+08	4617
ENSG0000(	0	0	0	5.992604	2.761296	2.465895	-2.6607	0.041814	0.083217	RP11-10N2	chr8	+	94753421	94756762	530
ENSG0000(	45.57484	27.69862	50.13772	13.48336	22.09037	17.26126	1.1939	0.009221	0.021616	RP11-10N2	chr8	+	94731802	94733395	939
ENSG0000(	0	0	0	2.996302	4.60216	0.821965	-2.206	0.099375	0.17452	RP11-386G	chr8	+	56074043	56077287	496
ENSG0000(	164.6909	143.3102	114.789	0.749076	5.522592	5.753754	5.0202	3.35E-27	4.52E-26	AC131025.	chr5	+	1.49E+08	1.49E+08	5131
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-394C	chr5	+	1.49E+08	1.49E+08	588
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	FER1L6-AS2	chr8	-	1.25E+08	1.25E+08	1746
ENSG0000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	PIGFP1	chr5	+	1.78E+08	1.78E+08	653
ENSG0000(	11.39371	24.08575	21.11062	73.4094	129.7809	87.95025	-2.3239	3.30E-09	1.73E-08	PCDHGA11	chr5	+	1.41E+08	1.41E+08	3936
ENSG0000(	0	2.408575	1.319414	0	6.443024	0	-0.47383	0.72087	0.81229	RP11-16P2	chr8	+	27590855	27613943	584
ENSG0000(	19.68005	12.04288	18.47179	6.74168	13.80648	16.4393	0.42397	0.4893	0.61839	RP11-347C	chr8	+	95962265	95963624	709
ENSG0000(	32.10955	30.10719	29.0271	0.749076	2.761296	5.753754	3.0984	3.18E-06	1.25E-05	RP11-61L2	chr7	-	1.43E+08	1.44E+08	2973
ENSG0000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	CTB-158E9.	chr5	+	1.54E+08	1.54E+08	1168
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-521N	chr8	+	27041838	27068011	585
ENSG0000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-203E	chr8	-	24027470	24034593	491
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-770E	chr8	-	49569820	49571454	594
ENSG0000(	2.071584	4.817151	2.638828	0.749076	1.840864	0	1.3452	0.27259	0.39337	FAM85B	chr8	-	8025341	8084136	792
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-613H	chr8	-	26921513	26922795	1283
ENSG0000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-122C	chr8	-	92555152	92919847	577
ENSG0000(	4.143168	0	0	2.247227	0	3.28786	-0.23802	0.85675	0.90907	RP11-252I:	chr5	+	1.8E+08	1.8E+08	687
ENSG0000(	24.85901	15.65574	29.0271	11.98521	17.48821	17.26126	0.55281	0.29922	0.42416	PCDHGB2	chr5	+	1.41E+08	1.41E+08	4602
ENSG0000(	0	2.408575	0	0	4.60216	0	-0.46148	0.73374	0.82196	KB-1205A7	chr8	+	99615481	99618568	301
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-402L	chr8	-	1.01E+08	1.01E+08	183
ENSG0000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	MAPRE1P1	chr8	-	1.37E+08	1.37E+08	797
ENSG0000(	0	0	0	1.498151	4.60216	2.465895	-2.2479	0.092142	0.1639	AC226119.	chr4	-	3916910	3957148	899
ENSG0000(	0	9.634302	2.638828	0.749076	0.920432	0.821965	1.6345	0.17948	0.28222	PRKRIRP7	chr8	-	79672377	79674666	2290
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	CTB-113P1	chr5	+	1.51E+08	1.51E+08	570
ENSG0000(	3.107376	0	0	2.247227	0	0	0.22117	0.87012	NA	KB-1980E6	chr8	+	1.03E+08	1.03E+08	975
ENSG0000(	1.035792	2.408575	5.277655	0	0	3.28786	0.93983	0.45787	0.58749	CTB-178M2	chr5	-	1.68E+08	1.68E+08	2181
ENSG0000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	GS1-39E22	chr5	-	1.35E+08	1.35E+08	771
ENSG0000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	RP11-382A	chr8	+	1.28E+08	1.28E+08	290
ENSG0000(	24.85901	14.45145	27.70769	60.67512	65.35067	64.11326	-1.4728	0.00017	0.000538	RP11-1149	chr8	+	23046792	23048188	637
ENSG0000(	0	0	0	2.996302	1.840864	0.821965	-1.6683	0.21867	NA	RP11-909N	chr8	+	1.44E+08	1.44E+08	544
ENSG0000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	RP11-10C8	chr8	+	13196083	13200263	3488
ENSG0000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	RP11-156K	chr8	+	17658854	17718578	510

ENSG0000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	CTB-77H17	chr5	-	1.67E+08	1.67E+08	489
ENSG0000(	18.64425	24.08575	15.83297	3.745378	11.96562	19.72716	0.68937	0.27822	0.40019	RP11-410L	chr8	-	1E+08	1E+08	380
ENSG0000(	555.1845	505.8008	568.6673	116.1067	170.2799	125.7606	1.9787	3.84E-27	5.17E-26	PCDHGB4	chr5	+	1.41E+08	1.41E+08	4578
ENSG0000(	3.107376	1.204288	0	1.498151	2.761296	0	0.036805	0.97762	0.98694	HMGN1P3	chr15	+	93254977	93256105	1129
ENSG0000(	12.4295	2.408575	5.277655	5.243529	0	0	1.5011	0.17659	0.27858	CTB-33O18	chr5	+	1.73E+08	1.73E+08	1777
ENSG0000(	2.071584	0	0	11.23613	13.80648	7.397684	-3.0785	0.003236	0.008319	CLDN23	chr8	+	8559448	8561616	2169
ENSG0000(	1.035792	0	0	0.749076	0.920432	1.64393	-0.70513	0.60322	NA	RP11-363L	chr8	-	31024594	31034683	643
ENSG0000(	0	0	0	8.988907	6.443024	0.821965	-3.1545	0.013518	0.030521	CTC-455F1	chr5	+	1.7E+08	1.7E+08	1337
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-333A	chr8	+	71383369	71397922	2367
ENSG0000(	0	0	0	0.749076	2.761296	0.821965	-1.3133	0.33155	NA	RP11-4K16	chr8	-	1.2E+08	1.2E+08	603
ENSG0000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP11-467K	chr11	+	9025709	9086701	960
ENSG0000(	0	0	0	0.749076	8.283888	2.465895	-2.6217	0.046471	0.091088	RP11-386G	chr8	-	56047763	56054918	813
ENSG0000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	KB-1639H6	chr8	+	1.04E+08	1.04E+08	247
ENSG0000(	2.071584	9.634302	2.638828	5.992604	5.522592	11.50751	-0.6062	0.4929	0.62189	CTB-178M2	chr5	-	1.68E+08	1.68E+08	503
ENSG0000(	10.35792	9.634302	6.597069	20.22504	16.56778	14.79537	-0.89509	0.15538	0.25117	ALG1L13P	chr8	-	8093525	8102189	765
ENSG0000(	327.3102	283.0076	211.1062	69.66403	118.7357	151.2415	1.2666	1.66E-06	6.71E-06	CTD-2336C	chr8	-	1710156	1712668	978
ENSG0000(	6.214751	2.408575	0	5.243529	0.920432	13.9734	-0.97234	0.35469	0.48439	CTC-756D1	chr8	-	23350522	23351711	715
ENSG0000(	0	0	0	4.494453	1.840864	0.821965	-1.9797	0.14229	0.23373	KB-1562D1	chr8	-	1.03E+08	1.03E+08	539
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-245A	chr8	-	1.25E+08	1.25E+08	331
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-213G	chr8	-	23583844	23600555	443
ENSG0000(	3.107376	1.204288	0	0	0.920432	2.465895	0.23267	0.86084	0.91151	CTB-167B5	chr7	+	87845975	87848541	576
ENSG0000(	473.3569	533.4995	600.3333	608.9984	600.1217	470.9859	-0.06535	0.68325	0.78324	ZNF260	chr19	-	37001597	37019562	5666
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-1D12	chr8	-	65713793	65730130	875
ENSG0000(	5.17896	6.021439	1.319414	17.22874	3.681728	13.15144	-1.2762	0.13294	0.22143	ALG1L10P	chr12	+	8380330	8384360	424
ENSG0000(	3.107376	1.204288	1.319414	2.996302	0.920432	0	0.35015	0.78362	0.8575	IGHEP2	chr9	+	5113549	5114804	1256
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-778D	chr8	-	1.07E+08	1.07E+08	489
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	PKMP4	chr8	+	76288944	76289249	306
ENSG0000(	0	0	0	4.494453	0	9.863579	-2.8543	0.029873	0.061942	KB-1562D1	chr8	-	1.02E+08	1.03E+08	491
ENSG0000(	0	2.408575	7.916483	0.749076	3.681728	0.821965	0.71345	0.55004	0.67142	RP11-363E	chr8	-	82192106	82193681	620
ENSG0000(	0	0	0	4.494453	1.840864	0.821965	-1.9797	0.14229	0.23373	RP11-326E	chr8	+	72067692	72116458	685
ENSG0000(	0	0	0	2.247227	4.60216	0	-1.7927	0.18635	0.29091	RP11-662B	chr8	+	28655659	28656986	548
ENSG0000(	0	0	1.319414	5.243529	1.840864	4.109825	-2.053	0.10523	0.18285	RP11-281C	chr5	+	1.78E+08	1.78E+08	674
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-775B	chr8	-	1.2E+08	1.2E+08	497
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-419C	chr8	-	36924959	36926936	639
ENSG0000(	0	0	0	1.498151	0	4.109825	-1.5377	0.25628	NA	RP11-328K	chr8	-	59904279	59905497	551
ENSG0000(	2.071584	0	2.638828	0	0	0.821965	1.2046	0.37464	NA	RP11-156K	chr8	+	17763265	17765396	634
ENSG0000(	1.035792	1.204288	0	0.749076	1.840864	0	-0.0892	0.94757	NA	RP3-388N1	chr8	-	94846682	94858971	528
ENSG0000(	0	2.408575	1.319414	3.745378	0.920432	0.821965	-0.39199	0.76022	0.84152	RP11-359B	chr8	-	33293786	33294218	433
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	DUXAP2	chr8	-	1.02E+08	1.02E+08	589
ENSG0000(	48.68222	43.35436	30.34652	13.48336	11.96562	39.45432	0.88492	0.076918	0.14053	CTD-2530N	chr8	-	22112089	22132675	515
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-697N	chr8	-	48504709	48505171	463
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-31K2	chr8	-	96960009	96960461	453
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-730G	chr8	-	75521933	75545555	677
ENSG0000(	0	0	0	2.996302	0.920432	4.109825	-2.1501	0.10895	0.18808	CTD-2024D	chr8	+	39424224	39437653	506

ENSG00000(	89.0781	121.6331	138.5384	1137.846	1077.826	979.7822	-3.1903	2.01E-75	9.83E-74	LYN	chr8	+	56792372	56923939	3020
ENSG00000(	1.035792	0	1.319414	0.749076	0	0.821965	0.26466	0.84506	NA	CTD-3083F	chr8	+	87515820	87517290	1471
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-388K	chr8	+	94271895	94310204	261
ENSG00000(	0	0	5.277655	0	2.761296	3.28786	-0.14174	0.91345	0.94699	MTND2P32	chr8	+	32872779	32874561	1038
ENSG00000(	73.54123	108.3859	84.44248	396.261	342.4007	397.0091	-2.084	9.87E-24	1.16E-22	PINX1	chr8	-	10622473	10697394	1545
ENSG00000(	2.071584	0	0	0	0.920432	4.109825	-0.66604	0.62173	0.73384	AC078852.	chr4	+	1350369	1351863	527
ENSG00000(	5.17896	1.204288	1.319414	0	3.681728	2.465895	0.26698	0.8245	0.88675	AC005740.	chr5	-	1.41E+08	1.41E+08	344
ENSG00000(	0	0	0	0.749076	1.840864	5.753754	-2.1777	0.10453	0.18184	RP11-675F	chr8	-	38409766	38416538	537
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-30J2(	chr8	+	1.38E+08	1.38E+08	774
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-21C4	chr8	-	65486863	65494445	2704
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	VENTXP6	chr8	+	74563524	74563837	314
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC011366.	chr5	+	1.09E+08	1.09E+08	518
ENSG00000(	1.035792	2.408575	1.319414	8.988907	7.363456	13.15144	-2.2461	0.018419	0.040293	CTD-3107N	chr8	-	30239635	30242917	1031
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	KB-1205A7	chr8	+	99645775	99646093	319
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	HMGN1P2{	chr17	+	58928743	58929106	364
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP11-386D	chr8	+	87719775	87777251	804
ENSG00000(	1434.572	1330.738	1683.572	373.7887	789.7307	620.5835	1.3123	7.81E-11	4.66E-10	PCDHGB7	chr5	+	1.41E+08	1.41E+08	4596
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-99H2	chr8	-	83010686	83072812	823
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	CTD-2647L	chr8	+	28968090	28998246	478
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CTB-7E3.1	chr5	-	1.66E+08	1.66E+08	566
ENSG00000(	7.250543	0	6.597069	6.74168	0	4.93179	0.18808	0.86379	0.91394	RP11-1007	chr8	+	42342118	42342537	420
ENSG00000(	1.035792	0	1.319414	0	0	0.821965	0.54471	0.68089	NA	MTND6P3	chr5	-	93904634	93905175	542
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-32D1	chr5	+	1.58E+08	1.58E+08	691
ENSG00000(	7.250543	6.021439	5.277655	1.498151	0	0	2.6552	0.021151	0.045627	CTD-2339F	chr8	+	58658708	58662758	2461
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP11-642D	chr8	+	1.07E+08	1.07E+08	716
ENSG00000(	0	0	0	0	1.840864	3.28786	-1.4188	0.29365	NA	RP11-53M:	chr8	+	55466921	55474487	787
ENSG00000(	0	1.204288	1.319414	1.498151	5.522592	4.109825	-1.5463	0.20315	0.31117	RP11-470N	chr8	+	40018977	40030131	531
ENSG00000(	0	0	0	3.745378	3.681728	15.61733	-3.7083	0.002503	0.006554	CTA-398F1(	chr8	-	8314419	8318847	510
ENSG00000(	9.322127	9.634302	18.47179	0	0	0	4.8672	2.49E-05	8.81E-05	RP4-798P1	chr1	-	1.78E+08	1.78E+08	6212
ENSG00000(	19.68005	22.88147	13.19414	15.73059	12.88605	9.863579	0.51124	0.37678	0.50741	RP11-48B3	chr8	-	81447241	81451370	3766
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	CTC-340I23	chr5	-	1.56E+08	1.56E+08	460
ENSG00000(	3.107376	2.408575	7.916483	0	0	0	3.2366	0.012342	0.028105	CTB-33O18	chr5	+	1.73E+08	1.73E+08	457
ENSG00000(	29.00217	25.29004	21.11062	33.7084	27.61296	22.19305	-0.14004	0.76002	0.84136	RP11-503E	chr8	-	42392672	42393447	708
ENSG00000(	0	0	1.319414	0	0	2.465895	-0.38078	0.77353	NA	RP11-255B	chr8	-	1.28E+08	1.28E+08	367
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	CTD-2373N	chr8	+	30501206	30501319	114
ENSG00000(	0	1.204288	0	2.247227	3.681728	0	-1.207	0.37141	0.50199	RP11-1149	chr8	+	81970758	81979979	431
ENSG00000(	2.071584	1.204288	6.597069	0.749076	0	0	2.2026	0.09039	0.16133	AB015752.	chr8	-	91546839	91632298	578
ENSG00000(	18.64425	6.021439	5.277655	23.97042	10.12475	10.68554	-0.52499	0.45404	0.58379	TYW1B	chr7	-	72023729	72298765	2008
ENSG00000(	0	0	1.319414	0	13.80648	2.465895	-2.3491	0.064467	0.12083	CTB-78F1.1	chr5	-	1.67E+08	1.67E+08	1124
ENSG00000(	0	0	0	2.247227	0	0.821965	-0.85594	0.51054	NA	CTC-558O2	chr5	+	1.68E+08	1.68E+08	810
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-585F	chr8	-	100584	100728	145
ENSG00000(	31.07376	48.17151	35.62417	0	0	0	6.4947	6.90E-10	3.83E-09	RP1-273G1	chr8	-	33831219	33867113	511
ENSG00000(	43.50326	71.05298	83.12307	37.45378	94.8045	50.13986	0.11404	0.76666	0.84615	RP11-598P	chr8	-	42981138	42981540	403
ENSG00000(	0	0	0	35.20655	55.22592	63.2913	-6.4639	4.84E-10	2.72E-09	RP11-120I2	chr8	+	84824948	85052518	640

ENSG00000(	0	0	0	2.996302	0.920432	1.64393	-1.649	0.22411	NA	RP11-92K1	chr8	+	81035087	81039905	364
ENSG00000(	48.68222	57.80581	26.38828	35.20655	21.16994	32.05663	0.57257	0.17994	0.28279	61E3.4	chr16	-	29392675	29415350	3653
ENSG00000(	1.035792	2.408575	1.319414	0.749076	4.60216	6.575719	-1.0156	0.37319	0.50373	RP11-43A1	chr8	-	675188	675877	316
ENSG00000(	1.035792	0	2.638828	0.749076	4.60216	3.28786	-0.87912	0.47487	0.60412	RP11-219B	chr8	-	86089757	86090385	468
ENSG00000(	25.8948	22.88147	50.13772	14.23244	18.40864	4.109825	1.361	0.017315	0.038153	PCDHGB1	chr5	+	1.41E+08	1.41E+08	4590
ENSG00000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	RP11-419K	chr8	-	1.31E+08	1.31E+08	683
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	KB-1043D8	chr8	+	97247655	97250262	382
ENSG00000(	2.071584	0	0	0	1.840864	0	0.093542	0.94384	NA	CTB-12O2.1	chr5	+	1.51E+08	1.52E+08	3591
ENSG00000(	0	3.612863	1.319414	7.490755	2.761296	0.821965	-0.88685	0.45351	0.58322	CTD-2284J1	chr8	-	87345503	87355543	1486
ENSG00000(	3.107376	0	1.319414	0.749076	1.840864	4.109825	-0.39706	0.74992	0.83399	RP11-242J1	chr4	-	1.86E+08	1.86E+08	802
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	KB-1639H6	chr8	-	1.04E+08	1.04E+08	414
ENSG00000(	2.071584	0	0	0.749076	1.840864	1.64393	-0.54615	0.68433	0.78413	RP11-300E	chr8	-	75938663	75941695	590
ENSG00000(	6.214751	6.021439	9.235896	0	0	0.821965	3.3468	0.004146	0.010444	PCDHGA3	chr5	+	1.41E+08	1.41E+08	4605
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-959I1	chr8	-	1.25E+08	1.25E+08	327
ENSG00000(	1.035792	6.021439	0	0	0	0	2.0906	0.12335	0.20852	RP11-662G	chr8	-	91818702	91871468	833
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTC-438O3	chr5	-	1.65E+08	1.65E+08	745
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-17A4	chr8	+	57358366	57464626	2643
ENSG00000(	0	2.408575	0	0	0	1.64393	0.21935	0.86915	NA	RP11-18A1	chr9	+	26746951	26786872	443
ENSG00000(	0	0	0	5.243529	3.681728	3.28786	-2.8004	0.030496	0.063065	RP11-473C	chr8	+	1.31E+08	1.31E+08	467
ENSG00000(	0	7.225726	1.319414	5.243529	3.681728	0	-0.05507	0.96343	0.97878	RP11-594N	chr8	-	79338338	79470738	2011
ENSG00000(	2.071584	0	2.638828	0	0	0	1.5584	0.24658	NA	KB-1458E1	chr8	-	99383583	99400475	435
ENSG00000(	0	0	2.638828	0	2.761296	0	-0.03456	0.97961	NA	RP11-382J1	chr8	+	22350144	22350557	414
ENSG00000(	2.071584	2.408575	7.916483	2.247227	4.60216	4.109825	0.13688	0.89178	0.93288	TDGF1P5	chr8	+	54985674	54986126	453
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-89M1	chr8	-	1.29E+08	1.3E+08	2055
ENSG00000(	0	0	0	0.749076	1.840864	0.821965	-1.0455	0.43461	NA	RP11-1144	chr8	+	72587535	72615021	808
ENSG00000(	2.071584	0	1.319414	23.97042	23.0108	41.92021	-4.1253	7.75E-07	3.25E-06	KRT8P3	chr8	+	62490779	62492230	1449
ENSG00000(	0	0	0	17.22874	24.85166	36.98842	-5.5578	2.78E-07	1.22E-06	RP11-89K1	chr8	+	1.28E+08	1.28E+08	574
ENSG00000(	0	0	0	0	2.761296	3.28786	-1.6293	0.2296	0.34285	RP11-150C	chr8	-	37454998	37457376	2379
ENSG00000(	0	0	0	7.490755	1.840864	12.32947	-3.6176	0.003389	0.008684	CTB-158E9.	chr5	-	1.54E+08	1.54E+08	1734
ENSG00000(	1.035792	0	0	0.749076	0	2.465895	-0.63474	0.6383	NA	IMPDH1P6	chr8	+	1.24E+08	1.24E+08	1514
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-706J1	chr8	+	77318889	77436591	1663
ENSG00000(	10.35792	4.817151	11.87472	0	0.920432	0	3.6562	0.001224	0.003382	MRPL9P1	chr8	-	77515475	77516087	613
ENSG00000(	0	1.204288	2.638828	0	0.920432	0	0.94343	0.48603	NA	RP11-267N	chr8	+	95545856	95546619	491
ENSG00000(	0	1.204288	0	0	2.761296	1.64393	-0.89024	0.51172	NA	RP11-473C	chr8	+	1.31E+08	1.31E+08	917
ENSG00000(	7.250543	14.45145	7.916483	0	0	0	4.5139	0.000136	0.000435	C8orf87	chr8	-	94146324	94179079	588
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-134C	chr8	-	2523591	2585991	582
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-495C	chr8	-	38558144	38562373	735
ENSG00000(	3.107376	3.612863	1.319414	0	1.840864	0	1.3998	0.27913	0.40133	hsa-mir-15	chr8	-	1.42E+08	1.42E+08	90
ENSG00000(	1.035792	3.612863	0	0	4.60216	3.28786	-0.51079	0.68451	0.78423	RP11-318K	chr8	+	56806154	56808298	673
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTC-308K2	chr5	+	1.72E+08	1.72E+08	182
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	RP11-1D12	chr8	-	65616331	65647016	769
ENSG00000(	3.107376	0	0	0	0	1.64393	0.41335	0.75876	NA	CKS1BP7	chr8	-	81557174	81557408	235
ENSG00000(	2.071584	2.408575	7.916483	3.745378	5.522592	14.79537	-0.85274	0.34956	0.47929	GS1-44D20	chr8	+	70041833	70042580	748
ENSG00000(	2.071584	0	0	1.498151	0	0.821965	-0.06236	0.96323	NA	CTC-367J1:	chr5	-	1.5E+08	1.5E+08	368

ENSG00000(	0	0	0	4.494453	1.840864	3.28786	-2.4341	0.065807	0.12305	RP11-865I(	chr8	-	69760977	69764998	515
ENSG00000(	0	0	2.638828	0	0	2.465895	0.027772	0.98358	NA	RP11-909N	chr8	+	1.44E+08	1.45E+08	417
ENSG00000(	3.107376	0	0	0	1.840864	0	0.36193	0.78835	NA	RP11-10A1	chr8	+	8998934	9002945	651
ENSG00000(	0	1.204288	1.319414	0.749076	0.920432	0.821965	-0.00512	0.99698	NA	RP11-760H	chr8	+	1.21E+08	1.21E+08	522
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	MTND1P6	chr8	+	32871599	32872544	946
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-1134	chr8	+	48100928	48101183	256
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-542A	chr5	+	1.58E+08	1.58E+08	706
ENSG00000(	8.286335	4.817151	3.958241	0.749076	4.60216	0.821965	1.2362	0.23341	0.34715	RP11-578C	chr8	-	79636031	79636371	341
ENSG00000(	1.035792	1.204288	2.638828	1.498151	5.522592	3.28786	-0.83339	0.46668	0.59593	RP11-195E	chr5	-	70328995	70330227	707
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-14I1	chr8	+	26298007	26300111	568
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	CTB-131B5	chr5	+	1.4E+08	1.4E+08	583
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-38H1	chr8	+	78311308	78449526	686
ENSG00000(	25.8948	15.65574	43.54065	0.749076	7.363456	3.28786	2.7207	9.67E-05	0.000316	HOXA-AS3	chr7	+	27169596	27195542	3987
ENSG00000(	1.035792	1.204288	2.638828	4.494453	1.840864	5.753754	-1.0434	0.35025	0.47991	RP11-181B	chr8	-	28273041	28277572	511
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-343P	chr8	-	1.36E+08	1.36E+08	318
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-34P1	chr5	+	1.6E+08	1.6E+08	333
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-32K4	chr8	+	65285885	65296344	2840
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP3-388N1	chr8	+	94861789	94862303	515
ENSG00000(	0	1.204288	0	0.749076	0.920432	3.28786	-1.0749	0.42573	0.55606	DUTP2	chr8	+	1.24E+08	1.24E+08	463
ENSG00000(	3.107376	0	2.638828	6.74168	12.88605	3.28786	-1.6375	0.10691	0.18533	RHPN1-AS1	chr8	-	1.44E+08	1.44E+08	1918
ENSG00000(	0	0	2.638828	0.749076	0	0	0.57076	0.66213	NA	RP11-56F1	chr9	+	27102628	27104726	564
ENSG00000(	0	1.204288	1.319414	0	4.60216	5.753754	-1.3791	0.27595	0.39744	CTD-2371C	chr11	-	9451903	9455033	597
ENSG00000(	0	2.408575	0	0.749076	0	0	0.55104	0.6711	NA	RP11-578F	chr15	-	28924551	28927398	546
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-179A	chr11	+	11139401	11205158	1833
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-109E	chr11	-	1.23E+08	1.23E+08	541
ENSG00000(	0	2.408575	3.958241	0	1.840864	3.28786	0.20069	0.87423	0.92104	RP11-613D	chr11	+	43942609	44022707	743
ENSG00000(	1.035792	3.612863	1.319414	0	0	0.821965	1.5446	0.25043	0.36783	RP11-182J1	chr15	-	85175129	85177218	845
ENSG00000(	0	0	0	10.48706	9.20432	9.041614	-4.1139	0.000474	0.001399	RP11-347E	chr11	+	1.1E+08	1.1E+08	720
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	ANO1-AS2	chr11	-	69918540	69921539	1004
ENSG00000(	1.035792	0	0	1.498151	11.04518	3.28786	-2.5305	0.041211	0.082156	RP11-21L1	chr11	-	14284392	14295237	240
ENSG00000(	2.071584	1.204288	0	0	1.840864	1.64393	-0.02642	0.98424	0.99091	RP11-261P	chr20	+	57285851	57286689	577
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	RP11-452H	chr11	+	78035804	78155095	437
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP11-351I2	chr8	-	12231875	12233055	1181
ENSG00000(	3.107376	1.204288	1.319414	7.490755	6.443024	15.61733	-2.0235	0.031542	0.064942	RP11-430H	chr11	+	45376922	45387672	872
ENSG00000(	30.03797	34.92434	19.79121	33.7084	52.46462	67.40112	-0.82952	0.047704	0.093164	RP11-110I1	chr11	-	1.19E+08	1.19E+08	523
ENSG00000(	75.61281	72.25726	44.86007	246.4459	231.9489	302.4831	-1.993	5.77E-16	4.82E-15	CTD-2562J1	chr11	+	74971171	74972069	506
ENSG00000(	9.322127	0	0	0	0	0.821965	1.8698	0.16415	0.26239	RP11-550A	chr8	-	1.26E+08	1.26E+08	722
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-33I1	chr8	-	61721294	61722165	301
ENSG00000(	3.107376	0	9.235896	1.498151	9.20432	4.93179	-0.28604	0.7821	0.85651	RP11-677I2	chr11	-	1.06E+08	1.06E+08	826
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	PBOV1	chr6	-	1.39E+08	1.39E+08	2499
ENSG00000(	3.107376	0	1.319414	0	1.840864	0	0.69183	0.6095	0.72336	RP11-718B	chr11	+	82546551	82548264	915
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-290F	chr11	-	6129365	6206806	816
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	SF3A3P2	chr11	-	1.23E+08	1.23E+08	1507
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	ALG9-IT1	chr11	-	1.12E+08	1.12E+08	684

ENSG0000(	0	0	0	4.494453	1.840864	4.109825	-2.5551	0.051964	0.10042	RCC2P6	chr11	+	62138618	62140640	1557
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-405K	chr11	+	25756317	25803305	575
ENSG0000(	12.4295	3.612863	5.277655	0	0.920432	1.64393	2.4381	0.024939	0.052853	RP11-867G	chr11	+	66080324	66086708	544
ENSG0000(	2.071584	4.817151	0	0	0	2.465895	0.89812	0.49764	0.62603	RP11-91P2	chr11	-	77540700	77583308	585
ENSG0000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-939C	chr11	-	75217982	75219436	386
ENSG0000(	16.57267	10.83859	10.55531	5.243529	11.96562	21.37109	-0.01145	0.98643	0.99167	RP11-755F	chr11	-	66027038	66029305	539
ENSG0000(	3.107376	2.408575	2.638828	2.247227	0	2.465895	0.57032	0.63339	0.74317	RP11-484D	chr11	+	43487942	43488421	480
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	PRKRIRP4	chr11	+	23499614	23501976	2266
ENSG0000(	22.78742	22.88147	18.47179	15.73059	30.37426	30.4127	-0.23808	0.63206	0.74198	RP11-849H	chr11	-	71576555	71639700	1781
ENSG0000(	128.4382	143.3102	147.7743	156.5568	181.3251	190.6959	-0.33233	0.11921	0.20266	AP5B1	chr11	-	65543364	65548273	4811
ENSG0000(	18.64425	18.06432	25.06886	19.47596	11.04518	9.041614	0.60274	0.29159	0.41566	RP11-522I2	chr9	+	86322509	86328293	1017
ENSG0000(	8.286335	7.225726	6.597069	0	5.522592	5.753754	0.84749	0.37348	0.50395	hsa-mir-21(	chr11	-	568089	568198	110
ENSG0000(	5.17896	0	1.319414	3.745378	11.96562	5.753754	-1.3798	0.1788	0.28147	AP000640.	chr11	-	59520488	59522448	879
ENSG0000(	0	1.204288	2.638828	4.494453	0.920432	0	-0.34004	0.79526	0.86632	SLC25A1P1	chr11	+	85645780	85646706	927
ENSG0000(	6.214751	2.408575	1.319414	0	1.840864	0	1.6616	0.1907	0.29614	RP11-23F2	chr11	+	4208370	4223885	462
ENSG0000(	0	0	1.319414	2.247227	0	0	-0.3289	0.80275	NA	PTP4A2P2	chr11	-	1.34E+08	1.34E+08	502
ENSG0000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	CTA-797E1(	chr11	+	70166034	70167521	422
ENSG0000(	1.035792	4.817151	3.958241	15.73059	8.283888	7.397684	-1.5075	0.08256	0.14943	RP11-380C	chr3	-	9334272	9404987	829
ENSG0000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	RP13-631K	chr11	+	12052422	12083332	3308
ENSG0000(	3.107376	0	3.958241	1.498151	2.761296	1.64393	0.1944	0.87103	0.91891	AP000487.	chr11	-	70204304	70204783	394
ENSG0000(	35.21692	25.29004	21.11062	13.48336	10.12475	12.32947	1.1387	0.031586	0.065016	CHMP4A	chr14	-	24678789	24683075	1393
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-748H	chr11	+	1.01E+08	1.01E+08	2371
ENSG0000(	4.143168	1.204288	5.277655	2.996302	9.20432	1.64393	-0.30852	0.76201	0.84276	RP11-677M	chr11	+	1.25E+08	1.25E+08	433
ENSG0000(	10.35792	14.45145	6.597069	26.21764	31.29469	20.54912	-1.2463	0.027558	0.05774	RP11-867G	chr11	+	66176629	66184608	948
ENSG0000(	1.035792	2.408575	3.958241	0	1.840864	3.28786	0.37667	0.75732	0.83948	RP11-472I2	chr11	+	43755309	43756114	806
ENSG0000(	0	1.204288	3.958241	0	1.840864	0	0.81113	0.54816	0.66983	RP11-113K	chr11	-	82751848	82752445	286
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-466I1	chr11	+	29181503	29288281	492
ENSG0000(	12.4295	2.408575	2.638828	12.73428	7.363456	3.28786	-0.35054	0.69153	0.78954	ABC11-484	chr8	-	12063268	12063898	631
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-728F	chr11	+	1.18E+08	1.18E+08	959
ENSG0000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-460B	chr11	-	29357425	29615842	448
ENSG0000(	142.9393	138.4931	94.99779	34.45748	43.2603	39.45432	1.6699	1.90E-08	9.36E-08	AP001816.	chr4	+	1.02E+08	1.02E+08	790
ENSG0000(	84.93494	103.5687	127.9831	98.1289	123.3379	111.7872	-0.07715	0.76567	0.84534	PABPC4L	chr4	-	1.35E+08	1.35E+08	4944
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	MTG1	chr10	+	1.35E+08	1.35E+08	1605
ENSG0000(	0	1.204288	5.277655	0	1.840864	0.821965	0.79876	0.54274	0.66528	RP1-130L2	chr11	+	33424762	33425151	390
ENSG0000(	0	0	1.319414	2.247227	3.681728	1.64393	-1.5522	0.23725	0.35188	RP11-463D	chr8	+	74582676	74645132	396
ENSG0000(	30.03797	34.92434	43.54065	6.74168	6.443024	3.28786	2.5921	4.12E-06	1.60E-05	RP4-791M1	chr1	-	1.45E+08	1.45E+08	869
ENSG0000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	NAV2-AS3	chr11	-	20000245	20002883	598
ENSG0000(	6.214751	0	2.638828	2.996302	0	0.821965	0.82844	0.50903	0.63644	RP11-84A1	chr1	+	32254731	32256923	537
ENSG0000(	3.107376	2.408575	2.638828	1.498151	0	0.821965	1.2297	0.3251	0.45264	OMP	chr11	+	76813886	76814377	492
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-727A	chr11	-	82920473	82924421	766
ENSG0000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	RP1-27O5.1	chr1	+	32930658	33066393	3447
ENSG0000(	20.71584	21.67718	23.74945	12.73428	20.2495	21.37109	0.27483	0.59441	0.71042	RP11-351I2	chr11	-	10324204	10325251	803
ENSG0000(	12.4295	22.88147	10.55531	2.247227	9.20432	9.041614	1.0856	0.13137	0.21909	AF131215.	chr8	-	10994408	10996117	1710
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-102F	chr8	+	70625625	70631957	552

ENSG00000(	10.35792	13.24716	14.51355	12.73428	23.0108	27.12484	-0.68975	0.23275	0.34643	RP11-1L12	chr11	-	27068733	27241660	879
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-196E	chr11	+	1.19E+08	1.2E+08	4476
ENSG00000(	0	2.408575	2.638828	1.498151	0.920432	0	0.61675	0.64273	0.75011	RP11-673F	chr11	+	78460295	78467525	320
ENSG00000(	2.071584	2.408575	2.638828	0.749076	2.761296	2.465895	0.19714	0.86553	0.91516	MTND2P26	chr11	-	1.03E+08	1.03E+08	1029
ENSG00000(	20.71584	4.817151	5.277655	3.745378	4.60216	5.753754	1.0267	0.21788	0.32922	RP11-484D	chr11	+	43411833	43417045	183
ENSG00000(	0	0	0	5.243529	0.920432	0.821965	-1.9273	0.15403	0.24947	PSMA2P1	chr11	-	87040449	87041094	646
ENSG00000(	0	0	0	0.749076	1.840864	1.64393	-1.2986	0.33698	NA	MAGEL2	chr15	-	23888691	23891175	2485
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	RP11-360K	chr11	+	96461317	96584822	1647
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP5-1173A	chr11	+	3357951	3361860	783
ENSG00000(	1.035792	1.204288	2.638828	5.243529	6.443024	7.397684	-1.6373	0.11094	0.19077	RP11-757C	chr11	+	71614240	71615127	888
ENSG00000(	21.75163	50.58008	44.86007	19.47596	14.72691	21.37109	1.0325	0.029154	0.060652	CTD-2010I1	chr11	-	6509416	6510607	686
ENSG00000(	0	0	0	0.749076	3.681728	0.821965	-1.5443	0.25498	NA	CSNK2A3	chr11	-	11373489	11374904	1416
ENSG00000(	49.71801	42.15007	35.62417	24.71949	37.73771	43.56414	0.26777	0.50153	0.62964	AP000662.	chr11	+	57405497	57420263	2790
ENSG00000(	5.17896	4.817151	10.55531	2.247227	0.920432	4.109825	1.2583	0.19193	0.29761	AP000487.	chr11	-	70128473	70209474	539
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RP11-22P4	chr11	+	28538379	28540888	747
ENSG00000(	10.35792	3.612863	9.235896	0.749076	0	0	3.4684	0.002871	0.007438	RP11-115C	chr11	+	1.27E+08	1.27E+08	408
ENSG00000(	0	0	0	2.996302	0.920432	0.821965	-1.4343	0.28996	NA	RP11-56A1	chr8	+	55561553	55782463	1014
ENSG00000(	10.35792	8.430014	17.15238	15.73059	15.64734	22.19305	-0.55508	0.35483	0.48452	RP11-676N	chr11	-	1.28E+08	1.28E+08	724
ENSG00000(	6.214751	2.408575	11.87472	5.243529	2.761296	5.753754	0.4898	0.58364	0.70115	AP003068.	chr11	-	64945077	64949305	1454
ENSG00000(	599.7235	645.4982	587.1391	281.6524	296.3791	380.5698	0.93155	8.53E-09	4.30E-08	RP11-395G	chr8	+	1.07E+08	1.07E+08	1318
ENSG00000(	0	1.204288	0	0	0	4.109825	-0.75943	0.57378	NA	RP11-700F	chr11	+	1.34E+08	1.34E+08	586
ENSG00000(	11.39371	14.45145	9.235896	23.97042	6.443024	9.863579	-0.19413	0.77456	0.85199	RP11-231C	chr16	-	29437121	29465435	2930
ENSG00000(	304.5228	351.652	278.3963	373.7887	312.9469	346.0472	-0.14405	0.39922	0.5303	WAC-AS1	chr10	-	28811581	28821672	2608
ENSG00000(	10.35792	1.204288	9.235896	0	0	0	3.8889	0.001841	0.004939	ARMS2	chr10	+	1.24E+08	1.24E+08	818
ENSG00000(	6.214751	0	1.319414	5.243529	6.443024	5.753754	-0.95878	0.35572	0.48531	CTD-2589M	chr11	+	46259933	46260818	653
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	COX6CP5	chr11	+	7999028	7999255	228
ENSG00000(	0	0	2.638828	0	0.920432	0	0.55591	0.6721	NA	RP11-5A11	chr8	-	1.05E+08	1.05E+08	376
ENSG00000(	1.035792	0	0	1.498151	2.761296	4.109825	-1.7455	0.18256	0.28613	RP11-713P	chr11	-	1.34E+08	1.34E+08	1130
ENSG00000(	0	0	3.958241	5.992604	0	13.15144	-1.7021	0.1533	0.24852	RP11-452H	chr11	+	78099107	78103451	365
ENSG00000(	4.143168	4.817151	2.638828	4.494453	0	0.821965	0.84175	0.46327	0.59257	RP11-702F	chr11	+	46138129	46138869	605
ENSG00000(	3.107376	0	3.958241	2.247227	1.840864	0.821965	0.37378	0.75959	0.84112	RP11-872D	chr11	+	57093077	57095432	311
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTD-2560E	chr11	-	45237366	45256843	567
ENSG00000(	1.035792	1.204288	1.319414	0.749076	5.522592	0	-0.52612	0.68237	0.78269	AP000783.	chr11	+	1.23E+08	1.23E+08	1103
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP5-945I17	chr11	-	35600978	35606858	537
ENSG00000(	7.250543	0	1.319414	8.239831	5.522592	2.465895	-0.71987	0.49666	0.62521	STT3A-AS1	chr11	-	1.25E+08	1.25E+08	429
ENSG00000(	2.071584	3.612863	1.319414	0	1.840864	3.28786	0.33191	0.78609	0.85956	RP5-916O1	chr11	-	35988560	35990226	1667
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-7I15.	chr11	+	77733979	77734767	277
ENSG00000(	4.143168	6.021439	11.87472	13.48336	8.283888	6.575719	-0.35077	0.64883	0.75525	RP11-727A	chr11	+	82891186	82895562	905
ENSG00000(	0	0	1.319414	0	0	4.109825	-0.74763	0.58005	NA	RP11-109L	chr11	-	1.17E+08	1.17E+08	301
ENSG00000(	466.1064	401.0278	414.2959	87.64184	276.1296	211.245	1.1247	0.012568	0.028566	PKD1P5	chr16	-	18458147	18495797	10291
ENSG00000(	79.75598	98.75159	79.16483	91.38722	80.99802	73.15488	0.06747	0.80683	0.87471	RP11-660L	chr11	+	71159720	71163203	680
ENSG00000(	72.50543	95.13873	157.0102	115.3576	84.67974	102.7456	0.090465	0.76269	0.84327	FPGT	chr1	+	74663922	74699770	3224
ENSG00000(	0	0	0	0.749076	1.840864	0	-0.68825	0.58858	NA	RP11-162D	chr8	+	54090131	54155243	826
ENSG00000(	9.322127	6.021439	2.638828	0.749076	0	0.821965	2.6145	0.02271	0.048563	RP11-47J1	chr11	-	12843982	12845214	489

ENSG00000(	4.143168	0	0	1.498151	0	0	0.68397	0.6136	NA	RP11-354A	chr8	+	82797612	82835428	466
ENSG00000(	15.53688	12.04288	5.277655	14.98151	12.88605	18.90519	-0.46618	0.46494	0.59399	GS1-393G1	chr8	-	1.46E+08	1.46E+08	444
ENSG00000(	9.322127	1.204288	5.277655	3.745378	4.60216	4.109825	0.30727	0.74716	0.83187	RP11-91P2	chr11	+	77561650	77562557	551
ENSG00000(	12.4295	7.225726	9.235896	2.996302	8.283888	2.465895	0.98027	0.23474	0.34893	RP11-50B3	chr11	-	1.26E+08	1.26E+08	362
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-659G	chr11	-	82674723	82750157	433
ENSG00000(	2.071584	1.204288	0	0	0.920432	1.64393	0.21609	0.87277	NA	RP11-1415	chr5	-	69435402	69503572	584
ENSG00000(	9.322127	12.04288	10.55531	6.74168	0	6.575719	1.0995	0.20111	0.30868	FLI1-AS1	chr11	-	1.29E+08	1.29E+08	1290
ENSG00000(	0	0	0	2.996302	0.920432	0	-1.1048	0.40628	NA	RP11-675N	chr11	-	92133357	92141342	775
ENSG00000(	0	1.204288	5.277655	0	1.840864	7.397684	-0.38321	0.75555	0.83826	RP11-35J1(	chr11	+	7726835	7731064	539
ENSG00000(	0	1.204288	1.319414	0	0	4.109825	-0.38581	0.7757	0.85283	RP1-145M2	chr11	-	34356665	34357550	886
ENSG00000(	8.286335	4.817151	2.638828	0	1.840864	2.465895	1.5003	0.17323	0.27454	CTD-2216N	chr11	+	1.23E+08	1.23E+08	701
ENSG00000(	12.4295	8.430014	2.638828	2.996302	8.283888	6.575719	0.37632	0.65554	0.76061	GLYATL1P2	chr11	+	58645775	58660933	902
ENSG00000(	2.071584	0	1.319414	8.239831	0.920432	6.575719	-1.6687	0.14628	0.239	CTD-2184C	chr14	-	60706839	60715483	2859
ENSG00000(	0	2.408575	1.319414	1.498151	4.60216	0.821965	-0.61827	0.62332	0.73502	RP11-351I2	chr11	-	10293599	10293806	208
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	FAM8A2P	chr11	-	56098823	56099964	1142
ENSG00000(	1973.184	1748.626	2157.242	1496.653	2047.961	1853.531	0.1231	0.37913	0.50984	MEX3A	chr1	-	1.56E+08	1.56E+08	6124
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-801G	chr11	-	1.09E+08	1.09E+08	320
ENSG00000(	0	0	1.319414	0	3.681728	0	-0.65657	0.62582	NA	CTD-2005H	chr11	+	86414141	86425134	432
ENSG00000(	8.286335	3.612863	7.916483	2.247227	12.88605	14.79537	-0.52529	0.52173	0.64732	RP11-691N	chr11	+	57509635	57560715	580
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-317J1	chr11	+	86142632	86333909	411
ENSG00000(	0	2.408575	0	0	3.681728	0	-0.28514	0.83342	0.89318	RP13-46H2	chr11	+	528907	529659	547
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-661A	chr8	+	1.45E+08	1.45E+08	431
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	OR10V3P	chr11	+	59508798	59509522	725
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	CTD-3076C	chr15	+	1.01E+08	1.01E+08	572
ENSG00000(	1.035792	4.817151	1.319414	0.749076	3.681728	2.465895	0.048972	0.96652	0.98029	RP11-867G	chr11	+	66101965	66107346	516
ENSG00000(	0	1.204288	0	0	1.840864	0	-0.18234	0.88799	NA	AP000889.	chr11	-	1.08E+08	1.08E+08	660
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	NAP1L1P1	chr11	+	1.26E+08	1.26E+08	1063
ENSG00000(	0	0	0	3.745378	2.761296	0	-1.7329	0.20153	0.30918	RP11-867G	chr11	-	66035106	66035600	272
ENSG00000(	0	0	0	0.749076	1.840864	3.28786	-1.711	0.20694	NA	TRIM53CP	chr11	-	49007423	49013433	1354
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CTD-2140G	chr11	-	22305276	22359791	635
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-50B3	chr11	-	1.26E+08	1.26E+08	202
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-148C	chr8	-	11410733	11411716	435
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	AC022182.	chr8	+	61822612	61879116	926
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	GVINP2	chr11	+	6769362	6771555	2194
ENSG00000(	4.143168	6.021439	6.597069	11.98521	9.20432	7.397684	-0.70986	0.36503	0.49488	RP11-320L	chr11	+	85994969	85995710	742
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-142C	chr11	-	58762912	58767162	1122
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTD-2537C	chr11	+	84431869	84511744	351
ENSG00000(	11.39371	7.225726	9.235896	1.498151	11.04518	6.575719	0.50614	0.53498	0.65921	FAR1-IT1	chr11	+	13690874	13691696	368
ENSG00000(	0	4.817151	2.638828	0.749076	0	0.821965	1.3577	0.30095	0.426	FDPSP4	chr15	-	43231508	43232556	1049
ENSG00000(	0	3.612863	0	1.498151	0	0	0.55191	0.68269	NA	SYS1-DBND	chr20	+	43991840	44039250	1313
ENSG00000(	7.250543	3.612863	7.916483	0	0	0	3.7978	0.002281	0.00602	RP11-672A	chr11	-	76365213	76367756	651
ENSG00000(	1.035792	0	5.277655	6.74168	4.60216	4.109825	-1.065	0.32423	0.45172	RP11-661A	chr8	-	1.45E+08	1.45E+08	701
ENSG00000(	5.17896	0	0	0	0	0.821965	1.2091	0.37233	0.50277	RP11-496I9	chr11	+	557595	560107	2210
ENSG00000(	0	10.83859	13.19414	3.745378	0	4.93179	1.1737	0.26526	0.38513	SLC22A18A	chr11	-	2909010	2924970	1659

ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-50B3	chr11	+	1.26E+08	1.26E+08	569
ENSG00000(	14.50109	12.04288	7.916483	14.23244	25.7721	17.26126	-0.68031	0.25562	0.37382	AP001372.	chr11	+	74204411	74209578	2493
ENSG00000(	2.071584	4.817151	6.597069	6.74168	2.761296	3.28786	0.042664	0.96471	0.97964	GVINP1	chr11	-	6735571	6767670	7057
ENSG00000(	6.214751	3.612863	3.958241	0	0	0	3.3141	0.009918	0.023091	AF131215.	chr8	-	10920157	10924599	639
ENSG00000(	0	1.204288	0	0.749076	0	0.821965	-0.12128	0.92635	NA	RP11-890B	chr11	-	1.31E+08	1.31E+08	2203
ENSG00000(	5.17896	3.612863	6.597069	0.749076	3.681728	0	1.4344	0.19602	0.30268	RP11-648C	chr11	-	86805776	86807627	1852
ENSG00000(	2.071584	0	2.638828	0	0	0	1.5584	0.24658	NA	RP11-203N	chr14	-	20812392	20815047	468
ENSG00000(	1.035792	4.817151	3.958241	1.498151	2.761296	5.753754	-0.03456	0.97411	0.98485	RP11-51B2	chr11	-	12559630	12562514	519
ENSG00000(	29.00217	33.72006	22.43003	66.66772	47.86246	70.68898	-1.0974	0.003773	0.009582	RP11-109L	chr11	+	1.17E+08	1.17E+08	822
ENSG00000(	3.107376	14.45145	0	15.73059	30.37426	28.76877	-1.9197	0.008653	0.020415	CTD-2523D	chr11	+	1.2E+08	1.2E+08	523
ENSG00000(	0	3.612863	1.319414	0	0	0.821965	1.2363	0.36215	NA	RP11-867G	chr11	-	66032248	66033137	479
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	NDUFA3P2	chr11	-	68256077	68256308	232
ENSG00000(	139.8319	152.9445	147.7743	396.261	301.9017	310.7027	-1.1915	9.37E-10	5.15E-09	MPV17L2	chr19	+	18303992	18307758	1959
ENSG00000(	0	1.204288	0	0	2.761296	0.821965	-0.69224	0.6093	NA	RP11-661A	chr8	-	1.45E+08	1.45E+08	498
ENSG00000(	29.00217	43.35436	55.41538	28.46487	19.32907	34.52253	0.60714	0.15763	0.25397	TMEM9B-A	chr11	+	8986222	8999074	1053
ENSG00000(	0	2.408575	2.638828	0	0.920432	4.93179	-0.1547	0.90423	0.94075	RP11-159H	chr11	+	27493276	27503980	1350
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-831A	chr11	-	1.2E+08	1.2E+08	518
ENSG00000(	0	2.408575	0	1.498151	1.840864	0	-0.24361	0.85744	NA	CTD-2516F	chr11	-	7590097	7593277	550
ENSG00000(	0	1.204288	1.319414	0	0.920432	0.821965	0.25429	0.85125	NA	RP11-1167	chr11	-	65751150	65751802	653
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-91I2(	chr8	-	61565061	61566120	430
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP13-870H	chr11	+	1049880	1055749	3139
ENSG00000(	1.035792	1.204288	1.319414	0.749076	3.681728	2.465895	-0.66598	0.58993	0.70675	RP11-770J	chr11	-	1.18E+08	1.18E+08	2074
ENSG00000(	14.50109	9.634302	2.638828	8.239831	8.283888	15.61733	-0.22441	0.76386	0.84398	RP11-23J9.	chr9	+	1E+08	1E+08	3161
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-687N	chr11	-	1.25E+08	1.25E+08	586
ENSG00000(	5.17896	0	2.638828	2.247227	0	1.64393	0.68519	0.58648	0.70381	RP11-682B	chr11	-	9332831	9333236	406
ENSG00000(	1.035792	6.021439	0	0	0	0	2.0906	0.12335	0.20852	RP11-802F	chr11	+	78902603	78904205	374
ENSG00000(	5.17896	2.408575	0	0	0	0	2.2334	0.099381	0.17452	CTC-378H2	chr19	+	42636707	42641251	759
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-10A7	chr11	-	1.09E+08	1.09E+08	457
ENSG00000(	24.85901	16.86003	22.43003	19.47596	15.64734	20.54912	0.19686	0.70142	0.7971	RP11-466P	chr5	-	75465911	75470171	1938
ENSG00000(	1.035792	0	3.958241	0	0.920432	0	1.2088	0.37284	NA	RP11-37O1	chr11	-	1.03E+08	1.03E+08	586
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-513D	chr8	+	38193499	38195069	434
ENSG00000(	7.250543	2.408575	3.958241	2.247227	2.761296	1.64393	0.86028	0.4086	0.53932	RP11-152H	chr11	+	8700636	8702460	537
ENSG00000(	69.39806	113.203	48.81831	99.62705	123.3379	118.3629	-0.5503	0.072583	0.13376	MEF2BNB	chr19	-	19287712	19303425	3698
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	RP11-712L	chr11	-	1.26E+08	1.26E+08	492
ENSG00000(	2.071584	0	5.277655	0.749076	3.681728	1.64393	0.20008	0.86824	0.9172	RP11-484D	chr11	-	43350298	43380846	787
ENSG00000(	6.214751	8.430014	9.235896	10.48706	10.12475	25.48091	-0.89025	0.19739	0.30446	RP11-110I1	chr11	-	1.19E+08	1.19E+08	208
ENSG00000(	16.57267	16.86003	25.06886	0.749076	3.681728	1.64393	2.9925	0.000127	0.000409	RP11-326C	chr11	-	310139	311141	392
ENSG00000(	140.8677	161.3746	246.7304	25.46857	100.3271	96.1699	1.2442	0.032636	0.066877	SCARNA9	chr11	+	93454679	93455031	353
ENSG00000(	6.214751	1.204288	2.638828	2.996302	0.920432	0	0.9887	0.41108	0.54181	RP11-632K	chr15	-	32786204	32792547	1226
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP4-791M1	chr1	+	1.45E+08	1.45E+08	406
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-263C	chr11	-	75653173	75653479	307
ENSG00000(	0	0	0	1.498151	0.920432	6.575719	-2.2833	0.087601	0.15723	RP11-529A	chr11	-	89785005	89786904	1459
ENSG00000(	0	0	0	10.48706	11.96562	7.397684	-4.164	0.00039	0.001166	RP11-259P	chr11	-	1.34E+08	1.34E+08	904
ENSG00000(	0	0	3.958241	0	0.920432	0	0.88424	0.51108	NA	RP11-684B	chr11	-	71217107	71217426	320

ENSG00000(	0	6.021439	1.319414	0	0.920432	1.64393	0.9668	0.45779	0.58744	RP11-37O1	chr11	-	1.03E+08	1.03E+08	674
ENSG00000(	7.250543	1.204288	2.638828	0	0	0	2.9248	0.026668	0.056111	RP11-619A	chr11	+	75901769	75906115	613
ENSG00000(	0	0	1.319414	138.579	136.2239	102.7456	-6.9889	5.09E-16	4.27E-15	LINC00678	chr11	-	27639173	27656174	798
ENSG00000(	10.35792	15.65574	13.19414	13.48336	17.48821	10.68554	-0.08366	0.8915	0.93263	AF131215.	chr8	-	10980891	10983574	1744
ENSG00000(	9.322127	1.204288	5.277655	4.494453	7.363456	0.821965	0.28352	0.77532	0.85267	RP11-677N	chr11	-	1.25E+08	1.25E+08	448
ENSG00000(	9.322127	12.04288	1.319414	2.247227	0.920432	0.821965	2.0456	0.048202	0.094011	ATP5F1P5	chr11	+	1.23E+08	1.23E+08	760
ENSG00000(	1.035792	0	0	0	0	2.465895	-0.37334	0.77636	NA	GNG5P3	chr11	+	1.12E+08	1.12E+08	207
ENSG00000(	1.035792	3.612863	3.958241	114.6086	129.7809	115.8971	-5.1839	2.25E-20	2.32E-19	RP11-494N	chr11	-	7726175	7927502	2503
ENSG00000(	7.250543	1.204288	3.958241	0	0	0	3.1038	0.017542	0.038603	RP11-831H	chr11	+	62373633	62373877	92
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP11-1081	chr11	+	18728084	18762115	874
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP11-680F	chr11	+	1.26E+08	1.26E+08	838
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-65M1	chr11	+	1.12E+08	1.12E+08	855
ENSG00000(	0	0	0	18.72689	7.363456	13.9734	-4.5869	6.17E-05	0.000207	RP11-429J1	chr8	-	1.45E+08	1.45E+08	1809
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	OR8B7P	chr11	-	1.24E+08	1.24E+08	919
ENSG00000(	24.85901	1.204288	15.83297	8.988907	19.32907	5.753754	0.28587	0.70914	0.80335	ALG1L9P	chr11	-	71511587	71515691	549
ENSG00000(	0	2.408575	1.319414	0.749076	1.840864	0	0.29487	0.82652	0.88831	RP11-794P	chr11	-	1.11E+08	1.11E+08	1155
ENSG00000(	1.035792	4.817151	0	0	0	2.465895	0.72054	0.59043	0.70703	RP11-350N	chr8	-	38258054	38259201	377
ENSG00000(	0	0	0	2.247227	3.681728	3.28786	-2.3723	0.073588	0.13539	HMGB1P24	chr17	-	35500531	35501387	685
ENSG00000(	1.035792	1.204288	0	0	9.20432	2.465895	-1.5642	0.21514	0.32584	FTLP6	chr11	-	66538717	66539138	422
ENSG00000(	2.071584	2.408575	0	2.247227	2.761296	4.109825	-0.74185	0.5306	0.65543	RSF1-IT2	chr11	-	77428757	77429456	566
ENSG00000(	853.4925	793.6256	895.882	1049.455	1120.166	1170.478	-0.3926	0.001629	0.004408	DPP3	chr11	+	66247484	66277130	3078
ENSG00000(	1.035792	3.612863	2.638828	0.749076	1.840864	7.397684	-0.36234	0.74807	0.83252	RP11-563P	chr11	-	1.04E+08	1.04E+08	562
ENSG00000(	0	0	3.958241	1.498151	0	0.821965	0.3778	0.78033	0.85524	CTD-2547H	chr11	-	76666461	76689663	568
ENSG00000(	1.035792	0	2.638828	2.247227	0.920432	0.821965	-0.0933	0.94314	0.96575	RP11-108C	chr11	-	1.12E+08	1.12E+08	783
ENSG00000(	0	1.204288	0	1.498151	3.681728	0	-1.0563	0.43559	0.56513	RP13-631K	chr11	+	12088476	12094561	899
ENSG00000(	13.46529	12.04288	1.319414	1.498151	1.840864	4.93179	1.4684	0.1197	0.20329	STX16-NPEI	chr20	+	57226490	57290466	3433
ENSG00000(	20.71584	22.88147	18.47179	8.988907	21.16994	7.397684	0.70071	0.23661	0.35113	ANKHD1-EI	chr5	+	1.4E+08	1.4E+08	8246
ENSG00000(	3.107376	0	0	1.498151	0	0	0.45456	0.7352	NA	KRTAP5-9	chr11	+	71259466	71260653	1188
ENSG00000(	4617.56	4514.875	4059.836	2652.477	2587.334	3274.708	0.63049	3.50E-07	1.53E-06	BRK1	chr3	+	10157276	10168874	1233
ENSG00000(	2.071584	1.204288	1.319414	0.749076	0	0	1.2903	0.34099	NA	AC139103.	chr8	+	1.46E+08	1.46E+08	1030
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-90K1	chr11	-	85627545	85634725	448
ENSG00000(	1.035792	0	0	0.749076	1.840864	0	-0.44174	0.74166	NA	AP000442.	chr11	-	59328619	59333547	769
ENSG00000(	0	6.021439	0	10.48706	8.283888	13.9734	-2.0706	0.033811	0.069014	AF131216.	chr8	-	11203257	11205011	1099
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-536I(	chr3	-	14313873	14345345	613
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-665E	chr11	+	87527116	87527416	301
ENSG00000(	11.39371	9.634302	10.55531	5.992604	6.443024	1.64393	1.0568	0.18605	0.29062	RP11-326C	chr11	+	287305	288987	812
ENSG00000(	5.17896	0	0	0	0	0	1.5469	0.24589	NA	RP11-708B	chr11	-	1.09E+08	1.09E+08	803
ENSG00000(	9.322127	19.2686	19.79121	10.48706	10.12475	9.863579	0.61971	0.32321	0.45056	RP11-802E	chr11	+	67818207	67821229	791
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP11-23J9.	chr9	+	1E+08	1E+08	6463
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	RP11-1167	chr11	-	65834748	65837090	502
ENSG00000(	0	0	1.319414	0.749076	4.60216	0	-1.0467	0.43967	0.56945	RP11-677N	chr11	-	14695152	14696101	950
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-677N	chr11	-	1.25E+08	1.25E+08	445
ENSG00000(	5.17896	4.817151	6.597069	1.498151	1.840864	0.821965	1.6263	0.1212	0.20558	RP11-297N	chr8	-	11655437	11660077	811
ENSG00000(	1.035792	1.204288	3.958241	0.749076	10.12475	9.041614	-1.3818	0.19013	0.29548	RP11-661A	chr8	+	1.45E+08	1.45E+08	1173

ENSG00000(	23.82321	14.45145	13.19414	22.47227	34.97642	32.8786	-0.7682	0.12488	0.2105	RP11-712L	chr11	-	1.26E+08	1.26E+08	509
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RP11-47J1	chr11	+	12870342	12870980	419
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP11-140L	chr11	+	14462333	14463223	512
ENSG00000(	2.071584	0	0	0.749076	0	0	0.47431	0.71145	NA	GRM5-AS1	chr11	+	88237744	88257222	4821
ENSG00000(	2.071584	0	6.597069	8.988907	1.840864	0.821965	-0.35469	0.7547	0.83776	RP11-843A	chr11	+	78244222	78269611	717
ENSG00000(	0	1.204288	0	1.498151	0	0	-0.08768	0.94524	NA	AF186192.	chr8	+	1.46E+08	1.46E+08	693
ENSG00000(	19.68005	12.04288	19.79121	4.494453	0.920432	0	2.8454	0.000785	0.002239	RP11-820L	chr11	-	1.22E+08	1.22E+08	959
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	RP11-495C	chr11	+	45673079	45674241	249
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-58K2	chr11	-	44627720	44629651	567
ENSG00000(	3.107376	0	1.319414	0	1.840864	0	0.69183	0.6095	0.72336	RP11-406D	chr11	-	28000216	28041122	806
ENSG00000(	0	2.408575	1.319414	0	0	4.93179	-0.24559	0.85438	0.90737	RP11-5L12	chr11	-	9263995	9267056	561
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-481A	chr8	-	11870545	11873043	425
ENSG00000(	2.071584	4.817151	1.319414	1.498151	4.60216	5.753754	-0.42288	0.69032	0.78869	RP11-21L2	chr11	-	76493625	76494106	336
ENSG00000(	230.9816	242.0618	449.9201	21.72319	270.607	95.34793	1.1166	0.18511	0.28965	KIAA0754	chr1	+	39876151	39882154	6004
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-159H	chr8	-	70771499	70772775	1277
ENSG00000(	0	0	2.638828	0.749076	0	0	0.57076	0.66213	NA	AP006621.	chr11	-	823634	832883	536
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTD-2572N	chr11	-	42204842	42275262	546
ENSG00000(	571.7571	464.8551	497.419	534.8399	400.3879	393.7212	0.20598	0.22327	0.33543	CHMP1B	chr18	+	11851395	11854448	3054
ENSG00000(	0	2.408575	0	0	5.522592	0	-0.6173	0.64862	0.75507	RP11-91P2	chr11	-	77626036	77626321	286
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP11-770G	chr11	-	65556522	65558339	494
ENSG00000(	2.071584	3.612863	6.597069	50.93714	47.86246	66.57916	-3.6085	4.45E-10	2.51E-09	RP11-110I1	chr11	-	1.19E+08	1.19E+08	1359
ENSG00000(	2.071584	4.817151	0	5.992604	5.522592	9.863579	-1.3562	0.17344	0.27482	RP11-303G	chr8	+	12437796	12438572	186
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-680F	chr11	+	1.26E+08	1.26E+08	496
ENSG00000(	0	4.817151	0	0.749076	0	0	1.1462	0.39668	NA	RP11-646J1	chr11	-	33836423	33843641	308
ENSG00000(	0	0	0	0.749076	0.920432	4.109825	-1.6737	0.21726	NA	OR8K2P	chr11	+	56102618	56103544	927
ENSG00000(	79.75598	61.41867	60.69303	141.5753	115.9744	151.2415	-1.0041	0.000159	0.000504	RP11-111N	chr11	-	76152382	76155724	2608
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTD-2562J1	chr11	-	74919099	74952218	538
ENSG00000(	0	0	0	0.749076	1.840864	0	-0.68825	0.58858	NA	RP11-290D	chr13	-	45911615	45911744	130
ENSG00000(	9.322127	0	2.638828	5.992604	12.88605	5.753754	-0.86248	0.36151	0.49119	AP000442.	chr11	+	59383902	59407334	601
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-438N	chr11	-	3994111	3995467	848
ENSG00000(	15.53688	28.90291	14.51355	12.73428	10.12475	27.12484	0.22382	0.70196	0.79743	AP006621.	chr11	+	781645	782105	284
ENSG00000(	0	0	0	2.247227	8.283888	11.50751	-3.6506	0.002968	0.007671	RP11-60I3.	chr9	-	1.03E+08	1.03E+08	544
ENSG00000(	0	0	0	1.498151	0	2.465895	-1.1271	0.39798	NA	RP11-659P	chr11	-	57811582	57827610	1890
ENSG00000(	5.17896	6.021439	3.958241	2.247227	0	1.64393	1.5268	0.16513	0.26367	RP4-791M1	chr1	+	1.45E+08	1.45E+08	573
ENSG00000(	14.50109	15.65574	6.597069	17.97781	27.61296	20.54912	-0.79371	0.16808	0.26763	EID3	chr12	+	1.05E+08	1.05E+08	1464
ENSG00000(	14.50109	13.24716	10.55531	8.239831	3.681728	8.219649	0.85344	0.22975	0.34303	CTD-2245C	chr11	+	1330999	1331937	939
ENSG00000(	4.143168	0	2.638828	6.74168	8.283888	4.109825	-1.2217	0.2302	0.34357	RPP14	chr3	+	58291974	58305920	3264
ENSG00000(	1.035792	3.612863	1.319414	0.749076	0	5.753754	-0.0939	0.9396	0.96348	KLHL22-IT1	chr22	-	20829490	20829598	109
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTD-2313N	chr11	+	71567323	71574704	237
ENSG00000(	8.286335	22.88147	18.47179	5.992604	0	3.28786	2.1373	0.008836	0.020787	RP11-754B	chr11	+	665910	678391	912
ENSG00000(	12.4295	2.408575	11.87472	0	9.20432	3.28786	0.95554	0.32042	0.44762	RP11-318C	chr11	+	8790325	8831778	850
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-428C	chr11	+	19321430	19329905	648
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-358N	chr11	+	89519113	89521006	1454
ENSG00000(	0	0	5.277655	1.498151	4.60216	0	-0.14701	0.91037	0.94496	RP5-1047A	chr8	+	1.46E+08	1.46E+08	439

ENSG0000(	0	0	1.319414	0	2.761296	0.821965	-0.69816	0.6064	NA	CTD-2609K	chr11	+	44093012	44093953	464
ENSG0000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP11-375D	chr11	+	41736118	41857992	563
ENSG0000(	47.64643	72.25726	39.58241	6.74168	7.363456	9.863579	2.6447	5.30E-08	2.50E-07	AP002954.	chr11	+	1.19E+08	1.19E+08	1388
ENSG0000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	CCDC166	chr8	-	1.45E+08	1.45E+08	1320
ENSG0000(	3.107376	6.021439	0	0	0	0	2.5044	0.063254	0.11894	CTD-2517M	chr8	-	1.46E+08	1.46E+08	2625
ENSG0000(	5.17896	8.430014	1.319414	0.749076	0	0	2.7963	0.02447	0.051967	RP11-106J2	chr16	-	70044654	70099848	1315
ENSG0000(	1.035792	1.204288	1.319414	1.498151	0.920432	0	0.3192	0.81133	0.87764	RP11-514F	chr11	+	36408071	36409800	151
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	GLYATL1P1	chr11	+	58746260	58761593	1607
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-626H	chr11	+	69831982	69861921	432
ENSG0000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	NANOGP8	chr15	-	35376394	35377311	916
ENSG0000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	SSU72P2	chr11	-	4263286	4263871	585
ENSG0000(	2.071584	0	2.638828	0.749076	1.840864	0	0.52207	0.69496	0.79211	RP11-750H	chr11	-	47404699	47430741	851
ENSG0000(	35.21692	45.76293	31.66593	54.68252	47.86246	51.78379	-0.44629	0.21944	0.33106	SNHG9	chr16	+	2014960	2015510	471
ENSG0000(	0	15.65574	3.958241	6.74168	1.840864	4.109825	0.50671	0.61705	0.72968	AP003068.	chr11	-	64941588	64943941	2354
ENSG0000(	5.17896	13.24716	5.277655	8.988907	2.761296	11.50751	0.015359	0.9849	0.99109	RP11-350N	chr8	+	38279407	38283614	534
ENSG0000(	0	0	2.638828	0	1.840864	0	0.2163	0.87177	NA	RP4-541C2	chr11	-	33686766	33718247	648
ENSG0000(	3.107376	0	1.319414	0.749076	4.60216	1.64393	-0.43349	0.72727	0.81727	OR7E2P	chr11	-	86568101	86568989	889
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-403D	chr8	-	68994439	69007316	774
ENSG0000(	0	0	0	2.247227	5.522592	1.64393	-2.3809	0.072827	0.13414	RP11-831A	chr11	-	1.2E+08	1.2E+08	562
ENSG0000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	DDX18P5	chr11	+	1.3E+08	1.3E+08	1306
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CARD17	chr11	-	1.05E+08	1.05E+08	466
ENSG0000(	3.107376	0	2.638828	0	0	1.64393	1.0069	0.45408	0.58381	SETP17	chr11	+	86005802	86006618	817
ENSG0000(	16.57267	8.430014	15.83297	29.21395	6.443024	20.54912	-0.44049	0.4881	0.61718	CTD-3065J2	chr8	-	1.45E+08	1.45E+08	1264
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-460B	chr11	+	29467034	29478940	563
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-304M	chr11	+	129279	186136	589
ENSG0000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-755E	chr11	+	92973299	92974334	400
ENSG0000(	2.071584	0	1.319414	3.745378	2.761296	4.109825	-1.2	0.31157	0.43784	RP11-727A	chr11	+	82997171	83134559	2643
ENSG0000(	1.035792	0	0	0.749076	5.522592	0	-1.2814	0.34334	0.47252	CTD-2655K	chr11	+	67889520	67897985	551
ENSG0000(	6.214751	3.612863	10.55531	5.243529	0	4.109825	0.92515	0.34791	0.47763	RP13-317D	chr11	-	462930	463899	664
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RFPL4AP1	chr19	+	56288919	56290266	850
ENSG0000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AP002954.	chr11	-	1.19E+08	1.19E+08	465
ENSG0000(	0	0	0	4.494453	1.840864	1.64393	-2.1524	0.10834	0.18723	RP11-142C	chr11	-	58701116	58826132	2810
ENSG0000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-164N	chr11	+	87831759	87849003	252
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-583F	chr11	+	18956532	18961268	707
ENSG0000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	CTD-2523D	chr11	+	1.2E+08	1.2E+08	559
ENSG0000(	1102.083	1327.125	1176.917	104.1215	58.90765	67.40112	3.9388	1.87E-97	1.37E-95	RP11-166D	chr11	-	1.22E+08	1.22E+08	3370
ENSG0000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	CTD-2005H	chr11	+	86438397	86476307	503
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-303G	chr8	+	12495937	12496111	175
ENSG0000(	0	1.204288	1.319414	0	0.920432	0	0.59762	0.65368	NA	RP5-916O1	chr11	+	35993978	36010557	494
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	TMPRSS4-A	chr11	-	1.18E+08	1.18E+08	304
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RRM1-AS1	chr11	-	4158346	4159487	346
ENSG0000(	7.250543	2.408575	0	0.749076	6.443024	0	0.33966	0.77993	0.85499	ABCC6P2	chr16	-	14914649	14918563	717
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-375D	chr11	+	41877470	41897547	533
ENSG0000(	0	2.408575	5.277655	5.243529	9.20432	0.821965	-0.80791	0.46129	0.59062	WTAPP1	chr11	+	1.03E+08	1.03E+08	2642

ENSG00000(	112.9013	92.73015	75.20659	72.66033	50.62376	110.9653	0.25939	0.41955	0.55028	AP006621.	chr11	+	777578	784297	765
ENSG00000(	0	1.204288	5.277655	0.749076	0.920432	1.64393	0.62517	0.62454	0.73612	RP11-708L	chr11	-	1.12E+08	1.12E+08	353
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP11-91I2(	chr8	+	61573379	61577089	529
ENSG00000(	0	0	2.638828	0.749076	1.840864	0	4.10E-05	0.99998	NA	RP11-757C	chr11	-	71649717	71650590	560
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-655C	chr11	-	58265361	58273231	585
ENSG00000(	1910	2197.825	2021.342	1606.018	1036.406	1204.179	0.669	1.31E-05	4.81E-05	EID1	chr15	+	49170083	49172380	2298
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-734C	chr11	-	57633770	57634751	982
ENSG00000(	3.107376	13.24716	1.319414	5.992604	2.761296	3.28786	0.46376	0.63247	0.74238	RP5-901A4	chr11	-	67792277	67797928	739
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	OR52B2	chr11	-	6190560	6191638	1079
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RP11-428C	chr11	+	19218322	19302973	516
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-756D	chr11	-	11780648	11780980	333
ENSG00000(	138.7961	164.9874	150.4132	172.2874	150.0304	142.1999	-0.03451	0.8729	0.92025	AF131215.	chr8	-	10965298	10967236	1939
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP11-160H	chr11	+	83354645	83436433	908
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP11-664H	chr11	-	81266952	81267467	516
ENSG00000(	50.7538	46.96722	23.74945	11.98521	6.443024	9.863579	2.0177	0.000101	0.000329	RP11-655N	chr11	-	67385750	67394775	831
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	CTD-2313N	chr11	+	71422786	71492229	1345
ENSG00000(	34.18113	34.92434	19.79121	17.22874	25.7721	12.32947	0.67047	0.18156	0.28475	RP11-755F	chr11	-	66012311	66013710	397
ENSG00000(	1.035792	2.408575	2.638828	3.745378	0.920432	1.64393	-0.06086	0.9591	0.97601	RP11-91I2(	chr8	-	61464516	61465595	689
ENSG00000(	1.035792	0	3.958241	2.247227	0	2.465895	0.030918	0.98095	0.9889	RP11-22P4	chr11	+	28373654	28548588	687
ENSG00000(	0	0	14.51355	0	0	0	2.9512	0.027906	0.05833	RP11-96B2	chr8	-	1.23E+08	1.24E+08	631
ENSG00000(	6.214751	3.612863	0	1.498151	0.920432	0.821965	1.1613	0.33939	0.46804	CTD-2530H	chr11	+	75294241	75305710	651
ENSG00000(	1.035792	0	0	0	0	1.64393	-0.12526	0.92174	NA	RP11-326C	chr11	+	327171	330122	827
ENSG00000(	2.071584	1.204288	3.958241	2.247227	1.840864	3.28786	-0.03273	0.97697	0.98658	H2AFZP4	chr11	-	70125027	70125403	377
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	RP11-708L	chr11	+	1.12E+08	1.12E+08	322
ENSG00000(	2.071584	2.408575	2.638828	8.988907	0.920432	2.465895	-0.65205	0.5496	0.67103	RP11-315C	chr11	+	1.02E+08	1.02E+08	692
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-484D	chr11	-	43400432	43407221	444
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	OR8Q1P	chr11	+	1.24E+08	1.24E+08	655
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	RP11-762B	chr11	-	1.23E+08	1.23E+08	454
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-299N	chr8	-	1.45E+08	1.45E+08	316
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	RP11-469N	chr11	+	1.35E+08	1.35E+08	455
ENSG00000(	5.17896	8.430014	7.916483	2.996302	4.60216	4.109825	0.77536	0.37393	0.50444	CTD-2337I	chr11	+	78803893	78809048	1897
ENSG00000(	0	0	1.319414	0.749076	7.363456	6.575719	-2.3571	0.058326	0.11105	NOX5	chr15	+	69222864	69355083	8592
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-700F	chr11	+	1.34E+08	1.34E+08	334
ENSG00000(	3.107376	16.86003	9.235896	1.498151	4.60216	5.753754	1.1483	0.1888	0.29384	RP11-37O1	chr11	-	1.03E+08	1.03E+08	1526
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-148C	chr8	-	11415975	11417529	594
ENSG00000(	1.035792	6.021439	0	0.749076	3.681728	1.64393	0.16722	0.89091	0.93231	AP000640.	chr11	+	59436785	59443514	683
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-567C	chr11	-	1.3E+08	1.3E+08	510
ENSG00000(	0	2.408575	3.958241	0	0.920432	2.465895	0.5769	0.6566	0.76149	RP11-619A	chr11	-	75922000	75927069	388
ENSG00000(	8.286335	8.430014	5.277655	0	0	0	4.0612	0.000876	0.00248	RP11-94A2	chr8	-	1.23E+08	1.23E+08	553
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-1134	chr8	+	48102395	48104885	2491
ENSG00000(	2.071584	6.021439	0	2.247227	0	3.28786	0.38433	0.75496	0.83789	RP13-726E	chr11	-	3502750	3602441	983
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CYCSP25	chr11	-	31302219	31302534	316
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	CTD-3064C	chr11	-	22282755	22283802	516
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP1-65P5.5	chr11	+	32154245	32165125	646

ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	AC084121.	chr8	-	7636113	7638935	1587
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	CYCSP29	chr11	-	1.09E+08	1.09E+08	318
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AP001258.	chr11	-	58909594	58910083	490
ENSG00000(	0	1.204288	2.638828	0	0	0	1.2853	0.33195	NA	RP11-718B	chr11	+	82502704	82528188	446
ENSG00000(	0	1.204288	1.319414	0	0.920432	0.821965	0.25429	0.85125	NA	RP11-770J	chr11	-	1.18E+08	1.18E+08	2086
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-124G	chr11	-	41540445	41735998	859
ENSG00000(	29.00217	38.53721	22.43003	15.73059	14.72691	18.08323	0.86117	0.078818	0.14347	C6orf3	chr6	+	1.12E+08	1.12E+08	2421
ENSG00000(	5.17896	3.612863	2.638828	0	0	0	3.0137	0.021287	0.045877	C8orf49	chr8	+	11618896	11620309	1414
ENSG00000(	0	0	0	0.749076	1.840864	2.465895	-1.5178	0.26323	NA	AC022182.	chr8	-	61850264	61852430	2167
ENSG00000(	0	0	0	2.996302	0	0.821965	-1.0802	0.41594	NA	HCAR3	chr12	-	1.23E+08	1.23E+08	2137
ENSG00000(	7.250543	0	0	0	0	0.821965	1.5733	0.24536	0.36178	TBX5-AS1	chr12	+	1.15E+08	1.15E+08	3620
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP13-631K	chr11	+	12108438	12110988	550
ENSG00000(	58.00435	56.60152	60.69303	24.71949	12.88605	7.397684	1.8945	2.73E-05	9.59E-05	PCDHA3	chr5	+	1.4E+08	1.4E+08	5260
ENSG00000(	0	1.204288	0	5.992604	0	2.465895	-1.6148	0.22444	0.33686	RSF1-IT1	chr11	-	77449725	77450613	632
ENSG00000(	1.035792	3.612863	2.638828	0	0	0	2.2878	0.090046	0.16086	RP11-732A	chr11	+	6651834	6656439	487
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AP000783.	chr11	+	1.23E+08	1.23E+08	2471
ENSG00000(	0	1.204288	5.277655	0	1.840864	7.397684	-0.38321	0.75555	0.83826	RP11-37O1	chr11	-	1.03E+08	1.03E+08	656
ENSG00000(	3.107376	0	0	2.247227	0.920432	0	0.002478	0.99854	0.99905	RP11-266A	chr11	+	23186446	23224707	685
ENSG00000(	3.107376	0	0	0.749076	0	0	0.76338	0.56438	NA	CTD-2011F	chr11	-	75848359	75848775	285
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AP002954.	chr11	+	1.19E+08	1.19E+08	425
ENSG00000(	32.10955	13.24716	25.06886	14.98151	23.0108	18.08323	0.32508	0.53761	0.66147	EBLN2	chr3	+	73110810	73112488	1679
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	OR8G3P	chr11	+	1.24E+08	1.24E+08	912
ENSG00000(	6.214751	1.204288	1.319414	0	3.681728	0	0.87945	0.48797	0.61714	CTD-2530H	chr11	-	75307189	75308315	546
ENSG00000(	0	0	1.319414	0	0.920432	2.465895	-0.65854	0.62673	NA	RP11-770J	chr11	-	1.18E+08	1.18E+08	579
ENSG00000(	22.78742	19.2686	14.51355	0	5.522592	7.397684	1.9625	0.010601	0.024498	CTD-2653D	chr20	+	46306645	46315041	2437
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CTD-2616J	chr19	+	51918978	51920679	729
ENSG00000(	5.17896	13.24716	5.277655	0	0.920432	0	3.4474	0.002845	0.00738	RP1-68D18	chr11	-	35231890	35236532	587
ENSG00000(	2.071584	4.817151	13.19414	2.996302	0.920432	0.821965	1.6699	0.10943	0.1887	RP11-573N	chr11	+	92885241	92885916	676
ENSG00000(	4.143168	0	0	3.745378	2.761296	2.465895	-0.75104	0.54154	0.66443	CTD-2531D	chr11	-	62189317	62194196	510
ENSG00000(	2.071584	0	0	0	1.840864	0.821965	-0.14076	0.91727	NA	CTD-2210P	chr11	+	45834770	45846809	469
ENSG00000(	2.071584	6.021439	1.319414	2.247227	0.920432	2.465895	0.56411	0.62055	0.73278	RP11-91P2	chr11	-	77577458	77581137	712
ENSG00000(	78.72018	67.44011	121.3861	47.19176	59.82808	43.56414	0.8156	0.01216	0.027726	RP11-890B	chr11	-	1.31E+08	1.31E+08	3994
ENSG00000(	5.17896	1.204288	0	0	0.920432	0.821965	1.1486	0.38642	0.51729	CTD-2517N	chr8	+	1.46E+08	1.46E+08	398
ENSG00000(	9.322127	8.430014	3.958241	6.74168	5.522592	7.397684	0.13704	0.86495	0.91473	RP11-539G	chr4	+	39640760	39668264	1061
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	ZDHHC20P	chr11	-	74939367	74939702	336
ENSG00000(	2.071584	3.612863	0	0	0	0	1.8175	0.17961	NA	RP11-144G	chr11	-	1.08E+08	1.08E+08	964
ENSG00000(	55.93276	74.66584	29.0271	19.47596	24.85166	27.94681	1.1199	0.009152	0.021471	RP11-867G	chr11	+	66115421	66132275	762
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-725K	chr11	+	1.03E+08	1.03E+08	355
ENSG00000(	1.035792	4.817151	3.958241	5.243529	4.60216	2.465895	-0.28696	0.77891	0.8545	RP11-736K	chr11	-	86603256	86636079	1156
ENSG00000(	4.143168	0	1.319414	5.243529	6.443024	6.575719	-1.3819	0.18827	0.29317	RP11-234B	chr12	-	4809583	4829268	1249
ENSG00000(	1.035792	1.204288	3.958241	0	0	0	2.0343	0.13352	0.22221	RP11-1H15	chr11	+	9860690	9950810	586
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-867C	chr11	+	65134909	65142770	564
ENSG00000(	0	8.430014	0	0	0	0	2.183	0.10757	0.18626	RP11-672A	chr11	-	76336506	76337878	831
ENSG00000(	2.071584	3.612863	0	0	0	2.465895	0.70466	0.59825	0.71377	RP11-513D	chr8	+	38133406	38134198	256

ENSG0000(	0	0	6.597069	0	1.840864	0	0.98308	0.46719	0.59644	CTD-2381F	chr11	-	11878037	11878406	370
ENSG0000(	10.35792	18.06432	9.235896	6.74168	6.443024	1.64393	1.2238	0.11461	0.19632	AC145124.	chr8	+	12051976	12053789	1361
ENSG0000(	8.286335	0	3.958241	0	1.840864	0	1.8411	0.14782	0.24095	RP11-587D	chr11	-	27717859	27899195	358
ENSG0000(	10.35792	3.612863	2.638828	5.992604	5.522592	5.753754	-0.02975	0.97322	0.98449	RP11-113K	chr11	-	82783444	82808238	436
ENSG0000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP11-203F	chr11	-	92481898	92500033	583
ENSG0000(	3.107376	0	0	0.749076	0	2.465895	-0.00771	0.99546	0.99707	RP11-535A	chr11	-	75514476	75526451	683
ENSG0000(	38.3243	20.47289	43.54065	21.72319	12.88605	11.50751	1.101	0.029828	0.061856	MIR3654	chr11	-	62327075	62359003	5064
ENSG0000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	RP11-445F	chr17	-	35218935	35293960	1462
ENSG0000(	26.93059	20.47289	47.4989	2.247227	5.522592	13.15144	2.0582	0.001039	0.002907	CTD-3074C	chr11	-	66240961	66247704	944
ENSG0000(	0	1.204288	2.638828	0	0.920432	0	0.94343	0.48603	NA	RP11-390K	chr11	-	47144655	47152352	332
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP4-607I7.	chr11	-	35154202	35159579	1102
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-780C	chr11	-	58684488	58696162	643
ENSG0000(	1.035792	0	0	0	0.920432	1.64393	-0.43567	0.74499	NA	A-575C2.4	chr16	+	28648975	28670003	2058
ENSG0000(	766.486	827.3457	919.6314	482.4047	431.6826	449.6148	0.87806	3.12E-10	1.78E-09	POLR2M	chr15	+	57884231	58074960	4199
ENSG0000(	3.107376	3.612863	0	0	0	0	2.0594	0.12904	0.21592	RP11-326C	chr11	-	303856	304144	289
ENSG0000(	0	0	0	4.494453	2.761296	4.93179	-2.7955	0.03088	0.063751	OR10V2P	chr11	+	59516284	59517047	764
ENSG0000(	1.035792	0	0	2.996302	1.840864	0.821965	-1.2739	0.34297	0.47206	CTA-797E1	chr11	-	70170977	70173315	367
ENSG0000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-727A	chr11	+	82920441	82920676	236
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP4-683L5	chr11	+	35440604	35442549	518
ENSG0000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-168K	chr11	+	1.27E+08	1.27E+08	572
ENSG0000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-617B	chr11	+	1.04E+08	1.04E+08	547
ENSG0000(	1.035792	1.204288	0	1.498151	4.60216	1.64393	-1.1648	0.35909	0.48869	RP11-351I2	chr8	-	12305522	12368787	929
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-810P	chr11	-	61844749	61849656	788
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-351I2	chr8	-	12236188	12237774	1587
ENSG0000(	2.071584	0	0	2.247227	0.920432	4.109825	-1.1046	0.39586	0.52694	RP11-770G	chr11	+	65513200	65539056	464
ENSG0000(	4.143168	2.408575	2.638828	8.988907	0.920432	3.28786	-0.4329	0.67843	0.77961	ZNF252P-A	chr8	+	1.46E+08	1.46E+08	3236
ENSG0000(	7.250543	16.86003	15.83297	28.46487	29.45382	24.65895	-1.0185	0.057288	0.10936	FDXACB1	chr11	-	1.12E+08	1.12E+08	2789
ENSG0000(	16.57267	4.817151	5.277655	0	0.920432	3.28786	2.2154	0.029944	0.062075	RP11-6B19	chr12	+	15933002	15935054	465
ENSG0000(	8.286335	19.2686	7.916483	10.48706	10.12475	0.821965	0.65563	0.41497	0.54549	RP11-114F	chr12	-	64836290	64837110	504
ENSG0000(	3.107376	0	2.638828	0.749076	0.920432	3.28786	0.15228	0.90318	0.9402	BRWD1-IT2	chr21	-	40685887	40686886	1000
ENSG0000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	CTD-2335A	chr15	+	89904810	89939471	2718
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AP000462.	chr11	+	1.15E+08	1.15E+08	818
ENSG0000(	5.17896	3.612863	2.638828	0	2.761296	8.219649	0.057579	0.95767	0.97502	RP11-188C	chr9	-	1.41E+08	1.41E+08	1023
ENSG0000(	4.143168	2.408575	1.319414	9.737982	1.840864	1.64393	-0.59906	0.57617	0.69451	RAB44	chr6	+	36688140	36699870	2238
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AP000439.	chr11	-	69253133	69259511	581
ENSG0000(	0	0	0	0	1.840864	2.465895	-1.2108	0.36631	NA	RP3-377H1	chr12	+	4948121	4951841	560
ENSG0000(	6.214751	0	1.319414	0	2.761296	0	0.92023	0.48551	0.61462	RP11-377D	chr12	+	13153385	13193613	2403
ENSG0000(	10.35792	19.2686	10.55531	1.498151	9.20432	0	1.7033	0.053977	0.10388	PCDHB17	chr5	+	1.41E+08	1.41E+08	3063
ENSG0000(	0	0	0	1.498151	1.840864	3.28786	-1.8914	0.16147	0.25903	RP11-564D	chr10	+	1.25E+08	1.25E+08	1530
ENSG0000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	RP11-196H	chr12	-	64540168	64541637	462
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC109992.	chr3	+	1.42E+08	1.42E+08	75
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-59N2	chr12	+	21912914	21919639	456
ENSG0000(	1.035792	0	3.958241	1.498151	0	1.64393	0.38883	0.76824	0.8474	AC093510.	chr5	+	89705817	89706485	662
ENSG0000(	2.071584	3.612863	3.958241	0	0	1.64393	1.688	0.18315	0.28693	FAM222A-A	chr12	-	1.1E+08	1.1E+08	871

ENSG00000(	5.17896	3.612863	6.597069	1.498151	0.920432	3.28786	1.1669	0.26129	0.38055	RP11-466C	chr11	-	63534956	63536113	229
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-256L	chr12	-	1.1E+08	1.1E+08	603
ENSG00000(	2.071584	0	1.319414	0	0	1.64393	0.51016	0.70682	NA	RERG-AS1	chr12	+	15304857	15308217	337
ENSG00000(	2.071584	2.408575	0	2.247227	7.363456	0	-0.75091	0.54366	0.66609	RP11-59H1	chr12	+	12878851	12982909	2375
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-212D	chr11	+	1.14E+08	1.14E+08	729
ENSG00000(	0	0	0	0.749076	4.60216	0	-1.4494	0.28352	NA	RP11-867G	chr11	+	94375073	94384797	644
ENSG00000(	6.214751	15.65574	1.319414	0	0	1.64393	2.8551	0.012672	0.028774	RP11-885B	chr12	-	2870366	2879621	550
ENSG00000(	1.035792	3.612863	3.958241	0	0.920432	0	1.9703	0.13225	0.22041	RP11-253I	chr12	+	12638287	12644515	412
ENSG00000(	1.035792	0	1.319414	0	0	0.821965	0.54471	0.68089	NA	RP11-45F1	chr11	+	72065560	72074599	550
ENSG00000(	1.035792	6.021439	1.319414	0	2.761296	0	1.0745	0.40299	0.53403	AC084125.	chr8	+	1.46E+08	1.46E+08	165
ENSG00000(	2.071584	0	1.319414	4.494453	29.45382	16.4393	-3.252	0.000653	0.001885	AC005013.	chr7	-	28992974	28998029	5050
ENSG00000(	3.107376	0	0	1.498151	1.840864	5.753754	-1.0168	0.41797	0.54866	RP1-127H1	chr12	+	1.2E+08	1.2E+08	451
ENSG00000(	0	1.204288	2.638828	0	0	0	1.2853	0.33195	NA	RP11-46H1	chr12	+	1.33E+08	1.33E+08	385
ENSG00000(	10.35792	13.24716	7.916483	7.490755	7.363456	14.79537	0.083766	0.90464	0.94101	RP11-667M	chr11	-	1.14E+08	1.14E+08	1030
ENSG00000(	906.3179	1178.998	799.5648	2265.204	1836.262	2133.821	-1.1084	2.52E-13	1.80E-12	SNHG1	chr11	-	62619460	62623386	2768
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-529H	chr4	-	88238322	88266362	349
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-443N	chr12	+	25956137	25957460	1229
ENSG00000(	10.35792	13.24716	13.19414	0	0	0.821965	4.155	0.000118	0.000379	RP11-508P	chr12	+	15154767	15159617	605
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	IFNG-AS1	chr12	+	68383225	68628466	1791
ENSG00000(	3.107376	6.021439	3.958241	32.95932	51.54419	35.34449	-3.0308	5.42E-07	2.31E-06	AC110619.	chr2	-	2.41E+08	2.41E+08	1667
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	RP11-571M	chr12	+	58120054	58122139	1500
ENSG00000(	9.322127	2.408575	7.916483	0	4.60216	6.575719	0.69514	0.48625	0.61536	RP11-757G	chr11	-	68708971	68710320	569
ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	RP11-625L	chr12	+	24857499	24927147	670
ENSG00000(	10.35792	4.817151	14.51355	23.22134	5.522592	9.863579	-0.36315	0.61677	0.72942	AC226150.	chr12	-	1.34E+08	1.34E+08	527
ENSG00000(	2.071584	0	0	0	2.761296	1.64393	-0.54588	0.68652	0.78557	RP11-283G	chr12	-	26383752	26472653	708
ENSG00000(	0	0	1.319414	0	8.283888	11.50751	-2.6536	0.031865	0.06552	RP11-22B2	chr12	-	9466998	9468769	586
ENSG00000(	0	0	0	0.749076	0	3.28786	-1.135	0.39451	NA	RP11-152F	chr15	-	82765134	82798350	1349
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	GS1-410F4	chr12	+	68323015	68363797	509
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AP000439.	chr11	-	69291901	69294708	726
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP3-454B2	chr12	-	6264201	6269885	653
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-436I	chr12	+	9188940	9189840	901
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-1029	chr12	+	64426192	64426445	254
ENSG00000(	0	3.612863	2.638828	0	0.920432	0	1.4705	0.2759	0.39742	RP11-809N	chr11	+	73163065	73163389	325
ENSG00000(	0	0	0	4.494453	0.920432	0	-1.4809	0.27346	NA	RMST	chr12	+	97825431	97958813	2598
ENSG00000(	1.035792	4.817151	0	0.749076	0	2.465895	0.53998	0.68012	0.78088	RP11-817J	chr11	+	1.03E+08	1.03E+08	721
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP1-34M23	chr1	-	35227027	35253698	560
ENSG00000(	0	1.204288	1.319414	0	1.840864	0	0.21033	0.87627	NA	RP11-196H	chr12	-	64502543	64514269	390
ENSG00000(	2.071584	0	0	0.749076	0.920432	0	0.15367	0.90884	NA	MTRNR2L8	chr11	-	10529434	10530723	1290
ENSG00000(	7.250543	2.408575	21.11062	0.749076	1.840864	5.753754	1.6101	0.08749	0.15706	RP11-157G	chr12	-	7591376	7592586	1211
ENSG00000(	12.4295	9.634302	19.79121	11.98521	3.681728	9.041614	0.68983	0.32238	0.44965	TAS2R20	chr12	-	11149094	11150474	1381
ENSG00000(	1.035792	1.204288	1.319414	0	1.840864	3.28786	-0.33915	0.79313	0.86485	AP000593.	chr11	+	72013183	72014009	578
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-804A	chr11	-	60581405	60589212	355
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-167N	chr11	-	73674702	73681332	1412
ENSG00000(	2.071584	0	3.958241	0	0	0	1.8862	0.16413	0.26236	AC061975.	chr17	-	26525465	26525619	150

ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-407A	chr12	-	1.27E+08	1.27E+08	802
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-735A	chr11	+	94782586	94784109	1524
ENSG00000(	14.50109	28.90291	10.55531	35.20655	31.29469	57.53754	-1.1593	0.018537	0.040514	PXN-AS1	chr12	+	1.21E+08	1.21E+08	1170
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	RP11-612B	chr12	+	26468648	26470746	475
ENSG00000(	4.143168	3.612863	7.916483	1.498151	11.04518	5.753754	-0.19034	0.83566	0.89487	RP11-444D	chr12	-	24366190	24715524	832
ENSG00000(	6.214751	1.204288	2.638828	0	0	0	2.7795	0.036317	0.073498	RP11-221N	chr12	+	65953371	65954669	443
ENSG00000(	5.17896	2.408575	5.277655	5.243529	6.443024	2.465895	-0.11401	0.90438	0.94085	DENND5B-A	chr12	+	31742857	31768600	1106
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-69C1	chr12	+	16846734	16848911	2178
ENSG00000(	1.035792	0	5.277655	2.247227	0.920432	0	0.60981	0.64037	0.74818	RP11-613N	chr9	-	37588410	38068684	2591
ENSG00000(	4.143168	2.408575	17.15238	2.247227	6.443024	4.109825	0.76748	0.40107	0.53228	LINC00346	chr13	-	1.12E+08	1.12E+08	585
ENSG00000(	2.071584	1.204288	1.319414	4.494453	0.920432	0	-0.16541	0.89657	0.93585	CTD-2102P	chr19	+	53313077	53313961	885
ENSG00000(	2.071584	2.408575	5.277655	5.992604	0.920432	2.465895	0.020722	0.98465	0.99106	RP11-685N	chr11	-	94206074	94206736	581
ENSG00000(	6.214751	2.408575	6.597069	3.745378	2.761296	6.575719	0.18593	0.84263	0.89965	U47924.19	chr12	+	7080084	7105520	1086
ENSG00000(	0	0	0	2.247227	1.840864	0	-1.1573	0.3864	NA	RP11-522N	chr12	+	1.24E+08	1.25E+08	557
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-405A	chr12	+	19928385	20162871	718
ENSG00000(	3.107376	6.021439	1.319414	0	5.522592	10.68554	-0.50379	0.63604	0.74482	RP11-264F	chr12	-	4361901	4384231	495
ENSG00000(	0	2.408575	2.638828	0	0	0	1.6365	0.22501	NA	RP11-662I	chr12	+	25102097	25113092	728
ENSG00000(	0	2.408575	0	0	0	2.465895	-0.0181	0.98928	NA	RP11-456I	chr11	+	73433394	73433739	210
ENSG00000(	10.35792	8.430014	6.597069	1.498151	7.363456	5.753754	0.72828	0.38855	0.5193	RP11-495K	chr12	-	1.32E+08	1.32E+08	666
ENSG00000(	6.214751	0	0	0	3.681728	1.64393	0.17531	0.89291	0.93378	RP11-173P	chr12	-	1.21E+08	1.21E+08	583
ENSG00000(	2.071584	0	0	0	0	4.109825	-0.45547	0.73699	0.82369	RP11-804A	chr11	-	60603469	60610438	501
ENSG00000(	0	0	0	0	0	4.93179	-1.2404	0.35057	NA	RP11-459D	chr12	+	18577597	18578074	478
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-408I	chr12	+	1.25E+08	1.25E+08	130
ENSG00000(	8.286335	9.634302	5.277655	7.490755	4.60216	4.93179	0.40111	0.62148	0.73365	RP5-940J5.	chr12	-	6641456	6642664	477
ENSG00000(	1.035792	0	0	2.247227	2.761296	2.465895	-1.6142	0.22086	0.33269	RP11-438L	chr12	+	8786963	8790204	2285
ENSG00000(	9.322127	7.225726	6.597069	2.996302	5.522592	1.64393	1.0562	0.23523	0.34954	RP11-513G	chr12	+	26471886	26574395	775
ENSG00000(	0	2.408575	1.319414	0	0	0	1.2548	0.34239	NA	RP11-43N5	chr12	-	68102827	68123255	3135
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-324E	chr12	-	1.23E+08	1.23E+08	28
ENSG00000(	12.4295	3.612863	29.0271	0.749076	1.840864	1.64393	2.9598	0.00117	0.003246	CYP2A6	chr19	-	41349443	41356352	1764
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	NXPE2P1	chr11	-	1.14E+08	1.14E+08	726
ENSG00000(	2.071584	4.817151	2.638828	3.745378	19.32907	5.753754	-1.3824	0.13017	0.21745	RP11-711N	chr2	+	74213653	74220867	710
ENSG00000(	3.107376	1.204288	2.638828	0	1.840864	7.397684	-0.30106	0.79821	0.86851	RP11-417L	chr12	-	1.32E+08	1.32E+08	426
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	PSMC1P9	chr12	+	18845696	18847030	1335
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CCDC177	chr14	-	70037483	70038032	550
ENSG00000(	0	0	0	0.749076	0	3.28786	-1.135	0.39451	NA	RP11-575F	chr12	-	1.28E+08	1.28E+08	505
ENSG00000(	1.035792	20.47289	1.319414	2.996302	2.761296	1.64393	1.3322	0.19802	0.30522	AC084117.	chr11	+	18427156	18428278	270
ENSG00000(	1.035792	0	1.319414	5.992604	30.37426	19.72716	-3.7873	9.99E-05	0.000326	HIST1H3G	chr6	-	26271146	26271612	467
ENSG00000(	1.035792	0	1.319414	2.247227	0	0	0.018495	0.9891	NA	RP11-501E	chr12	-	21600479	21601248	467
ENSG00000(	0	7.225726	0	0	5.522592	2.465895	-0.09231	0.94182	0.9649	CACNA1C-A	chr12	-	2329703	2332645	735
ENSG00000(	2.071584	4.817151	3.958241	3.745378	3.681728	0.821965	0.31288	0.76914	0.84814	CBX3P4	chr12	-	2896097	2903461	423
ENSG00000(	0	3.612863	5.277655	2.996302	3.681728	1.64393	0.054974	0.96128	0.97759	MRPL40P1	chr12	+	67745216	67745819	604
ENSG00000(	280.6996	272.169	349.6447	82.39831	71.7937	63.2913	2.0363	6.90E-21	7.25E-20	CTSO	chr4	-	1.57E+08	1.57E+08	2954
ENSG00000(	3.107376	6.021439	18.47179	0	0.920432	4.109825	2.0214	0.047754	0.093253	RP11-982N	chr14	+	1.05E+08	1.05E+08	1307
ENSG00000(	211.3015	221.5889	164.9267	280.9033	198.8133	202.2034	-0.18857	0.37901	0.50977	APOPT1	chr14	+	1.04E+08	1.04E+08	2523

ENSG00000(	16.57267	46.96722	27.70769	4.494453	14.72691	10.68554	1.5381	0.009119	0.021401	RP11-709A	chr12	-	27745394	27746972	928
ENSG00000(	43.50326	25.29004	18.47179	44.19546	37.73771	36.98842	-0.42287	0.32903	0.45674	TRAPPC2P1	chr19	+	57874879	57876721	1743
ENSG00000(	10.35792	3.612863	6.597069	2.996302	6.443024	12.32947	-0.06126	0.94179	0.9649	DYX1C1	chr15	-	55702723	55800432	1993
ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	A2MP1	chr12	-	9381129	9428413	4130
ENSG00000(	7.250543	4.817151	2.638828	4.494453	9.20432	2.465895	-0.097	0.91634	0.94893	C21orf119	chr21	+	33765439	33766254	816
ENSG00000(	20.71584	33.72006	14.51355	1.498151	11.04518	3.28786	1.9957	0.004711	0.01173	RP11-366L	chr12	-	66328557	66342259	454
ENSG00000(	308.666	338.4048	335.1311	280.1543	247.5962	230.1502	0.37077	0.030688	0.063405	ZNF432	chr19	-	52534632	52598991	4513
ENSG00000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	RP11-627G	chr11	+	1.14E+08	1.14E+08	679
ENSG00000(	31.07376	45.76293	38.263	21.72319	32.21512	29.59074	0.45227	0.27995	0.40221	RP13-942N	chr12	+	1.24E+08	1.24E+08	1920
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	LINC00696	chr3	-	52097076	52097567	492
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	RP11-691F	chr11	+	73853196	73853403	208
ENSG00000(	0	0	1.319414	0	2.761296	0	-0.44505	0.73801	NA	RP11-90D4	chr12	+	8474472	8482210	603
ENSG00000(	2.071584	1.204288	0	0	2.761296	0	0.15603	0.90836	0.94364	RP13-672B	chr12	+	1.33E+08	1.33E+08	574
ENSG00000(	0	2.408575	2.638828	0	0	1.64393	0.85739	0.5258	0.65076	RP11-783K	chr11	-	63996686	64001824	923
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	RP11-778H	chr12	+	24376205	24390899	573
ENSG00000(	2.071584	1.204288	0	2.996302	6.443024	4.109825	-1.5135	0.18774	0.29249	RP11-84E2	chr17	+	70026432	70034889	639
ENSG00000(	0	1.204288	1.319414	0	0	2.465895	0.003736	0.9978	NA	RP11-674J	chr12	-	16124824	16125543	720
ENSG00000(	0	7.225726	3.958241	5.243529	8.283888	3.28786	-0.50431	0.61628	0.72914	RP11-443D	chr12	+	1.1E+08	1.1E+08	539
ENSG00000(	4.143168	0	0	2.247227	1.840864	1.64393	-0.27698	0.82947	0.89062	Z95704.5	chr4	-	123966	125423	1452
ENSG00000(	0	1.204288	1.319414	0	0	0.821965	0.59385	0.65509	NA	RP11-809N	chr11	+	73221703	73221865	163
ENSG00000(	3.107376	1.204288	0	0	1.840864	0	0.67289	0.61944	0.7318	RP11-820K	chr12	+	31630440	31630921	482
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	SMLR1	chr6	+	1.31E+08	1.31E+08	2512
ENSG00000(	4.143168	2.408575	3.958241	5.243529	1.840864	3.28786	0.008451	0.99342	0.99585	RP11-264F	chr12	-	4357931	4385350	555
ENSG00000(	1.035792	0	0	0.749076	4.60216	0	-1.1147	0.41095	0.54179	ATF4P4	chr11	+	1.14E+08	1.14E+08	1930
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	GCSHP4	chr12	-	8293764	8295293	439
ENSG00000(	1.035792	3.612863	1.319414	5.243529	6.443024	8.219649	-1.4571	0.14501	0.23739	RP11-627K	chr12	+	31464551	31464963	316
ENSG00000(	64.2191	60.21439	67.2901	38.95193	25.7721	33.70056	0.93987	0.007634	0.018234	RP11-612B	chr12	-	26488797	26489883	172
ENSG00000(	7.250543	0	9.235896	1.498151	2.761296	0.821965	1.3453	0.22357	0.3358	TAS2R30	chr12	-	11285557	11287243	1687
ENSG00000(	0	4.817151	0	1.498151	0	0	0.79721	0.55675	0.67732	RP11-167N	chr11	-	73702328	73703225	898
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	LINC00507	chr12	+	1.28E+08	1.28E+08	1935
ENSG00000(	3.107376	10.83859	10.55531	0	0	0	4.1857	0.000571	0.001664	RP11-64D2	chr11	-	1.14E+08	1.14E+08	3837
ENSG00000(	0	0	1.319414	4.494453	2.761296	3.28786	-1.9833	0.11895	0.20232	RP11-881N	chr11	-	60685941	60692869	864
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	TSPAN9-IT1	chr12	+	3258963	3260642	562
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-439H	chr12	-	64900946	64927418	712
ENSG00000(	0	0	7.916483	0	1.840864	0.821965	0.95509	0.46957	0.59883	AC005255.	chr19	+	14903121	14903589	469
ENSG00000(	0	0	0	9.737982	7.363456	2.465895	-3.4892	0.004904	0.012171	RP11-1038	chr12	-	5475214	5476940	1727
ENSG00000(	1.035792	0	2.638828	2.247227	2.761296	0.821965	-0.45889	0.71833	0.81024	MTRNR2L3	chr20	-	55933496	55934878	1383
ENSG00000(	96.32865	156.5574	154.3714	118.3539	69.0324	87.95025	0.55068	0.05265	0.10157	ZNF10	chr12	+	1.34E+08	1.34E+08	4441
ENSG00000(	176.0846	217.9761	162.2879	577.5372	451.9321	408.5166	-1.3634	1.51E-12	1.02E-11	ZNF486	chr19	+	20278037	20311299	3837
ENSG00000(	0	0	0	15.73059	9.20432	22.19305	-4.8242	1.87E-05	6.70E-05	RP11-771K	chr12	-	31516415	31522235	868
ENSG00000(	2.071584	1.204288	3.958241	0	1.840864	0.821965	0.9862	0.43696	0.56663	RP11-283G	chr12	-	26364097	26488789	699
ENSG00000(	0	2.408575	2.638828	0	0	0	1.6365	0.22501	NA	SMIM3	chr5	+	1.5E+08	1.5E+08	2332
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-473N	chr12	-	16552208	16555340	3133
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RPL7AP3	chr14	-	35704386	35704857	472

ENSG00000(	0	3.612863	0	0	4.60216	0.821965	-0.33811	0.79989	0.86968	RP11-123C	chr12	-	67285656	67462942	192
ENSG00000(	1.035792	0	0	1.498151	0	0	-0.08447	0.94679	NA	RP11-324E	chr12	+	1.23E+08	1.23E+08	1731
ENSG00000(	0	0	1.319414	0	3.681728	0	-0.65657	0.62582	NA	RP11-989F	chr12	+	1.31E+08	1.31E+08	587
ENSG00000(	3.107376	1.204288	1.319414	0	0	0	1.9243	0.1561	NA	AP000647.	chr11	-	1.03E+08	1.03E+08	1127
ENSG00000(	0	1.204288	0	0	3.681728	0	-0.65196	0.62789	NA	DDX11L8	chr12	-	92239	93430	366
ENSG00000(	24.85901	31.31148	25.06886	0.749076	0	4.109825	3.6771	1.50E-06	6.09E-06	RP11-221N	chr12	+	65996649	66006777	612
ENSG00000(	488.8938	387.7806	430.1289	835.2192	736.3456	867.173	-0.89638	1.36E-09	7.36E-09	HMBS	chr11	+	1.19E+08	1.19E+08	2112
ENSG00000(	0	1.204288	3.958241	0	0	1.64393	0.86871	0.52045	0.64628	CACNA1C-A	chr12	-	2777666	2781386	609
ENSG00000(	5.17896	7.225726	9.235896	3.745378	2.761296	2.465895	1.0964	0.22608	0.33887	RP11-182J	chr15	-	85154920	85158200	1018
ENSG00000(	0	0	5.277655	0.749076	0.920432	0	0.8711	0.51947	0.64554	RP11-466C	chr11	-	63602139	63602415	277
ENSG00000(	17.60846	25.29004	7.916483	1.498151	7.363456	9.863579	1.3384	0.069919	0.12965	RP11-504G	chr11	-	18617006	18621230	943
ENSG00000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	RP11-754J	chr12	+	66957304	66957474	171
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-664H	chr12	+	20167714	20251802	431
ENSG00000(	0	0	0	0.749076	0	4.109825	-1.3462	0.31758	NA	RP11-277P	chr12	-	10485460	10490891	649
ENSG00000(	75.61281	92.73015	137.219	36.7047	39.57858	50.96182	1.2407	0.000136	0.000435	ZNF225	chr19	+	44616334	44637027	2538
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	AC005086.	chr7	-	1.02E+08	1.02E+08	219
ENSG00000(	3.107376	0	0	0	0.920432	0	0.70943	0.5938	NA	RP11-989F	chr12	-	1.31E+08	1.31E+08	317
ENSG00000(	1.035792	3.612863	2.638828	8.988907	24.85166	9.863579	-2.3007	0.007177	0.017244	RP11-512N	chr12	-	1.23E+08	1.23E+08	2215
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-4N23	chr12	+	13679788	13700516	382
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-407A	chr12	+	1.27E+08	1.27E+08	379
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	RP13-977J	chr12	+	1.33E+08	1.33E+08	391
ENSG00000(	0	2.408575	0	2.247227	0.920432	0	-0.20772	0.87831	NA	RP11-338E	chr12	-	65047840	65048799	482
ENSG00000(	3.107376	0	6.597069	0.749076	5.522592	1.64393	0.22968	0.84196	0.89907	HIST1H3F	chr6	-	26250370	26250835	466
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-153K	chr12	+	23252302	23344521	1629
ENSG00000(	6.214751	7.225726	5.277655	3.745378	6.443024	4.93179	0.28044	0.74461	0.82989	AL049542.	chr16	+	542366	542567	198
ENSG00000(	12.4295	8.430014	11.87472	2.996302	6.443024	11.50751	0.59542	0.42963	0.55973	RP11-611C	chr12	+	69221898	69222333	374
ENSG00000(	1.035792	2.408575	1.319414	2.247227	0	0	0.61104	0.6475	0.75399	SCARNA10	chr12	+	6619441	6619688	248
ENSG00000(	5.17896	3.612863	5.277655	5.243529	1.840864	4.109825	0.27207	0.77764	0.8535	RPL41P2	chr15	+	28560798	28561102	305
ENSG00000(	2.071584	2.408575	1.319414	2.996302	2.761296	5.753754	-0.78122	0.47475	0.604	ABCC6P1	chr16	+	18582484	18609650	2943
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-662N	chr12	+	1.31E+08	1.31E+08	1252
ENSG00000(	0	0	0	4.494453	5.522592	9.041614	-3.4747	0.004946	0.012264	RP11-800A	chr11	+	72959824	72960912	764
ENSG00000(	0	4.817151	1.319414	0	0	0	1.8904	0.16312	0.26107	RP1-7G5.5	chr12	-	1.1E+08	1.1E+08	343
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	HSPA8P5	chr12	+	4206617	4208685	2069
ENSG00000(	7.250543	7.225726	6.597069	13.48336	6.443024	17.26126	-0.75914	0.29513	0.41956	RP11-707G	chr11	+	73639578	73641417	383
ENSG00000(	1.035792	2.408575	0	0.749076	1.840864	4.93179	-0.76438	0.54191	0.66465	RP11-613F	chr11	-	18532590	18533022	433
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-711K	chr12	+	11365126	11404303	506
ENSG00000(	4.143168	15.65574	5.277655	12.73428	1.840864	8.219649	0.1082	0.89757	0.93636	RP11-1060	chr12	-	27849321	27863703	1110
ENSG00000(	1.035792	1.204288	5.277655	0	1.840864	0	1.2801	0.32814	0.45587	RP11-500N	chr12	+	4754662	4757193	572
ENSG00000(	18.64425	4.817151	6.597069	29.96302	19.32907	18.08323	-1.0782	0.086232	0.15516	AC020910.	chr19	-	35166998	35168486	1487
ENSG00000(	20.71584	7.225726	3.958241	3.745378	7.363456	9.041614	0.62199	0.43416	0.56393	RP11-347I	chr12	-	1.22E+08	1.22E+08	1626
ENSG00000(	55.93276	36.12863	21.11062	17.97781	15.64734	25.48091	0.91414	0.058317	0.11104	AC138123.	chr12	-	93477374	93477451	78
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	ASIC5	chr4	-	1.57E+08	1.57E+08	1692
ENSG00000(	3.107376	6.021439	0	0	0	0	2.5044	0.063254	0.11894	RP11-274J	chr12	-	64281159	64282378	1220
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-7N14	chr11	+	72121760	72123123	492

ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CYB5RL	chr1	-	54606897	54665746	2382
ENSG00000(	0	0	1.319414	2.247227	3.681728	0.821965	-1.4008	0.29128	0.4154	RP11-1038	chr12	+	5399646	5492819	992
ENSG00000(	2.071584	4.817151	0	1.498151	0	0	1.2514	0.34856	0.47826	RP1-102E2.	chr12	+	6503071	6504235	724
ENSG00000(	10.35792	3.612863	5.277655	1.498151	0.920432	6.575719	0.93193	0.34301	0.47208	TAS2R31	chr12	-	11182986	11184006	1021
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-705C	chr12	-	9799610	9800605	532
ENSG00000(	0	3.612863	0	5.243529	16.56778	9.863579	-2.5669	0.012296	0.028007	RP11-794G	chr11	-	61306988	61309731	1831
ENSG00000(	0	8.430014	0	0	0	0	2.183	0.10757	0.18626	RP11-809N	chr11	+	73116342	73121727	334
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	RP11-424N	chr12	+	16666379	16667305	927
ENSG00000(	4.143168	14.45145	3.958241	3.745378	6.443024	4.109825	0.58428	0.5037	0.63148	RP11-667N	chr11	+	1.14E+08	1.14E+08	158
ENSG00000(	0	0	5.277655	0.749076	0.920432	0	0.8711	0.51947	0.64554	RP11-363J2	chr2	-	2.04E+08	2.04E+08	427
ENSG00000(	1.035792	0	1.319414	150.5642	171.2004	120.0069	-6.7444	8.75E-19	8.38E-18	SALL3	chr18	+	76740275	76762677	3997
ENSG00000(	3.107376	2.408575	5.277655	5.243529	0	2.465895	0.35856	0.74784	0.83239	RP11-613F	chr11	-	18511790	18512502	713
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-856F	chr11	-	94607217	94658686	593
ENSG00000(	2.071584	3.612863	1.319414	1.498151	0.920432	7.397684	-0.3776	0.73841	0.82485	RP11-21A7	chr11	+	63849162	63854647	732
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RP11-625L	chr12	+	24983355	24989492	451
ENSG00000(	10.35792	20.47289	10.55531	0	2.761296	4.109825	2.304	0.007934	0.018868	RP11-554A	chr11	+	68779751	68785915	1490
ENSG00000(	0	0	0	0.749076	1.840864	0	-0.68825	0.58858	NA	RP11-977P	chr12	-	28974908	28978764	433
ENSG00000(	235.1248	225.2018	221.6615	262.1764	235.6306	247.4114	-0.12739	0.47388	0.60303	POLG2	chr17	-	62473902	62493154	1731
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	AC019294.	chr15	+	76030311	76031568	1258
ENSG00000(	3.107376	1.204288	1.319414	0.749076	0	0	1.521	0.25904	0.37777	RP11-212D	chr11	+	1.14E+08	1.14E+08	1060
ENSG00000(	1.035792	0	2.638828	8.988907	4.60216	2.465895	-1.6678	0.13812	0.22827	RP11-847H	chr12	+	34190373	34209675	794
ENSG00000(	25.8948	3.612863	14.51355	24.71949	28.53339	18.08323	-0.64584	0.28625	0.40959	AC156455.	chr12	+	1.23E+08	1.23E+08	893
ENSG00000(	4.143168	0	0	2.996302	1.840864	0.821965	-0.26458	0.83784	0.89629	RP11-113C	chr12	+	8472977	8522151	620
ENSG00000(	1.035792	0	2.638828	0	0.920432	0	0.90832	0.50205	NA	RP11-1060	chr12	-	27761666	27761979	314
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	NANOGNBP	chr12	-	1.34E+08	1.34E+08	421
ENSG00000(	4.143168	2.408575	0	2.996302	0	2.465895	0.18798	0.88055	0.92529	RP11-424N	chr12	+	16720345	16726874	603
ENSG00000(	0	0	0	1.498151	4.60216	0	-1.6319	0.22883	0.34221	RP11-274J	chr12	+	64272567	64273254	515
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	OR13A1	chr10	-	45798102	45811056	2078
ENSG00000(	6.214751	6.021439	3.958241	2.247227	1.840864	4.109825	0.83385	0.39322	0.524	RP13-977J	chr12	-	1.33E+08	1.33E+08	1477
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	RP11-75L1	chr12	+	9856673	9861946	560
ENSG00000(	3.107376	0	0	0	0.920432	2.465895	-0.04093	0.97587	0.98607	RP11-613F	chr11	-	18529155	18530367	630
ENSG00000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	RP11-266K	chr12	-	8407123	8461445	1013
ENSG00000(	13.46529	8.430014	7.916483	9.737982	3.681728	17.26126	-0.03609	0.96092	0.97731	RP11-286N	chr11	+	61196692	61253294	883
ENSG00000(	42.46747	59.0101	71.24834	28.46487	34.05598	36.98842	0.7763	0.036444	0.073716	RP11-705C	chr12	+	9787188	9811008	2612
ENSG00000(	1.035792	1.204288	0	0	1.840864	0.821965	-0.10652	0.9374	NA	RP11-522N	chr12	+	1.25E+08	1.25E+08	2256
ENSG00000(	0	1.204288	1.319414	0	1.840864	0.821965	-0.04333	0.97449	NA	RP11-667N	chr11	-	1.14E+08	1.14E+08	586
ENSG00000(	4.143168	1.204288	3.958241	0.749076	0	0	2.1519	0.098779	0.17359	AC093668.	chr7	-	1.02E+08	1.02E+08	916
ENSG00000(	6.214751	1.204288	2.638828	0	0	0.821965	2.2227	0.086024	0.15487	CYP2B7P1	chr19	+	41430124	41456565	2956
ENSG00000(	17.60846	9.634302	38.263	2.996302	4.60216	3.28786	2.3898	0.000927	0.002611	RP11-815J4	chr18	-	12073231	12076653	3365
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	MTRNR2L1	chr17	+	22022437	22023991	1555
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	RP11-582E	chr12	+	27274843	27300597	983
ENSG00000(	2.071584	2.408575	1.319414	5.243529	2.761296	2.465895	-0.67051	0.54524	0.6674	RP11-454H	chr3	+	1.01E+08	1.01E+08	1158
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-428I2	chr12	-	1.29E+08	1.29E+08	736
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-169D	chr11	+	72295616	72299023	664

ENSG0000(	0	0	1.319414	0.749076	0	0.821965	-0.12362	0.92519	NA	RP11-666F	chr12	+	26953776	26954235	460
ENSG0000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	DKFZP686I	chr7	-	42948872	42971773	2430
ENSG0000(	2.071584	8.430014	15.83297	0	0	0	4.2506	0.000479	0.00141	RERG-IT1	chr12	-	15265297	15267632	301
ENSG0000(	1.035792	2.408575	1.319414	0	0.920432	0	1.2549	0.35362	NA	RP11-144C	chr12	-	10983673	10984615	943
ENSG0000(	1.035792	4.817151	0	0	0	0	1.8349	0.17548	NA	RP11-429A	chr12	+	5132848	5134758	723
ENSG0000(	8.286335	12.04288	22.43003	6.74168	11.04518	9.041614	0.62141	0.3573	0.48676	TMEM75	chr8	-	1.29E+08	1.29E+08	1466
ENSG0000(	0	0	3.958241	2.996302	0	0	0.17782	0.89571	0.93537	RP11-144C	chr12	-	11348987	11349908	922
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-180N	chr12	-	12876231	12876945	150
ENSG0000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	A2ML1-AS1	chr12	-	8928815	8983543	452
ENSG0000(	111.8655	107.1816	131.9414	218.7301	303.7426	242.4797	-1.1173	2.70E-07	1.19E-06	RP11-424C	chr12	+	20704524	20705946	1423
ENSG0000(	85.97073	96.34302	75.20659	89.88907	58.90765	84.66239	0.13758	0.63508	0.74411	KLRAP1	chr12	-	10741077	10752434	2118
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-338E	chr12	-	64992858	65003239	254
ENSG0000(	1.035792	0	0	12.73428	15.64734	14.79537	-4.0158	0.000158	0.000502	RP11-599J	chr12	-	9550951	9567447	400
ENSG0000(	2.071584	0	1.319414	0.749076	0	0	0.90441	0.50226	NA	RP11-172C	chr11	+	1.14E+08	1.14E+08	1440
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-611C	chr12	-	69198791	69199259	469
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CCDC58P5	chr11	-	73561514	73562256	432
ENSG0000(	0	0	0	1.498151	2.761296	0.821965	-1.5229	0.26162	NA	TAS2R12	chr12	-	11047542	11048481	940
ENSG0000(	97.36444	115.6116	116.1084	77.15478	73.63456	88.77221	0.45095	0.082613	0.14952	ZNF350	chr19	-	52467596	52490109	2338
ENSG0000(	6.214751	1.204288	0	2.996302	0	2.465895	0.31809	0.79894	0.8689	RP11-727F	chr11	+	62599706	62601515	565
ENSG0000(	0	0	0	0.749076	0.920432	3.28786	-1.4827	0.27425	NA	CTD-2017C	chr14	-	1.02E+08	1.02E+08	599
ENSG0000(	5.17896	10.83859	7.916483	1.498151	1.840864	0.821965	2.1236	0.03064	0.063323	RP11-785H	chr12	-	11318689	11323952	385
ENSG0000(	0	3.612863	2.638828	0	0	0	1.93	0.15472	0.25026	PGA5	chr11	+	61008514	61018920	1519
ENSG0000(	1.035792	1.204288	0	0	3.681728	1.64393	-0.71243	0.59265	0.70878	CACNA1C-I	chr12	+	2378942	2398103	622
ENSG0000(	5.17896	0	0	0	2.761296	0	0.51241	0.70504	0.79994	RP11-167N	chr11	-	73706017	73707196	1180
ENSG0000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-45F1	chr11	+	72062391	72064254	560
ENSG0000(	3.107376	4.817151	2.638828	4.494453	18.40864	13.15144	-1.5698	0.062114	0.11705	RP13-941N	chr12	+	1.22E+08	1.22E+08	544
ENSG0000(	2.071584	0	3.958241	5.243529	9.20432	5.753754	-1.4519	0.15458	0.2502	RP11-680H	chr11	-	93921615	93922163	549
ENSG0000(	0	4.817151	5.277655	0	4.60216	5.753754	-0.03626	0.97493	0.98535	RP11-17G1	chr11	-	47292208	47293661	492
ENSG0000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	RP11-860B	chr12	-	27932754	27934000	679
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-695J	chr12	+	14720684	14772689	539
ENSG0000(	1.035792	0	0	1.498151	0	1.64393	-0.62149	0.64536	NA	RP11-159N	chr11	+	1.13E+08	1.13E+08	524
ENSG0000(	0	0	0	2.996302	0	0.821965	-1.0802	0.41594	NA	STH	chr17	+	44076616	44077060	445
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CACNA1C-A	chr12	-	2712516	2716606	444
ENSG0000(	103.5792	139.6974	137.219	219.4791	221.8241	180.0103	-0.70661	0.001352	0.003714	ZNF253	chr19	+	19976695	20005483	3519
ENSG0000(	2.071584	0	0	1.498151	0	1.64393	-0.28088	0.83599	NA	RP11-697H	chr11	+	63405149	63426434	423
ENSG0000(	4.143168	0	2.638828	0	0	0	2.0639	0.1282	0.21482	RP11-429A	chr12	+	5127631	5130879	604
ENSG0000(	3.107376	0	0	0.749076	0	0	0.76338	0.56438	NA	KLRF2	chr12	+	10034088	10048432	731
ENSG0000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-500N	chr12	-	4744515	4745306	631
ENSG0000(	181.2636	162.5788	170.2044	23.22134	22.09037	20.54912	2.9306	1.28E-24	1.55E-23	RP11-680F	chr15	+	29967194	29973161	2530
ENSG0000(	1.035792	0	0	0.749076	0.920432	3.28786	-1.1153	0.40909	0.53984	CAPNS2	chr16	+	55600584	55601599	1016
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-804A	chr11	-	60609279	60618554	491
ENSG0000(	1.035792	0	0	0	1.840864	0	-0.17777	0.89006	NA	AC084125.	chr8	-	1.46E+08	1.46E+08	168
ENSG0000(	1.035792	0	3.958241	1.498151	0	0	0.88795	0.51175	0.63886	RP11-21A7	chr11	+	63803442	63871125	650
ENSG0000(	0	4.817151	1.319414	0	0	3.28786	0.53263	0.68852	0.78725	AC138744.	chr17	+	62487640	62487906	267

ENSG00000(	2.071584	3.612863	3.958241	0	2.761296	4.93179	0.25305	0.82378	0.88627	RP11-214K	chr12	-	1.24E+08	1.24E+08	355
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	CACNA1C-I	chr12	+	2127379	2129698	687
ENSG00000(	0	2.408575	2.638828	0.749076	1.840864	0	0.57522	0.66486	0.76865	AC007401.	chr2	-	36816784	36818696	1911
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP11-405A	chr12	+	20094455	20095952	1498
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-661I	chr11	-	1.14E+08	1.14E+08	494
ENSG00000(	0	1.204288	2.638828	0	0.920432	0	0.94343	0.48603	NA	RP11-664D	chr12	+	3980900	4019504	678
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	SLC5A8	chr12	-	1.02E+08	1.02E+08	4178
ENSG00000(	53.86118	49.3758	40.90183	61.42419	27.61296	69.04505	-0.13206	0.7347	0.82247	NOL12	chr22	+	38077680	38089483	2852
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-284H	chr12	-	20514666	20523196	525
ENSG00000(	9.322127	9.634302	7.916483	4.494453	16.56778	9.863579	-0.17439	0.81201	0.8781	AP001877.	chr11	-	95556681	95557336	654
ENSG00000(	8.286335	26.49433	32.98534	0.749076	1.840864	0	4.1034	4.21E-06	1.63E-05	RP11-283G	chr12	-	26278088	26279550	566
ENSG00000(	29.00217	26.49433	22.43003	22.47227	20.2495	25.48091	0.18889	0.68579	0.78496	RP11-17G1	chr11	-	47241769	47243302	610
ENSG00000(	2.071584	3.612863	3.958241	0	2.761296	0	1.2691	0.31019	0.43627	RP11-707G	chr11	-	73632710	73633241	532
ENSG00000(	2.071584	2.408575	0	0	0	0	1.5041	0.26224	NA	RP11-986G	chr12	-	2861763	2862298	536
ENSG00000(	4.143168	1.204288	5.277655	0	2.761296	1.64393	0.96598	0.41199	0.54267	AC090571.	chr8	-	41818758	41820184	138
ENSG00000(	0	0	0	0	1.840864	3.28786	-1.4188	0.29365	NA	RP1-102E2	chr12	+	6586880	6589373	2494
ENSG00000(	0	2.408575	1.319414	0.749076	0	0	0.98048	0.46819	NA	RP11-467L	chr11	-	61580975	61582121	574
ENSG00000(	2.071584	10.83859	5.277655	1.498151	0	0	2.5795	0.028018	0.058541	RP11-221N	chr12	+	66038114	66057079	547
ENSG00000(	0	0	0	4.494453	0	2.465895	-1.83	0.17727	0.27944	RP11-817J	chr11	+	1.02E+08	1.02E+08	743
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP11-436I	chr12	+	9280379	9281241	863
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-783K	chr11	+	64013436	64015689	431
ENSG00000(	11.39371	4.817151	5.277655	0	0	0	4.0106	0.001093	0.003046	RP11-64D2	chr11	-	1.14E+08	1.14E+08	393
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-87C1	chr12	+	1.22E+08	1.22E+08	1361
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-6B19	chr12	-	15966427	15981208	417
ENSG00000(	0	0	1.319414	0	0	2.465895	-0.38078	0.77353	NA	RP11-417L	chr12	+	1.32E+08	1.32E+08	283
ENSG00000(	17.60846	4.817151	10.55531	7.490755	14.72691	24.65895	-0.45962	0.50082	0.62892	RP11-273B	chr12	-	7281675	7283794	749
ENSG00000(	0	1.204288	0	0.749076	0	0	0.1572	0.90001	NA	SNRPEP2	chr9	-	6748703	6748981	279
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-320N	chr12	+	4130143	4135824	542
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AP000462.	chr11	+	1.15E+08	1.15E+08	330
ENSG00000(	17.60846	14.45145	25.06886	1.498151	0	0	4.3034	5.93E-06	2.26E-05	RP11-359J	chr12	-	22613453	22616848	738
ENSG00000(	4.143168	4.817151	3.958241	0	8.283888	4.93179	-0.01352	0.98958	0.99397	TAS2R18	chr12	-	11311384	11312293	910
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-871F	chr12	-	17662287	17742926	1003
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-114G	chr12	+	22852793	23327057	1920
ENSG00000(	0	1.204288	5.277655	2.247227	1.840864	1.64393	0.09982	0.93496	0.96077	HP	chr16	+	72088491	72094954	3024
ENSG00000(	0	2.408575	0	0.749076	0	0	0.55104	0.6711	NA	RP11-268P	chr12	-	22762162	22777949	862
ENSG00000(	38.3243	31.31148	47.4989	35.20655	71.7937	46.852	-0.38237	0.33049	0.45829	RP11-705C	chr12	+	9811163	9814681	2508
ENSG00000(	6.214751	0	1.319414	0	0	1.64393	1.2968	0.32972	0.45754	RP13-200J	chr12	+	27649870	27651522	1418
ENSG00000(	7.250543	9.634302	6.597069	9.737982	8.283888	17.26126	-0.54445	0.44558	0.57514	RP11-800A	chr11	-	73018280	73020406	1695
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	AC005477.	chr14	-	72456191	72458326	2136
ENSG00000(	3.107376	0	0	0	0.920432	0	0.70943	0.5938	NA	RP11-993B	chr12	+	28111450	28122746	792
ENSG00000(	0	0	1.319414	0	2.761296	0	-0.44505	0.73801	NA	RP11-486F	chr2	+	2E+08	2E+08	831
ENSG00000(	0	1.204288	0	0	0.920432	0.821965	-0.17164	0.89643	NA	RP11-881N	chr11	+	60674261	60677214	810
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	Z98941.1	chr12	+	1.22E+08	1.22E+08	100
ENSG00000(	13.46529	13.24716	7.916483	4.494453	12.88605	9.041614	0.37708	0.59491	0.71086	RP11-864I	chr11	+	62313471	62315171	391

ENSG0000(	1.035792	0	3.958241	0	0	0	1.6134	0.2311	NA	RP11-667N	chr11	+	1.14E+08	1.14E+08	335
ENSG0000(	1.035792	0	0	0.749076	0	1.64393	-0.39004	0.77029	NA	RPL29P33	chr19	-	34787181	34787645	465
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP3-461F1	chr12	-	7148460	7148945	486
ENSG0000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	RP11-123C	chr12	-	67429288	67490186	775
ENSG0000(	0	0	0	0.749076	4.60216	2.465895	-2.0929	0.11949	0.203	U47924.27	chr12	+	7072409	7073610	350
ENSG0000(	4.143168	8.430014	3.958241	3.745378	2.761296	4.93179	0.45455	0.62556	0.73696	RP11-783K	chr11	-	64014411	64016966	853
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	PNMA6D	chrX	-	1.52E+08	1.52E+08	1479
ENSG0000(	154.333	158.966	174.1626	164.7966	214.4607	139.734	-0.08901	0.69166	0.7896	KIAA1147	chr7	-	1.41E+08	1.41E+08	7296
ENSG0000(	0	0	1.319414	0	3.681728	0	-0.65657	0.62582	NA	RP11-450K	chr12	+	1.23E+08	1.23E+08	1745
ENSG0000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	LRRC37A13	chr11	+	1.14E+08	1.14E+08	287
ENSG0000(	2019.794	2060.536	2195.505	2746.111	3099.095	2936.881	-0.48407	1.01E-05	3.74E-05	LSM14A	chr19	+	34663409	34720420	3651
ENSG0000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP11-259C	chr12	-	9139771	9149162	496
ENSG0000(	1.035792	2.408575	0	5.243529	7.363456	1.64393	-1.5373	0.18142	0.28461	NHLRC4	chr16	+	616996	619495	2097
ENSG0000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	CTD-2503I(	chr14	+	30122015	30127122	551
ENSG0000(	2.071584	4.817151	7.916483	0	1.840864	2.465895	1.3953	0.21159	0.32152	RP11-129B	chr12	+	95494307	95494821	515
ENSG0000(	26.93059	25.29004	46.17948	95.13259	96.64536	111.7872	-1.6117	1.36E-06	5.54E-06	RRN3P3	chr16	-	22430090	22449036	3269
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CLLU1	chr12	+	92815307	92824778	3897
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-2A1.1	chr12	+	42305058	42306014	465
ENSG0000(	10.35792	4.817151	2.638828	0	0	0.821965	3.0498	0.011578	0.026524	RP11-320N	chr2	+	10588820	10591453	1737
ENSG0000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	RP11-320P	chr12	+	70574118	70595784	578
ENSG0000(	5.17896	6.021439	11.87472	2.247227	1.840864	3.28786	1.4102	0.1279	0.21454	PGAM1P5	chr12	+	96043031	96067775	2148
ENSG0000(	212.3373	266.1476	295.5487	493.6408	468.4999	457.0125	-0.87516	2.91E-07	1.28E-06	RP11-701H	chr15	+	25277020	25281637	4618
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-13A1	chr12	-	89441964	89703330	599
ENSG0000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	RP11-58A1	chr12	+	58360841	58362182	633
ENSG0000(	20.71584	16.86003	26.38828	51.68621	57.98722	62.46933	-1.4007	0.000449	0.001329	TMPO-AS1	chr12	-	98906751	98910200	3357
ENSG0000(	3.107376	3.612863	3.958241	0	1.840864	0.821965	1.4791	0.21856	0.33004	RP11-117N	chr12	-	96780596	96780972	377
ENSG0000(	6.214751	0	10.55531	4.494453	3.681728	9.041614	-0.04035	0.96633	0.98027	RP11-996F	chr12	-	29433351	29470781	2380
ENSG0000(	1.035792	0	1.319414	0	5.522592	1.64393	-0.98836	0.45044	0.58016	hsa-mir-10	chr17	-	46656992	46659621	2630
ENSG0000(	0	0	0	0	1.840864	2.465895	-1.2108	0.36631	NA	HMGN2P6	chr14	-	25736270	25736542	273
ENSG0000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	RP11-274N	chr12	-	74642417	74677449	529
ENSG0000(	22.78742	16.86003	34.30476	0	0	0	5.8701	6.81E-08	3.18E-07	RP1-170O1	chr7	-	27203154	27219632	765
ENSG0000(	3.107376	2.408575	0	0.749076	4.60216	0.821965	-0.08351	0.94627	0.96752	RP11-390N	chr12	-	79354038	79439424	716
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-567C	chr12	+	90501516	90506556	926
ENSG0000(	0	1.204288	0	0	0.920432	4.109825	-1.0194	0.45216	0.58187	RP11-603K	chr12	+	93277549	93278476	928
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-850P	chr12	+	94208912	94209885	434
ENSG0000(	0	0	1.319414	0	0.920432	1.64393	-0.44377	0.74139	NA	FAM205B	chr9	-	34832292	34838583	4009
ENSG0000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	RP11-512N	chr12	-	1.02E+08	1.02E+08	564
ENSG0000(	1.035792	2.408575	1.319414	0	0	0	1.6865	0.21314	NA	LIMS1	chr2	-	1.11E+08	1.11E+08	3202
ENSG0000(	344.9187	321.5448	343.0476	400.0063	336.8781	395.3651	-0.16585	0.30138	0.42651	GATC	chr12	+	1.21E+08	1.21E+08	2081
ENSG0000(	91.14969	103.5687	84.44248	0	0	0	7.6825	1.51E-14	1.16E-13	RP11-54A9	chr12	+	76653619	76698911	1083
ENSG0000(	2.071584	0	0	0	0	2.465895	-0.09123	0.94581	NA	RP11-136F	chr12	-	78524117	78524784	668
ENSG0000(	48.68222	46.96722	47.4989	0	8.283888	13.15144	2.6148	1.26E-05	4.62E-05	RP11-689B	chr12	+	1.09E+08	1.09E+08	600
ENSG0000(	0	2.408575	7.916483	6.74168	11.04518	7.397684	-1.1366	0.22997	0.34327	RP11-554E	chr12	+	1.02E+08	1.02E+08	374
ENSG0000(	4.143168	6.021439	0	0	0.920432	3.28786	0.91451	0.45707	0.58688	RP11-328C	chr12	+	42853168	42859930	2791

ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-438N	chr12	-	1.14E+08	1.14E+08	266
ENSG00000(	1.035792	0	0	2.996302	0	0	-0.53136	0.68956	NA	RP11-611E	chr12	-	70340323	70340861	434
ENSG00000(	7.250543	4.817151	0	2.996302	9.20432	2.465895	-0.2033	0.84266	0.89965	RP11-24B2	chr12	-	92378756	92536690	2201
ENSG00000(	7.250543	8.430014	3.958241	1.498151	0	9.041614	0.74632	0.46076	0.59019	RP11-133N	chr12	+	49988931	49989471	541
ENSG00000(	4.143168	3.612863	5.277655	2.247227	1.840864	0.821965	1.1234	0.29829	0.42319	RP11-416A	chr12	-	51518411	51519164	754
ENSG00000(	5.17896	10.83859	1.319414	5.243529	3.681728	9.863579	-0.09793	0.91314	0.94683	RP11-486A	chr12	-	93710911	93771512	814
ENSG00000(	0	0	5.277655	0	0.920432	0.821965	0.84842	0.53029	0.65508	RP3-405J1(	chr12	+	50613387	50623767	325
ENSG00000(	2.071584	0	0	0.749076	0.920432	0	0.15367	0.90884	NA	RP11-946L	chr12	-	29296129	29301608	593
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP11-767I2	chr12	-	58959743	59175529	1975
ENSG00000(	17.60846	15.65574	10.55531	24.71949	11.96562	17.26126	-0.28439	0.6244	0.73601	RP11-96H1	chr12	+	46777462	46850051	829
ENSG00000(	0	0	0	0	2.761296	1.64393	-1.2339	0.35779	NA	MIR3179-1	chr16	+	14995356	14996031	676
ENSG00000(	494.0727	567.2195	539.6402	637.4633	645.2228	562.224	-0.20479	0.14951	0.24336	ZNF271	chr18	+	32870246	32890730	5124
ENSG00000(	24.85901	22.88147	22.43003	49.43899	44.18074	51.78379	-1.0263	0.010444	0.024176	RP11-521B	chr14	-	1.06E+08	1.06E+08	445
ENSG00000(	2.071584	1.204288	1.319414	0	2.761296	0	0.46027	0.72992	0.81911	RP11-317N	chr14	+	36343063	36344509	601
ENSG00000(	17.60846	12.04288	14.51355	3.745378	7.363456	4.109825	1.4353	0.044826	0.088322	RP11-231I2	chr12	-	1.17E+08	1.17E+08	4196
ENSG00000(	1.035792	7.225726	2.638828	0	0.920432	0	2.2724	0.077003	0.14065	RP11-1060	chr12	-	94288741	94337379	540
ENSG00000(	2.071584	2.408575	0	3.745378	11.96562	8.219649	-1.9561	0.055563	0.10648	RP11-298I3	chr14	+	23398818	23424771	591
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-701B	chr12	+	85065377	85065805	429
ENSG00000(	24.85901	18.06432	27.70769	2.996302	12.88605	7.397684	1.5276	0.014947	0.033385	RP3-405J1(	chr12	-	50579363	50585146	4713
ENSG00000(	0	0	0	4.494453	0	0	-1.1446	0.38559	NA	FAHD2P1	chr12	+	71065698	71066636	939
ENSG00000(	20.71584	12.04288	10.55531	14.98151	14.72691	14.79537	-0.02616	0.96494	0.97974	RP11-977G	chr12	+	56693926	56708592	437
ENSG00000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	RP11-317N	chr14	+	36350207	36350915	709
ENSG00000(	72.50543	45.76293	154.3714	0	20.2495	6.575719	2.6246	0.018023	0.039512	ZBED6	chr1	+	2.04E+08	2.04E+08	4250
ENSG00000(	0	1.204288	0	0	3.681728	0	-0.65196	0.62789	NA	RP11-511B	chr12	-	93397191	93609455	721
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-650K	chr12	+	1.04E+08	1.04E+08	674
ENSG00000(	0	1.204288	0	1.498151	0	0	-0.08768	0.94524	NA	RP11-290L	chr12	+	76358220	76360842	358
ENSG00000(	0	0	0	0.749076	2.761296	0	-0.97685	0.45852	NA	MGAM	chr7	+	1.42E+08	1.42E+08	9172
ENSG00000(	30.03797	43.35436	58.05421	26.21764	21.16994	13.9734	1.0588	0.018671	0.040787	RP11-983P	chr12	-	53408380	53448222	2863
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	CRIP1	chr14	+	1.06E+08	1.06E+08	980
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-511B	chr12	+	93392994	93413596	898
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-386G	chr12	+	49483991	49487095	717
ENSG00000(	43.50326	30.10719	55.41538	22.47227	11.96562	9.863579	1.4804	0.002225	0.005881	RP11-631N	chr12	+	62996532	63007855	555
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-74K1	chr12	+	94533853	94535113	1261
ENSG00000(	6.214751	12.04288	10.55531	1.498151	11.96562	1.64393	0.83778	0.33848	0.46708	FNTB	chr14	+	65453438	65529368	2834
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-438E	chr12	+	45838549	45839221	673
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-547C	chr12	-	43373057	43390289	552
ENSG00000(	8.286335	12.04288	6.597069	0	0	0.821965	3.6849	0.001121	0.003117	RP11-328C	chr12	-	42825467	42827159	775
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	MIR3179-2	chr16	+	16394007	16394683	677
ENSG00000(	0	1.204288	1.319414	0	6.443024	0.821965	-0.94928	0.46962	0.59883	RP11-762I7	chr12	-	56151059	56221330	1807
ENSG00000(	1.035792	0	0	0	2.761296	0	-0.44657	0.73574	NA	MIR3180-4	chr16	+	15248760	15250877	2118
ENSG00000(	3.107376	1.204288	5.277655	0	0.920432	0.821965	1.6868	0.17833	0.2808	CTD-2547E	chr16	+	21358460	21363459	255
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RP11-645C	chr16	+	21950186	21956451	813
ENSG00000(	16.57267	19.2686	19.79121	13.48336	5.522592	10.68554	0.84501	0.16686	0.26587	RP11-2H8.2	chr12	-	72187635	72193407	1431
ENSG00000(	3.107376	0	1.319414	2.247227	1.840864	0	0.083694	0.94915	0.96942	RP11-263K	chr12	+	82906456	82909596	3141

ENSG00000(	16.57267	6.021439	21.11062	15.73059	4.60216	12.32947	0.37993	0.58029	0.69841	RP1-197B1	chr12	+	48099868	48136077	3299
ENSG00000(	11.39371	1.204288	6.597069	8.239831	6.443024	9.041614	-0.26198	0.75503	0.83793	RP11-114F	chr12	+	1.06E+08	1.06E+08	753
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-150C	chr12	+	59314420	59458019	555
ENSG00000(	5.17896	4.817151	1.319414	15.73059	6.443024	12.32947	-1.4245	0.086058	0.15492	ZNF878	chr19	-	12154620	12167127	1737
ENSG00000(	14.50109	3.612863	1.319414	0	0	1.64393	2.6034	0.027284	0.057237	RP11-290L	chr12	+	76424274	76425158	569
ENSG00000(	3.107376	2.408575	3.958241	0	0	0	2.7139	0.040995	0.081822	RP11-310I2	chr12	+	29672664	29682907	349
ENSG00000(	1.035792	2.408575	0	2.247227	0	0	0.30524	0.82195	NA	RP11-161H	chr12	-	49836207	49836435	229
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	RP11-121G	chr12	+	81664454	81706201	1080
ENSG00000(	0	2.408575	9.235896	6.74168	43.2603	19.72716	-2.3524	0.004312	0.010822	RP11-359N	chr12	+	79933983	79944315	816
ENSG00000(	7.250543	20.47289	13.19414	6.74168	8.283888	3.28786	1.0653	0.14688	0.23985	RP11-983P	chr12	+	53405888	53407705	536
ENSG00000(	0	0	0	2.996302	8.283888	2.465895	-2.9457	0.021969	0.04718	RP11-175P	chr12	-	1.01E+08	1.01E+08	928
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP3-521E1	chr12	+	1.13E+08	1.13E+08	751
ENSG00000(	3.107376	3.612863	0	0.749076	1.840864	0	0.8996	0.48922	0.61833	RP11-474P	chr12	-	46778016	46780774	562
ENSG00000(	33.14534	39.74149	27.70769	5.992604	10.12475	5.753754	2.1202	0.000106	0.000343	RP11-585P	chr12	-	75877904	75883600	812
ENSG00000(	1.035792	13.24716	0	0	0	0	3.1005	0.019393	0.042212	RP11-571N	chr12	-	58117544	58119448	1795
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-956E	chr12	+	69843250	69854504	423
ENSG00000(	8.286335	7.225726	6.597069	20.97412	15.64734	17.26126	-1.2054	0.060735	0.11484	RP11-762I7	chr12	-	56155334	56156412	529
ENSG00000(	17.60846	24.08575	6.597069	1.498151	20.2495	12.32947	0.47858	0.5186	0.64491	RP11-278C	chr12	-	32879317	32880321	1005
ENSG00000(	2.071584	1.204288	0	4.494453	1.840864	6.575719	-1.453	0.21205	0.32207	RP11-486A	chr12	+	93708585	93709717	1133
ENSG00000(	1.035792	0	0	0	0	1.64393	-0.12526	0.92174	NA	RP11-498N	chr12	-	72102951	72104154	577
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP4-601P9	chr12	+	1.15E+08	1.15E+08	435
ENSG00000(	0	0	7.916483	0	2.761296	0	0.87846	0.51167	0.63882	RP11-20E2	chr12	+	76956074	77009211	250
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-843B	chr12	-	32257051	32260462	407
ENSG00000(	3.107376	13.24716	0	4.494453	7.363456	7.397684	-0.19596	0.83683	0.89561	RP3-405J1(	chr12	-	50611445	50612126	354
ENSG00000(	6.214751	8.430014	5.277655	0.749076	8.283888	1.64393	0.78967	0.4125	0.54297	RP11-834C	chr12	-	54555849	54558236	754
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	HSPA8P14	chr12	+	1.12E+08	1.12E+08	1805
ENSG00000(	0	0	1.319414	5.992604	1.840864	1.64393	-1.8224	0.15868	0.25548	OR7E47P	chr12	+	52473480	52502045	1422
ENSG00000(	7.250543	1.204288	7.916483	6.74168	5.522592	2.465895	0.13046	0.88889	0.93101	RP11-321F	chr12	-	1.02E+08	1.02E+08	379
ENSG00000(	0	0	0	0	1.840864	2.465895	-1.2108	0.36631	NA	RP11-144F	chr12	-	1.07E+08	1.07E+08	570
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-793H	chr12	+	53907768	53911392	2297
ENSG00000(	17.60846	12.04288	5.277655	8.988907	5.522592	6.575719	0.67664	0.35892	0.4886	RP11-44N2	chr14	+	1.06E+08	1.06E+08	965
ENSG00000(	3.107376	10.83859	7.916483	1.498151	5.522592	2.465895	1.0468	0.26166	0.381	RP11-84G2	chr12	+	80328681	80334448	1190
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-123N	chr12	-	79187306	79187894	589
ENSG00000(	1.035792	10.83859	9.235896	0	1.840864	1.64393	2.07	0.057564	0.10982	RP11-863H	chr12	-	62876129	62878712	848
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	GSTP1P1	chr12	+	56294084	56294402	319
ENSG00000(	11.39371	7.225726	10.55531	0	1.840864	0	3.2359	0.002285	0.006029	RP11-496I2	chr14	-	19719545	19720589	1045
ENSG00000(	0	4.817151	0	3.745378	1.840864	0.821965	-0.28451	0.82347	0.88612	RP11-153N	chr12	+	56904786	56906487	1702
ENSG00000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	RP11-128P	chr12	-	1.08E+08	1.08E+08	507
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-718L	chr12	+	98711519	98712127	609
ENSG00000(	0	6.021439	10.55531	2.247227	3.681728	1.64393	0.90245	0.39722	0.52828	ZNF625	chr19	-	12251032	12267546	1678
ENSG00000(	6.214751	8.430014	18.47179	0	4.60216	4.109825	1.6875	0.063467	0.11929	GALNT4	chr12	-	89913185	89918583	5399
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP3-473L9	chr12	+	1.12E+08	1.12E+08	314
ENSG00000(	4.143168	3.612863	3.958241	13.48336	15.64734	26.30288	-2.0619	0.004686	0.011677	RP11-968A	chr12	+	54656399	54672847	735
ENSG00000(	0	0	2.638828	1.498151	0	0	0.308	0.81734	NA	RP11-677C	chr12	+	29542227	29640421	963

ENSG00000(	0	0	1.319414	0.749076	18.40864	8.219649	-3.1676	0.006927	0.016696	RP11-359N	chr12	-	79893899	79894467	243
ENSG00000(	15.53688	24.08575	23.74945	6.74168	6.443024	4.109825	1.7579	0.00591	0.014428	RP11-680A	chr12	-	53692449	53694098	637
ENSG00000(	1.035792	0	3.958241	0	2.761296	1.64393	0.11352	0.93056	0.95822	RP11-320P	chr12	-	70612912	70615642	629
ENSG00000(	641.1552	609.3696	573.945	492.8917	434.4439	462.7662	0.39129	0.005602	0.013748	RP11-349A	chr14	-	58732083	58764852	2475
ENSG00000(	4.143168	0	1.319414	0	0.920432	0	1.3284	0.32679	0.45453	RP11-1103	chr14	-	30907198	31042835	609
ENSG00000(	1.035792	0	0	1.498151	0.920432	0.821965	-0.68763	0.61221	NA	RP11-474B	chr12	-	1.06E+08	1.06E+08	549
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-278C	chr12	-	32845438	32845782	345
ENSG00000(	24.85901	27.69862	48.81831	21.72319	54.30549	23.83698	0.020823	0.96511	0.97979	RP11-701H	chr15	-	25272883	25277194	427
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-497G	chr12	+	1.17E+08	1.17E+08	366
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-352N	chr12	-	45912101	46004403	725
ENSG00000(	2.071584	0	0	0	3.681728	0	-0.35836	0.79134	NA	RP3-521E1	chr12	+	1.13E+08	1.13E+08	878
ENSG00000(	0	0	1.319414	0	4.60216	2.465895	-1.3607	0.31016	0.43627	RP11-579D	chr12	+	49182930	49184318	473
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-1100	chr12	-	52470625	52475868	647
ENSG00000(	1.035792	6.021439	0	0	0	2.465895	0.90775	0.49399	0.62281	CBX3P5	chr12	-	95680094	95680614	521
ENSG00000(	0	0	0	20.97412	23.93123	34.52253	-5.5767	2.28E-07	1.01E-06	RP3-416H2	chr12	-	52638832	52641232	1693
ENSG00000(	6.214751	9.634302	5.277655	17.22874	14.72691	5.753754	-0.76888	0.2964	0.42085	RP11-341G	chr12	-	1.04E+08	1.04E+08	738
ENSG00000(	0	3.612863	2.638828	0.749076	0	0	1.5384	0.25501	0.3732	RP11-175P	chr12	+	1.01E+08	1.01E+08	418
ENSG00000(	80.79177	60.21439	65.97069	32.21025	23.93123	21.37109	1.389	0.000145	0.000463	RP11-620J1	chr12	-	58325311	58329958	759
ENSG00000(	2.071584	8.430014	3.958241	22.47227	27.61296	34.52253	-2.4048	0.000227	0.000702	LBX2-AS1	chr2	+	74729722	74731805	2083
ENSG00000(	589.3656	452.8122	341.7282	262.1764	207.0972	208.7791	1.0246	6.06E-07	2.57E-06	PRR24	chr19	+	47778142	47778979	838
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-256L	chr12	+	96419101	96421749	656
ENSG00000(	5.17896	4.817151	1.319414	0.749076	4.60216	6.575719	-0.04363	0.96638	0.98027	RP11-396F	chr12	+	39300253	39303394	526
ENSG00000(	66.29068	85.50443	87.08131	78.65293	87.44104	113.4312	-0.22748	0.42295	0.55348	CNPY2	chr12	-	56703626	56710120	1209
ENSG00000(	0	4.817151	0	0	1.840864	0	0.69806	0.6069	0.72127	RP11-818F	chr12	-	1.05E+08	1.05E+08	701
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-370I1	chr12	+	48744728	48836194	562
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-139E	chr12	+	45594600	45595334	735
ENSG00000(	27.96638	33.72006	18.47179	104.8706	43.2603	73.15488	-1.4297	0.000489	0.001438	RP11-977G	chr12	+	56702652	56703233	437
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-540D	chr12	+	81156933	81164496	1260
ENSG00000(	106.6866	98.75159	124.0249	172.2874	156.4734	143.0219	-0.51694	0.024506	0.052037	RP11-350F	chr12	-	44112796	44117803	5008
ENSG00000(	1.035792	4.817151	0	0	0	0	1.8349	0.17548	NA	RP11-474L	chr12	-	88451653	88452355	703
ENSG00000(	3.107376	2.408575	1.319414	0.749076	0	0	1.7622	0.18631	0.29091	RP11-650K	chr12	+	1.04E+08	1.04E+08	413
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-486C	chr14	-	70892529	71014181	565
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-186F	chr12	-	71976073	71977632	527
ENSG00000(	0	0	0	0	0.920432	3.28786	-1.1769	0.37857	NA	RP11-370I1	chr12	-	48749575	48750397	823
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTB-193M1	chr16	+	15702331	15704420	530
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-630C	chr12	+	42157991	42159383	351
ENSG00000(	12.4295	22.88147	7.916483	7.490755	10.12475	3.28786	0.97529	0.1759	0.27779	FNBP1P1	chr2	+	74347807	74350345	1994
ENSG00000(	1.035792	3.612863	2.638828	0	1.840864	0	1.2659	0.33268	0.46072	MRS2P2	chr12	-	72243008	72244208	1201
ENSG00000(	0	0	1.319414	0	2.761296	3.28786	-1.196	0.37513	0.50574	RP11-575G	chr12	+	1.01E+08	1.01E+08	1454
ENSG00000(	0	0	2.638828	0	0	0.821965	0.55859	0.66971	NA	RP11-603J1	chr12	-	56544580	56552004	540
ENSG00000(	12.4295	21.67718	14.51355	20.97412	8.283888	20.54912	-0.04271	0.9426	0.96532	RP11-611E	chr12	-	70297813	70637140	883
ENSG00000(	0	3.612863	1.319414	9.737982	5.522592	4.93179	-1.6757	0.11069	0.19049	RP4-601P9	chr12	+	1.15E+08	1.15E+08	1330
ENSG00000(	0	0	2.638828	2.996302	1.840864	0.821965	-0.71043	0.58981	0.70665	RP11-1143	chr12	+	69678177	69679265	1089
ENSG00000(	2.071584	0	1.319414	2.996302	3.681728	0	-0.62422	0.62863	0.73909	RP11-596D	chr14	+	31717834	31771945	975

ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-368J:	chr16	+	22557019	22588186	2661
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-547C	chr12	+	43359925	43361156	256
ENSG00000(	0	0	3.958241	0.749076	6.443024	3.28786	-1.0136	0.41205	0.54268	RP11-199A	chr12	-	52106253	52107390	1138
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	MTND1P24	chr12	-	42093193	42094053	861
ENSG00000(	2.071584	0	9.235896	2.247227	0	3.28786	0.73274	0.54102	0.66393	RP11-266E	chr12	+	1.06E+08	1.06E+08	2503
ENSG00000(	0	2.408575	0	0.749076	0.920432	0.821965	-0.02765	0.98373	NA	RP11-461I1.	chr12	-	44642215	44642787	573
ENSG00000(	1.035792	3.612863	0	0	0	0	1.5346	0.25314	NA	RP11-263K	chr12	+	82862235	82862727	493
ENSG00000(	6.214751	3.612863	0	4.494453	3.681728	4.93179	-0.31791	0.75985	0.84128	RP3-462E2	chr12	+	1.12E+08	1.12E+08	569
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	RP11-256L	chr12	+	96390299	96405267	862
ENSG00000(	0	0	0	0	1.840864	3.28786	-1.4188	0.29365	NA	RP11-769N	chr12	-	62533780	62539424	477
ENSG00000(	1.035792	3.612863	0	0	0	0	1.5346	0.25314	NA	RP11-497G	chr12	+	1.17E+08	1.17E+08	876
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-61E1	chr12	+	1.05E+08	1.05E+08	289
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	RP11-114F	chr12	-	1.06E+08	1.06E+08	632
ENSG00000(	7.250543	6.021439	3.958241	1.498151	7.363456	22.19305	-0.74117	0.39369	0.5245	RP1-78O14	chr12	-	79734985	79897176	1155
ENSG00000(	5.17896	9.634302	6.597069	5.243529	4.60216	4.109825	0.54427	0.52192	0.64752	RP11-210N	chr12	+	44130431	44134870	582
ENSG00000(	0	0	7.916483	0	0	0.821965	1.6394	0.22538	0.33808	RP11-454K	chr14	+	45846471	45858489	548
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-269C	chr14	+	30409951	30449418	821
ENSG00000(	1.035792	2.408575	0	0	0.920432	0	0.86086	0.52404	NA	RP3-432I18	chr12	+	47986991	47987223	233
ENSG00000(	1.035792	2.408575	1.319414	1.498151	0.920432	0	0.59797	0.64969	0.75609	RP11-461F	chr12	+	77271973	77274132	571
ENSG00000(	5.17896	7.225726	6.597069	3.745378	2.761296	0	1.2756	0.21022	0.31997	RP11-386G	chr12	+	49392150	49412988	2114
ENSG00000(	0	0	0	5.992604	0	1.64393	-1.9442	0.15139	0.24591	RP11-482D	chr12	-	1.07E+08	1.07E+08	809
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-541G	chr12	-	97666470	97669987	576
ENSG00000(	1037.863	1064.59	1056.85	1154.325	1468.089	1118.694	-0.24267	0.075318	0.1381	CUX1	chr7	+	1.01E+08	1.02E+08	13762
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-155I9	chr12	+	30473767	30474550	562
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-248E	chr12	+	88210263	88211608	554
ENSG00000(	0	1.204288	3.958241	0.749076	0	0	1.306	0.33572	NA	RP11-290L	chr12	+	76451318	76451895	578
ENSG00000(	20.71584	12.04288	13.19414	23.22134	21.16994	39.45432	-0.82484	0.11853	0.2018	RP11-48B1	chr17	-	3566357	3599488	5905
ENSG00000(	0	0	1.319414	5.992604	2.761296	1.64393	-1.9467	0.12818	0.21482	RP11-554D	chr12	+	1.08E+08	1.08E+08	949
ENSG00000(	8.286335	22.88147	10.55531	2.247227	4.60216	1.64393	2.0747	0.011088	0.025521	RP11-620J:	chr12	+	58230875	58236528	610
ENSG00000(	2.071584	2.408575	1.319414	3.745378	0.920432	0.821965	0.049724	0.96729	0.98074	RP11-161H	chr12	+	49783299	49783945	647
ENSG00000(	0	1.204288	0	5.243529	14.72691	4.109825	-3.1082	0.007475	0.017892	RP11-359N	chr12	+	79952562	79952946	385
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	QRSL1P3	chr14	+	36235001	36236316	1316
ENSG00000(	2.071584	12.04288	5.277655	2.996302	2.761296	8.219649	0.40001	0.66509	0.76874	RP11-133N	chr12	-	49970623	49971288	570
ENSG00000(	1.035792	2.408575	0	0	1.840864	0	0.46673	0.73084	NA	RP11-115H	chr12	+	1.17E+08	1.17E+08	214
ENSG00000(	0	0	0	1.498151	0.920432	0.821965	-0.99775	0.45448	NA	RP11-579D	chr12	+	49121218	49159569	635
ENSG00000(	1.035792	0	0	3.745378	0	0	-0.7218	0.59124	NA	RP11-61E1	chr12	-	1.05E+08	1.06E+08	641
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-756H	chr12	+	57824899	57827718	548
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	RP11-350G	chr12	-	1.01E+08	1.01E+08	557
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-210N	chr15	-	80726136	80737493	1891
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	HMGA1P3	chr12	-	1.11E+08	1.11E+08	324
ENSG00000(	0	7.225726	5.277655	0	0	1.64393	1.9129	0.13245	0.2207	RP11-603K	chr12	+	93251855	93253049	1195
ENSG00000(	0	4.817151	1.319414	0	2.761296	3.28786	0.01323	0.99164	0.99499	RP11-386G	chr12	+	49521565	49541652	897
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-762H	chr12	-	48779200	48780048	849
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-543H	chr12	-	81488154	81519624	882

ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-350G	chr12	+	1.01E+08	1.01E+08	1256
ENSG0000(	2.071584	3.612863	1.319414	0.749076	0.920432	0	1.3334	0.30255	0.42768	RP11-493P	chr12	+	1.16E+08	1.16E+08	501
ENSG0000(	0	0	0	0.749076	0.920432	1.64393	-1.0185	0.44577	NA	AC005086.	chr7	+	1.02E+08	1.02E+08	243
ENSG0000(	2.071584	8.430014	7.916483	0.749076	6.443024	3.28786	0.69423	0.47748	0.60659	RP11-530C	chr12	+	80217558	80219276	667
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-530C	chr12	+	80083924	80172231	354
ENSG0000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	CTD-2021H	chr12	-	71441182	71512027	565
ENSG0000(	40.39588	45.76293	46.17948	47.19176	41.41944	55.89361	-0.12816	0.71772	0.80996	RP11-644F	chr12	+	56122888	56124467	1274
ENSG0000(	10.35792	19.2686	3.958241	4.494453	2.761296	11.50751	0.75801	0.3473	0.47692	BCDIN3D-A	chr12	+	50222325	50234926	3078
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-781A	chr12	+	78169563	78177356	376
ENSG0000(	0	0	0	5.992604	0	0.821965	-1.772	0.19153	0.29714	RP11-554D	chr12	-	1.08E+08	1.08E+08	679
ENSG0000(	48.68222	46.96722	39.58241	2.996302	0	5.753754	3.6997	1.86E-09	9.93E-09	RP11-114H	chr12	-	75956982	76377795	748
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-443B	chr1	-	2.35E+08	2.35E+08	846
ENSG0000(	10.35792	12.04288	7.916483	0	3.681728	0.821965	2.3735	0.014299	0.032113	RP11-753H	chr12	+	54747576	54860769	546
ENSG0000(	7.250543	9.634302	6.597069	0.749076	0	4.109825	1.8748	0.064612	0.12106	RP11-114H	chr12	-	76087790	76092596	742
ENSG0000(	11.39371	2.408575	2.638828	0	1.840864	2.465895	1.5421	0.16561	0.26428	RP11-474P	chr12	+	46765246	46767561	627
ENSG0000(	5.17896	1.204288	6.597069	5.243529	3.681728	8.219649	-0.35147	0.70653	0.80128	RP11-686G	chr12	+	1.12E+08	1.12E+08	485
ENSG0000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	RP11-121E	chr12	+	91755973	91762383	894
ENSG0000(	6.214751	3.612863	11.87472	9.737982	9.20432	10.68554	-0.42245	0.5763	0.69458	RP11-977B	chr12	-	49627352	49658539	674
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-809C	chr12	+	1.17E+08	1.17E+08	732
ENSG0000(	0	0	1.319414	0	0	4.93179	-0.89929	0.50711	0.63465	RP11-43D4	chr12	+	1.05E+08	1.05E+08	411
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-89M2	chr12	-	72439929	72451157	819
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-804F	chr12	-	38937979	38983614	678
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-61A1	chr16	-	66875336	66887351	434
ENSG0000(	11.39371	12.04288	17.15238	2.247227	0	2.465895	2.6899	0.002207	0.005837	RP11-347C	chr16	-	30215637	30220392	1693
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-541G	chr12	+	97379434	97579387	573
ENSG0000(	0	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-956A	chr12	-	32380344	32381088	745
ENSG0000(	16.57267	31.31148	11.87472	4.494453	11.96562	5.753754	1.3512	0.041641	0.082916	RP11-864J2	chr12	+	1.08E+08	1.08E+08	1680
ENSG0000(	3.107376	2.408575	0	0	0	0	1.7825	0.18787	NA	RP11-753H	chr12	+	54747445	54891472	564
ENSG0000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-18O1	chr12	-	1.03E+08	1.03E+08	507
ENSG0000(	0	3.612863	0	1.498151	0.920432	0	0.29588	0.82721	0.88863	RP11-511H	chr12	-	1.02E+08	1.02E+08	308
ENSG0000(	0	0	0	1.498151	0	5.753754	-1.8682	0.16834	0.26796	RP11-588H	chr12	+	70861860	70932859	1942
ENSG0000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-511B	chr12	+	93568142	93575608	1269
ENSG0000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-1105	chr12	-	94665926	94670971	493
ENSG0000(	0	1.204288	7.916483	0	0	4.109825	0.7307	0.57198	0.69073	RP11-394J2	chr12	-	96616575	96617751	525
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-753N	chr12	+	90674671	90694117	574
ENSG0000(	1.035792	0	1.319414	0	0	2.465895	-0.03351	0.98027	NA	RP11-146E	chr14	+	19812176	19859970	586
ENSG0000(	4.143168	2.408575	1.319414	0	0	0.821965	1.9103	0.14768	0.24079	RP11-977G	chr12	-	56556143	56584068	403
ENSG0000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	RP1-228P1	chr12	-	48399060	48405010	550
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-90E9	chr12	+	99188263	99188742	480
ENSG0000(	2.071584	0	0	0	3.681728	0.821965	-0.55725	0.6805	0.78116	RP11-478C	chr12	-	1.11E+08	1.11E+08	946
ENSG0000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-624G	chr12	-	44402423	44403946	1524
ENSG0000(	0	8.430014	3.958241	0	0	0	2.9411	0.026937	0.056601	RP11-136F	chr12	-	78445961	78485517	475
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CLEC5A	chr7	-	1.42E+08	1.42E+08	3511
ENSG0000(	5.17896	1.204288	2.638828	4.494453	2.761296	3.28786	-0.17366	0.86891	0.91759	RP11-511H	chr12	-	1.02E+08	1.02E+08	568

ENSG00000(	4.143168	2.408575	0	0	0	0	2.023	0.13594	0.22523	RP11-362K	chr12	+	58937907	59206842	1447
ENSG00000(	0	0	0	6.74168	1.840864	7.397684	-3.1811	0.012083	0.027572	RP1-46F2.3	chr12	-	1.11E+08	1.11E+08	590
ENSG00000(	13.46529	18.06432	11.87472	3.745378	0.920432	3.28786	2.1911	0.00599	0.01461	RP11-114H	chr12	-	76082574	76082876	303
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-167N	chr12	-	95770984	95774672	201
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-219B	chr8	-	86134675	86157946	790
ENSG00000(	0	1.204288	7.916483	0	0	2.465895	1.1642	0.37348	0.50395	RP11-977G	chr12	-	56661577	56663888	542
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-510I5	chr12	-	96816104	96879220	379
ENSG00000(	0	2.408575	3.958241	0	0	0.821965	1.5251	0.25862	0.37731	RP11-370I1	chr12	-	48727538	48727684	147
ENSG00000(	2.071584	0	1.319414	1.498151	0.920432	2.465895	-0.33465	0.79574	0.86664	RP11-887P	chr12	-	94101567	94131599	1587
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-297L	chr12	+	38475848	38477884	577
ENSG00000(	6.214751	0	5.277655	2.996302	0.920432	3.28786	0.52365	0.6401	0.74805	POLR2KP1	chr12	+	49987874	49988041	168
ENSG00000(	1.035792	0	2.638828	2.247227	3.681728	0.821965	-0.61064	0.62732	0.73837	RP11-103B	chr12	+	1.18E+08	1.18E+08	1053
ENSG00000(	793.4166	926.0973	881.3684	580.5336	639.7002	491.535	0.60176	3.58E-05	0.000124	CHURC1	chr14	+	65381079	65411309	3381
ENSG00000(	147.0825	172.2131	175.482	131.8373	75.47542	144.6658	0.48167	0.06408	0.12021	RP11-658F	chr11	+	66433507	66435845	2339
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-317N	chr14	+	36289043	36289426	384
ENSG00000(	21.75163	16.86003	11.87472	28.46487	19.32907	16.4393	-0.3272	0.54594	0.66805	RP11-488C	chr14	-	77248083	77253067	1677
ENSG00000(	4.143168	2.408575	5.277655	1.498151	1.840864	4.109825	0.54163	0.60752	0.72173	RP11-981P	chr12	+	89954906	89987798	854
ENSG00000(	4.143168	3.612863	2.638828	0	0	1.64393	1.798	0.15204	0.24685	RP11-887P	chr12	+	94229943	94231814	779
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-554E	chr12	-	1.02E+08	1.02E+08	1034
ENSG00000(	7.250543	3.612863	14.51355	5.243529	2.761296	8.219649	0.56176	0.50461	0.63233	RP11-644F	chr12	+	56109820	56118487	3382
ENSG00000(	0	0	0	0	0	4.93179	-1.2404	0.35057	NA	RP11-690J1	chr12	-	98506792	98686223	521
ENSG00000(	1.035792	6.021439	1.319414	3.745378	3.681728	1.64393	-0.09511	0.93142	0.9588	C17orf49	chr17	+	6917814	6920844	2343
ENSG00000(	2.071584	3.612863	1.319414	0	0	0	2.2408	0.097211	0.17127	RP11-769N	chr12	-	62628171	62629296	1126
ENSG00000(	9.322127	10.83859	1.319414	6.74168	8.283888	8.219649	-0.08727	0.91527	0.94835	RP11-603J1	chr12	-	56513817	56523403	882
ENSG00000(	4.143168	7.225726	0	4.494453	6.443024	0	0.055448	0.96081	0.97728	RP1-267L1	chr12	+	1.13E+08	1.13E+08	596
ENSG00000(	1.035792	4.817151	0	0.749076	0.920432	1.64393	0.54461	0.67161	0.77391	RP4-816N1	chr12	-	2906043	2922068	439
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-118A	chr12	+	43549118	43556913	836
ENSG00000(	0	0	3.958241	1.498151	0.920432	0	0.35495	0.79324	0.86489	RP11-161H	chr12	-	49686414	49718359	4166
ENSG00000(	3.107376	4.817151	5.277655	4.494453	0	2.465895	0.71505	0.50954	0.63685	RP11-115H	chr12	-	1.17E+08	1.17E+08	493
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-116N	chr14	+	36367188	36532949	477
ENSG00000(	1.035792	0	0	0	2.761296	0	-0.44657	0.73574	NA	RP11-536G	chr12	-	96189123	96252617	467
ENSG00000(	2.071584	0	10.55531	12.73428	7.363456	10.68554	-1.1529	0.20157	0.30921	RP11-968A	chr12	+	54670415	54738867	567
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-148B	chr12	+	1.17E+08	1.17E+08	600
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-23J18	chr12	-	47529281	47532153	404
ENSG00000(	1.035792	1.204288	0	1.498151	0	0	0.24225	0.85676	NA	MIR3180-1	chr16	-	15003744	15005202	1459
ENSG00000(	4.143168	4.817151	0	0.749076	2.761296	1.64393	0.6141	0.60514	0.71987	RP11-651L	chr12	-	1.07E+08	1.07E+08	312
ENSG00000(	0	2.408575	0	1.498151	0	0	0.25968	0.84497	NA	RP11-778J1	chr12	-	94914866	94915645	780
ENSG00000(	2.071584	2.408575	1.319414	2.247227	4.60216	2.465895	-0.52033	0.64402	0.75121	PCNPP1	chr12	-	1.12E+08	1.12E+08	511
ENSG00000(	8.286335	3.612863	9.235896	4.494453	3.681728	5.753754	0.53025	0.53854	0.66234	RP11-1105	chr12	-	94671534	94676620	796
ENSG00000(	11.39371	20.47289	11.87472	2.247227	7.363456	4.109825	1.5493	0.038322	0.077124	RTEL1	chr20	+	62289163	62328416	5030
ENSG00000(	2.071584	0	0	0	0	1.64393	0.14412	0.91322	NA	SLC25A3P2	chr12	+	1.12E+08	1.12E+08	880
ENSG00000(	12.4295	25.29004	10.55531	2.996302	0.920432	1.64393	2.7607	0.000855	0.002425	RP4-647C1	chr14	-	73710726	73712687	1683
ENSG00000(	0	1.204288	0	3.745378	3.681728	3.28786	-2.0315	0.11016	0.1898	RP11-517C	chr14	+	58865275	58893843	436
ENSG00000(	1.035792	0	0	2.996302	0	0	-0.53136	0.68956	NA	RP11-33N1	chr14	+	89866339	89875813	341

ENSG00000(	0	0	0	1.498151	3.681728	4.109825	-2.3711	0.073996	0.13605	CTD-2313J:	chr15	-	93331144	93331702	449
ENSG00000(	6.214751	8.430014	3.958241	2.996302	0	1.64393	1.6056	0.12665	0.21281	AC068831.	chr15	-	91495469	91498455	1858
ENSG00000(	4.143168	3.612863	1.319414	2.996302	9.20432	6.575719	-0.87027	0.36629	0.49631	EGFL8	chr6	+	32121622	32139755	4181
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-1070	chr14	+	96039899	96048293	1334
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-58E2	chr14	-	50505863	50555913	534
ENSG00000(	0	0	6.597069	0	0.920432	0	1.3953	0.30352	0.42861	RP11-65I1:	chr2	+	1.14E+08	1.14E+08	582
ENSG00000(	2.071584	0	2.638828	0	0	3.28786	0.29715	0.82454	0.88675	RP11-831F	chr14	-	50174385	50175510	568
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-326E	chr14	+	49840684	49841101	418
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP11-516J:	chr14	-	76747286	76776409	520
ENSG00000(	1.035792	0	0	1.498151	3.681728	4.93179	-1.9804	0.12439	0.20983	ZNF578	chr19	+	52956829	53015407	5255
ENSG00000(	3.107376	8.430014	0	0	1.840864	0	1.7597	0.16919	0.2691	RP11-404P	chr14	+	96677197	96681155	460
ENSG00000(	1.035792	0	1.319414	2.247227	0	0.821965	-0.21621	0.87308	NA	RP11-665C	chr14	-	55729485	55738793	554
ENSG00000(	0	0	1.319414	0	0.920432	0.821965	-0.17431	0.89516	NA	RP11-356C	chr14	+	38033252	38048330	738
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-32B5	chr15	-	21987458	21987995	538
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-526N	chr14	-	80359423	80440512	446
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-662J:	chr14	+	40855456	40855998	453
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-486C	chr14	+	70653840	70696904	576
ENSG00000(	11.39371	3.612863	2.638828	5.992604	7.363456	10.68554	-0.37441	0.65551	0.7606	RP11-471B	chr14	-	90868867	90871579	300
ENSG00000(	2.071584	0	0	3.745378	0.920432	3.28786	-1.2085	0.34899	0.47864	CTD-2568P	chr14	+	60864475	60864999	525
ENSG00000(	2.071584	1.204288	1.319414	4.494453	0	1.64393	-0.29608	0.8133	0.87876	RP11-1085	chr14	-	57099962	57115376	421
ENSG00000(	79.75598	79.48299	42.22124	135.5827	124.2583	184.9421	-1.1222	0.000126	0.000405	PDF	chr16	-	69362524	69364498	1158
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-255N	chr15	-	95577613	95578966	715
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-711D	chr12	+	1.22E+08	1.22E+08	552
ENSG00000(	1.035792	2.408575	1.319414	0	0	4.93179	-0.03575	0.97816	0.98728	RP11-173A	chr14	+	75124752	75125293	542
ENSG00000(	462.999	441.9736	522.4879	464.4268	591.8378	420.846	-0.04873	0.7703	0.84906	LINC00641	chr14	-	21668238	21675059	5425
ENSG00000(	2.071584	0	0	0.749076	1.840864	4.109825	-1.0044	0.44384	0.57349	RP3-414A1	chr14	-	73983937	73987352	937
ENSG00000(	1.035792	0	1.319414	0	0.920432	2.465895	-0.28162	0.83495	NA	RP11-307P	chr14	+	61246696	61247313	618
ENSG00000(	0	0	2.638828	1.498151	0	0	0.308	0.81734	NA	RP11-895N	chr14	+	91885793	91886095	303
ENSG00000(	0	0	0	0	2.761296	1.64393	-1.2339	0.35779	NA	RP11-109N	chr14	-	73534816	73535326	511
ENSG00000(	6.214751	4.817151	10.55531	0.749076	6.443024	2.465895	1.0116	0.2842	0.40715	RP11-649E	chr14	-	50096009	50096608	401
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-903H	chr14	-	21161639	21175279	915
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-757H	chr14	+	81288868	81289140	273
ENSG00000(	0	7.225726	1.319414	0.749076	0	3.28786	0.72094	0.56962	0.68872	RP11-361H	chr14	+	76702160	76729817	520
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	RP11-665C	chr14	-	55792552	55806219	363
ENSG00000(	14.50109	6.021439	11.87472	5.992604	7.363456	9.041614	0.49705	0.49515	0.62387	RP11-298I:	chr14	+	23451907	23468287	1021
ENSG00000(	0	7.225726	0	3.745378	3.681728	6.575719	-0.74448	0.51088	0.63812	CTD-2555K	chr14	-	23171820	23235771	662
ENSG00000(	0	1.204288	0	0	0	4.93179	-0.92783	0.49356	0.6225	RP11-164J:	chr15	+	42640301	42704515	3881
ENSG00000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	DCAF8	chr1	-	1.6E+08	1.6E+08	2635
ENSG00000(	4.143168	0	0	1.498151	0.920432	1.64393	0.043155	0.97386	0.9848	RP11-1012	chr14	-	68126537	68157084	670
ENSG00000(	3.107376	3.612863	5.277655	5.243529	4.60216	2.465895	-0.04025	0.967	0.98061	CHMP4BP1	chr14	+	55765362	55765949	588
ENSG00000(	2.071584	0	0	1.498151	0	0.821965	-0.06236	0.96323	NA	RP11-84C1	chr14	-	21463996	21467322	1398
ENSG00000(	30.03797	24.08575	26.38828	170.7892	155.553	129.8705	-2.4664	4.96E-16	4.16E-15	RP11-192H	chr17	-	26782770	26941215	3604
ENSG00000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	LINC00640	chr14	+	51800111	51832275	708
ENSG00000(	0	0	0	5.992604	0.920432	3.28786	-2.4893	0.059925	0.11359	AC144835.	chr15	+	98563824	98565007	686

ENSG00000(	3.107376	2.408575	5.277655	0	0	1.64393	1.8354	0.14247	0.23399	SPESP1	chr15	+	69110560	69239150	1431
ENSG00000(	1.035792	7.225726	1.319414	2.996302	0.920432	4.93179	0.079999	0.9425	0.9653	RP11-193F	chr14	-	61385958	61386873	916
ENSG00000(	38348.12	33167.29	164162.8	3289.94	19998.23	24685.25	2.0306	0.019232	0.041891	RN7SL1	chr14	+	50053297	50053596	300
ENSG00000(	1.035792	2.408575	1.319414	0	0	1.64393	0.85879	0.52286	0.64815	RP11-467L	chr15	+	20721492	20725870	735
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	RP11-862P	chr14	-	67435755	67436533	514
ENSG00000(	12.4295	14.45145	9.235896	19.47596	7.363456	27.94681	-0.56835	0.36896	0.49932	DIO3OS	chr14	-	1.02E+08	1.02E+08	3108
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	CTD-2062F	chr14	+	1.01E+08	1.01E+08	323
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RP11-783L	chr14	+	66578299	66592565	608
ENSG00000(	0	1.204288	0	0	1.840864	0.821965	-0.461	0.73167	NA	RP11-493G	chr14	+	77825766	77826259	494
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	RP11-796G	chr14	+	1.02E+08	1.02E+08	639
ENSG00000(	0	0	0	0.749076	0	3.28786	-1.135	0.39451	NA	RP5-892G5	chr14	+	74659292	74659526	235
ENSG00000(	3.107376	7.225726	21.11062	2.996302	7.363456	4.93179	0.92108	0.27253	0.39334	RP11-203N	chr14	+	20919464	20920077	478
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	RP11-363J	chr14	-	69705883	69727284	578
ENSG00000(	10.35792	2.408575	5.277655	9.737982	5.522592	4.93179	-0.13541	0.87457	0.92127	RP11-638I	chr14	+	1.01E+08	1.01E+08	552
ENSG00000(	10.35792	6.021439	3.958241	0	0	0	3.9248	0.00149	0.004052	NT5CP1	chr14	-	74037863	74038371	509
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-829H	chr14	-	31345385	31359014	1991
ENSG00000(	4.143168	1.204288	0	1.498151	3.681728	4.109825	-0.55963	0.63442	0.74381	RP11-111A	chr14	+	39944044	39982984	857
ENSG00000(	2.071584	3.612863	2.638828	2.996302	11.96562	4.109825	-1.005	0.30508	0.43042	ASB9P1	chr15	+	93338877	93339669	793
ENSG00000(	8.286335	1.204288	7.916483	0.749076	5.522592	1.64393	0.95889	0.35237	0.48209	BANF1P1	chr14	+	69403319	69403581	263
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTD-2134A	chr14	-	1.04E+08	1.04E+08	582
ENSG00000(	0	0	2.638828	0	0	1.64393	0.26729	0.84149	NA	RP11-280K	chr14	+	52231994	52292140	5982
ENSG00000(	0	0	0	2.996302	8.283888	8.219649	-3.4924	0.004758	0.011836	RP11-1053	chr14	+	42211842	42212166	325
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	FRMD6-AS2	chr14	-	51921230	52066670	581
ENSG00000(	1.035792	0	0	1.498151	0	0	-0.08447	0.94679	NA	RP11-12J1(	chr10	-	1.26E+08	1.26E+08	3422
ENSG00000(	2.071584	0	0	0.749076	1.840864	1.64393	-0.54615	0.68433	0.78413	RP4-755D9	chrX	+	1.19E+08	1.19E+08	2102
ENSG00000(	0	0	0	1.498151	1.840864	0	-0.93652	0.47589	NA	RP11-16B1	chr14	-	60435834	60558501	502
ENSG00000(	1.035792	0	1.319414	0	0.920432	0	0.55201	0.67753	NA	SPECC1L	chr22	+	24666866	24838324	6204
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP11-159L	chr14	-	31204132	31291908	430
ENSG00000(	12.4295	12.04288	10.55531	8.239831	8.283888	11.50751	0.30234	0.65262	0.75842	AC005519.	chr14	-	74755830	74761128	1367
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	CTD-2376I	chr14	-	1.01E+08	1.01E+08	548
ENSG00000(	2.071584	0	0	1.498151	0.920432	3.28786	-0.84301	0.52432	0.6494	RP11-72M	chr14	-	66679528	66976112	1206
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	CTD-2313J	chr15	+	93305987	93306980	526
ENSG00000(	9.322127	18.06432	11.87472	8.988907	18.40864	4.109825	0.30028	0.66756	0.77083	RP11-723P	chr14	-	69334574	69336668	1130
ENSG00000(	8.286335	0	5.277655	1.498151	1.840864	3.28786	0.82647	0.45333	0.58309	RHOQP1	chr14	+	50066712	50067290	579
ENSG00000(	0	0	1.319414	0	0	2.465895	-0.38078	0.77353	NA	RP11-99E1	chr14	-	77177001	77227731	540
ENSG00000(	0	2.408575	1.319414	0	0.920432	0	0.92035	0.49653	NA	PTTG4P	chr14	-	71552199	71552550	352
ENSG00000(	4.143168	7.225726	6.597069	0	1.840864	0	2.502	0.030413	0.062919	RP11-1070	chr14	+	95982473	95984248	993
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-98L1	chr14	+	76480022	76480486	465
ENSG00000(	0	3.612863	0	0	1.840864	0.821965	0.23964	0.85959	0.91076	RP11-638I	chr14	+	1.01E+08	1.01E+08	293
ENSG00000(	5.17896	9.634302	7.916483	7.490755	8.283888	10.68554	-0.20705	0.78302	0.85708	NBEAP1	chr15	-	20862967	20893737	3036
ENSG00000(	0	4.817151	0	0	1.840864	0.821965	0.48581	0.71839	0.81024	RP11-545N	chr14	+	39577546	39577911	366
ENSG00000(	0	0	0	13.48336	4.60216	6.575719	-3.855	0.001399	0.00383	RP11-108N	chr14	-	57532978	57579378	1111
ENSG00000(	0	0	0	2.247227	11.04518	7.397684	-3.5562	0.00401	0.010133	CTD-3051D	chr14	-	1.05E+08	1.05E+08	1045
ENSG00000(	0	0	0	0.749076	7.363456	0.821965	-2.23	0.09643	0.17025	RP11-84C1	chr14	-	21451314	21453225	578

ENSG00000(	2.071584	2.408575	0	36.7047	30.37426	37.81039	-4.0769	8.84E-08	4.08E-07	RP11-7F17	chr14	+	77425981	77432145	581
ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	RP3-414A1	chr14	-	74083412	74100644	621
ENSG00000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	RP11-299L	chr14	+	81879314	81879583	270
ENSG00000(	0	0	0	4.494453	0	0	-1.1446	0.38559	NA	DNAJC19P9	chr14	+	45759239	45759589	351
ENSG00000(	4.143168	3.612863	5.277655	0	0.920432	1.64393	1.7646	0.13076	0.21828	RP11-368J:	chr15	-	93608815	93609835	1021
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CTD-2509G	chr14	-	65733356	65734408	483
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-725G	chr14	+	95665376	95665682	181
ENSG00000(	1.035792	3.612863	0	0	0.920432	0	1.1485	0.39729	NA	RP11-362L	chr14	+	1.01E+08	1.01E+08	441
ENSG00000(	1.035792	2.408575	1.319414	0	0	2.465895	0.55563	0.6771	0.77848	CTD-2325P	chr14	-	69150128	69152282	461
ENSG00000(	1.035792	1.204288	0	5.243529	8.283888	0	-1.7685	0.15229	0.24723	COX7A2P1	chr14	-	68119017	68119331	315
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-76E1	chr15	-	94368287	94368388	102
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-857B	chr14	-	45346077	45366280	693
ENSG00000(	124.295	150.536	139.8579	111.6123	146.3487	115.0751	0.15242	0.51494	0.64162	RP4-773N1	chr1	+	1.11E+08	1.11E+08	4216
ENSG00000(	16.57267	18.06432	23.74945	32.95932	43.2603	54.24968	-1.1336	0.010719	0.024743	CTD-2298J:	chr14	-	42057064	42074059	530
ENSG00000(	0	0	1.319414	0	0.920432	3.28786	-0.84165	0.53503	NA	RP11-242P	chr14	-	80128009	80257606	394
ENSG00000(	0	1.204288	0	4.494453	0	0.821965	-1.0889	0.4216	0.55217	RPL21P5	chr14	-	31580775	31581445	472
ENSG00000(	7.250543	15.65574	9.235896	4.494453	2.761296	6.575719	1.0923	0.1691	0.26902	BCL2L2-PA	chr14	+	23776044	23794578	1366
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	CTD-2302E	chr14	+	64068227	64068532	306
ENSG00000(	3.107376	3.612863	2.638828	8.988907	0	0.821965	-0.06763	0.95283	0.97191	RP11-950C	chr14	-	75471422	75475184	489
ENSG00000(	7.250543	4.817151	17.15238	0	1.840864	2.465895	2.3313	0.017994	0.039454	UBE2CP1	chr14	-	31152251	31152804	554
ENSG00000(	0	1.204288	0	0	2.761296	0	-0.43954	0.74062	NA	RP11-517C	chr14	+	58930689	58930854	166
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP5-1021I:	chr14	+	74318674	74398981	3695
ENSG00000(	81.82756	113.203	68.60952	13.48336	16.56778	4.93179	2.8472	2.24E-11	1.39E-10	RP11-509A	chr15	+	20549989	20564419	906
ENSG00000(	6.214751	6.021439	18.47179	35.95563	23.93123	25.48091	-1.4277	0.014485	0.032467	ARHGAP5-A	chr14	-	32544625	32545999	1375
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-104E	chr14	+	25064929	25126980	636
ENSG00000(	5.17896	0	5.277655	3.745378	0	0	0.9838	0.43704	0.5667	RP11-517C	chr14	-	58836741	58862359	399
ENSG00000(	0	2.408575	1.319414	2.996302	1.840864	1.64393	-0.5691	0.65018	0.75641	TRIM34	chr11	+	5640994	5665628	2493
ENSG00000(	56.96855	49.3758	39.58241	38.20285	36.81728	45.20807	0.2787	0.44284	0.57245	RP4-693M:	chr14	-	74164806	74167054	693
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-964E	chr14	-	37116288	37128006	2613
ENSG00000(	41.43168	24.08575	54.09597	5.243529	5.522592	4.109825	2.8657	5.19E-07	2.22E-06	HIF1A-AS2	chr14	-	62182276	62217815	533
ENSG00000(	0	3.612863	3.958241	0	0	0	2.2049	0.10381	0.18087	RP11-1042	chr14	+	60981837	61021634	868
ENSG00000(	3.107376	0	1.319414	0	3.681728	0	0.17804	0.89441	0.93468	RP11-543C	chr14	-	1E+08	1E+08	493
ENSG00000(	0	0	0	0.749076	4.60216	3.28786	-2.2366	0.094412	0.1672	RP11-299L	chr14	-	81908331	81916501	637
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-386N	chr15	+	93124059	93143775	1980
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-74M:	chr12	+	57216769	57268052	3942
ENSG00000(	26.93059	46.96722	38.263	32.21025	23.0108	27.94681	0.41242	0.33339	0.46146	CTD-2002H	chr14	+	58731380	58736399	576
ENSG00000(	8.286335	0	1.319414	1.498151	0	0.821965	1.355	0.28841	0.41205	RP11-854K	chr15	+	21365634	21372686	1147
ENSG00000(	14.50109	9.634302	26.38828	1.498151	0.920432	4.93179	2.4895	0.0021	0.005573	RP4-773N1	chr1	+	1.11E+08	1.11E+08	4870
ENSG00000(	1.035792	0	0	1.498151	0.920432	0	-0.39626	0.76684	NA	RP6-65G23	chr14	+	71165415	71178870	602
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-81F1	chr14	+	37257849	37276368	526
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	SALL4P7	chr14	-	60960484	60963603	3120
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-436N	chr14	-	1E+08	1E+08	386
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-1033	chr14	-	52577840	52596343	349
ENSG00000(	0	0	0	4.494453	1.840864	2.465895	-2.3009	0.084026	0.15172	LINC00871	chr14	+	46410146	46971026	866

ENSG00000(	17.60846	19.2686	11.87472	17.22874	11.04518	15.61733	0.14438	0.80326	0.87237	LINC00638	chr14	+	1.05E+08	1.05E+08	2518
ENSG00000(	0	1.204288	2.638828	0	0.920432	0	0.94343	0.48603	NA	RP11-433J(	chr14	+	97059070	97062099	3030
ENSG00000(	37.28851	10.83859	31.66593	20.22504	11.96562	12.32947	0.80171	0.15495	0.25057	RP11-85K1	chr14	-	35390064	35451738	603
ENSG00000(	1.035792	0	5.277655	6.74168	5.522592	9.863579	-1.5348	0.13058	0.21806	RP11-537P	chr14	+	37641093	37643016	1924
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CT60	chr15	+	21145767	21198632	3401
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-218E	chr14	-	51422977	51428720	4714
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	C20orf141	chr20	+	2795633	2796479	730
ENSG00000(	21.75163	14.45145	17.15238	0	0	0	5.4173	1.12E-06	4.61E-06	RP11-566J(	chr14	-	1.01E+08	1.01E+08	722
ENSG00000(	6.214751	2.408575	5.277655	6.74168	11.96562	4.93179	-0.66817	0.43708	0.56673	AC068831.	chr15	+	91509575	91531854	1525
ENSG00000(	3.107376	3.612863	1.319414	3.745378	1.840864	6.575719	-0.48227	0.64651	0.75329	RP11-66N2	chr14	+	24030306	24037282	3243
ENSG00000(	2.071584	3.612863	0	0	3.681728	1.64393	0.084589	0.94703	0.96796	ITPK1-AS1	chr14	+	93533797	93538497	4701
ENSG00000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	RP11-547D	chr14	+	53620072	53624246	1076
ENSG00000(	56.96855	57.80581	63.33186	10.48706	21.16994	6.575719	2.1701	1.79E-06	7.24E-06	RP11-603B	chr15	+	22566922	22570823	378
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTD-2341N	chr14	+	86401054	86596117	736
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-982N	chr14	-	1.05E+08	1.05E+08	503
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	SUB1P2	chr14	+	74772128	74772766	266
ENSG00000(	13.46529	27.69862	14.51355	14.98151	9.20432	16.4393	0.42542	0.47017	0.59927	RP11-73E1	chr14	+	35343549	35345665	2117
ENSG00000(	5.17896	4.817151	0	0	1.840864	4.109825	0.56541	0.63793	0.74625	ENO1P2	chr15	+	92964090	92965965	974
ENSG00000(	2.071584	0	0	0.749076	0	0	0.47431	0.71145	NA	RP11-386N	chr15	-	93277053	93277425	373
ENSG00000(	0	0	1.319414	8.239831	3.681728	7.397684	-2.8116	0.017543	0.038603	RP11-406A	chr14	+	83108964	83173169	789
ENSG00000(	1.035792	0	0	2.247227	0.920432	0.821965	-0.89377	0.50979	NA	RP11-80A1	chr14	+	24970800	24977894	698
ENSG00000(	0	3.612863	1.319414	0	0	2.465895	0.5493	0.68345	0.78343	RP11-218E	chr14	+	51378944	51380076	535
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	CTD-2223C	chr14	-	1.05E+08	1.05E+08	462
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-2G1.:	chr14	-	48865711	48960970	487
ENSG00000(	0	1.204288	1.319414	0	0	1.64393	0.26393	0.84486	NA	RP11-356K	chr14	+	89816629	89831043	601
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-794A	chr14	+	54937427	54937936	385
ENSG00000(	5.17896	9.634302	1.319414	0	0	0	3.5058	0.006057	0.014762	CTD-3049N	chr15	-	94261771	94614049	3480
ENSG00000(	0	0	0	0	0	7.397684	-1.7322	0.20085	0.30837	CTD-2509G	chr14	-	65703198	65785508	574
ENSG00000(	33.14534	28.90291	54.09597	17.22874	37.73771	23.01502	0.56027	0.22091	0.33273	CTD-2292N	chr14	-	20728639	20732467	3829
ENSG00000(	0	6.021439	1.319414	0.749076	0.920432	0	1.2978	0.32461	0.45208	RAP1AP	chr14	+	74949688	74950138	451
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTD-2007A	chr14	-	88100723	88121638	555
ENSG00000(	5.17896	7.225726	15.83297	0	0.920432	3.28786	2.2878	0.022181	0.047587	RP11-255N	chr15	-	95623324	95676088	573
ENSG00000(	19.68005	8.430014	30.34652	15.73059	15.64734	21.37109	0.13563	0.81269	0.87847	HIF1A-AS1	chr14	-	62147759	62162541	652
ENSG00000(	19.68005	10.83859	6.597069	3.745378	1.840864	0.821965	2.2266	0.010729	0.024761	RP11-492D	chr15	+	20359029	20366079	1141
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-813I2	chr14	+	56214926	56239921	459
ENSG00000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	RP11-404P	chr14	+	96689445	96689684	240
ENSG00000(	7.250543	7.225726	1.319414	5.992604	11.96562	7.397684	-0.58658	0.48733	0.61652	RP11-507K	chr14	+	89017941	89018837	718
ENSG00000(	3.107376	1.204288	0	5.243529	7.363456	4.93179	-1.5727	0.1438	0.2357	KIAA0391	chr14	+	35591755	35786680	3857
ENSG00000(	3.107376	2.408575	1.319414	0	2.761296	1.64393	0.47075	0.70348	0.79871	LINC00520	chr14	-	56247864	56263406	883
ENSG00000(	0	0	0	0.749076	2.761296	0	-0.97685	0.45852	NA	RP11-895N	chr14	+	91884610	91887520	303
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-589N	chr14	-	53265622	53265779	158
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	OR11H7	chr14	+	20697561	20698500	940
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP11-1152	chr14	-	88176763	88338635	826
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	RP11-255G	chr14	-	51858846	51863853	572

ENSG0000(	1.035792	0	2.638828	5.243529	1.840864	1.64393	-0.91159	0.45603	0.58577	CTD-2555C	chr14	-	64825486	64846036	572
ENSG0000(	0	0	0	0	2.761296	3.28786	-1.6293	0.2296	0.34285	RP11-219E	chr14	+	21252047	21252452	294
ENSG0000(	6.214751	0	1.319414	0.749076	9.20432	4.109825	-0.66678	0.5523	0.67323	CTD-3051D	chr14	+	1.05E+08	1.05E+08	3254
ENSG0000(	0	1.204288	3.958241	0	0	0	1.651	0.221	NA	RP11-109N	chr14	-	73525139	73526123	494
ENSG0000(	0	1.204288	0	8.239831	3.681728	10.68554	-3.0461	0.008933	0.021002	RP11-408B	chr12	+	85711838	85736690	519
ENSG0000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-293N	chr14	+	75726114	75738653	704
ENSG0000(	3.107376	1.204288	2.638828	2.996302	5.522592	0	-0.20999	0.85792	0.90972	AC005041.	chr2	-	74725815	74726494	412
ENSG0000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	CTD-2555K	chr14	-	23192685	23195781	767
ENSG0000(	1.035792	1.204288	3.958241	5.992604	2.761296	3.28786	-0.78975	0.46917	0.59843	CTD-2555C	chr14	-	64889653	64915275	550
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-537P	chr14	-	37566267	37567768	828
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-349A	chr14	+	58567703	58568292	590
ENSG0000(	3.107376	7.225726	1.319414	0	0	0	3.0022	0.022253	0.047711	CTD-2566J	chr14	-	68591721	68596913	537
ENSG0000(	29.00217	54.19295	25.06886	11.23613	13.80648	34.52253	0.82891	0.1137	0.19491	MC1R	chr16	+	89978527	89987385	3637
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-355I	chr14	-	62536236	62547872	322
ENSG0000(	0	0	0	5.992604	0	0	-1.4779	0.2718	0.39245	RP11-286C	chr14	+	51288598	51290219	392
ENSG0000(	0	0	1.319414	2.247227	2.761296	0.821965	-1.2421	0.3531	0.4828	RP11-894P	chr14	+	1.04E+08	1.04E+08	553
ENSG0000(	0	0	0	2.996302	2.761296	0	-1.5727	0.24592	NA	RP11-247L	chr14	+	50863731	50865063	501
ENSG0000(	6.214751	2.408575	2.638828	0	2.761296	1.64393	1.0537	0.36461	0.4944	RP11-982N	chr14	-	1.05E+08	1.05E+08	716
ENSG0000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP11-594C	chr14	-	87819414	88039366	544
ENSG0000(	2.071584	3.612863	1.319414	0	0	0	2.2408	0.097211	0.17127	RP11-561B	chr14	-	35831438	35832834	624
ENSG0000(	10.35792	12.04288	3.958241	6.74168	6.443024	9.041614	0.23255	0.76196	0.84274	EIF4EBP1P2	chr14	+	21887779	21888119	341
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP3-514A2	chr14	-	73019288	73061833	654
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-304L	chr14	-	55351567	55352931	1013
ENSG0000(	6.214751	16.86003	9.235896	0	0	0	4.6338	8.08E-05	0.000267	RP11-270N	chr14	+	76437267	76437930	580
ENSG0000(	5.17896	0	2.638828	0	0	0	2.2696	0.093866	0.16642	RP11-713N	chr12	+	25164349	25173827	559
ENSG0000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	CTD-2277K	chr14	+	62278692	62437037	664
ENSG0000(	0	0	2.638828	0	0.920432	0	0.55591	0.6721	NA	RP11-32B5	chr15	-	21893090	21903057	382
ENSG0000(	0	0	1.319414	4.494453	0	1.64393	-1.2226	0.36443	0.49424	CTD-3035D	chr14	-	91288709	91294472	384
ENSG0000(	401.8873	435.9522	424.8512	534.0909	481.3859	484.9593	-0.24935	0.087175	0.15666	CEP95	chr17	+	62502706	62538579	3641
ENSG0000(	11.39371	14.45145	9.235896	1.498151	5.522592	4.93179	1.4195	0.075649	0.13866	RP5-1021I	chr14	-	74362867	74404817	3548
ENSG0000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	CTD-2643K	chr15	+	94576887	94577406	520
ENSG0000(	2.071584	0	0	0	1.840864	0	0.093542	0.94384	NA	RP11-248B	chr14	+	60625694	60626042	349
ENSG0000(	6.214751	7.225726	10.55531	23.97042	39.57858	44.38611	-2.0842	0.000181	0.00057	HNRPCP	chr14	+	58987941	58988706	766
ENSG0000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	CTD-2128A	chr14	-	85828801	85983278	558
ENSG0000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-355I	chr14	-	62570096	62583893	737
ENSG0000(	21.75163	1.204288	11.87472	8.239831	3.681728	2.465895	1.127	0.19446	0.30067	RP11-638I	chr14	+	1.01E+08	1.01E+08	533
ENSG0000(	3.107376	0	1.319414	6.74168	10.12475	11.50751	-2.2081	0.024876	0.052732	RP11-19E1	chr2	-	1.2E+08	1.2E+08	695
ENSG0000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-260N	chr14	+	1.05E+08	1.05E+08	854
ENSG0000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	CTD-2134A	chr14	+	1.04E+08	1.04E+08	127
ENSG0000(	3.107376	0	1.319414	0	0	0	1.4805	0.26902	NA	RP11-114N	chr14	+	81448332	81449982	1651
ENSG0000(	12.4295	0	1.319414	2.996302	1.840864	0	1.1146	0.35279	0.48249	ZMYND19P	chr14	+	78162934	78163720	787
ENSG0000(	22.78742	12.04288	9.235896	45.69361	30.37426	42.74218	-1.3649	0.005755	0.014088	FOXN3-AS1	chr14	+	89883698	89886137	1077
ENSG0000(	5.17896	3.612863	2.638828	2.247227	4.60216	4.93179	-0.02168	0.98253	0.99003	CTD-2313J	chr15	-	93349000	93351797	464
ENSG0000(	1.035792	0	5.277655	0	0	0	1.9229	0.15616	0.25219	RP11-463J	chr14	-	52382863	52385289	529

ENSG00000(	1.035792	1.204288	5.277655	2.247227	2.761296	1.64393	0.11684	0.91943	0.95101	RP11-58E2	chr14	-	50474031	50507947	2301
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP5-1163L	chr14	-	71498403	71498687	285
ENSG00000(	0	0	0	2.247227	4.60216	2.465895	-2.3811	0.072509	0.13365	CTD-3006G	chr14	-	27727923	28314492	674
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-991C	chr14	-	95426614	95429313	737
ENSG00000(	4.143168	0	2.638828	0	0.920432	0	1.5854	0.23844	0.35335	RP11-1078	chr14	+	91033839	91036320	559
ENSG00000(	8.286335	6.021439	7.916483	6.74168	4.60216	9.863579	0.059074	0.94042	0.96402	RP11-317N	chr14	-	36288430	36295971	2867
ENSG00000(	0	1.204288	5.277655	2.996302	0	0	0.63671	0.63161	0.74163	RP11-407N	chr14	-	39734907	39736265	1359
ENSG00000(	18.64425	8.430014	9.235896	0	0	1.64393	3.5981	0.000476	0.001403	RP11-696D	chr14	-	63764844	63766265	880
ENSG00000(	7.250543	6.021439	17.15238	0	3.681728	0.821965	2.3492	0.017087	0.037694	RP4-647C1	chr14	-	73738890	73740789	777
ENSG00000(	145.0109	116.8159	122.7055	128.841	132.5422	151.2415	-0.09832	0.667	0.7705	TUBB3	chr16	+	89987800	90005169	3715
ENSG00000(	2.071584	2.408575	3.958241	0	0	2.465895	1.1772	0.3551	0.48466	RP11-857B	chr14	-	45368111	45381066	360
ENSG00000(	2.071584	0	1.319414	1.498151	2.761296	0	-0.18492	0.88909	0.9311	CTD-2540L	chr14	+	71061269	71062487	1219
ENSG00000(	36.25272	38.53721	51.45714	0	0	0	6.6246	2.41E-10	1.38E-09	RP11-1042	chr14	+	61107448	61109307	572
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC004507.	chr5	-	1.26E+08	1.26E+08	2977
ENSG00000(	10.35792	8.430014	13.19414	0.749076	0	0	3.9606	0.000335	0.001012	LINC00519	chr14	-	51771134	51795104	682
ENSG00000(	0	0	2.638828	0.749076	2.761296	4.93179	-1.1359	0.37502	0.50565	RP11-363J2	chr14	-	69649737	69680809	1826
ENSG00000(	8.286335	7.225726	10.55531	5.992604	9.20432	4.93179	0.34259	0.65616	0.76109	RP11-1017	chr14	-	1.03E+08	1.03E+08	566
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-903H	chr14	+	21202737	21203170	434
ENSG00000(	1.035792	3.612863	3.958241	0	0	0	2.5341	0.058511	0.11133	RP5-1163L	chr14	-	71511092	71511357	266
ENSG00000(	5.17896	10.83859	3.958241	4.494453	0	2.465895	1.242	0.22096	0.33276	RP11-829H	chr14	+	31487652	31488002	351
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-305B	chr14	-	44464984	44853748	257
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-326A	chr15	-	93844645	93844876	232
ENSG00000(	1.035792	2.408575	2.638828	0.749076	0	0	1.6037	0.23235	0.34601	CTD-2207P	chr14	-	75081396	75083350	667
ENSG00000(	2.071584	0	2.638828	2.247227	3.681728	0	-0.21809	0.86446	0.91436	EIF1AXP2	chr14	-	65995548	65996292	413
ENSG00000(	1.035792	0	1.319414	2.247227	1.840864	0	-0.4528	0.73609	0.82343	RP11-638I2	chr14	-	1.01E+08	1.01E+08	331
ENSG00000(	3.107376	4.817151	7.916483	4.494453	6.443024	0	0.43941	0.6672	0.77059	RP11-507K	chr14	+	88965678	88981433	492
ENSG00000(	0	0	2.638828	2.247227	0.920432	0	-0.16072	0.90567	NA	UBE2F	chr2	+	2.39E+08	2.39E+08	2902
ENSG00000(	26.93059	12.04288	13.19414	26.96672	6.443024	25.48091	-0.16286	0.7907	0.86303	RP11-368P	chr14	+	53503473	53504969	366
ENSG00000(	0	0	0	2.247227	0.920432	1.64393	-1.4644	0.28023	NA	TMEM179	chr14	-	1.05E+08	1.05E+08	2510
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-125H	chr14	+	67665779	67667044	1266
ENSG00000(	0	0	0	0.749076	1.840864	0	-0.68825	0.58858	NA	NF1P2	chr15	-	22133181	22152165	2505
ENSG00000(	2.071584	3.612863	2.638828	0	0	0	2.5105	0.060897	0.11506	RP11-398E	chr14	-	45232360	45252032	2904
ENSG00000(	2.071584	3.612863	6.597069	0	3.681728	0.821965	1.1145	0.336	0.46429	RP11-114N	chr14	-	81573377	81636758	601
ENSG00000(	80.79177	186.6646	382.63	8.988907	141.7465	73.97684	1.3205	0.1588	0.25562	RPPH1	chr14	-	20811207	20811844	638
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-671J2	chr14	-	35011023	35011650	545
ENSG00000(	2.071584	1.204288	0	2.996302	2.761296	4.93179	-1.2237	0.30292	0.42804	RP3-449M8	chr14	-	74940710	74941567	589
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	RP11-566K	chr16	-	89986235	89989070	985
ENSG00000(	0	0	0	0.749076	0.920432	0.821965	-0.73223	0.57364	NA	RP11-1017	chr14	-	1.02E+08	1.02E+08	238
ENSG00000(	1.035792	0	2.638828	2.996302	3.681728	10.68554	-1.7625	0.11385	0.19508	RP11-109N	chr14	+	73427303	73428701	289
ENSG00000(	7.250543	13.24716	6.597069	0	0.920432	0	3.6646	0.001168	0.003243	FPGT-TNNI3	chr1	+	74663926	75009666	7566
ENSG00000(	10.35792	2.408575	2.638828	0	0	2.465895	1.9424	0.10213	0.17846	CTD-2062F	chr14	+	1.01E+08	1.01E+08	553
ENSG00000(	1.035792	2.408575	1.319414	1.498151	1.840864	2.465895	-0.20823	0.86423	0.9142	ENSAP2	chr14	-	83159048	83159399	352
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-718G	chr14	+	70742013	70758576	448
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-666E	chr14	+	82207346	82496693	559

ENSG00000(	0	2.408575	6.597069	0	2.761296	2.465895	0.55006	0.65507	0.76036	CTD-2325P	chr14	-	69093883	69095162	279
ENSG00000(	1.035792	0	5.277655	0	0	0	1.9229	0.15616	0.25219	RP11-409I:	chr14	+	58045350	58048038	708
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CTD-2058B	chr14	-	38503492	38663486	785
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	CHORDC2P	chr14	-	90203309	90204735	1090
ENSG00000(	0	1.204288	0	0.749076	0	0	0.1572	0.90001	NA	RP11-736L	chr14	+	43769466	43769798	333
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-1140	chr14	+	51555675	51558006	1131
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	DUXAP1	chr2	+	84977893	84978355	463
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	RP11-488C	chr14	-	77388183	77390992	756
ENSG00000(	1.035792	0	0	4.494453	2.761296	12.32947	-2.8551	0.017364	0.038249	ACTN1-AS1	chr14	+	69446399	69454180	599
ENSG00000(	7.250543	4.817151	6.597069	5.992604	1.840864	3.28786	0.63784	0.48735	0.61652	RP5-1021I:	chr14	+	74254063	74269973	573
ENSG00000(	3.107376	1.204288	0	0	0	2.465895	0.45149	0.73826	0.82477	RP11-371E	chr14	+	93651318	93684932	570
ENSG00000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	CTD-3051D	chr14	+	1.05E+08	1.05E+08	584
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	LINC00639	chr14	-	39218545	39417477	4494
ENSG00000(	19.68005	14.45145	17.15238	14.23244	15.64734	13.9734	0.21951	0.69631	0.7931	RP11-247L	chr14	-	50793244	50794627	446
ENSG00000(	0	3.612863	2.638828	0	0	0	1.93	0.15472	0.25026	FOXN3-AS2	chr14	+	90042560	90043821	1262
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	POC1B-GAL	chr12	-	89913185	89920039	5436
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	PTBP1P	chr14	+	65745985	65747884	1601
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP1-261D1	chr14	-	71797059	71797455	397
ENSG00000(	3.107376	1.204288	3.958241	1.498151	1.840864	0	0.92967	0.44987	0.57966	RP11-488C	chr14	-	77240627	77247861	749
ENSG00000(	4.143168	1.204288	1.319414	0.749076	0.920432	5.753754	-0.10034	0.93231	0.95944	RP11-407N	chr14	-	39644089	39645084	530
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-134E	chr14	-	32741061	32741510	450
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-356C	chr14	-	38025363	38036300	379
ENSG00000(	5.17896	4.817151	5.277655	6.74168	2.761296	6.575719	-0.07228	0.93555	0.96121	CTD-2017C	chr14	-	1.02E+08	1.02E+08	448
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-173D	chr14	-	35627110	35628305	1196
ENSG00000(	48.68222	63.82725	56.73479	4.494453	2.761296	7.397684	3.3829	5.39E-11	3.25E-10	RP11-603B	chr15	+	22546089	22546799	711
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-1074	chr14	-	39854608	39856306	1699
ENSG00000(	0	9.634302	1.319414	2.996302	2.761296	2.465895	0.31369	0.78138	0.85605	RP11-270N	chr14	-	76280845	76314041	448
ENSG00000(	0	0	0	0	8.283888	0	-1.8662	0.16883	0.26865	RP11-242P	chr14	-	80077761	80099654	551
ENSG00000(	0	0	1.319414	0	1.840864	0.821965	-0.46629	0.72905	NA	RP11-406H	chr14	+	50915525	50923460	502
ENSG00000(	24.85901	16.86003	15.83297	7.490755	14.72691	4.109825	1.0769	0.094342	0.16713	RP11-973N	chr14	-	64980872	65007086	558
ENSG00000(	7.250543	13.24716	10.55531	0.749076	3.681728	5.753754	1.4323	0.095737	0.16918	RP11-840I:	chr14	+	65548752	65560930	796
ENSG00000(	6.214751	2.408575	0	3.745378	7.363456	12.32947	-1.1822	0.22557	0.33832	SMIM6	chr17	+	73642323	73644057	957
ENSG00000(	1.035792	1.204288	3.958241	0	2.761296	0	0.7407	0.57266	0.69137	RP11-545N	chr14	+	39560105	39560305	201
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	TVP23BP1	chr15	+	27210064	27215532	617
ENSG00000(	11.39371	31.31148	18.47179	2.247227	0.920432	0.821965	3.4785	2.69E-05	9.46E-05	RP11-545N	chr12	-	57538403	57541402	645
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-99L1	chr14	-	44861734	44862919	263
ENSG00000(	16.57267	6.021439	7.916483	27.7158	43.2603	31.23467	-1.6457	0.002711	0.007059	LINC00648	chr14	-	48234157	48264295	2885
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-219E	chr14	-	21338437	21341751	549
ENSG00000(	1.035792	4.817151	1.319414	4.494453	3.681728	1.64393	-0.36308	0.74359	0.82919	RP11-950C	chr14	+	75593856	75603633	367
ENSG00000(	1.035792	2.408575	2.638828	2.247227	3.681728	0	0.023498	0.9847	0.99107	CTD-2240H	chr14	-	95651454	95652191	594
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-903H	chr14	-	21188901	21191286	2104
ENSG00000(	0	6.021439	1.319414	5.243529	10.12475	0.821965	-0.90533	0.41288	0.54341	RP1-261D1	chr14	-	71759442	71788531	513
ENSG00000(	0	1.204288	1.319414	0.749076	0.920432	2.465895	-0.44614	0.73696	0.82369	CAP2P1	chr14	-	89756549	89757938	1390
ENSG00000(	5.17896	0	0	0	0.920432	0	1.173	0.38696	0.51775	RP11-100N	chr15	+	27667527	27673484	318

ENSG00000(	8.286335	6.021439	2.638828	74.90755	126.0992	73.97684	-3.8377	1.28E-14	9.87E-14	RP6-65G23	chr14	+	71276922	71282120	629
ENSG00000(	1.035792	0	1.319414	1.498151	3.681728	3.28786	-1.2555	0.31635	0.44316	RP11-831F	chr14	+	50144087	50144611	525
ENSG00000(	3.107376	3.612863	7.916483	0	0	0.821965	2.7612	0.025403	0.053729	ADAM20P1	chr14	-	70935598	70950473	3034
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	CTD-2017C	chr14	-	1.02E+08	1.02E+08	729
ENSG00000(	0	2.408575	0	3.745378	0	6.575719	-1.3655	0.28861	0.41229	RP11-203N	chr14	+	20906141	20909427	890
ENSG00000(	1.035792	0	2.638828	1.498151	0	0	0.60883	0.65358	NA	RP11-1078	chr14	+	91108982	91115238	1237
ENSG00000(	4.143168	4.817151	14.51355	0	4.60216	2.465895	1.4599	0.14519	0.23766	DDX18P1	chr14	+	69550115	69552106	1992
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	RP11-100N	chr15	-	27728181	27787137	1100
ENSG00000(	1.035792	3.612863	0	7.490755	8.283888	4.109825	-1.6893	0.10903	0.18821	RP11-299G	chr15	+	1.02E+08	1.02E+08	2590
ENSG00000(	1.035792	0	0	2.247227	0	0	-0.31629	0.80869	NA	RP11-1180	chr15	+	23181938	23182642	705
ENSG00000(	0	4.817151	2.638828	0	0	0	2.1804	0.10782	0.18657	RP11-379K	chr15	-	80846950	80855285	2520
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP11-69H1	chr15	+	22278010	22413497	2317
ENSG00000(	0	0	0	1.498151	0.920432	1.64393	-1.2565	0.35231	NA	RP11-154B	chr15	-	90936722	90941113	458
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTD-2184D	chr15	+	52374499	52378771	462
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	UBE2CP4	chr15	+	31712331	31712865	535
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-420N	chr15	+	55972583	55973661	364
ENSG00000(	51.7896	48.17151	64.65128	5.992604	3.681728	0.821965	3.7677	2.58E-11	1.59E-10	RP11-424I2	chr15	+	1.02E+08	1.02E+08	645
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTD-2647E	chr15	+	50171801	50175722	1284
ENSG00000(	0	3.612863	0	0.749076	0.920432	0.821965	0.29541	0.8266	0.88831	RP11-253N	chr15	-	69726805	69727459	655
ENSG00000(	0	1.204288	1.319414	0	0.920432	3.28786	-0.43245	0.74748	0.83213	AC109631.	chr15	-	38750961	38751741	781
ENSG00000(	1.035792	9.634302	1.319414	0	0	0	2.9829	0.023826	0.050764	RP11-158N	chr15	+	86314221	86314394	174
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	HMBOX1-IT	chr8	+	28807193	28813472	347
ENSG00000(	4.143168	8.430014	6.597069	5.243529	6.443024	0.821965	0.53124	0.56711	0.6863	RP11-718C	chr15	+	45997276	46223267	861
ENSG00000(	5.17896	4.817151	5.277655	1.498151	3.681728	0.821965	1.1223	0.27872	0.40082	RP11-56B1	chr15	-	52179757	52193320	510
ENSG00000(	3.107376	7.225726	1.319414	0	0	0	3.0022	0.022253	0.047711	RP11-342N	chr15	-	67435072	67439277	472
ENSG00000(	1.035792	1.204288	7.916483	2.996302	8.283888	8.219649	-0.81867	0.4045	0.53542	PRKXP1	chr15	-	1.01E+08	1.01E+08	1122
ENSG00000(	92.18548	81.89156	112.1502	7.490755	12.88605	6.575719	3.3441	2.59E-16	2.20E-15	ITGB3	chr17	+	45331212	45421658	3995
ENSG00000(	0	1.204288	9.235896	0	5.522592	8.219649	-0.32038	0.78054	0.85532	RP5-991G2	chr16	+	72840887	72843538	498
ENSG00000(	1.035792	3.612863	1.319414	0.749076	2.761296	0.821965	0.33512	0.78651	0.85986	RP11-64K1	chr15	-	40756392	40758925	729
ENSG00000(	1.035792	9.634302	5.277655	1.498151	5.522592	0.821965	0.84143	0.4239	0.55444	CTD-3065B	chr15	-	91139072	91139679	474
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	CTD-2071N	chr15	+	78079535	78081016	742
ENSG00000(	0	2.408575	0	2.247227	1.840864	0	-0.41398	0.75953	0.84108	RP11-227D	chr15	+	49017535	49018024	490
ENSG00000(	0	0	2.638828	1.498151	4.60216	3.28786	-1.2766	0.31035	0.43643	CTD-3076C	chr15	+	1.01E+08	1.01E+08	2393
ENSG00000(	17.60846	18.06432	10.55531	1.498151	7.363456	7.397684	1.4049	0.056326	0.10773	SLC35G6	chr17	+	7384721	7386383	1195
ENSG00000(	0	4.817151	1.319414	0	0	0	1.8904	0.16312	0.26107	RP11-1008	chr15	+	38276967	38354541	1147
ENSG00000(	3.107376	0	2.638828	0	0	0	1.8293	0.17689	NA	RP11-64K1	chr15	+	70894463	70894855	393
ENSG00000(	0	1.204288	2.638828	2.247227	0	0.821965	0.15864	0.90563	0.94172	AC022819.	chr15	-	99824830	99825781	952
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	CTD-2555C	chr14	+	1.03E+08	1.03E+08	1603
ENSG00000(	1.035792	2.408575	2.638828	0	0	0	2.0265	0.13497	0.22409	RP11-349G	chr15	-	65767656	65767952	297
ENSG00000(	9.322127	13.24716	10.55531	8.239831	7.363456	3.28786	0.74055	0.32078	0.44795	CTD-2611K	chr15	-	1.02E+08	1.02E+08	1798
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-361D	chr15	+	59980716	59981617	402
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC002306.	chr19	+	19716690	19719991	1928
ENSG00000(	1.035792	0	3.958241	0	0.920432	0	1.2088	0.37284	NA	RP11-182J1	chr15	-	85056472	85070180	492
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-684B	chr15	+	36338283	36341730	632

ENSG00000(	4.143168	13.24716	15.83297	5.992604	0	4.109825	1.4702	0.10212	0.17846	RP11-265N	chr15	-	63836446	63893788	1807
ENSG00000(	74.57702	61.41867	67.2901	77.90386	54.30549	76.44274	-0.03843	0.89996	0.9378	RP11-50C1	chr15	+	58879706	58883875	542
ENSG00000(	0	0	7.916483	0	0	0	2.0802	0.12493	0.21053	RP11-643N	chr15	+	62352702	62354633	1921
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	CTD-2339L	chr15	+	40935131	40939055	516
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-838N	chr18	-	3347774	3350557	404
ENSG00000(	0	2.408575	2.638828	2.996302	0	0	0.40828	0.76055	0.8417	RP11-325L	chr15	+	65397872	65398138	267
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	NDUFA3P4	chr15	+	90929046	90929295	250
ENSG00000(	0	0	0	7.490755	11.96562	12.32947	-4.2554	0.000265	0.000812	RP11-60L3	chr15	+	74495046	74513896	1344
ENSG00000(	1.035792	0	0	0	3.681728	0	-0.68494	0.60991	NA	CTD-2501E	chr15	+	60822172	60837358	434
ENSG00000(	4.143168	0	3.958241	0	2.761296	0	1.0032	0.44253	0.57218	RP11-522B	chr15	+	96897466	96946964	563
ENSG00000(	2.071584	0	0	2.247227	2.761296	2.465895	-1.1442	0.37542	0.50599	RP11-815J	chr15	-	86164495	86170920	568
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP13-126C	chr15	-	29262399	29269667	751
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-62C7	chr15	+	39311434	39317119	574
ENSG00000(	0	0	2.638828	0	0	0.821965	0.55859	0.66971	NA	RP11-122D	chr15	-	37168580	37179236	750
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CTD-2632K	chr15	+	77952394	77960416	663
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-26L2	chr16	-	55293881	55367500	763
ENSG00000(	2.071584	2.408575	5.277655	0	0	0	2.7419	0.038825	0.07795	RP11-696L	chr15	+	69126169	69127088	920
ENSG00000(	9.322127	13.24716	15.83297	12.73428	16.56778	3.28786	0.21754	0.75546	0.83825	RP11-3D4.1	chr15	-	34150918	34157026	447
ENSG00000(	0	0	3.958241	4.494453	1.840864	3.28786	-0.94696	0.44165	0.57145	RP11-133K	chr15	+	40509629	40568597	2767
ENSG00000(	1.035792	2.408575	1.319414	0	0	4.109825	0.12885	0.92194	0.95276	RP11-687N	chr11	+	1.25E+08	1.25E+08	356
ENSG00000(	25.8948	8.430014	10.55531	14.98151	14.72691	7.397684	0.27102	0.67877	0.77981	RP11-617F	chr15	-	90617747	90625439	1168
ENSG00000(	2.071584	0	0	2.247227	0.920432	0	-0.28364	0.8344	NA	CTA-339C1	chr7	-	1.01E+08	1.01E+08	622
ENSG00000(	47.64643	37.33292	22.43003	0	7.363456	2.465895	3.2635	1.95E-06	7.83E-06	RP11-561C	chr15	+	85734669	85757136	7790
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP11-313P	chr15	-	52000192	52007417	387
ENSG00000(	3.107376	6.021439	7.916483	5.243529	2.761296	0	0.88017	0.3959	0.52694	RP11-562A	chr15	-	50789392	50790941	667
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-37J1	chr15	-	29525877	29527341	1465
ENSG00000(	3.107376	0	1.319414	0	0.920432	0	1.1063	0.4148	NA	TUBBP8	chr15	+	29904774	29906478	1232
ENSG00000(	4.143168	1.204288	0	0	1.840864	0	0.87886	0.51457	0.64135	ZHX1-C8ORF	chr8	-	1.24E+08	1.24E+08	1255
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-108K	chr15	+	51608038	51614193	776
ENSG00000(	0	0	0	0	3.681728	0.821965	-1.2455	0.35322	NA	RP11-382A	chr15	+	83713120	83713523	404
ENSG00000(	5.17896	0	0	0	0	0	1.5469	0.24589	NA	CTD-3065B	chr15	-	91147457	91157790	807
ENSG00000(	14.50109	7.225726	3.958241	19.47596	9.20432	9.863579	-0.52749	0.46391	0.59319	RP11-752G	chr15	-	83394625	83407656	1662
ENSG00000(	6.214751	9.634302	3.958241	21.72319	25.7721	22.19305	-1.7048	0.006493	0.015724	CTD-2116N	chr15	-	64472547	64665980	1683
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	RP11-561C	chr15	+	85815758	85816205	368
ENSG00000(	3.107376	8.430014	13.19414	0.749076	3.681728	13.15144	0.41953	0.64508	0.75221	RP11-454L	chr14	-	55861658	55861951	294
ENSG00000(	3.107376	1.204288	13.19414	11.98521	3.681728	2.465895	-0.0696	0.94161	0.9649	RP11-293N	chr14	-	75890386	75894444	4059
ENSG00000(	7.250543	2.408575	3.958241	4.494453	2.761296	17.26126	-0.72911	0.42217	0.55266	RP11-468E	chr14	+	24608654	24609653	747
ENSG00000(	1.035792	9.634302	1.319414	0	0	0	2.9829	0.023826	0.050764	RP11-762H	chr15	+	78585628	78588391	449
ENSG00000(	0	0	0	0.749076	1.840864	0.821965	-1.0455	0.43461	NA	RP11-69H1	chr15	-	22318882	22319785	904
ENSG00000(	6.214751	8.430014	6.597069	1.498151	2.761296	5.753754	0.94618	0.29976	0.42463	RP11-102L	chr15	+	38795054	38797182	2129
ENSG00000(	4.143168	12.04288	1.319414	0.749076	0	0	2.9987	0.014418	0.032348	CTD-2184D	chr15	+	52408771	52414328	874
ENSG00000(	22.78742	16.86003	18.47179	10.48706	7.363456	17.26126	0.69006	0.24295	0.35881	RP11-152F	chr15	+	82944773	82974312	1160
ENSG00000(	301.4154	292.6419	291.5904	541.5816	453.773	531.8113	-0.78387	5.47E-07	2.33E-06	RP11-64K1	chr15	+	40617417	40618916	594
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-516C	chr15	-	44739775	44741542	1768

ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	RP11-323I:	chr15	-	35391223	35461899	1342
ENSG00000(	0	1.204288	0	0.749076	0	0	0.1572	0.90001	NA	RP11-20G1	chr15	-	99967214	99971233	395
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	RP11-519G	chr15	-	45722850	45734006	729
ENSG00000(	2.071584	0	5.277655	2.996302	0	0.821965	0.60678	0.63435	0.74377	RP11-761I4	chr15	+	81616718	81654378	769
ENSG00000(	0	0	0	1.498151	1.840864	4.93179	-2.195	0.10101	0.17689	RP11-566K	chr15	-	23095170	23115256	608
ENSG00000(	19.68005	20.47289	30.34652	2.996302	0	0.821965	3.7041	4.43E-06	1.71E-05	RP11-624L	chr15	-	39157523	39719396	1378
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-798K	chr15	-	67278699	67351591	741
ENSG00000(	4.143168	7.225726	9.235896	0	0	0	3.9404	0.00138	0.003783	RP11-4G2.:	chr15	-	96571318	96590159	561
ENSG00000(	20.71584	6.021439	13.19414	3.745378	13.80648	7.397684	0.64443	0.37788	0.50857	RP11-15E1	chr17	+	58603654	58628159	557
ENSG00000(	0	0	0	2.247227	0	0.821965	-0.85594	0.51054	NA	RP11-63A2	chr15	+	89495914	89496691	470
ENSG00000(	0	1.204288	0	13.48336	4.60216	9.863579	-3.3488	0.003108	0.008006	RP11-519G	chr15	+	45740625	45805965	2399
ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	RP11-90E5	chr15	+	1.01E+08	1.01E+08	1781
ENSG00000(	3.107376	7.225726	3.958241	0.749076	0.920432	0	2.2632	0.055649	0.10661	RP11-327J:	chr15	+	96714810	96717568	639
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-307C	chr15	+	77817882	77826452	3814
ENSG00000(	20.71584	24.08575	22.43003	2.247227	2.761296	4.93179	2.5679	0.000177	0.000556	CTD-2054N	chr15	+	1E+08	1E+08	665
ENSG00000(	8.286335	4.817151	2.638828	0	2.761296	4.109825	0.98748	0.35512	0.48466	RP11-64K1	chr15	-	40745643	40746838	584
ENSG00000(	6.214751	8.430014	2.638828	0	0	0	3.6561	0.003694	0.009398	RP11-424I:	chr15	+	1.02E+08	1.02E+08	556
ENSG00000(	13.46529	28.90291	29.0271	5.243529	27.61296	6.575719	0.81418	0.20684	0.31596	CTD-2647L	chr8	+	28913452	28914202	552
ENSG00000(	4.143168	1.204288	6.597069	0	1.840864	1.64393	1.3387	0.25506	0.37323	RP11-815J:	chr15	-	86162854	86214179	660
ENSG00000(	2.071584	1.204288	0	3.745378	8.283888	9.863579	-2.1454	0.044138	0.087167	RP11-1069	chr15	-	63124323	63176233	2978
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTD-2240J:	chr15	+	81702858	81711358	658
ENSG00000(	1.035792	3.612863	2.638828	0	0	0	2.2878	0.090046	0.16086	RP11-505E	chr15	-	1.02E+08	1.02E+08	491
ENSG00000(	1.035792	7.225726	0	2.996302	0	1.64393	0.56096	0.65477	0.76009	DCAF13P3	chr15	+	51236860	51238193	1334
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-925D	chr15	+	58444805	58446606	1802
ENSG00000(	3.107376	0	0	0	1.840864	0	0.36193	0.78835	NA	RP11-346D	chr15	-	38431796	38519088	2471
ENSG00000(	1.035792	4.817151	3.958241	0	0	0	2.7313	0.039906	0.079846	RP11-192N	chr15	-	1.01E+08	1.01E+08	1222
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	GH1	chr17	-	61994560	61996179	830
ENSG00000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	H3F3AP1	chr15	-	40243576	40243909	334
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-758N	chr15	-	33129184	33129527	344
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-244F	chr15	+	63245372	63246323	952
ENSG00000(	0	0	0	0.749076	3.681728	2.465895	-1.924	0.15425	0.24976	RP11-16O9	chr15	+	41635278	41636423	476
ENSG00000(	5.17896	0	2.638828	2.247227	8.283888	4.93179	-0.77387	0.46478	0.59382	RP11-323I:	chr15	+	35384682	35385413	732
ENSG00000(	6.214751	1.204288	7.916483	2.996302	1.840864	1.64393	1.0111	0.33131	0.45921	RP11-430B	chr15	+	52325904	52327822	381
ENSG00000(	3.107376	2.408575	7.916483	2.247227	2.761296	10.68554	-0.20398	0.83319	0.89318	RP11-30K9	chr15	+	59107471	59109927	526
ENSG00000(	0	0	1.319414	1.498151	0	1.64393	-0.61204	0.65104	NA	EFTUD1P1	chr15	+	84748920	84795356	1798
ENSG00000(	4.143168	0	0	0.749076	0	2.465895	0.22234	0.86887	0.91759	ISCA1P4	chr15	-	41240934	41241067	134
ENSG00000(	7.250543	7.225726	2.638828	4.494453	0.920432	6.575719	0.43837	0.64626	0.75323	RP11-158N	chr15	-	86287340	86293512	964
ENSG00000(	13.46529	0	9.235896	5.992604	12.88605	10.68554	-0.32654	0.69867	0.79517	RP11-3D4.:	chr15	-	34147101	34149010	543
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-34F1	chr15	+	68125063	68166204	346
ENSG00000(	2.071584	0	0	0	1.840864	0.821965	-0.14076	0.91727	NA	RP11-139F	chr15	+	35692892	35693969	1078
ENSG00000(	3.107376	2.408575	3.958241	0	0	0.821965	2.1634	0.094809	0.16773	HERC2P7	chr15	+	23388289	23392657	726
ENSG00000(	2.071584	0	0	2.996302	7.363456	4.93179	-2.0267	0.087202	0.15669	RP11-158N	chr15	-	86298172	86299468	855
ENSG00000(	1.035792	2.408575	3.958241	6.74168	11.96562	8.219649	-1.6348	0.075408	0.13825	RP11-2E17	chr15	-	80487826	80544555	6890
ENSG00000(	5.17896	0	0	0	1.840864	0	0.78341	0.56357	0.68317	RP11-109D	chr15	-	45333914	45350905	542

ENSG00000(	0	1.204288	0	0.749076	6.443024	0	-1.3804	0.30486	0.43016	RP11-593F	chr15	-	76467232	76473827	2354
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-265N	chr15	+	39459940	39472231	696
ENSG00000(	1.035792	0	0	0	1.840864	0	-0.17777	0.89006	NA	RP11-35O1	chr15	-	99190180	99190600	334
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	RP11-566K	chr15	+	23096869	23105332	3940
ENSG00000(	7.250543	10.83859	1.319414	26.21764	29.45382	24.65895	-1.9112	0.002541	0.006646	RP11-253N	chr15	-	69689243	69707368	1778
ENSG00000(	4.143168	0	1.319414	0	0.920432	0.821965	0.97843	0.46421	0.59339	UBE2Q2P3	chr15	+	83023847	83088805	809
ENSG00000(	78.72018	71.05298	73.88717	11.23613	22.09037	37.81039	1.6194	7.60E-05	0.000252	THTPA	chr14	+	24025216	24029480	2860
ENSG00000(	2.071584	0	1.319414	0	0	0.821965	0.88094	0.51378	NA	RP11-37C7	chr15	-	40105424	40107630	567
ENSG00000(	2.071584	0	1.319414	0	0	0.821965	0.88094	0.51378	NA	CTC-378H2	chr19	+	42656721	42661675	1955
ENSG00000(	0	8.430014	0	0	0	0.821965	1.7274	0.20056	0.30811	CTD-2650P	chr15	-	52303196	52311292	865
ENSG00000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	NPM1P43	chr15	-	73454120	73455269	786
ENSG00000(	7.250543	13.24716	10.55531	7.490755	2.761296	12.32947	0.40839	0.59165	0.70798	RP11-752G	chr15	+	83412975	83419041	1091
ENSG00000(	1.035792	8.430014	6.597069	3.745378	2.761296	0.821965	0.91396	0.37927	0.51	RP11-276N	chr15	-	82245644	82288007	526
ENSG00000(	0	0	0	0.749076	7.363456	1.64393	-2.379	0.074077	0.13615	RP11-489D	chr15	-	33595858	33602860	479
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP11-16E1	chr15	+	31508223	31516648	468
ENSG00000(	0	0	0	4.494453	1.840864	1.64393	-2.1524	0.10834	0.18723	RP11-265N	chr15	-	39480639	39486510	1961
ENSG00000(	8.286335	7.225726	5.277655	0	0	0	3.9736	0.001213	0.003354	RP11-561C	chr15	-	85857898	85858747	470
ENSG00000(	5.17896	4.817151	2.638828	0	3.681728	2.465895	0.84185	0.44782	0.57756	RP11-815J	chr15	+	86244340	86246002	746
ENSG00000(	4.143168	13.24716	7.916483	16.47966	5.522592	11.50751	-0.38787	0.60204	0.71723	RP5-914P2	chr20	+	49547521	49561316	572
ENSG00000(	0	0	2.638828	0	5.522592	2.465895	-1.0063	0.44366	0.57332	RP11-625H	chr15	-	62929371	62937490	2425
ENSG00000(	11.39371	9.634302	3.958241	0	0	0	4.2436	0.000447	0.001324	RP11-321G	chr15	+	63682335	63729347	816
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	ANP32BP3	chr15	-	81409976	81410681	706
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-752G	chr15	+	83316521	83361572	2138
ENSG00000(	1.035792	2.408575	0	0	0	2.465895	0.25271	0.85215	NA	RP11-540C	chr15	+	41303795	41305498	414
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AHCYP7	chr15	+	50709582	50710889	1308
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	NDUFAF4P1	chr15	+	49448526	49449044	519
ENSG00000(	0	0	0	3.745378	0	2.465895	-1.6796	0.21567	0.32631	RP11-227D	chr15	-	49021277	49022041	540
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	KRT8P9	chr15	+	71151053	71152501	1449
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-321F	chr15	+	66874528	66978132	833
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP13-996F	chr15	-	83141718	83182928	1349
ENSG00000(	0	1.204288	1.319414	0	2.761296	0	-0.06147	0.96386	NA	RP11-650L	chr15	-	78772399	78774162	325
ENSG00000(	9.322127	0	6.597069	0	3.681728	0.821965	1.3961	0.23227	0.34592	RP11-654A	chr15	-	99497378	99646030	588
ENSG00000(	22.78742	9.634302	27.70769	7.490755	5.522592	19.72716	0.81926	0.20755	0.31682	CTD-2008A	chr15	-	45118569	45176892	1133
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-26F2	chr15	-	23128188	23145997	1064
ENSG00000(	1.035792	1.204288	1.319414	0	0.920432	0.821965	0.58234	0.66567	NA	RP11-39M2	chr15	+	61473448	61488137	476
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-219B	chr15	+	60973768	60979087	589
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-930C	chr14	-	56770208	56777479	517
ENSG00000(	21.75163	14.45145	21.11062	11.23613	11.96562	8.219649	0.82624	0.16165	0.25928	RP11-323F	chr15	-	57151866	57210697	3017
ENSG00000(	0	0	0	17.97781	24.85166	22.19305	-5.3025	1.17E-06	4.81E-06	CTD-2147F	chr15	+	97839111	97975324	565
ENSG00000(	4.143168	0	1.319414	6.74168	3.681728	1.64393	-0.85677	0.45298	0.5827	RP11-154J2	chr15	-	48604550	48624053	752
ENSG00000(	40.39588	36.12863	58.05421	48.68991	62.58938	49.3179	-0.25346	0.47808	0.60716	MRPL46	chr15	-	89002707	89010650	5561
ENSG00000(	34.18113	32.51577	26.38828	663.6809	706.8918	721.6852	-4.4506	1.10E-90	7.02E-89	RP11-244F	chr15	-	63338233	63341586	3354
ENSG00000(	3.107376	13.24716	5.277655	2.247227	1.840864	0	1.9459	0.063853	0.1199	RP11-616K	chr15	-	44679518	44682649	655
ENSG00000(	0	0	1.319414	2.996302	1.840864	3.28786	-1.6472	0.20681	0.31593	RP11-643G	chr14	+	68077703	68080581	619

ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-352D	chr15	+	69571014	69587661	561
ENSG00000(	4.143168	1.204288	0	1.498151	2.761296	5.753754	-0.64591	0.58122	0.69922	RP11-74D7	chr15	+	34282887	34284249	1203
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-661D	chr14	-	1.03E+08	1.03E+08	567
ENSG00000(	16.57267	7.225726	18.47179	0	0.920432	0.821965	3.821	0.000118	0.000381	RP11-182J	chr15	+	84841242	84850986	499
ENSG00000(	4.143168	6.021439	2.638828	0	0	0	3.1879	0.013883	0.031284	HNRNPA1P	chr15	+	67920190	67921473	966
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	CTD-2501E	chr15	+	60850279	60850600	322
ENSG00000(	2.071584	7.225726	6.597069	0.749076	0	2.465895	1.7626	0.11774	0.20071	RP11-685G	chr15	-	76631950	76634404	758
ENSG00000(	1.035792	2.408575	3.958241	6.74168	8.283888	21.37109	-2.0371	0.02212	0.047475	RP11-365N	chr14	+	1.03E+08	1.03E+08	828
ENSG00000(	0	7.225726	2.638828	1.498151	0	2.465895	0.90737	0.46304	0.59241	ANP32AP1	chr15	+	35474000	35530398	1074
ENSG00000(	5.17896	4.817151	3.958241	5.243529	4.60216	7.397684	-0.26527	0.76533	0.84506	CTD-2651B	chr15	-	45543884	45571449	630
ENSG00000(	0	3.612863	2.638828	0.749076	4.60216	7.397684	-0.80833	0.47671	0.60599	RP11-540C	chr15	+	41309005	41320091	444
ENSG00000(	9.322127	14.45145	7.916483	14.23244	5.522592	12.32947	-0.02346	0.97314	0.98445	RP11-680F	chr15	+	30114834	30116284	1451
ENSG00000(	20.71584	6.021439	13.19414	2.996302	14.72691	18.08323	0.15924	0.82523	0.88728	RP11-330L	chr15	-	64982366	64995393	707
ENSG00000(	0	0	0	5.243529	0.920432	6.575719	-2.8132	0.030575	0.063206	LINC00052	chr15	+	88120160	88122917	1786
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	RP11-272D	chr15	-	73547675	73548450	531
ENSG00000(	7.250543	2.408575	5.277655	12.73428	24.85166	6.575719	-1.4073	0.06945	0.12886	RNF31	chr14	+	24620427	24636611	4798
ENSG00000(	0	2.408575	3.958241	8.239831	8.283888	1.64393	-1.2524	0.2394	0.35441	RP11-295H	chr15	-	49657321	49658882	1562
ENSG00000(	4.143168	7.225726	1.319414	0.749076	0	3.28786	1.2435	0.28498	0.40804	RP11-138H	chr15	+	71041271	71046516	472
ENSG00000(	5.17896	2.408575	0	0	0	0	2.2334	0.099381	0.17452	RP11-111A	chr15	+	40780240	40850183	2242
ENSG00000(	6.214751	1.204288	0	0	0	0	2.1793	0.10812	0.18693	RP13-262C	chr15	-	84967471	84976535	205
ENSG00000(	3.107376	0	0	3.745378	0	0.821965	-0.30013	0.82331	0.88603	RP11-526I	chr15	+	1.01E+08	1.01E+08	632
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-778C	chr11	-	1.2E+08	1.2E+08	2128
ENSG00000(	0	2.408575	5.277655	1.498151	0	0	1.3526	0.3084	0.43435	RP11-522B	chr15	-	96936375	96948419	562
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CTD-2034I	chr15	+	81719789	82047558	564
ENSG00000(	1.035792	1.204288	1.319414	0	0	2.465895	0.28943	0.83013	0.89104	RP11-158N	chr15	-	86269346	86270458	569
ENSG00000(	0	1.204288	1.319414	0	5.522592	1.64393	-0.94979	0.46769	0.59699	RP11-325E	chr15	-	49469807	49470938	598
ENSG00000(	0	0	0	3.745378	3.681728	0.821965	-2.1818	0.10344	0.18036	CYCSP2	chr15	+	41401076	41401376	301
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-182J	chr15	+	85043609	85045612	546
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC140725.	chr15	-	1.03E+08	1.03E+08	712
ENSG00000(	16.57267	24.08575	22.43003	10.48706	19.32907	13.15144	0.5332	0.33444	0.46243	RP11-56B1	chr15	-	52211270	52222824	1041
ENSG00000(	3.107376	8.430014	21.11062	20.97412	11.96562	11.50751	-0.43848	0.53211	0.65663	RP11-762H	chr15	-	78582869	78583563	695
ENSG00000(	0	12.04288	3.958241	0	2.761296	0	1.802	0.14312	0.23479	CTD-2329K	chr15	-	44808848	44809681	498
ENSG00000(	0	1.204288	1.319414	0	0.920432	0	0.59762	0.65368	NA	RP11-16B9	chr15	+	62126951	62144351	399
ENSG00000(	6.214751	8.430014	21.11062	0	0	3.28786	2.8442	0.004488	0.011225	RP11-671N	chr15	+	84949210	84950212	389
ENSG00000(	0	0	14.51355	0	0	0	2.9512	0.027906	0.05833	BLID	chr11	-	1.22E+08	1.22E+08	862
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-39M2	chr15	+	61504112	61506430	481
ENSG00000(	0	1.204288	1.319414	0	2.761296	3.28786	-0.78465	0.55166	0.6727	RP11-430B	chr15	+	52472290	52498071	1972
ENSG00000(	5.17896	14.45145	11.87472	0	12.88605	3.28786	0.85109	0.35064	0.48031	TYRO3P	chr15	-	76551327	76554031	2705
ENSG00000(	6.214751	12.04288	5.277655	8.988907	4.60216	12.32947	-0.13175	0.86481	0.91464	RP11-66B2	chr15	-	1.01E+08	1.01E+08	3213
ENSG00000(	0	0	0	4.494453	0	0	-1.1446	0.38559	NA	RP11-521C	chr15	-	40367405	40370905	864
ENSG00000(	0	0	1.319414	0	0.920432	0.821965	-0.17431	0.89516	NA	RP11-150L	chr15	-	35590450	35591641	1192
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	RP11-552E	chr15	-	47896077	47898549	472
ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	RP11-20G1	chr15	-	99935384	99936798	323
ENSG00000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	RP11-554D	chr15	+	61056105	61057824	806

ENSG00000(	0	2.408575	1.319414	2.996302	1.840864	4.93179	-1.0347	0.38883	0.51944	PRELID1P4	chr15	-	35413774	35414285	512
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-640I2	chr15	+	46633552	46633797	246
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	CTD-2034I4	chr15	+	81846344	81989121	684
ENSG00000(	1.035792	0	6.597069	0	1.840864	0	1.2205	0.35868	0.48835	RP11-516C	chr15	-	44694883	44719342	625
ENSG00000(	4.143168	9.634302	14.51355	0	4.60216	1.64393	1.8674	0.054868	0.1054	CTD-2647L	chr8	+	28910034	28911276	307
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-138E	chr15	+	49230433	49240228	666
ENSG00000(	32.10955	56.60152	21.11062	23.22134	31.29469	57.53754	-0.02526	0.95702	0.97461	AC074212.	chr19	+	46268043	46273064	1420
ENSG00000(	22.78742	1.204288	11.87472	0	1.840864	0.821965	3.0917	0.002819	0.007316	YLPM1	chr14	+	75283941	75322378	696
ENSG00000(	0	0	0	14.23244	1.840864	0.821965	-3.1542	0.014262	0.032046	RP11-499F	chr15	-	81926228	81934531	476
ENSG00000(	2.071584	4.817151	0	0	0.920432	0	1.6018	0.23337	0.34712	EEF1A1P22	chr15	-	53229336	53230715	1380
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-522B	chr15	-	96931443	96932285	843
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-507B	chr15	-	61592525	61927648	450
ENSG00000(	3.107376	0	3.958241	0	3.681728	1.64393	0.2952	0.81363	0.87897	RP11-540C	chr15	+	41291472	41297063	500
ENSG00000(	0	2.408575	0	0	0	0.821965	0.52892	0.68442	NA	RP11-562A	chr15	-	50786215	50789277	297
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP11-390N	chr15	-	54340785	54343073	2289
ENSG00000(	0	0	0	0.749076	0.920432	2.465895	-1.2662	0.34855	NA	RP11-654A	chr15	-	99423888	99436764	263
ENSG00000(	160.5477	192.686	121.3861	182.0254	240.2328	182.4762	-0.34319	0.1339	0.22274	RP11-156E	chr17	-	40004770	40007699	2930
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-467H	chr7	+	76673038	76827943	617
ENSG00000(	1.035792	7.225726	0	0	2.761296	0.821965	0.82061	0.52068	0.6465	CTD-2262B	chr15	+	85958459	85958864	406
ENSG00000(	1.035792	2.408575	2.638828	2.247227	0.920432	0.821965	0.41206	0.73848	0.82485	RP11-56B1	chr15	-	52151382	52153490	1800
ENSG00000(	0	0	1.319414	1.498151	0	0	-0.08979	0.94423	NA	RP11-182J1	chr15	+	84924665	84924766	102
ENSG00000(	7.250543	15.65574	7.916483	4.494453	11.04518	12.32947	0.13774	0.85029	0.9047	AC100830.	chr15	+	64993447	65011801	1609
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-184D	chr15	-	36231368	36544458	701
ENSG00000(	0	0	2.638828	0	1.840864	1.64393	-0.22543	0.86786	0.91696	RP6-33F8.1	chrX	-	83755033	83757461	475
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-279F	chr15	+	69884468	69988089	2121
ENSG00000(	8.286335	1.204288	9.235896	0.749076	8.283888	8.219649	0.11086	0.90664	0.94247	C15orf37	chr15	+	80215113	80217194	2082
ENSG00000(	10.35792	14.45145	11.87472	5.243529	5.522592	9.041614	0.82047	0.25026	0.36765	RP11-680F	chr15	-	30020390	30021735	1346
ENSG00000(	0	1.204288	0	6.74168	6.443024	3.28786	-2.6076	0.031283	0.064476	RP11-253N	chr15	+	69683531	69684488	694
ENSG00000(	0	1.204288	1.319414	0.749076	0.920432	0	0.27611	0.83862	NA	RP11-643G	chr14	+	68081646	68083343	1698
ENSG00000(	10.35792	19.2686	10.55531	1.498151	0	0	3.7806	0.000184	0.000578	RP11-351N	chr15	-	81188532	81202118	638
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-797A	chr15	+	77336022	77337502	264
ENSG00000(	0	0	1.319414	0	2.761296	1.64393	-0.88471	0.51431	NA	RP11-245C	chr15	+	85229115	85230177	487
ENSG00000(	0	2.408575	11.87472	0.749076	0.920432	0.821965	1.8075	0.13239	0.22061	RP11-325E	chr15	+	49393988	49395461	743
ENSG00000(	8.286335	10.83859	1.319414	3.745378	11.96562	0.821965	0.28295	0.76579	0.84543	PIGHP1	chr15	+	59968956	59969520	565
ENSG00000(	43.50326	52.98866	44.86007	5.243529	10.12475	21.37109	1.8788	0.000184	0.000578	RP11-89K1	chr15	-	1.02E+08	1.02E+08	625
ENSG00000(	19.68005	16.86003	15.83297	5.243529	13.80648	6.575719	0.98516	0.12607	0.21211	RP11-151N	chr15	+	44850027	44851386	653
ENSG00000(	12.4295	15.65574	9.235896	5.243529	5.522592	5.753754	1.087	0.13523	0.22445	DNM1P47	chr15	+	1.02E+08	1.02E+08	15043
ENSG00000(	9.322127	19.2686	6.597069	32.95932	25.7721	28.76877	-1.2574	0.022442	0.048068	CTD-2314G	chr5	-	50668570	50679166	6762
ENSG00000(	0	0	0	1.498151	3.681728	0.821965	-1.734	0.20077	0.30831	CTD-2147F	chr15	-	97913601	97971182	1357
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	RP11-323I1	chr15	+	35373345	35373714	370
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	RP11-307C	chr15	+	77934106	77943997	1720
ENSG00000(	4.143168	12.04288	18.47179	0	0.920432	6.575719	1.8784	0.049183	0.095702	RP11-707P	chr15	+	51749483	51752779	1053
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-485C	chr15	+	49075387	49076318	406
ENSG00000(	10.35792	10.83859	18.47179	23.22134	17.48821	18.90519	-0.57295	0.31476	0.44145	IQCH-AS1	chr15	-	67695957	67814182	5753

ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-507B	chr15	-	61931548	62007370	395
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP11-343B	chr15	-	89340644	89341965	571
ENSG00000(	2.071584	2.408575	2.638828	5.243529	1.840864	4.109825	-0.53779	0.61548	0.72859	RP11-493E	chr15	+	90419772	90420517	746
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-707P	chr15	+	51706294	51791030	560
ENSG00000(	0	8.430014	2.638828	0	1.840864	2.465895	0.97698	0.4238	0.55434	RP11-702L	chr15	+	64762452	64763563	391
ENSG00000(	35.21692	67.44011	31.66593	0	0.920432	1.64393	5.1439	7.54E-11	4.50E-10	RP11-182J	chr15	+	84944427	84950601	970
ENSG00000(	25.8948	4.817151	13.19414	33.7084	22.09037	33.70056	-0.96712	0.087861	0.15762	RP11-120K	chr15	+	50849798	50852697	606
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTD-2315E	chr15	+	90645881	90676674	352
ENSG00000(	8.286335	1.204288	2.638828	1.498151	3.681728	3.28786	0.44618	0.67328	0.77548	RP11-293M	chr14	+	75761107	75763341	715
ENSG00000(	0	0	0	1.498151	6.443024	0	-1.9753	0.14478	0.23706	CTD-3118D	chr15	-	29665806	29669160	3355
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	FKBP1AP2	chr15	-	73435577	73435859	283
ENSG00000(	2.071584	0	0	9.737982	22.09037	13.15144	-3.5339	0.000384	0.001149	RP11-499F	chr15	-	81952823	82163466	569
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP13-262C	chr15	-	84839930	84841946	546
ENSG00000(	0	8.430014	2.638828	0	1.840864	0	1.6826	0.19208	0.29779	RP11-236L	chr15	-	96592504	96607655	571
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	LINC00593	chr15	+	70127573	70135459	1483
ENSG00000(	6.214751	13.24716	9.235896	4.494453	7.363456	5.753754	0.64178	0.4081	0.53893	RP11-227D	chr15	+	48938148	48944213	1943
ENSG00000(	3.107376	1.204288	0	0	0.920432	6.575719	-0.50806	0.69128	0.7894	HSP90B2P	chr15	+	99797837	99800220	2384
ENSG00000(	7.250543	1.204288	5.277655	2.247227	6.443024	3.28786	0.18329	0.85271	0.90607	CTD-2184D	chr15	+	52416758	52432443	895
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-150L	chr15	+	35574797	35575181	385
ENSG00000(	0	3.612863	0	3.745378	0	0	-0.0396	0.9767	0.98648	CTD-3032H	chr16	+	54968825	54988577	359
ENSG00000(	6.214751	7.225726	6.597069	1.498151	0	0.821965	2.4213	0.025598	0.054089	CTD-2184D	chr15	-	52348872	52392720	635
ENSG00000(	0	2.408575	0	0	3.681728	0	-0.28514	0.83342	0.89318	RP11-429B	chr15	+	90061754	90135187	501
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	LINC00594	chr15	+	40664026	40664677	401
ENSG00000(	53.86118	52.98866	30.34652	40.45008	46.94203	59.18147	-0.08624	0.81718	0.88154	CTD-3110H	chr15	-	50651647	50652391	612
ENSG00000(	0	2.408575	0	0	0	1.64393	0.21935	0.86915	NA	LINC00677	chr14	-	1.04E+08	1.04E+08	486
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-930C	chr14	+	56777598	56811719	573
ENSG00000(	13.46529	31.31148	35.62417	0	2.761296	0.821965	4.0576	7.98E-07	3.34E-06	RP11-758N	chr15	-	33009471	33011208	1738
ENSG00000(	3.107376	0	2.638828	0	0	0	1.8293	0.17689	NA	RP11-94P1	chr15	+	77496920	77497442	245
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP5-823G1	chr20	-	52069597	52120853	542
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	CTD-2643K	chr15	-	94448634	94651167	3173
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTD-3032H	chr16	-	54971698	54972583	557
ENSG00000(	108.7581	109.5902	102.9143	15.73059	24.85166	18.08323	2.4251	5.25E-13	3.66E-12	RP11-671M	chr15	+	84855504	84866136	4910
ENSG00000(	1.035792	1.204288	0	113.1104	97.56579	83.01846	-6.1886	2.84E-15	2.29E-14	RP11-1069	chr15	+	63188011	63191742	1225
ENSG00000(	6.214751	2.408575	5.277655	0	0	0	3.3146	0.009977	0.023207	RP11-182J	chr15	+	85113880	85123406	2606
ENSG00000(	1.035792	1.204288	2.638828	0	1.840864	7.397684	-0.67084	0.58168	0.69947	RP5-977B1	chr20	-	35141012	35154533	593
ENSG00000(	43.50326	32.51577	38.263	5.243529	12.88605	4.109825	2.2816	3.26E-05	0.000113	RP11-59H7	chr15	+	59413233	59425449	633
ENSG00000(	3.107376	3.612863	6.597069	1.498151	0	2.465895	1.331	0.2387	0.35363	RP11-356M	chr15	-	59640847	59652088	497
ENSG00000(	5.17896	1.204288	3.958241	1.498151	0	3.28786	0.82876	0.47965	0.60868	RP11-387D	chr15	-	91163239	91260372	657
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-475A	chr15	-	36731173	36763217	3042
ENSG00000(	0	1.204288	0	0	0.920432	1.64393	-0.43846	0.74402	NA	RP11-315C	chr15	-	46391391	46392590	800
ENSG00000(	6.214751	9.634302	14.51355	5.992604	3.681728	7.397684	0.74051	0.34046	0.46923	RP11-138H	chr15	-	71141222	71142109	755
ENSG00000(	0	1.204288	2.638828	2.996302	0	0	0.1676	0.90131	0.93875	CTD-3065B	chr15	+	91177957	91178265	309
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-356M	chr15	-	59693420	59694203	784
ENSG00000(	0	0	2.638828	1.498151	0.920432	0.821965	-0.19167	0.88706	NA	RP11-83J1(	chr15	-	35141338	35142596	1259

ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	FKSG62	chr15	-	47425693	47426320	628
ENSG00000(	3.107376	1.204288	2.638828	0	0	1.64393	1.2819	0.32874	0.45648	RP11-505E	chr15	-	1.02E+08	1.02E+08	720
ENSG00000(	2.071584	0	0	0	2.761296	0	-0.15346	0.90925	NA	RP11-625H	chr15	-	62975115	62982647	577
ENSG00000(	565.5424	687.6483	844.4248	971.551	1208.527	844.158	-0.52695	0.00219	0.005796	CTA-204B4	chr8	-	1.42E+08	1.42E+08	9346
ENSG00000(	0	1.204288	3.958241	0	0	0	1.651	0.221	NA	RP11-20G1	chr15	-	99936818	99941520	198
ENSG00000(	0	0	0	0	3.681728	3.28786	-1.8162	0.1806	0.28356	RP11-138H	chr15	+	87585285	87590392	509
ENSG00000(	1.035792	6.021439	5.277655	2.247227	6.443024	2.465895	0.11628	0.90908	0.94406	RP11-158N	chr15	-	86293567	86296132	494
ENSG00000(	10.35792	20.47289	15.83297	0	1.840864	0	3.9388	5.82E-05	0.000196	RP11-327J	chr15	+	96779014	96779932	447
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-299G	chr15	+	1.02E+08	1.02E+08	639
ENSG00000(	6.214751	2.408575	6.597069	0.749076	0	2.465895	1.7185	0.12849	0.2152	RP11-90B9	chr15	-	83690988	83693088	454
ENSG00000(	7.250543	1.204288	6.597069	5.243529	11.96562	13.15144	-0.89607	0.28168	0.40426	RP5-991G2	chr16	+	72699069	72821143	462
ENSG00000(	3.107376	3.612863	6.597069	0	0	0.821965	2.633	0.034875	0.070927	RP11-429D	chr15	-	59558919	59563361	448
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	RP11-507J	chr15	+	51038906	51042026	304
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-182J	chr15	+	84977316	84980581	1212
ENSG00000(	16.57267	12.04288	5.277655	9.737982	6.443024	4.109825	0.68438	0.36403	0.49381	RP11-45P1	chr14	-	1.04E+08	1.04E+08	694
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-544D	chr1	-	2.39E+08	2.39E+08	3011
ENSG00000(	188.5141	199.9118	158.3297	547.5742	480.4655	571.2656	-1.5406	2.42E-19	2.38E-18	RP11-673C	chr15	-	71457109	71457754	646
ENSG00000(	5.17896	6.021439	2.638828	0.749076	0	0.821965	2.2539	0.057967	0.11048	CTD-2270L	chr16	-	23457791	23458603	813
ENSG00000(	177.1204	130.0631	153.052	6.74168	13.80648	4.109825	4.1626	4.41E-27	5.93E-26	CTB-85P21	chr5	+	1.44E+08	1.44E+08	3379
ENSG00000(	1.035792	0	3.958241	0	0	0.821965	1.2459	0.35843	NA	RP11-114H	chr15	+	78285747	78287631	483
ENSG00000(	3.107376	0	0	2.996302	0.920432	6.575719	-1.1801	0.34153	0.4704	RP11-400N	chr2	-	2.34E+08	2.34E+08	2285
ENSG00000(	1.035792	1.204288	7.916483	56.18067	43.2603	34.52253	-3.5533	4.92E-08	2.33E-07	RP11-355I2	chr14	+	62577593	62579268	1676
ENSG00000(	4.143168	3.612863	0	5.992604	6.443024	4.93179	-0.94162	0.35208	0.48182	RP11-96D1	chr16	+	68350704	68352939	428
ENSG00000(	0	0	0	2.247227	5.522592	2.465895	-2.5145	0.056285	0.10767	RP11-23E1	chr16	+	71147255	71147903	483
ENSG00000(	2.071584	7.225726	0	0	0	0	2.5144	0.062241	0.11725	RP11-554A	chr11	+	68923378	68927220	573
ENSG00000(	12.4295	15.65574	15.83297	9.737982	14.72691	15.61733	0.12503	0.83507	0.89446	CTD-2256P	chr5	-	10352813	10353713	901
ENSG00000(	6.214751	8.430014	3.958241	1.498151	1.840864	1.64393	1.5889	0.11469	0.19641	SLC22A31	chr16	-	89262406	89268072	1672
ENSG00000(	8.286335	3.612863	2.638828	5.243529	0.920432	1.64393	0.733	0.48048	0.60957	CTD-2012K	chr16	-	67595314	67596212	899
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-382A	chr15	+	83594636	83772195	754
ENSG00000(	127.4024	95.13873	116.1084	89.88907	92.96363	87.95025	0.32175	0.20439	0.31278	CTD-2196E	chr16	+	23683453	23686820	372
ENSG00000(	3.107376	4.817151	1.319414	0	0.920432	0	2.0818	0.10915	0.18834	RP11-426C	chr16	-	29228491	29231352	2099
ENSG00000(	5.17896	0	0	0.749076	0	1.64393	0.63911	0.63479	0.74395	AC002519.	chr16	+	31799523	31801961	2439
ENSG00000(	4.143168	0	5.277655	0	0	0	2.5467	0.058592	0.11145	RP11-863P	chr16	-	88211655	88212547	756
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-5N23	chr10	+	6628186	6628882	697
ENSG00000(	4.143168	13.24716	1.319414	0	0	0	3.7084	0.003372	0.008646	RP11-300A	chr15	-	29901880	29903416	1537
ENSG00000(	3.107376	1.204288	1.319414	1.498151	0	0	1.0923	0.41313	0.54357	RP5-1024G	chr1	+	53686335	53689925	3591
ENSG00000(	12.4295	33.72006	25.06886	78.65293	59.82808	49.3179	-1.3772	0.001091	0.003041	AC083843.	chr8	-	1.36E+08	1.36E+08	6253
ENSG00000(	7.250543	7.225726	21.11062	14.23244	6.443024	19.72716	-0.18943	0.78345	0.85736	RP11-467D	chr7	-	39987121	39989354	2234
ENSG00000(	10.35792	13.24716	9.235896	2.996302	0	0	2.8161	0.004697	0.0117	RP11-63E9	chr6	+	1.42E+08	1.42E+08	3996
ENSG00000(	0	0	0	8.239831	6.443024	4.109825	-3.4561	0.005241	0.012934	RP11-284N	chr1	-	1.11E+08	1.11E+08	3481
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	TCEB1P2	chr15	+	41849225	41849633	332
ENSG00000(	10.35792	6.021439	13.19414	0	0	0.821965	3.8166	0.000639	0.001846	LA16c-380	chr16	-	760746	761277	446
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-429P	chr16	-	50080340	50100135	498
ENSG00000(	0	0	0	3.745378	0.920432	2.465895	-1.9861	0.14078	0.23194	HERC2P10	chr15	+	31107474	31136356	2393

ENSG00000(	11.39371	4.817151	10.55531	0	0	0	4.354	0.000277	0.000848	RP11-467L	chr16	+	64398684	64634150	548
ENSG00000(	3.107376	13.24716	3.958241	0	0	0	3.8756	0.001851	0.004965	RP11-95H3	chr16	-	65175659	65210616	750
ENSG00000(	0	2.408575	2.638828	1.498151	0.920432	0.821965	0.3939	0.76105	0.84198	RAB43P1	chr16	-	46660316	46660904	589
ENSG00000(	2.071584	2.408575	0	0	0	0	1.5041	0.26224	NA	RP11-439I:	chr16	+	64769828	64770707	456
ENSG00000(	59.04014	73.46155	63.33186	2.247227	10.12475	16.4393	2.6826	5.41E-08	2.54E-07	SH3RF3-AS:	chr2	-	1.1E+08	1.1E+08	1604
ENSG00000(	91.14969	84.30014	67.2901	265.9218	171.2004	219.4646	-1.4209	9.18E-09	4.61E-08	RP11-488L	chr1	-	2.47E+08	2.47E+08	1246
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-177N	chr16	-	47595218	47596391	1174
ENSG00000(	0	1.204288	3.958241	2.996302	4.60216	0	-0.40343	0.74783	0.83239	RP11-525K	chr16	-	80188950	80597032	1476
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AL022344.	chr10	-	43246626	43247593	968
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-170L	chr16	-	31882208	31882445	238
ENSG00000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	CTD-3037G	chr16	-	12650210	12651551	563
ENSG00000(	37.28851	44.55865	31.66593	76.40571	49.70333	38.63235	-0.52775	0.17196	0.27296	RP11-46C2	chr16	-	89281638	89284061	2424
ENSG00000(	0	10.83859	2.638828	0	0.920432	5.753754	0.74523	0.5311	0.65583	CTD-2382E	chr15	+	42213615	42221081	771
ENSG00000(	4.143168	0	1.319414	0	0.920432	1.64393	0.68293	0.60593	0.72063	RP11-923I:	chr12	+	52242007	52246513	427
ENSG00000(	34.18113	18.06432	36.94359	34.45748	41.41944	49.3179	-0.47609	0.25952	0.37828	CTA-204B4	chr8	-	1.42E+08	1.42E+08	2231
ENSG00000(	3.107376	1.204288	0	0	0	0	1.4526	0.27741	NA	RP11-1H8.4	chr15	+	34848071	34849021	951
ENSG00000(	2.071584	0	0	5.243529	0	4.93179	-1.4325	0.26702	0.38713	RP11-697E	chr15	+	90788645	90789043	399
ENSG00000(	18.64425	2.408575	5.277655	1.498151	3.681728	9.041614	0.79142	0.38518	0.51603	RP11-715J:	chr16	-	2514951	2518214	3264
ENSG00000(	2.071584	0	1.319414	0	2.761296	0	0.17644	0.89641	0.93579	CTD-3037G	chr16	-	12654613	12704901	698
ENSG00000(	73.54123	38.53721	52.77655	68.16587	80.07758	71.51095	-0.40098	0.22283	0.33496	RP5-991G2	chr16	+	72823142	72825522	2381
ENSG00000(	1.035792	2.408575	1.319414	1.498151	4.60216	0.821965	-0.38406	0.75111	0.83484	RP11-602N	chr15	-	34665742	34666804	1063
ENSG00000(	2.071584	2.408575	0	0	0	0	1.5041	0.26224	NA	RP11-616N	chr16	-	1209548	1210176	476
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-298D	chr16	-	83759281	83759982	702
ENSG00000(	9.322127	3.612863	1.319414	0	0.920432	0	2.6693	0.032308	0.066303	RP11-410E	chr2	-	1.87E+08	1.87E+08	2202
ENSG00000(	3.107376	2.408575	6.597069	5.992604	7.363456	6.575719	-0.64031	0.47524	0.60449	RP11-1H8.:	chr15	-	34781203	34782772	1570
ENSG00000(	10.35792	2.408575	7.916483	0	0.920432	2.465895	2.0959	0.051993	0.10047	RP11-2E11	chr7	-	1.3E+08	1.3E+08	2902
ENSG00000(	6.214751	0	2.638828	2.996302	0	0.821965	0.82844	0.50903	0.63644	AC022819.	chr15	-	99697436	99701345	3910
ENSG00000(	4.143168	1.204288	1.319414	0	0	1.64393	1.2314	0.35084	0.48052	RP11-16E2	chr15	-	66063514	66064477	964
ENSG00000(	0	0	0	0	0	6.575719	-1.5834	0.24075	0.35606	CTA-363E6.	chr16	-	19354969	19413015	1937
ENSG00000(	0	2.408575	0	0	7.363456	1.64393	-1.1749	0.36945	0.49987	RP11-44F1	chr16	+	53482660	53483502	706
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	CTD-2323K	chr15	-	75805111	75805381	271
ENSG00000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	CTD-2651B	chr15	-	45490715	45491337	623
ENSG00000(	3.107376	2.408575	7.916483	1.498151	1.840864	3.28786	0.8207	0.43552	0.56513	RP11-304L	chr16	+	2141437	2145426	600
ENSG00000(	0	0	5.277655	1.498151	0	0.821965	0.63413	0.63761	0.74607	RP11-519C	chr15	-	52940831	52942063	540
ENSG00000(	0	0	0	18.72689	11.04518	20.54912	-4.9298	1.02E-05	3.79E-05	RP11-438D	chr12	-	33557810	33558831	1022
ENSG00000(	5.17896	9.634302	6.597069	2.996302	0.920432	4.109825	1.2033	0.20014	0.30776	CTD-3203P	chr16	-	27224631	27226314	1684
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-292F	chr10	+	47656084	47657233	1150
ENSG00000(	41.43168	62.62296	43.54065	55.43159	44.18074	63.2913	-0.14334	0.68301	0.78314	RP1-39G22	chr1	-	40722099	40723639	1541
ENSG00000(	5.17896	13.24716	7.916483	4.494453	4.60216	0	1.3172	0.16095	0.25838	RP11-490G	chr1	-	98432561	98434370	1810
ENSG00000(	0	0	5.277655	0	3.681728	0	0.28395	0.83336	0.89318	RP11-170L	chr16	-	31905863	31906304	442
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC009133.	chr16	-	29817817	29819053	547
ENSG00000(	17.60846	24.08575	32.98534	101.8743	79.15715	55.07165	-1.6393	2.61E-05	9.19E-05	RP11-4O1.:	chr9	-	1.15E+08	1.15E+08	4488
ENSG00000(	0	1.204288	0	2.247227	1.840864	0	-0.82823	0.54155	NA	IL21R-AS1	chr16	-	27458990	27464714	2615
ENSG00000(	69.39806	78.2787	91.03955	92.13629	76.39586	77.2647	-0.04715	0.86658	0.91591	RP11-121C	chr4	-	47842139	47846356	4218

ENSG00000(	2.071584	0	0	0	0.920432	1.64393	-0.11897	0.93001	NA	RP11-673C	chr15	-	71439989	71481381	823
ENSG00000(	4.143168	3.612863	3.958241	0	3.681728	0.821965	1.075	0.35277	0.48249	RP11-2E17	chr15	+	80458265	80459322	556
ENSG00000(	96.32865	121.6331	69.92893	2.247227	6.443024	2.465895	4.5552	2.57E-19	2.53E-18	RP11-999E	chr14	-	58460263	58461243	981
ENSG00000(	19.68005	34.92434	19.79121	11.98521	9.20432	8.219649	1.2723	0.025432	0.053785	AC009120.	chr16	-	74339100	74369244	679
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	LINC00261	chr20	-	22541191	22559280	4912
ENSG00000(	66.29068	50.58008	44.86007	5.992604	9.20432	14.79537	2.3633	5.71E-07	2.43E-06	RP11-553L	chr3	-	1.14E+08	1.14E+08	1679
ENSG00000(	5.17896	4.817151	9.235896	2.996302	3.681728	4.109825	0.72205	0.42557	0.55595	AL121578.	chrX	+	37765400	37808658	710
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	MRPS21P8	chr16	+	49798365	49798599	235
ENSG00000(	0	0	2.638828	0	1.840864	0	0.2163	0.87177	NA	CDC37P1	chr16	-	28711615	28712861	959
ENSG00000(	0	0	2.638828	2.996302	0	0	-0.1113	0.93449	NA	RP11-335G	chr1	-	25662920	25663956	459
ENSG00000(	2.071584	1.204288	1.319414	92.13629	50.62376	40.27628	-4.8465	1.99E-11	1.24E-10	RP11-549B	chr18	+	29265618	29266786	1169
ENSG00000(	4.143168	0	0	5.243529	1.840864	3.28786	-0.91625	0.45034	0.58014	RP11-382A	chr15	+	83847934	84108197	418
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RP11-261B	chr15	+	30515220	30517767	2548
ENSG00000(	42.46747	42.15007	32.98534	41.94823	44.18074	43.56414	-0.13445	0.71593	0.80851	RP11-305E	chr10	-	30591755	30594995	3241
ENSG00000(	0	1.204288	2.638828	0	0	0	1.2853	0.33195	NA	RP11-252K	chr16	-	75355788	75358946	427
ENSG00000(	11.39371	12.04288	9.235896	8.239831	13.80648	13.15144	-0.09342	0.88715	0.92967	RP3-467N1	chr6	+	1.01E+08	1.01E+08	1517
ENSG00000(	18.64425	13.24716	25.06886	4.494453	11.96562	10.68554	1.0144	0.10912	0.18832	TGFBR3L	chr19	+	7981030	7983982	1260
ENSG00000(	16.57267	10.83859	5.277655	14.23244	9.20432	9.863579	-0.01433	0.98338	0.99047	AC027601.	chr17	+	79202507	79207783	4506
ENSG00000(	75.61281	46.96722	63.33186	85.39461	66.2711	58.35951	-0.17203	0.59431	0.71037	RP11-469N	chr2	+	2.02E+08	2.02E+08	2666
ENSG00000(	0	0	3.958241	0	4.60216	2.465895	-0.54474	0.67697	0.77848	RP11-732A	chr11	+	1.02E+08	1.02E+08	1957
ENSG00000(	2.071584	0	1.319414	2.247227	0.920432	0	0.057564	0.96577	0.98014	RP13-20L1	chr17	-	80338986	80340566	360
ENSG00000(	2.071584	3.612863	0	0	0	0	1.8175	0.17961	NA	RP11-329J	chr16	+	47296652	47297411	760
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	LSM3P5	chr16	+	78389426	78389731	306
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-510N	chr16	-	71573737	71575728	409
ENSG00000(	0	0	0	2.247227	1.840864	0	-1.1573	0.3864	NA	RP11-1035	chr16	+	18814405	18823503	361
ENSG00000(	14.50109	14.45145	5.277655	10.48706	20.2495	17.26126	-0.44257	0.4887	0.61779	RP11-505K	chr16	+	84150656	84151176	521
ENSG00000(	6.214751	13.24716	5.277655	3.745378	1.840864	6.575719	0.89778	0.30338	0.42851	LA16c-306	chr16	+	933780	935090	530
ENSG00000(	39.36009	37.33292	34.30476	44.19546	26.69253	27.94681	0.16037	0.69675	0.79349	RP11-49C2	chr16	+	70610204	70611571	399
ENSG00000(	0	0	13.19414	0	1.840864	4.109825	0.79504	0.5213	0.64696	MRPS21P7	chr16	+	49741917	49742154	238
ENSG00000(	23.82321	33.72006	18.47179	56.92974	52.46462	69.86702	-1.2093	0.002038	0.005424	RP11-490N	chr2	-	36581892	36582257	366
ENSG00000(	34.18113	25.29004	31.66593	208.9921	150.0304	156.1733	-2.4671	8.47E-17	7.34E-16	HOXB7	chr17	-	46684594	46724385	3929
ENSG00000(	21.75163	30.10719	27.70769	0.749076	5.522592	3.28786	2.8757	2.76E-05	9.71E-05	RP11-401P	chr16	-	50585735	50587851	1146
ENSG00000(	12822.07	12959.34	15237.91	4139.391	6933.614	5350.992	1.3162	4.59E-17	4.03E-16	LINC00657	chr20	-	34633544	34638882	5339
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	CTC-527H2	chr16	+	48634087	48634555	469
ENSG00000(	15.53688	18.06432	14.51355	165.5457	204.3359	156.1733	-3.3961	8.71E-25	1.07E-23	RP11-266L	chr16	-	25151898	25160353	5666
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-178D	chr15	-	55734833	55735555	723
ENSG00000(	2.071584	2.408575	1.319414	0.749076	7.363456	0.821965	-0.44656	0.70417	0.79928	CTD-2524L	chr15	+	72110737	72115725	630
ENSG00000(	0	2.408575	9.235896	1.498151	2.761296	0.821965	0.88543	0.4499	0.57966	RP11-407G	chr16	+	57281262	57282404	358
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-454K	chr14	+	45838418	45840042	1625
ENSG00000(	1.035792	12.04288	2.638828	2.247227	7.363456	1.64393	0.40506	0.69217	0.79003	LA16c-390I	chr16	+	1501761	1502654	570
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	CTC-527H2	chr16	+	48671054	48672630	539
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	ABCB10P4	chr15	-	28751771	28753954	2184
ENSG00000(	461.9632	537.1123	344.367	323.6006	373.6954	406.8726	0.28357	0.1236	0.20877	RP11-611L	chr7	+	6694495	6696063	1569
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-7O14	chr16	+	51796430	51807084	812

ENSG00000(	1.035792	0	0	0	0	1.64393	-0.12526	0.92174	NA	RP11-231E	chr2	-	1.39E+08	1.39E+08	2764
ENSG00000(	10.35792	2.408575	18.47179	2.996302	4.60216	10.68554	0.68709	0.40858	0.53932	RP11-388N	chr16	+	31207452	31208284	833
ENSG00000(	4.143168	15.65574	11.87472	5.992604	11.96562	2.465895	0.57238	0.47403	0.60317	RP5-968P1	chr1	-	27018623	27020622	2000
ENSG00000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	RP11-18F1	chr16	-	80661448	80662276	829
ENSG00000(	95.29286	113.203	93.67838	51.68621	47.86246	56.71558	0.93959	0.000985	0.002766	CTA-445C9	chr22	-	26917949	26921002	3054
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-439I	chr16	+	64772226	64772467	242
ENSG00000(	1.035792	2.408575	0	0	0	0.821965	0.89411	0.50769	NA	RP11-182J	chr7	+	36359384	36360088	705
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	NSFP1	chr17	+	44450221	44564507	1471
ENSG00000(	17.60846	6.021439	10.55531	12.73428	16.56778	15.61733	-0.35737	0.57567	0.69405	RP11-254F	chr2	-	10179219	10180790	1572
ENSG00000(	8.286335	10.83859	11.87472	3.745378	1.840864	6.575719	1.2024	0.14043	0.23142	RP11-66N1	chrX	+	1.53E+08	1.53E+08	755
ENSG00000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	RP11-2C24	chr16	-	30832389	30833431	600
ENSG00000(	9.322127	9.634302	3.958241	5.992604	9.20432	17.26126	-0.4485	0.55136	0.6725	MIR4519	chr16	+	30886543	30906541	1429
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-615I	chr16	-	68607685	68623415	547
ENSG00000(	2.071584	1.204288	0	2.996302	1.840864	3.28786	-0.90076	0.46393	0.59319	RP11-42I1(	chr16	+	48657347	48778553	854
ENSG00000(	0	4.817151	2.638828	5.992604	0	0.821965	0.065951	0.95765	0.97502	RP11-92G1	chr1	+	2.01E+08	2.01E+08	736
ENSG00000(	3.107376	0	5.277655	0	0.920432	0	1.8394	0.16661	0.26557	ADAM3B	chr16	-	49551673	49552512	840
ENSG00000(	10.35792	12.04288	11.87472	9.737982	10.12475	22.19305	-0.27989	0.66548	0.76904	RP11-33B1	chr4	+	1.2E+08	1.2E+08	901
ENSG00000(	0	1.204288	0	2.996302	0.920432	0	-0.78586	0.56226	NA	RP11-1E4.1	chr8	-	9907995	9911764	3770
ENSG00000(	3.107376	0	2.638828	6.74168	5.522592	5.753754	-1.3423	0.19604	0.30268	RP11-715J	chr16	-	2502582	2502978	397
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-220I	chr9	-	37078810	37079773	964
ENSG00000(	1.035792	0	5.277655	0	0	1.64393	1.0768	0.42266	0.55313	RP11-568N	chr2	-	64749321	64751227	1907
ENSG00000(	9.322127	3.612863	7.916483	20.22504	10.12475	14.79537	-1.0329	0.1406	0.23167	RP11-10O1	chr15	-	74770411	74782627	3385
ENSG00000(	1.035792	0	0	0	0	1.64393	-0.12526	0.92174	NA	AOC4	chr17	+	41017939	41026386	2289
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTC-543D1	chr19	+	9628826	9630017	1192
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RP11-146F	chr16	+	30638297	30638499	203
ENSG00000(	96.32865	81.89156	81.80365	47.19176	32.21512	44.38611	1.0533	0.000843	0.00239	CTD-2574D	chr16	-	29930957	29933226	2270
ENSG00000(	0	0	0	2.247227	0	0.821965	-0.85594	0.51054	NA	CTC-420A1	chr16	+	61952225	61974601	714
ENSG00000(	0	0	0	7.490755	2.761296	17.26126	-3.9741	0.000977	0.002743	RP6-201G1	chrX	-	67233312	67234743	1432
ENSG00000(	6.214751	10.83859	10.55531	18.72689	28.53339	28.76877	-1.3994	0.016038	0.035578	RP5-1142A	chr16	+	88785023	88786867	1845
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-923I	chr12	-	52203489	52204384	896
ENSG00000(	11.39371	14.45145	14.51355	0	0	0	5.0018	1.16E-05	4.28E-05	RP4-791K1	chr20	-	47980414	47984296	3883
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	ULK4P2	chr15	+	30864941	30892918	798
ENSG00000(	1.035792	0	1.319414	0	2.761296	0	-0.09868	0.94199	NA	LA16c-312I	chr16	+	1458835	1462249	379
ENSG00000(	10.35792	13.24716	13.19414	7.490755	17.48821	13.9734	-0.07373	0.90849	0.94369	CTD-2270L	chr16	+	23464079	23468927	730
ENSG00000(	1.035792	4.817151	0	4.494453	0	0	0.22257	0.86602	0.91547	RP11-764E	chr2	+	1.95E+08	1.95E+08	1028
ENSG00000(	4.143168	14.45145	1.319414	2.996302	2.761296	3.28786	0.96525	0.32236	0.44965	RP11-361N	chr15	+	72897524	72904667	1194
ENSG00000(	2.071584	4.817151	0	0	0	0	2.0839	0.12453	0.21	RP11-322D	chr16	-	57086417	57092409	672
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTD-2258A	chr16	-	66484901	66485254	354
ENSG00000(	0	0	2.638828	0	2.761296	0	-0.03456	0.97961	NA	RP11-407G	chr16	-	57125125	57126215	472
ENSG00000(	1.035792	1.204288	1.319414	0	1.840864	0.821965	0.26006	0.84549	0.90132	RP11-394B	chr16	+	70780960	70781829	551
ENSG00000(	64.2191	51.78437	31.66593	35.95563	20.2495	27.12484	0.80612	0.054502	0.10477	CTC-471J1.	chr19	-	52561743	52566956	675
ENSG00000(	2.071584	0	0	4.494453	0	0.821965	-0.72959	0.5882	0.70538	RP11-521C	chr2	+	1.28E+08	1.28E+08	4476
ENSG00000(	0	0	0	2.996302	4.60216	0	-1.9381	0.15258	0.24764	CTD-2323K	chr15	+	75773002	75773177	176
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-863P	chr16	+	88120993	88121538	213

ENSG00000(	1.035792	0	0	3.745378	6.443024	15.61733	-3.2408	0.0051	0.012614	RP11-146F	chr16	+	30597228	30619914	482
ENSG00000(	30.03797	36.12863	30.34652	29.21395	28.53339	23.83698	0.23564	0.58108	0.69911	CTD-3126B	chr16	-	2694085	2695215	572
ENSG00000(	4.143168	4.817151	1.319414	7.490755	8.283888	13.15144	-1.3058	0.1299	0.21711	RP5-902P8	chr1	-	1185157	1186714	1558
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-432I9	chr16	+	71688930	71698115	406
ENSG00000(	3.107376	1.204288	3.958241	0	0	0	2.4855	0.063943	0.12003	RP11-439I1	chr16	+	64770691	64771183	493
ENSG00000(	3.107376	7.225726	1.319414	2.996302	1.840864	8.219649	-0.13616	0.89305	0.93379	RP11-229P	chr9	-	1.4E+08	1.4E+08	820
ENSG00000(	3.107376	6.021439	0	11.23613	15.64734	17.26126	-2.0144	0.014704	0.032894	RP11-83N9	chr9	-	1.39E+08	1.39E+08	1274
ENSG00000(	2.071584	2.408575	2.638828	0	3.681728	0.821965	0.48545	0.69434	0.79163	RP11-357N	chr16	-	54032225	54033881	739
ENSG00000(	81.82756	56.60152	87.08131	65.16957	48.7829	67.40112	0.30725	0.32934	0.45707	RP1-239B2	chr11	+	17402196	17405078	2883
ENSG00000(	20.71584	32.51577	9.235896	14.23244	23.0108	16.4393	0.21834	0.69967	0.79573	RP11-424G	chrY	-	21853827	21856492	2666
ENSG00000(	0	1.204288	0	0.749076	0.920432	0.821965	-0.45539	0.73631	NA	RP11-441F	chr16	+	56334528	56336816	1777
ENSG00000(	4.143168	0	2.638828	0	0	0	2.0639	0.1282	0.21482	CTD-2026K	chr15	+	75928480	75931580	572
ENSG00000(	0	0	1.319414	2.247227	1.840864	5.753754	-1.8743	0.14502	0.23739	RP11-680F	chr11	-	1.26E+08	1.26E+08	1080
ENSG00000(	6.214751	4.817151	5.277655	2.247227	5.522592	0	0.89319	0.39124	0.52201	RP13-395E	chr15	-	32605327	32607855	2529
ENSG00000(	1.035792	1.204288	2.638828	11.98521	5.522592	4.93179	-1.851	0.066773	0.1246	RP11-303E	chr16	-	81050397	81069364	789
ENSG00000(	483.7148	505.8008	527.7655	131.8373	115.054	110.9653	2.0731	2.02E-33	3.44E-32	GS1-465N1	chr7	+	19037466	19042039	4574
ENSG00000(	11.39371	4.817151	9.235896	15.73059	32.21512	23.01502	-1.387	0.023985	0.051075	RP11-347C	chr16	+	30366762	30367848	415
ENSG00000(	3.107376	0	2.638828	0.749076	0	8.219649	-0.44777	0.71838	0.81024	RP11-483P	chr16	-	83823572	83841439	577
ENSG00000(	1.035792	4.817151	0	3.745378	4.60216	3.28786	-0.76382	0.49903	0.62731	RP11-391L	chr16	-	81509628	81510124	497
ENSG00000(	11.39371	34.92434	11.87472	0	3.681728	9.863579	1.8982	0.019656	0.042716	RP11-526J	chr9	-	1.12E+08	1.12E+08	5646
ENSG00000(	18.64425	28.90291	14.51355	19.47596	32.21512	26.30288	-0.31217	0.53359	0.65808	RP4-659J6.	chr7	+	1.4E+08	1.4E+08	2380
ENSG00000(	29.00217	28.90291	17.15238	12.73428	13.80648	20.54912	0.65227	0.21346	0.32378	RP11-856B	chr11	-	65335953	65337894	1942
ENSG00000(	32.10955	34.92434	34.30476	11.23613	40.49901	45.20807	0.066939	0.8911	0.93241	RP11-708J	chr3	-	47420579	47422489	1911
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-274H	chr6	+	4492041	4496003	2272
ENSG00000(	0	0	5.277655	222.4754	255.8801	263.0288	-6.8264	6.28E-28	8.76E-27	RP11-588K	chr4	+	1.57E+08	1.57E+08	2615
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC000032.	chr1	-	1.1E+08	1.1E+08	491
ENSG00000(	0	1.204288	0	0	3.681728	3.28786	-1.3798	0.30408	0.42927	SUB1P4	chr16	+	23548382	23548877	339
ENSG00000(	5.17896	18.06432	2.638828	2.996302	3.681728	8.219649	0.70276	0.4246	0.55514	RP11-143K	chr17	+	71171622	71172772	1151
ENSG00000(	8.286335	13.24716	14.51355	2.996302	3.681728	0	2.1352	0.015866	0.035246	RP11-401P	chr16	+	50700122	50705550	5214
ENSG00000(	0	6.021439	0	2.996302	3.681728	8.219649	-1.0112	0.37442	0.50492	RP11-384N	chr16	+	72118756	72121342	369
ENSG00000(	1.035792	0	0	2.247227	0.920432	0	-0.62282	0.6445	NA	RP4-676L2	chr8	-	29209937	29210687	751
ENSG00000(	0	0	0	0	7.363456	2.465895	-2.277	0.090564	0.16156	RP11-185C	chr16	-	25836031	25837651	1094
ENSG00000(	89.0781	67.44011	38.263	379.0322	186.8477	284.3999	-2.091	2.16E-12	1.44E-11	RP5-1085F	chr20	+	31444848	31446557	1710
ENSG00000(	3.107376	1.204288	2.638828	0	0	0.821965	1.748	0.189	0.29408	RP11-467J	chr16	+	52976051	52977376	867
ENSG00000(	15.53688	13.24716	3.958241	5.243529	4.60216	18.08323	0.21875	0.77593	0.8529	RP11-368I	chr16	-	89749028	89752977	721
ENSG00000(	363.563	486.5322	360.2	252.4385	298.22	429.8877	0.30211	0.14732	0.24036	RP11-304L	chr16	-	2204798	2205359	342
ENSG00000(	9.322127	7.225726	6.597069	23.22134	38.65814	46.852	-2.1199	0.000151	0.000482	RP11-480A	chr3	-	1.96E+08	1.96E+08	3508
ENSG00000(	3.107376	8.430014	6.597069	10.48706	15.64734	4.93179	-0.71001	0.37071	0.50123	RP11-666N	chr18	-	18526867	18528428	1562
ENSG00000(	0	0	0	0.749076	8.283888	2.465895	-2.6217	0.046471	0.091088	RP11-44F2	chr4	-	76006912	76009927	785
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CTD-2311N	chr15	+	74643109	74656961	3337
ENSG00000(	58.00435	77.07441	46.17948	47.94084	37.73771	38.63235	0.53391	0.13011	0.21738	RP11-452L	chr16	-	31468032	31471057	3026
ENSG00000(	11.39371	8.430014	2.638828	2.996302	4.60216	9.863579	0.33753	0.69431	0.79163	CTD-2323K	chr15	-	75819491	75893546	789
ENSG00000(	6.214751	7.225726	0	7.490755	5.522592	1.64393	-0.09229	0.92715	0.95612	RP11-425D	chr6	+	1.1E+08	1.1E+08	872
ENSG00000(	2.071584	0	2.638828	14.23244	4.60216	6.575719	-2.0207	0.045724	0.089835	RP11-817C	chr15	+	75660496	75661925	1430

ENSG00000(	29.00217	39.74149	18.47179	28.46487	26.69253	54.24968	-0.31436	0.49619	0.62478	RP11-77H9	chr16	+	8941962	8954274	2288
ENSG00000(	1.035792	2.408575	2.638828	0.749076	0.920432	0.821965	0.85949	0.49881	0.6271	RP11-101E	chr16	-	22094577	22103552	515
ENSG00000(	1.035792	4.817151	2.638828	0	0	3.28786	0.91638	0.46996	0.5991	RP11-109G	chr4	-	79694808	79697127	2320
ENSG00000(	40.39588	26.49433	44.86007	8.988907	22.09037	32.8786	0.78119	0.11884	0.20218	AC137932.	chr16	+	89363916	89364724	402
ENSG00000(	5.17896	7.225726	5.277655	1.498151	1.840864	1.64393	1.5204	0.13325	0.22191	RP11-329J	chr16	+	47178234	47196658	494
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	TPSP2	chr16	-	1336352	1338838	610
ENSG00000(	24.85901	24.08575	32.98534	12.73428	22.09037	23.01502	0.48669	0.32364	0.451	RP11-600F	chr14	-	1.04E+08	1.04E+08	4063
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP3-369A1	chr6	-	24797549	24799117	814
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-24M:	chr15	+	76030161	76055662	1597
ENSG00000(	2.071584	7.225726	0	4.494453	3.681728	0.821965	0.039308	0.97239	0.98395	CTD-2033A	chr16	-	69790439	69791840	1402
ENSG00000(	9.322127	9.634302	15.83297	3.745378	0	4.109825	1.8623	0.033685	0.068781	RP11-715J:	chr16	+	2526559	2527062	504
ENSG00000(	8.286335	21.67718	9.235896	20.97412	18.40864	22.19305	-0.62432	0.2862	0.40954	RP11-395I(	chr4	+	40168295	40169451	1157
ENSG00000(	1.035792	0	1.319414	0	2.761296	0	-0.09868	0.94199	NA	RP11-429P	chr16	-	50092061	50093142	1082
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-973H	chr18	-	12774650	12775922	1273
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-203B	chr4	-	1.47E+08	1.47E+08	4159
ENSG00000(	24.85901	21.67718	27.70769	12.73428	9.20432	12.32947	1.0638	0.048671	0.094792	RP11-645C	chr16	-	21805416	21807080	1665
ENSG00000(	0	0	0	2.247227	2.761296	0	-1.3959	0.30129	NA	RP11-27M:	chr16	-	10670356	10672040	435
ENSG00000(	5.17896	8.430014	2.638828	0	8.283888	2.465895	0.51078	0.62396	0.73559	LA16c-306	chr16	-	950520	955224	3175
ENSG00000(	18.64425	16.86003	26.38828	27.7158	34.97642	29.59074	-0.56254	0.22813	0.3414	RP11-48B3	chr8	+	81453535	81455339	1805
ENSG00000(	6.214751	2.408575	19.79121	4.494453	9.20432	5.753754	0.48242	0.56141	0.6815	COX6CP1	chr16	-	11997780	11997994	215
ENSG00000(	1.035792	6.021439	0	0	0	0	2.0906	0.12335	0.20852	RP11-467J:	chr16	+	52968725	52969547	823
ENSG00000(	21.75163	22.88147	19.79121	5.243529	2.761296	6.575719	2.0013	0.002149	0.005696	RP11-412D	chr12	-	1.07E+08	1.07E+08	1469
ENSG00000(	5.17896	0	0	1.498151	0	0	0.88387	0.51475	0.64144	RP11-111J(	chr2	-	18728652	18729470	819
ENSG00000(	0	0	1.319414	0.749076	0.920432	0	-0.15244	0.90808	NA	RP11-345J4	chr16	+	29460512	29460946	152
ENSG00000(	532.397	650.3154	563.3897	264.4237	307.4243	276.1802	1.0392	3.85E-11	2.35E-10	RP11-395B	chr7	+	1.01E+08	1.01E+08	3921
ENSG00000(	0	2.408575	0	0	2.761296	0	-0.08034	0.95255	NA	RP11-386N	chr15	-	93135809	93139692	3810
ENSG00000(	0	1.204288	0	5.243529	11.04518	0.821965	-2.5793	0.03598	0.072903	HEXA-AS1	chr15	+	72668454	72671129	2676
ENSG00000(	21.75163	33.72006	32.98534	11.23613	31.29469	13.15144	0.64844	0.21644	0.32736	RP11-473I:	chr16	-	9199691	9201031	731
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-152P	chr16	-	8941507	8942581	430
ENSG00000(	0	0	1.319414	0.749076	1.840864	0	-0.44914	0.73845	NA	RP11-382A	chr15	+	83691323	83759534	499
ENSG00000(	7.250543	0	1.319414	6.74168	0.920432	1.64393	-0.07853	0.94618	0.9675	CTD-2288F	chr16	+	18938185	18948365	463
ENSG00000(	10.35792	21.67718	18.47179	25.46857	7.363456	8.219649	0.26442	0.68291	0.78312	RP11-436A	chr3	+	1.81E+08	1.81E+08	2312
ENSG00000(	18.64425	4.817151	7.916483	5.992604	1.840864	2.465895	1.417	0.10148	0.17761	RP11-4F5.2	chr15	+	95024040	95027181	3142
ENSG00000(	3.107376	0	2.638828	2.247227	0.920432	5.753754	-0.46979	0.69129	0.7894	RP11-533E	chr1	-	1.8E+08	1.8E+08	1257
ENSG00000(	2.071584	7.225726	1.319414	16.47966	16.56778	23.83698	-2.2141	0.003377	0.008656	CTD-2313J:	chr15	-	93322987	93324722	1736
ENSG00000(	1.035792	2.408575	3.958241	0	2.761296	0	0.94086	0.46642	0.59569	CTD-2639E	chr19	+	49429428	49429701	274
ENSG00000(	6.214751	9.634302	2.638828	8.239831	12.88605	9.041614	-0.63083	0.41805	0.54874	RP11-264B	chr16	-	28986294	28990145	467
ENSG00000(	4.143168	12.04288	2.638828	5.992604	5.522592	4.109825	0.2359	0.79055	0.86291	RP11-521I:	chr8	-	1.02E+08	1.02E+08	1142
ENSG00000(	14.50109	9.634302	0	7.490755	1.840864	4.109825	0.72694	0.44607	0.57565	CTD-2526A	chr17	-	78427535	78428529	995
ENSG00000(	0	0	1.319414	3.745378	0	1.64393	-1.0885	0.42102	0.55162	AQP4-AS1	chr18	+	24235706	24770662	2392
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-646E	chr3	-	1.82E+08	1.82E+08	1180
ENSG00000(	1.035792	3.612863	1.319414	0	6.443024	0	-0.06015	0.96238	0.97823	CTD-2583P	chr16	+	12839730	12851692	786
ENSG00000(	0	0	3.958241	0	3.681728	2.465895	-0.40879	0.75635	0.83891	RP11-429P	chr16	-	50134250	50155854	666
ENSG00000(	1.035792	0	10.55531	7.490755	7.363456	4.93179	-0.67369	0.50236	0.63035	LINC00562	chr13	-	48504290	48506757	2468

ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	WBP11P1	chr18	+	30091626	30094597	2972
ENSG00000(	26.93059	28.90291	23.74945	23.22134	25.7721	26.30288	0.08015	0.85942	0.91067	RP11-71H1	chr3	+	1.24E+08	1.24E+08	2538
ENSG00000(	2.071584	1.204288	1.319414	0	0	0	1.6469	0.22376	NA	LA16c-313I	chr16	-	728504	729777	1220
ENSG00000(	1.035792	0	3.958241	2.996302	0	0.821965	0.21524	0.86981	0.91828	AC012065.	chr2	+	20877569	20879005	1437
ENSG00000(	2.071584	12.04288	0	0.749076	7.363456	0	0.61368	0.60237	0.71748	RP11-594N	chr8	+	79518187	79521940	3754
ENSG00000(	71.46964	93.93444	43.54065	167.7929	174.8821	155.3514	-1.2347	7.48E-06	2.82E-05	RP11-119F	chr10	+	70458257	70460551	2295
ENSG00000(	0	0	0	59.17697	63.50981	102.7456	-6.9651	8.61E-12	5.51E-11	RP11-800A	chr11	+	72950020	72953380	3361
ENSG00000(	178.1562	178.2346	178.1209	135.5827	169.3595	170.1467	0.17073	0.41171	0.54242	RP11-384K	chr4	+	1.2E+08	1.2E+08	4395
ENSG00000(	5.17896	6.021439	10.55531	2.996302	0.920432	5.753754	0.99465	0.28377	0.40671	RP11-403B	chr15	-	20935076	20961512	1602
ENSG00000(	3.107376	0	0	0.749076	0.920432	0	0.44463	0.74281	NA	RP11-505K	chr16	+	84152898	84154758	1015
ENSG00000(	15.53688	8.430014	9.235896	8.988907	16.56778	4.109825	0.1654	0.81875	0.88294	RP11-438B	chr9	-	27937615	27944495	6881
ENSG00000(	199.9078	180.6432	138.5384	17.22874	14.72691	30.4127	3.0128	3.91E-21	4.14E-20	RP11-923I	chr12	+	52203789	52206648	2860
ENSG00000(	11.39371	4.817151	2.638828	0.749076	9.20432	8.219649	0.07126	0.93874	0.9628	CTD-2542L	chr16	+	85625872	85629326	3455
ENSG00000(	0	0	0	11.23613	4.60216	10.68554	-3.973	0.000881	0.002492	RP3-406A7	chr6	-	1.37E+08	1.37E+08	374
ENSG00000(	0	0	1.319414	2.996302	0.920432	11.50751	-2.4128	0.052361	0.1011	RP13-735L	chr12	+	9520060	9550213	4388
ENSG00000(	12.4295	19.2686	14.51355	12.73428	13.80648	25.48091	-0.16547	0.77576	0.85283	LA16c-316	chr16	-	1408901	1411406	435
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP5-912I13	chr7	+	1.55E+08	1.55E+08	1861
ENSG00000(	1.035792	0	3.958241	0	0	0	1.6134	0.2311	NA	RP11-626G	chr16	+	19098178	19109432	841
ENSG00000(	0	0	0	15.73059	19.32907	13.9734	-4.8996	1.14E-05	4.20E-05	RP11-297N	chr16	-	9847272	9851895	4624
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-202D	chr18	-	51105993	51107429	1037
ENSG00000(	0	1.204288	0	0	1.840864	0	-0.18234	0.88799	NA	RP11-20I23	chr16	-	2621571	2622354	287
ENSG00000(	20.71584	34.92434	11.87472	0	1.840864	0	4.4771	1.61E-06	6.54E-06	LA16c-366	chr16	+	971033	984495	1408
ENSG00000(	2.071584	2.408575	3.958241	0.749076	1.840864	0.821965	0.96162	0.42224	0.55269	RP11-96D1	chr16	-	68290065	68294346	457
ENSG00000(	3.107376	7.225726	6.597069	4.494453	13.80648	6.575719	-0.49811	0.55031	0.67158	RP11-22P6	chr16	-	28890278	28891241	558
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	CTD-3057C	chr16	-	87978664	87978808	145
ENSG00000(	6.214751	6.021439	1.319414	0	0.920432	0.821965	2.1577	0.072159	0.13317	RP11-304L	chr16	+	2169208	2170249	627
ENSG00000(	14.50109	7.225726	21.11062	16.47966	29.45382	19.72716	-0.5881	0.307	0.43274	RP11-449H	chr16	-	25096913	25122876	766
ENSG00000(	0	2.408575	2.638828	0	0	0	1.6365	0.22501	NA	TPRKBP2	chr16	-	28122494	28122968	475
ENSG00000(	2.071584	2.408575	0	0	0	0	1.5041	0.26224	NA	RP11-367F	chr9	+	93759336	93764153	1395
ENSG00000(	0	0	3.958241	3.745378	0.920432	1.64393	-0.4769	0.71141	0.80495	RP1-67M12	chr6	-	22135186	22147422	1940
ENSG00000(	8.286335	10.83859	7.916483	6.74168	9.20432	8.219649	0.15259	0.83481	0.89423	C16orf95	chr16	-	87117168	87351022	1650
ENSG00000(	0	0	0	16.47966	31.29469	13.15144	-5.1819	2.72E-06	1.08E-05	FTLP14	chr16	+	68856490	68856973	484
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-284F	chr1	+	1.56E+08	1.56E+08	1828
ENSG00000(	41.43168	31.31148	30.34652	36.7047	23.93123	16.4393	0.40705	0.37252	0.503	RP11-541N	chr10	-	1.06E+08	1.06E+08	2388
ENSG00000(	6.214751	3.612863	9.235896	5.992604	11.96562	4.109825	-0.18699	0.82218	0.88522	RP4-561L2	chr1	+	94312730	94314495	1766
ENSG00000(	3.107376	0	0	2.996302	1.840864	4.109825	-1.0101	0.41879	0.54947	RP4-536B2	chr16	+	87870138	87871269	522
ENSG00000(	0	0	0	10.48706	0.920432	0	-2.4573	0.067008	0.12501	RP11-27M2	chr16	-	10608699	10622059	502
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-8P11	chr15	+	74060555	74061978	519
ENSG00000(	5.17896	8.430014	5.277655	7.490755	7.363456	9.041614	-0.30935	0.69584	0.7928	RP11-834C	chr12	-	54538853	54541009	2157
ENSG00000(	0	2.408575	5.277655	0.749076	0.920432	1.64393	0.8197	0.5129	0.63984	RP11-923I	chr12	+	52217287	52229280	1027
ENSG00000(	5.17896	4.817151	0	0	1.840864	3.28786	0.71713	0.55364	0.67452	RP11-85A1	chr10	+	1.01E+08	1.01E+08	864
ENSG00000(	205.0868	185.4603	294.2293	117.6049	186.8477	105.2115	0.73562	0.004113	0.01037	CTD-2196E	chr16	+	23681332	23684448	2463
ENSG00000(	0	0	0	0	0	8.219649	-1.8685	0.1683	0.26795	RP11-1081	chr8	-	54301261	54303432	2172
ENSG00000(	1.035792	0	3.958241	0	0.920432	0	1.2088	0.37284	NA	RP11-166B	chr16	-	12070708	12071707	601

ENSG00000(	3.107376	0	1.319414	9.737982	4.60216	4.109825	-1.6237	0.13068	0.21821	RP11-265N	chr15	+	42864125	42864631	507
ENSG00000(	0	1.204288	0	0	0.920432	3.28786	-0.84421	0.53376	NA	RP11-219B	chr8	-	86084312	86089297	1264
ENSG00000(	0	0	0	2.247227	0.920432	1.64393	-1.4644	0.28023	NA	AC002310.	chr16	-	30548523	30549552	723
ENSG00000(	4.143168	6.021439	3.958241	21.72319	12.88605	13.15144	-1.6238	0.025604	0.054095	RP11-55K1	chr16	-	81344336	81347028	2693
ENSG00000(	0	1.204288	0	5.243529	0	3.28786	-1.6299	0.21952	0.33112	RP4-536B2	chr16	-	87807094	87812980	575
ENSG00000(	1.035792	2.408575	0	0	0	0.821965	0.89411	0.50769	NA	CTD-3193C	chr19	-	7983537	7984042	506
ENSG00000(	0	0	2.638828	0	3.681728	0.821965	-0.43351	0.74815	0.83257	RP11-271N	chr13	-	25874262	25875576	1315
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC004381.	chr16	-	20754985	20777942	351
ENSG00000(	310.7376	289.0291	416.9348	44.19546	60.74851	46.852	2.7272	2.22E-31	3.52E-30	RP13-259F	chr11	-	1.07E+08	1.07E+08	5329
ENSG00000(	3.107376	0	11.87472	0	0	0	3.2213	0.014229	0.031982	CTD-2199C	chr5	-	10195233	10197740	2508
ENSG00000(	0	2.408575	2.638828	0	0	0	1.6365	0.22501	NA	RP11-426C	chr16	+	29127448	29229181	580
ENSG00000(	7.250543	6.021439	9.235896	3.745378	2.761296	0	1.5022	0.12687	0.21314	RP11-293B	chr16	-	33489492	33500971	1178
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-109E	chr4	+	42659513	42659945	433
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-510N	chr16	+	71547766	71551752	440
ENSG00000(	6.214751	13.24716	3.958241	2.996302	0	1.64393	1.9066	0.060515	0.11448	RP11-483P	chr16	+	83831266	83834245	2980
ENSG00000(	3.107376	8.430014	7.916483	11.23613	11.96562	7.397684	-0.60928	0.42655	0.55673	RP11-73K9	chr4	-	1.13E+08	1.13E+08	2036
ENSG00000(	33.14534	50.58008	36.94359	24.71949	34.05598	45.20807	0.20988	0.60939	0.72335	FAM157C	chr16	+	90168679	90244752	2184
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	LA16c-381	chr16	+	1161627	1163399	1773
ENSG00000(	82.86335	74.66584	79.16483	33.7084	25.7721	36.98842	1.272	0.000132	0.000424	RP11-1006	chr15	+	72882032	72884186	2155
ENSG00000(	5.17896	2.408575	2.638828	6.74168	12.88605	7.397684	-1.2155	0.16314	0.26107	RP5-1085F	chr20	-	31430934	31442063	459
ENSG00000(	924.9622	898.3986	721.7193	539.3344	510.8398	526.0575	0.69026	1.40E-06	5.73E-06	RP11-252A	chr16	-	74481325	74483790	2466
ENSG00000(	13.46529	3.612863	11.87472	10.48706	2.761296	2.465895	0.77345	0.36262	0.4923	LA16c-429	chr16	-	1891021	1893548	220
ENSG00000(	1.035792	0	0	0	0.920432	1.64393	-0.43567	0.74499	NA	CTB-134F1	chr16	+	58150789	58153257	415
ENSG00000(	22.78742	9.634302	7.916483	8.239831	5.522592	1.64393	1.2666	0.10565	0.18348	MT1L	chr16	+	56651388	56652730	411
ENSG00000(	24.85901	9.634302	10.55531	35.95563	23.0108	10.68554	-0.58502	0.33232	0.46041	RP11-49I1	chr18	-	33759959	33767411	609
ENSG00000(	0	0	0	1.498151	3.681728	0	-1.4292	0.2903	NA	RP11-728K	chr7	+	1.5E+08	1.5E+08	3044
ENSG00000(	38.3243	28.90291	32.98534	84.64554	70.87326	64.93523	-1.1162	0.001193	0.003302	CTD-2382E	chr15	+	42189688	42190773	441
ENSG00000(	5.17896	1.204288	3.958241	0.749076	0.920432	2.465895	1.0086	0.38394	0.51463	RP11-63M	chr16	+	66772166	66773229	536
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AP000220.	chr21	-	26818547	26818693	147
ENSG00000(	37.28851	52.98866	38.263	41.94823	22.09037	34.52253	0.36741	0.36836	0.49865	RP13-516N	chr17	+	80251592	80252786	1195
ENSG00000(	219.5879	210.7504	304.7846	92.13629	135.3035	127.4046	1.0438	6.71E-06	2.54E-05	ERVK13-1	chr16	-	2710350	2723445	5578
ENSG00000(	0	2.408575	1.319414	0	0.920432	0.821965	0.58326	0.66656	NA	RP11-546B	chr15	+	42605885	42606584	498
ENSG00000(	0	0	0	2.247227	3.681728	5.753754	-2.7194	0.03674	0.074289	RP11-16N1	chr3	-	1.6E+08	1.6E+08	1715
ENSG00000(	1.035792	0	0	0	2.761296	0.821965	-0.71844	0.59551	NA	RP11-390D	chr15	-	72333535	72333994	460
ENSG00000(	0	0	0	0	5.522592	9.041614	-2.861	0.029479	0.061219	RP11-615I	chr16	-	68679283	68680071	550
ENSG00000(	60.07593	39.74149	46.17948	5.992604	2.761296	6.575719	3.106	5.25E-09	2.70E-08	CTD-2541J	chr18	-	65149028	65152203	3176
ENSG00000(	16.57267	19.2686	15.83297	14.98151	10.12475	12.32947	0.43833	0.45111	0.58071	RP11-382A	chr15	-	83782369	83783318	396
ENSG00000(	0	1.204288	0	3.745378	0	0	-0.68738	0.60971	NA	CTB-113P1	chr5	+	1.51E+08	1.51E+08	1567
ENSG00000(	0	0	0	0	2.761296	3.28786	-1.6293	0.2296	0.34285	TPST2P1	chr15	-	36918875	36919976	1102
ENSG00000(	3.107376	0	0	1.498151	1.840864	4.109825	-0.79894	0.53145	0.65613	LINC00515	chr21	-	26955082	26955638	557
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-592N	chr15	+	71634663	71640810	698
ENSG00000(	15.53688	10.83859	9.235896	18.72689	11.04518	22.19305	-0.51105	0.40131	0.53251	RP11-930P	chr8	-	41685683	41687452	1770
ENSG00000(	4.143168	6.021439	13.19414	25.46857	21.16994	20.54912	-1.4622	0.02016	0.043683	RP11-390B	chr10	-	17683283	17685877	2595
ENSG00000(	1.035792	1.204288	3.958241	1.498151	0	4.109825	0.081146	0.9477	0.96852	RP11-817C	chr15	-	75647551	75648087	343

ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	CTA-363E6.	chr16	-	19488238	19499221	633
ENSG00000(	0	3.612863	2.638828	2.247227	0.920432	1.64393	0.24386	0.84405	0.90056	RP11-432I9	chr16	-	71657611	71660719	465
ENSG00000(	0	0	2.638828	0.749076	0	0	0.57076	0.66213	NA	CTD-2055G	chr16	+	80770257	80776202	452
ENSG00000(	134.6529	115.6116	208.4674	2.247227	6.443024	0.821965	5.4335	2.80E-27	3.81E-26	AC012531.	chr12	+	54413694	54416373	2680
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	HMGN2P4(	chr15	+	68546887	68547277	391
ENSG00000(	13.46529	12.04288	15.83297	0.749076	0	0.821965	3.84	0.000101	0.00033	RP1-140K8	chr6	-	3905144	3912213	7070
ENSG00000(	0	1.204288	0	0.749076	6.443024	0	-1.3804	0.30486	0.43016	RP11-382A	chr15	+	83681413	83730597	421
ENSG00000(	0	0	0	4.494453	9.20432	0	-2.7729	0.035572	0.072164	RP11-491F	chr16	+	49321341	49324138	654
ENSG00000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	RP11-327F	chr16	-	50817770	50837249	787
ENSG00000(	15.53688	13.24716	13.19414	2.996302	6.443024	0	1.9418	0.020213	0.043788	RP11-23N2	chr15	+	52870039	52890906	635
ENSG00000(	2.071584	3.612863	0	0	0	0	1.8175	0.17961	NA	RP11-775C	chr15	-	81283145	81285599	2455
ENSG00000(	0	0	2.638828	3.745378	0	2.465895	-0.76616	0.56465	0.68414	RP11-413H	chr16	+	56443232	56445595	549
ENSG00000(	6.214751	0	1.319414	1.498151	0	7.397684	-0.15735	0.89726	0.93627	RP11-452L	chr16	+	31519792	31520569	647
ENSG00000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	RP11-23E1	chr16	-	33336283	33337443	560
ENSG00000(	18.64425	14.45145	32.98534	7.490755	5.522592	5.753754	1.6987	0.007563	0.018079	RP11-1166	chr16	+	31987124	32015049	1670
ENSG00000(	234.089	209.5461	209.7868	49.43899	76.39586	70.68898	1.7261	5.77E-13	4.01E-12	SNAI3-AS1	chr16	+	88729706	88753594	2096
ENSG00000(	0	3.612863	2.638828	3.745378	2.761296	4.109825	-0.61505	0.58651	0.70381	RP11-375I2	chr3	-	1.34E+08	1.34E+08	1946
ENSG00000(	6.214751	6.021439	5.277655	0	0	4.109825	1.6233	0.14808	0.24126	RP11-21M2	chr16	+	22376442	22380368	423
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-46C2	chr16	-	89323587	89333938	555
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	KB-1000E4	chr8	-	98253970	98254432	463
ENSG00000(	41.43168	37.33292	36.94359	2.247227	16.56778	7.397684	2.0682	0.000298	0.000905	RP11-1299	chr4	+	99580055	99585701	5647
ENSG00000(	3.107376	0	2.638828	2.996302	3.681728	2.465895	-0.50068	0.6655	0.76904	RP11-303E	chr16	-	81087270	81121256	773
ENSG00000(	56.96855	51.78437	34.30476	20.97412	15.64734	16.4393	1.3942	0.001255	0.003464	RP11-250B	chr6	+	81176675	81178797	2123
ENSG00000(	0	0	2.638828	0	2.761296	4.109825	-0.8534	0.51942	0.64554	LA16c-385I	chr16	+	1562980	1564676	682
ENSG00000(	5.17896	4.817151	1.319414	5.243529	3.681728	9.041614	-0.5611	0.55063	0.67183	RP1-178F1	chr17	+	18171394	18172142	749
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP11-133K	chr15	+	40524283	40528308	4026
ENSG00000(	0	0	1.319414	0	3.681728	1.64393	-1.056	0.43528	0.56498	AF213884.	chr4	-	1.03E+08	1.03E+08	479
ENSG00000(	5.17896	10.83859	2.638828	8.239831	0	0.821965	0.82718	0.43449	0.56417	CTA-250D1	chr22	-	42318027	42319104	1078
ENSG00000(	0	2.408575	0	0	1.840864	0	0.16879	0.89944	NA	RP11-315D	chr15	-	68560130	68570332	396
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-69H7	chr15	-	75519094	75526292	720
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-152L	chr15	-	92691982	92874267	1304
ENSG00000(	7.250543	4.817151	1.319414	0	0.920432	0.821965	2.1409	0.07513	0.13782	AL136419.	chr14	-	24678852	24685193	2108
ENSG00000(	0	0	0	0	5.522592	3.28786	-2.1349	0.11377	0.19496	RP11-278A	chr16	-	87773369	87781312	346
ENSG00000(	1.035792	8.430014	6.597069	0.749076	0	1.64393	2.0401	0.07777	0.14187	RP11-1006	chr15	+	72908151	72910591	2441
ENSG00000(	0	7.225726	1.319414	0.749076	3.681728	0.821965	0.50912	0.67715	0.77849	RP11-510J1	chr16	+	81993524	81996298	2775
ENSG00000(	5.17896	3.612863	0	0.749076	0	0.821965	1.5861	0.21927	0.33085	RP11-326L	chr15	-	76242805	76243485	681
ENSG00000(	4.143168	2.408575	27.70769	20.97412	3.681728	14.79537	-0.20774	0.79684	0.86752	CTB-36H16	chr5	+	1.22E+08	1.22E+08	2178
ENSG00000(	8.286335	10.83859	2.638828	2.247227	7.363456	2.465895	0.76094	0.40386	0.53493	RP11-358N	chr15	-	57539158	57540091	934
ENSG00000(	8.286335	2.408575	2.638828	0	0	0.821965	2.6264	0.036211	0.073321	AC026150.	chr15	+	30832296	30838172	701
ENSG00000(	10.35792	4.817151	1.319414	1.498151	0.920432	0.821965	1.8492	0.09429	0.16705	RP11-439E	chr1	+	2.47E+08	2.47E+08	2968
ENSG00000(	0	0	0	1.498151	6.443024	3.28786	-2.637	0.044147	0.087167	RP11-449J1	chr16	+	77467279	77478233	579
ENSG00000(	0	7.225726	0	9.737982	8.283888	8.219649	-1.5541	0.12416	0.20951	LINC00543	chr13	+	28527663	28529507	1845
ENSG00000(	35.21692	46.96722	22.43003	53.18436	52.46462	78.90863	-0.79799	0.037751	0.0761	CTA-29F11.	chr22	-	47157791	47158460	670
ENSG00000(	0	1.204288	0	11.98521	11.96562	7.397684	-3.528	0.001456	0.003968	RP11-747H	chr14	-	92223103	92226142	3040

ENSG0000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RP11-266L	chr16	+	25027299	25032344	4007
ENSG0000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	AC009133.	chr16	+	29756568	29759620	1656
ENSG0000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	VN1R67P	chr16	-	31812906	31813818	913
ENSG0000(	1.035792	0	3.958241	0	0	0.821965	1.2459	0.35843	NA	RP11-165N	chr16	+	12466669	12467756	435
ENSG0000(	0	0	0	16.47966	19.32907	13.15144	-4.8963	1.17E-05	4.30E-05	AC005307.	chr19	-	28909390	28920397	1570
ENSG0000(	3.107376	3.612863	5.277655	9.737982	13.80648	27.12484	-1.9095	0.011899	0.027195	SLC7A5P1	chr16	-	29624425	29624961	537
ENSG0000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP11-106N	chr15	-	72577068	72668322	4374
ENSG0000(	2.071584	0	1.319414	0.749076	0	0	0.90441	0.50226	NA	RP11-264L	chr16	-	78529823	78540465	719
ENSG0000(	4.143168	10.83859	1.319414	3.745378	0	1.64393	1.2434	0.25852	0.37724	RP11-72I8.	chr16	+	15188268	15203054	2598
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-18F1	chr16	-	80600691	80606705	1338
ENSG0000(	0	0	0	0.749076	2.761296	0	-0.97685	0.45852	NA	RP11-2F9.4	chr15	-	22433890	22436177	545
ENSG0000(	0	0	0	16.47966	11.04518	13.9734	-4.6579	4.02E-05	0.000138	RP11-366L	chr2	-	1.83E+08	1.83E+08	3813
ENSG0000(	5.17896	9.634302	15.83297	11.98521	5.522592	11.50751	0.052452	0.94232	0.96521	RP11-255C	chr3	+	1.79E+08	1.79E+08	1566
ENSG0000(	0	3.612863	5.277655	3.745378	0.920432	0.821965	0.48187	0.68756	0.78648	RP11-329J	chr16	+	47230222	47236340	764
ENSG0000(	0	6.021439	1.319414	3.745378	0	0	0.58698	0.6545	0.75999	RP11-421N	chr18	-	65945039	65945480	442
ENSG0000(	10.35792	14.45145	3.958241	2.247227	2.761296	7.397684	1.0831	0.20584	0.31463	RP11-482N	chr16	+	87526161	87549241	555
ENSG0000(	18.64425	19.2686	10.55531	24.71949	23.0108	13.9734	-0.32642	0.55464	0.67542	CTD-2196E	chr16	+	23579994	23581017	1024
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-143N	chr16	-	20597872	20618429	2438
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CES1P2	chr16	+	55762027	55784023	1242
ENSG0000(	70.43385	57.80581	68.60952	51.68621	23.0108	21.37109	1.0041	0.011669	0.0267	RP11-226L	chr1	-	1.6E+08	1.6E+08	1842
ENSG0000(	2.071584	6.021439	0	11.98521	0	3.28786	-0.70973	0.53401	0.65849	RP11-352G	chr15	-	66607252	66624041	500
ENSG0000(	16.57267	14.45145	6.597069	10.48706	8.283888	21.37109	-0.07942	0.90444	0.94085	CTD-2083E	chr5	-	214013	217394	2881
ENSG0000(	3.107376	1.204288	2.638828	0.749076	1.840864	0.821965	0.74287	0.54572	0.66785	CTD-2008P	chr17	-	26590660	26593395	2736
ENSG0000(	29.00217	30.10719	14.51355	15.73059	18.40864	24.65895	0.32037	0.53215	0.65665	hsa-mir-94(	chr16	+	2318156	2323419	543
ENSG0000(	9.322127	6.021439	9.235896	0.749076	2.761296	1.64393	1.941	0.042456	0.084294	ARHGAP23	chr16	-	33709886	33739634	1937
ENSG0000(	0	0	2.638828	2.996302	0.920432	0	-0.3324	0.80596	0.87421	RP11-480G	chr16	+	46823810	46825952	1836
ENSG0000(	0	2.408575	0	1.498151	0	0.821965	0.014238	0.99162	NA	AC026150.	chr15	+	30808282	30810070	1156
ENSG0000(	6.214751	0	5.277655	2.247227	3.681728	0.821965	0.60634	0.59176	0.708	RP11-797A	chr15	-	77334178	77335533	1356
ENSG0000(	0	0	1.319414	2.996302	0	0	-0.52076	0.6968	NA	RP11-298D	chr16	-	83754724	83806541	906
ENSG0000(	0	0	0	0.749076	0.920432	0.821965	-0.73223	0.57364	NA	RP11-21M2	chr16	+	22386180	22389501	1415
ENSG0000(	2.071584	4.817151	2.638828	0	0	2.465895	1.3254	0.29156	0.41564	RP11-982N	chr14	-	1.05E+08	1.05E+08	3816
ENSG0000(	29.00217	13.24716	11.87472	5.992604	11.96562	4.109825	1.2274	0.071693	0.13248	RP5-882C2	chr17	+	42298769	42301078	1796
ENSG0000(	4.143168	2.408575	1.319414	3.745378	5.522592	7.397684	-0.88729	0.37146	0.50203	RP11-1348	chr16	-	28831891	28833354	540
ENSG0000(	0	0	0	1.498151	0.920432	0.821965	-0.99775	0.45448	NA	RP11-354N	chr16	-	68848233	68857429	562
ENSG0000(	2.071584	0	0	0	1.840864	0.821965	-0.14076	0.91727	NA	RP11-90M2	chr15	-	43093166	43094603	1438
ENSG0000(	0	1.204288	0	0	2.761296	0	-0.43954	0.74062	NA	RP11-294K	chr1	+	2.02E+08	2.02E+08	1395
ENSG0000(	4.143168	2.408575	1.319414	0	0	0.821965	1.9103	0.14768	0.24079	RP6-170F5	chrX	+	1.11E+08	1.11E+08	4595
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	Z84812.4	chr16	-	67514	85195	773
ENSG0000(	386.3504	354.0606	315.3399	545.327	419.717	427.4218	-0.39716	0.019027	0.041491	RP11-566E	chr2	+	2.17E+08	2.17E+08	3148
ENSG0000(	4.143168	7.225726	17.15238	29.21395	17.48821	27.94681	-1.3404	0.02972	0.061649	RP11-61J1	chr1	+	2.13E+08	2.13E+08	1899
ENSG0000(	6.214751	4.817151	9.235896	38.20285	33.13555	24.65895	-2.1455	0.000226	0.000699	RP11-872J	chr14	-	96967147	96968658	1512
ENSG0000(	37.28851	28.90291	18.47179	48.68991	60.74851	64.93523	-1.0069	0.010124	0.023514	RP11-161N	chr16	-	1025761	1031596	3726
ENSG0000(	4.143168	4.817151	2.638828	1.498151	10.12475	5.753754	-0.48141	0.61575	0.72879	CTD-2007L	chr11	-	68380367	68384179	563
ENSG0000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	CTD-2547L	chr14	+	91724643	91725347	705

ENSG0000(	12.4295	6.021439	7.916483	21.72319	20.2495	9.041614	-0.88134	0.18325	0.28707	RP11-107F	chr15	-	42063130	42064930	334
ENSG0000(	0	0	0	2.996302	0	0.821965	-1.0802	0.41594	NA	RP11-319G	chr16	+	78931062	78933541	2480
ENSG0000(	116.0087	130.0631	129.3026	63.67142	60.74851	69.86702	0.93949	0.000265	0.000813	GS1-358P8	chrX	+	24563633	24568583	4951
ENSG0000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	HMGB3P32	chr16	+	57637049	57637609	561
ENSG0000(	3.107376	1.204288	0	4.494453	6.443024	2.465895	-1.222	0.28033	0.40256	RP11-524C	chr14	+	21852451	21853079	629
ENSG0000(	1.035792	4.817151	10.55531	0.749076	8.283888	2.465895	0.42438	0.67802	0.77926	GHc-362H1	chrX	+	1.03E+08	1.03E+08	4484
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTD-3253I1	chr16	-	82986835	83023903	1493
ENSG0000(	67.32647	83.09585	81.80365	45.69361	34.05598	55.07165	0.76752	0.01834	0.04013	AC124789.	chr17	-	36606638	36608688	702
ENSG0000(	0	1.204288	0	0.749076	6.443024	0.821965	-1.5862	0.23068	0.34407	RP11-256I9	chr16	-	65224876	65268817	1337
ENSG0000(	34.18113	26.49433	43.54065	11.23613	11.04518	6.575719	1.7792	0.000645	0.001863	RP11-434B	chr2	-	8861264	8862816	1553
ENSG0000(	0	0	1.319414	0	0.920432	3.28786	-0.84165	0.53503	NA	RP11-531A	chr8	+	73859385	73862680	3296
ENSG0000(	58.00435	52.98866	72.56776	18.72689	10.12475	18.08323	1.9086	4.28E-06	1.66E-05	CTC-205M6	chr5	-	1.8E+08	1.8E+08	3088
ENSG0000(	3.107376	0	2.638828	0	0	0	1.8293	0.17689	NA	RP11-578F	chr15	-	29008586	29009297	712
ENSG0000(	159.512	164.9874	163.6073	298.1321	284.4135	361.6646	-0.94803	5.39E-07	2.30E-06	FBXL19-AS1	chr16	-	30930640	30934590	3951
ENSG0000(	18.64425	25.29004	40.90183	77.15478	45.10117	56.71558	-1.068	0.009008	0.021169	RP11-264B	chr16	-	28968008	28978204	573
ENSG0000(	40.39588	44.55865	29.0271	1.498151	0.920432	4.109825	3.8436	7.21E-09	3.67E-08	RP11-439E	chr1	+	2.47E+08	2.47E+08	3472
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-254F	chr16	+	84861869	84862848	260
ENSG0000(	0	0	0	2.247227	5.522592	4.93179	-2.8445	0.027666	0.057936	RP11-615I2	chr16	-	68684959	68685851	893
ENSG0000(	2.071584	0	3.958241	0.749076	2.761296	3.28786	-0.12814	0.91565	0.94854	RP11-22H5	chr16	+	82806924	82863243	4037
ENSG0000(	0	0	0	1.498151	2.761296	0	-1.199	0.3707	NA	CTA-331F8.	chr16	-	58631493	58631849	357
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-459F	chr16	+	58231016	58251709	330
ENSG0000(	12.4295	6.021439	11.87472	7.490755	5.522592	12.32947	0.23761	0.74499	0.83024	RP11-394I1	chr2	+	1.75E+08	1.75E+08	1884
ENSG0000(	0	0	0	0	5.522592	0	-1.3606	0.30939	NA	CTD-2373J(	chr5	-	89684285	89685180	896
ENSG0000(	25.8948	12.04288	32.98534	11.98521	16.56778	18.08323	0.5794	0.29221	0.41641	RP11-680G	chr16	-	15111963	15114345	2383
ENSG0000(	5.17896	3.612863	2.638828	0.749076	4.60216	3.28786	0.35018	0.73971	0.82569	RP11-715J1	chr16	-	2506253	2509980	789
ENSG0000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-345N	chr16	+	79710005	79841819	1494
ENSG0000(	0	0	0	5.243529	0	5.753754	-2.4763	0.063647	0.11953	RP11-211G	chr11	+	69186231	69187279	371
ENSG0000(	0	0	1.319414	2.247227	0	0.821965	-0.59149	0.66171	NA	RP11-483I1	chr1	+	1.09E+08	1.09E+08	1566
ENSG0000(	2.071584	0	0	0	3.681728	0	-0.35836	0.79134	NA	RP11-346C	chr16	+	73126248	73127673	1079
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-10K1	chr16	-	5128169	5128606	438
ENSG0000(	30.03797	22.88147	15.83297	6.74168	9.20432	12.32947	1.2286	0.036424	0.073682	AC009120.	chr16	+	74347235	74349532	513
ENSG0000(	0	1.204288	0	2.247227	2.761296	4.93179	-1.9239	0.13413	0.2231	RP11-96D1	chr16	-	68246304	68255574	460
ENSG0000(	13.46529	12.04288	23.74945	0	4.60216	0.821965	2.8501	0.001055	0.002949	RP11-554A	chr11	+	68870961	68876562	622
ENSG0000(	1.035792	0	3.958241	3.745378	0	0	0.21954	0.86941	0.91803	RP11-314C	chr16	-	80862632	80926492	2218
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	DNM1P30	chr15	-	30443075	30445612	452
ENSG0000(	7.250543	15.65574	17.15238	0.749076	0.920432	0	3.7534	0.000177	0.000556	ADPGK-AS1	chr15	+	73075176	73090540	2730
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-95M1	chr3	-	14840838	14852921	3830
ENSG0000(	0	1.204288	0	5.992604	0.920432	2.465895	-1.8267	0.15988	0.2571	RP1-310O1	chr20	+	30586850	30591190	4341
ENSG0000(	1.035792	0	2.638828	1.498151	1.840864	1.64393	-0.30218	0.81389	0.87912	RP11-105C	chr16	-	22623864	22624804	375
ENSG0000(	3.107376	0	0	5.243529	1.840864	4.93179	-1.3608	0.25945	0.37821	AC008088.	chr17	-	20433355	20434194	840
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-93O1	chr16	+	46683038	46683761	398
ENSG0000(	59.04014	78.2787	59.37362	1.498151	5.522592	3.28786	4.1086	3.90E-14	2.92E-13	LINC00565	chr13	-	1.15E+08	1.15E+08	2331
ENSG0000(	5.17896	9.634302	3.958241	0	0	1.64393	2.6142	0.023466	0.05005	RP11-196G	chr16	+	31054471	31061201	461
ENSG0000(	13.46529	33.72006	29.0271	139.3281	115.054	147.9537	-2.3801	2.61E-12	1.74E-11	RP11-363E	chr9	+	19453207	19455171	1965

ENSG00000(	51.7896	42.15007	59.37362	40.45008	29.45382	48.49593	0.36125	0.32949	0.45725	CCPG1	chr15	-	55632230	55700708	6822
ENSG00000(	200.9436	167.396	174.1626	93.63444	106.7701	85.48435	0.92103	4.86E-05	0.000166	RP11-57H1	chr10	+	1.15E+08	1.15E+08	4237
ENSG00000(	58.00435	67.44011	81.80365	1.498151	3.681728	0	5.0395	1.87E-15	1.51E-14	RP11-731J	chr4	+	47433977	47440976	7000
ENSG00000(	91.14969	74.66584	55.41538	55.43159	46.94203	36.98842	0.66	0.049628	0.096463	RP1-228H1	chr1	+	40929991	40932436	2446
ENSG00000(	0	0	0	0	6.443024	0	-1.5465	0.25144	0.36902	RP11-538I	chr16	+	77268774	77324831	652
ENSG00000(	4.143168	4.817151	2.638828	0	6.443024	0.821965	0.54709	0.63035	0.74045	AC137934.	chr16	+	90252405	90289086	2056
ENSG00000(	26.93059	24.08575	19.79121	27.7158	40.49901	64.11326	-0.87028	0.052756	0.10175	AC004463.	chr22	+	19158908	19160345	1438
ENSG00000(	7.250543	6.021439	14.51355	4.494453	10.12475	7.397684	0.3047	0.69131	0.7894	RP11-459F	chr16	+	58163433	58193037	577
ENSG00000(	2.071584	0	0	1.498151	0	0	0.18632	0.88758	NA	RP11-327F	chr16	-	50774821	50776726	640
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-214L	chr18	-	53548919	53587430	2310
ENSG00000(	5.17896	1.204288	3.958241	0	4.60216	3.28786	0.32122	0.77668	0.85308	RP11-65L3	chr2	+	1.79E+08	1.79E+08	2058
ENSG00000(	0	1.204288	1.319414	5.992604	0	3.28786	-1.2697	0.3198	0.44694	RP11-483P	chr16	-	83963401	83964828	388
ENSG00000(	3.107376	6.021439	3.958241	5.992604	2.761296	0	0.45602	0.67131	0.77386	FTO-IT1	chr16	+	54073305	54074638	1223
ENSG00000(	4.143168	1.204288	1.319414	9.737982	9.20432	7.397684	-1.6752	0.072413	0.13355	RP4-593C1	chr1	+	1.78E+08	1.78E+08	600
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-467J	chr16	-	53044307	53045198	892
ENSG00000(	0	0	2.638828	0	0	2.465895	0.027772	0.98358	NA	RP4-575N6	chr1	+	1.02E+08	1.02E+08	592
ENSG00000(	19.68005	14.45145	13.19414	13.48336	14.72691	16.4393	0.087267	0.87924	0.92454	LINC00622	chr1	-	1.2E+08	1.2E+08	1570
ENSG00000(	54.89697	31.31148	52.77655	95.13259	50.62376	80.55256	-0.69289	0.053038	0.10227	RP11-27M	chr2	-	2.42E+08	2.42E+08	4000
ENSG00000(	0	4.817151	1.319414	0	0	0	1.8904	0.16312	0.26107	RP11-463C	chr16	-	86598751	86601367	319
ENSG00000(	0	0	3.958241	0	0	0.821965	0.91937	0.49384	NA	RP11-384P	chr9	+	33697457	33700984	3528
ENSG00000(	25.8948	40.94578	35.62417	14.23244	12.88605	14.79537	1.242	0.010145	0.023557	RP11-552M	chr1	-	1.12E+08	1.12E+08	2023
ENSG00000(	7.250543	4.817151	9.235896	5.992604	3.681728	12.32947	-0.04852	0.95249	0.97169	KB-1836B5	chr8	+	37920399	37921309	911
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-426C	chr16	-	29273594	29275800	561
ENSG00000(	4.143168	0	0	0.749076	0	0	1.0202	0.44849	NA	LA16c-425	chr16	-	1629243	1630309	404
ENSG00000(	0	3.612863	13.19414	2.247227	2.761296	4.109825	0.69887	0.50754	0.63502	RP11-30L1	chr8	-	54955549	54958189	440
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	LINC00557	chr13	+	95612295	95613573	1279
ENSG00000(	48.68222	40.94578	59.37362	23.97042	17.48821	17.26126	1.3045	0.001705	0.004597	RP11-690D	chr11	-	1.03E+08	1.03E+08	5113
ENSG00000(	0	0	1.319414	0	2.761296	0	-0.44505	0.73801	NA	RP11-190D	chr16	-	78271259	78275115	443
ENSG00000(	3.107376	1.204288	7.916483	2.996302	3.681728	0	0.67324	0.55013	0.67146	RP11-504A	chr1	-	56713966	56724243	1352
ENSG00000(	27.96638	36.12863	29.0271	0.749076	3.681728	7.397684	2.8051	1.64E-05	5.93E-05	RP11-333I	chr2	+	47004922	47007384	2463
ENSG00000(	2.071584	0	1.319414	0	0	2.465895	0.24177	0.8585	NA	RP11-77H9	chr16	+	9056563	9060847	427
ENSG00000(	0	2.408575	3.958241	1.498151	1.840864	0	0.59183	0.64742	0.75398	LA16c-395	chr16	+	1630528	1660329	485
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP3-518E1	chr1	+	1.75E+08	1.75E+08	847
ENSG00000(	1.035792	0	1.319414	5.992604	5.522592	2.465895	-1.8912	0.10784	0.18659	DOCK9-AS2	chr13	+	99740073	99740879	807
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP4-647J2	chr7	-	44998598	45000508	1911
ENSG00000(	1.035792	1.204288	1.319414	0	0.920432	0.821965	0.58234	0.66567	NA	RP11-534L	chr1	+	2.07E+08	2.07E+08	509
ENSG00000(	0	7.225726	2.638828	0.749076	2.761296	4.109825	0.27932	0.80847	0.87565	RP11-546B	chr15	+	42500611	42519188	823
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	RP1-140C1	chr6	+	1.71E+08	1.71E+08	5187
ENSG00000(	7.250543	21.67718	32.98534	9.737982	11.96562	17.26126	0.6193	0.31741	0.44424	CTB-58E17.	chr17	+	36858705	36861000	2296
ENSG00000(	4.143168	3.612863	2.638828	4.494453	8.283888	10.68554	-1.0176	0.25375	0.37178	AC004158.	chr16	-	72459384	72698908	2194
ENSG00000(	20.71584	33.72006	13.19414	13.48336	8.283888	11.50751	0.96996	0.097418	0.17162	RP1-90J20.	chr6	+	3025025	3027659	2635
ENSG00000(	3.107376	3.612863	5.277655	2.247227	5.522592	3.28786	0.10052	0.91927	0.95096	RP11-111K	chr7	-	42940871	42942238	1368
ENSG00000(	6.214751	0	1.319414	0	4.60216	4.109825	-0.12406	0.91841	0.9507	GS1-279B7	chr1	-	1.85E+08	1.85E+08	635
ENSG00000(	0	0	0	1.498151	0	4.109825	-1.5377	0.25628	NA	RP11-84D1	chr1	-	25294914	25297356	2443

ENSG0000(	1.035792	1.204288	1.319414	1.498151	0	0	0.62497	0.64477	NA	CTD-3247F	chr8	-	22536526	22541522	4997
ENSG0000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP11-209D	chr17	-	19911364	19912547	1184
ENSG0000(	0	1.204288	2.638828	0	0	0	1.2853	0.33195	NA	RP11-574H	chr5	-	1.2E+08	1.2E+08	517
ENSG0000(	2.071584	9.634302	1.319414	0	0	0	3.1431	0.01615	0.035809	RP11-417E	chr6	-	1.7E+08	1.7E+08	542
ENSG0000(	62.14751	57.80581	71.24834	1.498151	2.761296	0.821965	4.938	6.64E-15	5.20E-14	CTD-2319I	chr17	-	58160927	58169246	630
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AP006547.	chr8	+	1.44E+08	1.44E+08	692
ENSG0000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP11-810K	chr15	-	21095535	21095935	401
ENSG0000(	1.035792	4.817151	0	1.498151	1.840864	1.64393	0.16606	0.89389	0.93429	RP11-357N	chr16	-	54067909	54088495	281
ENSG0000(	155.3688	201.116	122.7055	92.88537	64.43024	74.79881	1.0333	0.000106	0.000345	RP11-145F	chr3	+	1.5E+08	1.5E+08	2974
ENSG0000(	10.35792	15.65574	21.11062	3.745378	5.522592	5.753754	1.5254	0.031228	0.064382	RP11-274H	chr3	-	1.46E+08	1.46E+08	2095
ENSG0000(	1.035792	2.408575	0	1.498151	0.920432	0	0.28377	0.83341	NA	SULT1A3	chr16	+	30205754	30215631	2369
ENSG0000(	3.107376	0	0	1.498151	0	0.821965	0.22369	0.86904	NA	RP11-6O2.4	chr15	-	99669037	99672011	2562
ENSG0000(	4.143168	13.24716	15.83297	4.494453	9.20432	2.465895	0.93604	0.24686	0.36366	RP11-454F	chr16	+	53332136	53333704	1569
ENSG0000(	0	0	1.319414	2.996302	0	0	-0.52076	0.6968	NA	RP11-252E	chr16	+	75153456	75178098	510
ENSG0000(	64.2191	40.94578	50.13772	310.8664	221.8241	269.6045	-2.3425	1.30E-20	1.34E-19	RP11-303E	chr16	+	81064375	81065090	716
ENSG0000(	5.17896	10.83859	1.319414	4.494453	5.522592	0	0.65718	0.52785	0.65258	RP5-931K2	chr20	-	10381657	10384178	2522
ENSG0000(	6.214751	6.021439	2.638828	0	0	0	3.4271	0.007291	0.017484	RP11-1000	chr15	+	32828248	32879814	543
ENSG0000(	16.57267	1.204288	7.916483	2.247227	8.283888	7.397684	0.47682	0.58822	0.70538	RP11-264B	chr16	+	28986125	29002096	5296
ENSG0000(	6.214751	10.83859	3.958241	23.22134	17.48821	19.72716	-1.4293	0.027106	0.056926	RP11-7K24	chr6	-	42059976	42061997	2022
ENSG0000(	40.39588	42.15007	54.09597	24.71949	55.22592	32.05663	0.28428	0.48532	0.61449	RP11-701H	chr15	+	25332808	25334043	1236
ENSG0000(	0	2.408575	1.319414	0	0	0	1.2548	0.34239	NA	RP11-554A	chr11	-	68914696	68939032	990
ENSG0000(	22.78742	15.65574	15.83297	32.95932	26.69253	29.59074	-0.68824	0.15267	0.24768	RP1-223E5	chr6	-	13614343	13615387	1045
ENSG0000(	0	1.204288	3.958241	0	0	1.64393	0.86871	0.52045	0.64628	RP11-5N19	chr15	-	56484551	56485460	910
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-179B	chr10	-	60085374	60086790	1417
ENSG0000(	7.250543	0	1.319414	2.247227	10.12475	3.28786	-0.66094	0.53964	0.66319	RP11-252A	chr16	+	74401360	74403724	2365
ENSG0000(	3.107376	2.408575	0	0	0	0	1.7825	0.18787	NA	RP1-166H4	chr6	-	45541083	45544507	1513
ENSG0000(	5.17896	0	2.638828	0	0	0	2.2696	0.093866	0.16642	RP11-1H8.1	chr15	+	34701826	34702795	970
ENSG0000(	1.035792	9.634302	2.638828	0	0	3.28786	1.4406	0.23566	0.35001	RP11-93I21	chr4	-	1.25E+08	1.25E+08	1771
ENSG0000(	29.00217	25.29004	18.47179	17.97781	23.93123	15.61733	0.33641	0.50251	0.63047	KB-1460A1	chr8	-	1.02E+08	1.02E+08	2825
ENSG0000(	119.1161	124.0416	117.4278	217.981	153.7121	133.9803	-0.48589	0.046243	0.090686	RP11-61A1	chr16	+	66923072	66924996	1903
ENSG0000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	RP11-435I2	chr16	+	28425024	28426339	1029
ENSG0000(	60.07593	43.35436	39.58241	51.68621	57.06678	74.79881	-0.34699	0.31622	0.44303	RP11-355C	chr9	+	1.26E+08	1.26E+08	1993
ENSG0000(	3.107376	1.204288	1.319414	7.490755	0	3.28786	-0.70055	0.55039	0.67161	RP11-690I2	chr2	+	2.33E+08	2.33E+08	2507
ENSG0000(	2.071584	2.408575	0	0	0	0	1.5041	0.26224	NA	LINC00563	chr13	-	46870580	46871979	1400
ENSG0000(	21.75163	18.06432	14.51355	44.19546	34.97642	21.37109	-0.85266	0.081723	0.14804	RP11-819C	chr11	-	1.07E+08	1.07E+08	4140
ENSG0000(	8.286335	1.204288	31.66593	2.247227	9.20432	4.93179	1.1763	0.17428	0.27592	RP4-545K1	chrX	+	1.01E+08	1.01E+08	651
ENSG0000(	0	0	0	2.996302	1.840864	0	-1.3549	0.31496	NA	ATP5J2P6	chr15	-	66707271	66707536	266
ENSG0000(	6.214751	7.225726	2.638828	0	3.681728	8.219649	0.37106	0.7173	0.80967	RP11-298D	chr16	-	83743784	83751503	566
ENSG0000(	0	0	0	0.749076	6.443024	5.753754	-2.8161	0.03047	0.063028	RP11-734K	chr2	+	9246722	9249994	3273
ENSG0000(	2.071584	9.634302	3.958241	1.498151	4.60216	0	1.093	0.31794	0.44484	RP11-173B	chr13	-	76178836	76210130	549
ENSG0000(	33.14534	37.33292	25.06886	19.47596	17.48821	30.4127	0.49014	0.28991	0.41377	RP11-141C	chr16	-	22298029	22300059	669
ENSG0000(	10.35792	3.612863	1.319414	0	4.60216	1.64393	1.0516	0.3438	0.47305	RP11-325K	chr16	+	56974940	56975638	699
ENSG0000(	1.035792	0	1.319414	176.0328	304.663	211.245	-7.3453	8.39E-23	9.49E-22	TMEM178B	chr7	+	1.41E+08	1.41E+08	10558
ENSG0000(	7.250543	13.24716	10.55531	173.0365	154.6326	137.2681	-3.8423	2.55E-24	3.08E-23	RP3-523K2	chr6	+	54807965	54809897	1933

ENSG0000(	0	10.83859	2.638828	0	0.920432	0	2.4351	0.058492	0.1113	RP11-333C	chr2	+	12855541	12856353	813
ENSG0000(	19.68005	22.88147	7.916483	19.47596	22.09037	12.32947	-0.07989	0.89062	0.93212	RP11-104N	chr16	-	89558425	89570868	871
ENSG0000(	2.071584	0	2.638828	0.749076	0	0	1.2345	0.36288	NA	RP11-496D	chr4	+	24661479	24673191	2195
ENSG0000(	3.107376	15.65574	2.638828	2.247227	0	8.219649	0.84581	0.40907	0.53984	RP11-304L	chr16	-	2144831	2147027	596
ENSG0000(	3.107376	2.408575	5.277655	0	0	5.753754	0.65805	0.58385	0.70137	AC135050.	chr16	+	31076816	31080567	504
ENSG0000(	13.46529	26.49433	35.62417	11.23613	3.681728	18.08323	1.1134	0.072409	0.13355	RP11-795F	chr18	+	77797387	77853362	5187
ENSG0000(	27.96638	26.49433	32.98534	65.16957	34.97642	34.52253	-0.61444	0.14588	0.23859	RP11-18F1	chr16	-	80631803	80636416	4614
ENSG0000(	3.107376	1.204288	3.958241	7.490755	2.761296	0	-0.24916	0.82683	0.8884	RP11-93O1	chr16	-	46694608	46695503	321
ENSG0000(	0	0	2.638828	2.996302	0	2.465895	-0.63956	0.63267	0.74257	RP4-798A1	chr1	+	16841140	16842249	1110
ENSG0000(	11.39371	3.612863	21.11062	8.988907	9.20432	8.219649	0.40879	0.57417	0.69285	RP11-37C7	chr15	+	40074772	40077818	3047
ENSG0000(	2.071584	0	1.319414	0.749076	2.761296	12.32947	-1.6414	0.16012	0.25743	CTD-2517N	chr8	-	1.46E+08	1.46E+08	3368
ENSG0000(	21.75163	19.2686	25.06886	24.71949	32.21512	21.37109	-0.23598	0.62064	0.73278	RP11-20I23	chr16	-	2619044	2621937	459
ENSG0000(	8.286335	9.634302	2.638828	5.243529	4.60216	3.28786	0.5762	0.51469	0.64144	RP11-303E	chr16	+	81088906	81090031	593
ENSG0000(	8.286335	1.204288	3.958241	0	0.920432	0	2.5856	0.039316	0.078807	RP11-114H	chr15	+	78268384	78285399	3716
ENSG0000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-296I1	chr16	+	70236257	70236362	106
ENSG0000(	0	0	0	11.98521	3.681728	5.753754	-3.6374	0.003019	0.007796	RP11-2A4.4	chr3	+	1.38E+08	1.38E+08	4706
ENSG0000(	0	0	1.319414	1.498151	0	1.64393	-0.61204	0.65104	NA	RP11-697E	chr15	+	90792788	90815440	3838
ENSG0000(	0	0	0	1.498151	1.840864	0	-0.93652	0.47589	NA	CTD-2583P	chr16	+	12853139	12855019	927
ENSG0000(	30.03797	6.021439	6.597069	5.992604	2.761296	8.219649	1.2129	0.12504	0.21068	RP11-723C	chr3	-	1.29E+08	1.29E+08	811
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-58A1	chr16	+	86679907	86702529	508
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-775H	chr4	-	1.37E+08	1.37E+08	1444
ENSG0000(	33.14534	27.69862	48.81831	21.72319	44.18074	27.94681	0.22045	0.61677	0.72942	RP11-517B	chr3	-	1.31E+08	1.31E+08	3473
ENSG0000(	19.68005	18.06432	11.87472	0	0	0	5.3082	2.17E-06	8.68E-06	RP11-68I18	chr1	-	1.51E+08	1.51E+08	1536
ENSG0000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RP11-252A	chr16	+	74456018	74469152	574
ENSG0000(	56.96855	78.2787	30.34652	40.45008	23.0108	36.98842	0.70276	0.090838	0.16197	RP11-356C	chr16	-	90176982	90234633	589
ENSG0000(	0	1.204288	0	0.749076	0.920432	0	-0.14992	0.90929	NA	RP11-169E	chr16	+	47007900	47012894	516
ENSG0000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-844G	chr15	+	56615391	56615917	527
ENSG0000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	CTD-2015G	chr16	+	86755697	86771432	550
ENSG0000(	11.39371	16.86003	5.277655	136.3317	224.5854	140.556	-3.8024	2.12E-22	2.37E-21	RP11-13L2	chr3	+	1.4E+08	1.4E+08	5692
ENSG0000(	0	0	0	23.97042	18.40864	33.70056	-5.5149	3.44E-07	1.50E-06	RP11-532F	chr15	-	41128006	41136585	643
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-317P	chr1	-	1.83E+08	1.83E+08	1492
ENSG0000(	0	0	1.319414	1.498151	6.443024	6.575719	-2.3763	0.054599	0.10494	RP11-341N	chr2	-	2.43E+08	2.43E+08	1104
ENSG0000(	7.250543	6.021439	6.597069	2.996302	5.522592	8.219649	0.22595	0.78974	0.86243	RP11-1007	chr15	-	72757469	72758603	1135
ENSG0000(	36.25272	28.90291	36.94359	33.7084	23.0108	35.34449	0.14209	0.73538	0.82299	CTA-445C9	chr22	+	26908503	26910534	2032
ENSG0000(	10.35792	1.204288	0	92.13629	91.12277	129.8705	-4.0685	9.81E-06	3.65E-05	RP3-512B1	chr6	-	7540684	7541571	888
ENSG0000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	RP11-16L1	chr15	-	36933387	36961298	565
ENSG0000(	0	1.204288	3.958241	0	0.920432	2.465895	0.36186	0.7837	0.85755	RP11-863P	chr16	-	88112767	88120989	559
ENSG0000(	1.035792	0	2.638828	2.247227	0	0.821965	0.12831	0.9237	0.95381	CTD-2380F	chr16	-	19772494	19777421	686
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-989E	chr16	-	33344309	33348279	3971
ENSG0000(	0	0	0	0.749076	2.761296	0.821965	-1.3133	0.33155	NA	RP3-496C2	chr22	-	40439072	40440534	1463
ENSG0000(	8.286335	3.612863	3.958241	12.73428	9.20432	19.72716	-1.2615	0.092124	0.1639	AC004449.	chr19	-	637105	637537	433
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	LINC00561	chr13	-	76506531	76509268	2738
ENSG0000(	29.00217	16.86003	19.79121	5.992604	9.20432	9.041614	1.3737	0.022608	0.048375	LA16c-361	chr16	-	1801560	1802263	565
ENSG0000(	1.035792	3.612863	3.958241	17.22874	8.283888	13.9734	-1.9897	0.017565	0.038644	RP1-80N2.3	chr6	-	6680542	6683866	3325

ENSG0000(	0	2.408575	3.958241	0	0.920432	0	1.4877	0.27008	0.39054	RP3-507I15	chrX	-	1.4E+08	1.4E+08	354
ENSG0000(	1.035792	0	0	2.996302	9.20432	2.465895	-2.4562	0.04793	0.093551	RP11-510C	chr1	-	75588203	75589612	1410
ENSG0000(	3.107376	0	0	0	0	2.465895	0.17171	0.89908	NA	RP11-195F	chr9	-	34661900	34666026	3264
ENSG0000(	6.214751	8.430014	0	2.996302	4.60216	13.9734	-0.46396	0.62665	0.73784	RP11-166B	chr16	+	12002065	12002773	384
ENSG0000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	RP11-344A	chr15	+	58012493	58013126	634
ENSG0000(	21.75163	13.24716	6.597069	11.98521	12.88605	16.4393	0.024755	0.96874	0.98169	RP11-629C	chr8	+	1.35E+08	1.35E+08	679
ENSG0000(	857.6357	759.9056	630.6798	879.4147	771.322	829.3626	-0.1399	0.33831	0.4669	ZNF865	chr19	+	56116771	56128635	4005
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTD-2006K	chr17	+	72595979	72603368	3493
ENSG0000(	0	0	0	3.745378	0	3.28786	-1.8467	0.17329	0.27459	RP11-38G5	chr15	-	80135889	80136646	758
ENSG0000(	2.071584	0	0	4.494453	0.920432	4.93179	-1.5152	0.22868	0.34209	RP11-510J	chr16	-	82077941	82173236	829
ENSG0000(	0	2.408575	7.916483	15.73059	5.522592	4.109825	-1.1377	0.24287	0.35875	AC009166.	chr16	+	51183150	51183730	487
ENSG0000(	0	0	0	5.243529	0	0	-1.3189	0.32312	NA	ANKRD26P	chr16	-	46503253	46603009	4741
ENSG0000(	4.143168	1.204288	1.319414	0	0	0	2.1615	0.11037	0.19002	RP11-304L	chr16	+	2162336	2163343	456
ENSG0000(	3.107376	7.225726	0	14.23244	4.60216	5.753754	-1.0655	0.2634	0.38316	CTD-2302E	chr14	+	64010287	64011382	1096
ENSG0000(	1.035792	0	1.319414	0	1.840864	0	0.17192	0.89859	NA	RP11-517C	chr16	+	84529205	84531101	596
ENSG0000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	GOLGA8T	chr15	+	30427352	30437770	1896
ENSG0000(	1.035792	0	0	1.498151	2.761296	0	-0.89883	0.50763	NA	AC009120.	chr16	+	74316313	74321417	475
ENSG0000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-545A	chr1	-	1.8E+08	1.8E+08	3294
ENSG0000(	0	2.408575	3.958241	5.992604	3.681728	6.575719	-1.1312	0.28549	0.40867	RP3-388M	chr22	+	44208336	44213274	1463
ENSG0000(	0	1.204288	0	2.996302	0.920432	1.64393	-1.2169	0.36451	0.49432	RP11-318L	chr1	+	2.12E+08	2.12E+08	262
ENSG0000(	20.71584	16.86003	18.47179	2.996302	8.283888	4.93179	1.6889	0.012127	0.027665	AC137932.	chr16	+	89387541	89391518	1205
ENSG0000(	23.82321	28.90291	15.83297	14.23244	34.97642	18.90519	0.020729	0.96848	0.98169	RP4-714D9	chr1	+	1E+08	1.01E+08	5067
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-673E	chr11	-	1.26E+08	1.26E+08	1909
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CTD-2515H	chr15	-	57819385	57821207	800
ENSG0000(	3.107376	10.83859	6.597069	2.996302	8.283888	14.79537	-0.31302	0.70577	0.80057	CTD-2196E	chr16	-	23698370	23699665	473
ENSG0000(	2.071584	0	3.958241	1.498151	1.840864	2.465895	0.032243	0.97889	0.98772	RP11-44I1(	chr16	+	48593572	48621314	438
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-389C	chr5	-	71735730	71738214	2485
ENSG0000(	4.143168	3.612863	3.958241	0	1.840864	2.465895	1.1192	0.32904	0.45674	RP11-325K	chr16	+	56974190	56975254	601
ENSG0000(	3.107376	8.430014	2.638828	0	0	0	3.3279	0.009717	0.02266	MUC22	chr6	+	30978251	31003179	6019
ENSG0000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-554A	chr11	+	68771862	68772568	366
ENSG0000(	0	2.408575	1.319414	0	0	0	1.2548	0.34239	NA	ULK4P1	chr15	-	32698798	32727193	875
ENSG0000(	5.17896	2.408575	0	10.48706	7.363456	11.50751	-1.6476	0.073833	0.13581	CTD-3105H	chr19	-	12456763	12458752	1990
ENSG0000(	6.214751	8.430014	5.277655	2.996302	7.363456	6.575719	0.21763	0.797	0.86766	RP11-517C	chr16	-	84492865	84500967	2998
ENSG0000(	9.322127	1.204288	2.638828	0.749076	0.920432	0	2.1223	0.080881	0.14675	RP11-295N	chr16	+	53202434	53203362	510
ENSG0000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	RP11-389G	chr3	+	97478367	97480374	2008
ENSG0000(	2.071584	0	0	0	0.920432	0	0.46104	0.72109	NA	RP11-276H	chr16	-	12187484	12189164	502
ENSG0000(	109.7939	78.2787	139.8579	0.749076	2.761296	1.64393	5.701	2.66E-21	2.85E-20	RP11-524D	chrX	+	99928327	99928978	652
ENSG0000(	1.035792	2.408575	0	0.749076	4.60216	0	-0.37507	0.77577	0.85283	RP11-343H	chr16	-	56742684	56763880	1018
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-160C	chr15	+	78952986	79027837	1432
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP4-584D1	chr7	+	1.5E+08	1.5E+08	837
ENSG0000(	29.00217	16.86003	5.277655	65.16957	102.168	99.45776	-2.2884	1.52E-07	6.85E-07	RP11-923I	chr12	-	52214243	52216199	1957
ENSG0000(	71.46964	73.46155	88.40072	28.46487	33.13555	41.09825	1.1649	0.000494	0.001453	RP5-1014C	chr1	+	92864531	92867613	3083
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC002550.	chr16	+	19717673	19726705	1379
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-359E	chr1	-	2.12E+08	2.12E+08	711

ENSG00000(	0	0	1.319414	0.749076	0	4.109825	-0.96956	0.47459	0.60383	LARP4P	chr15	+	36909290	36911466	2177
ENSG00000(	99.43602	90.32158	117.4278	62.92235	44.18074	54.24968	0.91235	0.001736	0.004675	RP11-174G	chr12	-	14915438	14920865	5428
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC140542.	chr16	-	47883225	47921041	1325
ENSG00000(	90.1139	136.0845	94.99779	95.88167	92.96363	64.93523	0.335	0.23845	0.35335	RP5-1057J	chr1	-	23607802	23613245	5444
ENSG00000(	13.46529	14.45145	10.55531	0	0	0	4.9318	1.70E-05	6.14E-05	RP11-863P	chr16	-	88210904	88219696	1313
ENSG00000(	8.286335	0	0	0.749076	0.920432	2.465895	0.6997	0.58164	0.69945	CTD-2049C	chr16	-	27690261	27730104	679
ENSG00000(	1.035792	0	5.277655	0	0.920432	1.64393	0.79954	0.54315	0.66568	RP11-65J3.	chr9	-	1.32E+08	1.32E+08	1934
ENSG00000(	5.17896	2.408575	5.277655	6.74168	9.20432	2.465895	-0.44363	0.6294	0.73967	RP11-318A	chr17	+	74668024	74669740	1717
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	EIF4BP5	chr16	-	47599001	47600795	1795
ENSG00000(	8.286335	8.430014	6.597069	3.745378	11.04518	11.50751	-0.14847	0.847	0.90252	RP11-498D	chr16	-	71952815	71959638	762
ENSG00000(	54.89697	61.41867	35.62417	68.16587	51.54419	53.42772	-0.18288	0.59844	0.71389	RP11-378A	chr2	+	2.19E+08	2.19E+08	2046
ENSG00000(	5.17896	0	1.319414	5.992604	2.761296	16.4393	-1.5846	0.11979	0.20343	CTD-2568A	chr19	-	51279398	51289467	495
ENSG00000(	17.60846	27.69862	7.916483	20.97412	15.64734	24.65895	-0.19058	0.73614	0.82346	AC006538.	chr19	-	2727741	2729325	1585
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-510N	chr16	-	71444343	71460367	530
ENSG00000(	12.4295	1.204288	3.958241	0	1.840864	1.64393	1.8405	0.10186	0.17806	RP3-465N2	chr1	-	25592593	25593627	459
ENSG00000(	0	1.204288	0	4.494453	2.761296	4.93179	-2.2003	0.079583	0.14471	CTD-3185P	chr15	-	66782086	66784447	1078
ENSG00000(	19.68005	18.06432	17.15238	8.988907	10.12475	9.041614	0.91738	0.12556	0.21136	CTA-14H9.5	chr6	+	26527291	26527632	342
ENSG00000(	21.75163	42.15007	19.79121	20.22504	20.2495	25.48091	0.33135	0.49851	0.62683	RP11-698N	chr11	+	35835882	35839557	3676
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-626G	chr16	+	19077313	19078016	704
ENSG00000(	3.107376	15.65574	5.277655	13.48336	13.80648	4.93179	-0.38969	0.61815	0.7305	CTD-2165H	chr5	-	14661917	14664713	2797
ENSG00000(	2.071584	1.204288	11.87472	2.247227	11.04518	0	0.1487	0.89075	0.93222	MANEA-AS1	chr6	-	96023059	96025326	2268
ENSG00000(	0	1.204288	1.319414	2.996302	1.840864	2.465895	-1.0563	0.40463	0.5355	RP11-455F	chr16	+	30118996	30121862	553
ENSG00000(	0	0	3.958241	0	0.920432	0	0.88424	0.51108	NA	RP11-474B	chr16	+	47333358	47351725	870
ENSG00000(	15.53688	12.04288	2.638828	7.490755	15.64734	16.4393	-0.33927	0.63358	0.74324	RP11-529H	chr14	-	92511119	92516990	671
ENSG00000(	36.25272	31.31148	29.0271	200.0032	143.5874	109.3213	-2.1942	6.03E-12	3.90E-11	RP11-368I7	chr16	+	89778264	89784573	1753
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-64K1	chr15	+	40666599	40668192	1594
ENSG00000(	0	3.612863	0	0	0	0.821965	0.85103	0.52479	NA	RP11-632K	chr15	-	32781468	32783787	1262
ENSG00000(	0	1.204288	3.958241	5.992604	2.761296	4.93179	-1.1375	0.30976	0.43598	RP11-578F	chr15	+	29034810	29101361	1069
ENSG00000(	12.4295	6.021439	9.235896	1.498151	0.920432	0.821965	2.5905	0.008207	0.019442	RP11-395N	chr2	+	2.28E+08	2.28E+08	1026
ENSG00000(	9.322127	8.430014	1.319414	4.494453	10.12475	3.28786	0.10245	0.90863	0.94374	CTD-2012K	chr16	-	67583117	67597861	798
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	RP11-345N	chr16	-	79750622	79804460	772
ENSG00000(	0	3.612863	2.638828	0	0	3.28786	0.55256	0.67644	0.77809	RP11-165N	chr16	-	12460839	12466439	539
ENSG00000(	0	0	0	0	4.60216	2.465895	-1.83	0.17727	0.27944	RP11-354N	chr16	+	68720302	68720573	272
ENSG00000(	1.035792	0	1.319414	0	0	2.465895	-0.03351	0.98027	NA	CTD-2012K	chr16	-	67572460	67574009	530
ENSG00000(	4.143168	1.204288	2.638828	0	2.761296	0.821965	0.83991	0.49795	0.62626	LA16c-329I	chr16	-	1763528	1764209	468
ENSG00000(	2.071584	1.204288	0	0.749076	0.920432	0.821965	0.24805	0.8531	NA	RP11-578F	chr15	+	28577383	28581755	716
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-378I(	chr9	+	19926092	19929935	3844
ENSG00000(	1.035792	0	0	2.247227	0.920432	0.821965	-0.89377	0.50979	NA	AC009120.	chr16	-	74088050	74330660	966
ENSG00000(	4.143168	2.408575	0	2.996302	2.761296	5.753754	-0.61307	0.58129	0.69922	TEN1-CDK3	chr17	+	73975312	74002080	3897
ENSG00000(	3.107376	2.408575	7.916483	6.74168	5.522592	11.50751	-0.74564	0.39139	0.5221	RP6-24A23	chrX	-	1.08E+08	1.08E+08	4996
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-543N	chr16	-	83416612	83431775	563
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-455F	chr16	-	30194826	30196278	520
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RP11-529J	chr15	+	23675986	23680359	736
ENSG00000(	7.250543	6.021439	7.916483	1.498151	7.363456	2.465895	0.80413	0.37705	0.50769	RP11-57A1	chr16	-	28671017	28752102	361

ENSG00000(	1.035792	0	0	2.247227	9.20432	5.753754	-2.6794	0.027611	0.057841	RP1-168L1	chr6	+	1.67E+08	1.67E+08	1636
ENSG00000(	5.17896	6.021439	15.83297	12.73428	16.56778	12.32947	-0.59608	0.38578	0.51666	RP11-1007	chr15	-	72700119	72767509	2325
ENSG00000(	55.93276	62.62296	40.90183	0	0	0	6.9407	1.82E-11	1.14E-10	RP11-709B	chr15	-	68591128	68593343	2216
ENSG00000(	1.035792	0	0	1.498151	1.840864	0	-0.6672	0.62173	NA	AC144833.	chr15	+	27607456	27611544	4089
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTD-2349B	chr16	+	19125324	19184900	809
ENSG00000(	13.46529	16.86003	15.83297	35.95563	20.2495	23.83698	-0.77159	0.13768	0.22766	RP11-16P6	chr2	-	2.23E+08	2.23E+08	2815
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	DPPA2P4	chr16	+	56720763	56721964	878
ENSG00000(	0	0	0	1.498151	1.840864	2.465895	-1.7134	0.20614	NA	LA16c-390I	chr16	-	1517674	1522685	307
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP4-616B8	chr20	-	37590568	37590754	187
ENSG00000(	0	1.204288	0	1.498151	0.920432	0	-0.40353	0.76332	NA	CTC-297N7	chr17	-	10561859	10562399	541
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	CTD-2083E	chr5	+	195893	196456	564
ENSG00000(	0	0	0	21.72319	24.85166	28.76877	-5.5111	3.26E-07	1.42E-06	RP11-22C1	chr8	-	95649513	95651695	2183
ENSG00000(	38.3243	34.92434	46.17948	21.72319	8.283888	25.48091	1.0597	0.026861	0.056456	RP11-399C	chr10	+	90775593	90776816	1224
ENSG00000(	2.071584	0	1.319414	4.494453	0	0	-0.2364	0.86035	0.91124	RP11-217B	chr15	+	89878284	89879392	1109
ENSG00000(	4.143168	7.225726	0	3.745378	6.443024	2.465895	-0.11104	0.91489	0.94808	RP11-709D	chr16	-	4684330	4690624	1543
ENSG00000(	15.53688	1.204288	0	0	0	2.465895	1.9174	0.12261	0.20757	RP11-109D	chr9	+	72287665	72288629	965
ENSG00000(	1.035792	0	3.958241	0	0	0	1.6134	0.2311	NA	CTD-2576D	chr16	+	17228361	17232593	641
ENSG00000(	0	3.612863	2.638828	4.494453	1.840864	2.465895	-0.39769	0.73289	0.8214	RP11-981G	chr8	+	10291182	10295822	4641
ENSG00000(	14.50109	12.04288	10.55531	61.42419	59.82808	87.12828	-2.416	1.97E-08	9.65E-08	RP11-509E	chr2	+	25380063	25382006	1944
ENSG00000(	41.43168	33.72006	35.62417	75.65663	46.94203	65.75719	-0.75258	0.03598	0.072903	RP5-1129J	chr7	+	1.52E+08	1.52E+08	1764
ENSG00000(	1.035792	3.612863	7.916483	2.996302	1.840864	9.041614	-0.14295	0.88708	0.92967	RP11-106M	chr15	+	72571208	72644135	3148
ENSG00000(	0	1.204288	0	0.749076	0	9.863579	-1.8289	0.16602	0.26473	UBE2MP1	chr16	-	34404063	34404612	550
ENSG00000(	5.17896	4.817151	10.55531	5.243529	1.840864	1.64393	1.0391	0.27104	0.39176	RP11-1024	chr3	+	30739153	30741068	1916
ENSG00000(	4.143168	0	0	2.247227	0.920432	3.28786	-0.39653	0.75652	0.83898	RP11-96D1	chr16	-	68270748	68271570	533
ENSG00000(	7.250543	2.408575	9.235896	0	4.60216	13.15144	0.077995	0.93677	0.96178	RP11-61F1	chr16	+	84627999	84630432	2434
ENSG00000(	29.00217	38.53721	42.22124	15.73059	7.363456	18.08323	1.3525	0.006494	0.015724	RP11-452L	chr16	-	31460856	31464814	449
ENSG00000(	9.322127	13.24716	5.277655	8.988907	9.20432	13.9734	-0.18781	0.7902	0.86265	RP11-77K1	chr16	-	75492150	75493915	852
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-578F	chr15	-	28964523	28983577	557
ENSG00000(	1.035792	0	0	0.749076	1.840864	0	-0.44174	0.74166	NA	RP11-77H9	chr16	+	8963108	8963889	498
ENSG00000(	33.14534	39.74149	43.54065	20.22504	25.7721	27.12484	0.65353	0.12023	0.20411	PAN3-AS1	chr13	-	28710980	28712330	1351
ENSG00000(	9.322127	7.225726	1.319414	33.7084	34.97642	18.90519	-2.1254	0.000867	0.002456	RP11-757F	chr3	+	1.12E+08	1.12E+08	1937
ENSG00000(	0	0	0	0	1.840864	4.109825	-1.6043	0.23668	0.35119	CTD-2515H	chr15	-	57769682	57770527	255
ENSG00000(	45.57484	60.21439	72.56776	78.65293	74.55499	96.99186	-0.48938	0.11247	0.19314	RP11-448G	chr4	-	10069713	10074643	3510
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	RP13-514E	chr4	-	86933449	86935027	1579
ENSG00000(	12.4295	3.612863	7.916483	0	4.60216	2.465895	1.51	0.12732	0.21373	RP11-317P	chr1	+	1.83E+08	1.83E+08	1376
ENSG00000(	94.25706	118.0202	80.48424	83.14739	106.7701	84.66239	0.095009	0.72704	0.81717	LA16c-358I	chr16	-	1367892	1372846	3107
ENSG00000(	56.96855	67.44011	38.263	74.90755	80.07758	80.55256	-0.52164	0.099268	0.17439	RP11-46D6	chr16	-	46656773	46658363	1591
ENSG00000(	0	7.225726	3.958241	2.247227	0.920432	8.219649	-0.03675	0.97336	0.98455	RP11-432I9	chr16	+	71757083	71758133	777
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-403P	chr16	+	66583183	66585092	1910
ENSG00000(	3.107376	0	1.319414	5.992604	11.04518	5.753754	-1.9019	0.064788	0.12133	DLGAP1-AS	chr18	+	4264602	4295405	2594
ENSG00000(	3.107376	1.204288	2.638828	32.95932	20.2495	24.65895	-3.1806	1.85E-05	6.66E-05	RP11-408H	chr18	-	28638806	28639359	554
ENSG00000(	4.143168	9.634302	3.958241	5.243529	9.20432	9.041614	-0.36145	0.66013	0.76457	CTB-31O20	chr19	-	1874881	1876168	1288
ENSG00000(	3.107376	0	1.319414	2.996302	2.761296	4.93179	-0.93592	0.42193	0.55238	RP11-343C	chr16	-	69477143	69478193	722
ENSG00000(	7.250543	4.817151	1.319414	0	3.681728	0	1.4009	0.24234	0.35803	AC002400.	chr16	+	23512226	23512951	726

ENSG00000(	10.35792	2.408575	6.597069	1.498151	4.60216	0.821965	1.2636	0.20857	0.31805	RP13-487P	chr15	-	25590780	25592382	1603
ENSG00000(	3.107376	7.225726	1.319414	2.247227	6.443024	4.93179	-0.17829	0.85727	0.90929	RP11-15N2	chr3	+	99898411	99900574	2164
ENSG00000(	112.9013	87.913	130.622	19.47596	23.93123	22.19305	2.3043	3.71E-12	2.44E-11	RP11-244C	chr9	-	1.25E+08	1.25E+08	3779
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-319G	chr16	+	79028242	79038627	793
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-3M1.	chr16	-	48198863	48201149	426
ENSG00000(	18.64425	24.08575	19.79121	20.22504	16.56778	25.48091	0.002098	0.99669	0.99805	RP11-16E1	chr8	+	64128539	64130592	2054
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-665J	chr15	-	74445141	74471567	554
ENSG00000(	0	0	7.916483	0	0	0	2.0802	0.12493	0.21053	RP11-16E2	chr15	-	66058798	66059736	428
ENSG00000(	6.214751	0	2.638828	0	6.443024	0	0.33615	0.7908	0.86307	CTD-2555A	chr16	-	89179583	89181687	2105
ENSG00000(	0	0	0	17.22874	28.53339	27.94681	-5.4701	4.44E-07	1.91E-06	RP11-320A	chr15	-	89532750	89533476	727
ENSG00000(	12.4295	10.83859	15.83297	2.996302	12.88605	17.26126	0.22579	0.74716	0.83187	RP11-467J	chr16	-	53069602	53086785	464
ENSG00000(	2.071584	3.612863	15.83297	1.498151	13.80648	7.397684	-0.07609	0.93302	0.95994	RP11-29G8	chr13	+	76123909	76381256	4128
ENSG00000(	0	0	0	1.498151	2.761296	2.465895	-1.9136	0.15629	0.25228	RP11-810K	chr15	-	21098712	21099309	598
ENSG00000(	80.79177	72.25726	69.92893	101.8743	76.39586	88.77221	-0.25751	0.35704	0.48654	RP11-296I	chr16	-	70253477	70279519	2631
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP11-1H8.	chr15	+	34786621	34788101	1481
ENSG00000(	16.57267	14.45145	6.597069	14.23244	16.56778	17.26126	-0.3212	0.59852	0.71391	RP11-166B	chr16	-	11974932	11976426	1495
ENSG00000(	8.286335	8.430014	1.319414	0	7.363456	2.465895	0.74395	0.47728	0.60641	RP11-680G	chr16	+	85391069	85393055	289
ENSG00000(	4.143168	0	2.638828	1.498151	0	0.821965	0.96993	0.45714	0.58691	RP11-524C	chr6	+	22221010	22222624	1615
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-744I	chr7	-	1.41E+08	1.41E+08	474
ENSG00000(	8.286335	3.612863	5.277655	7.490755	0	3.28786	0.54898	0.58655	0.70381	RP11-384L	chr3	-	32278180	32280070	1891
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-553K	chr1	-	1.99E+08	1.99E+08	416
ENSG00000(	3.107376	7.225726	6.597069	0	1.840864	0	2.4056	0.03986	0.079789	RP1-168P1	chr16	-	89458783	89478972	420
ENSG00000(	0	1.204288	1.319414	5.992604	1.840864	5.753754	-1.8159	0.12477	0.21035	RP11-259G	chr17	+	44344403	44346060	491
ENSG00000(	79.75598	74.66584	92.35896	17.97781	25.7721	16.4393	2.0048	3.01E-08	1.45E-07	RP11-21L2	chr11	+	76511408	76515599	4192
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	RP11-665A	chr15	-	28820165	28824546	725
ENSG00000(	20.71584	15.65574	21.11062	2.996302	0	7.397684	2.2319	0.00366	0.009316	RP4-614O4	chr20	-	33855688	33867846	529
ENSG00000(	17.60846	24.08575	15.83297	32.95932	24.85166	28.76877	-0.57245	0.23343	0.34716	RP11-457N	chr6	+	26686469	26688192	1724
ENSG00000(	13.46529	13.24716	3.958241	131.8373	187.7681	181.6542	-3.9136	2.58E-24	3.11E-23	RP11-923I	chr12	+	52211683	52213934	2094
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	AC002310.	chr16	-	30598983	30599241	259
ENSG00000(	166.7625	158.966	135.8996	48.68991	54.30549	42.74218	1.6515	2.87E-10	1.64E-09	CTC-462L7.	chr17	+	53246184	53250993	4810
ENSG00000(	0	8.430014	1.319414	1.498151	0.920432	0	1.3218	0.30033	0.42535	RP11-178L	chr16	-	87430310	87433901	513
ENSG00000(	148.1182	131.2674	109.5113	11.23613	8.283888	13.15144	3.503	2.53E-22	2.82E-21	TPBGL	chr11	+	74951950	74954742	2793
ENSG00000(	0	4.817151	7.916483	11.23613	0	1.64393	-0.04043	0.97152	0.98345	CTB-31N19	chr16	+	21638063	21638723	661
ENSG00000(	44.53905	55.39724	80.48424	32.95932	32.21512	17.26126	1.0991	0.006447	0.015627	RP11-353B	chr15	+	49944336	49948429	4094
ENSG00000(	9.322127	12.04288	15.83297	6.74168	0	0	2.0612	0.030828	0.063656	CTD-2636A	chr5	+	43287703	43290941	2125
ENSG00000(	178.1562	185.4603	174.1626	440.4564	437.2052	422.49	-1.2686	2.38E-14	1.81E-13	MIR4720	chr16	+	81416874	81424489	7616
ENSG00000(	0	1.204288	1.319414	0.749076	0	0	0.61214	0.64459	NA	AP000265.	chr21	-	33632115	33633896	1782
ENSG00000(	2.071584	3.612863	1.319414	0	3.681728	0.821965	0.46898	0.70575	0.80057	RP11-20I23	chr16	-	2604061	2606061	2001
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	YBX3P1	chr16	-	31579707	31580796	1090
ENSG00000(	9.322127	8.430014	10.55531	5.243529	11.96562	13.9734	-0.12528	0.86013	0.91114	RP11-6O2.	chr15	+	99679522	99685575	2677
ENSG00000(	0	0	1.319414	1.498151	0	0	-0.08979	0.94423	NA	RP11-79H2	chr8	+	79749764	79752757	2994
ENSG00000(	0	1.204288	0	1.498151	0	2.465895	-0.80408	0.55336	NA	HMGN2P4	chr16	-	35037240	35037651	412
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-189E	chr16	+	49500017	49503786	3673
ENSG00000(	126.3666	140.9017	121.3861	0.749076	1.840864	4.93179	5.4758	8.68E-26	1.11E-24	RP11-554A	chr11	-	68768233	68769516	1284

ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-91I8.	chr18	-	6641970	6642477	508
ENSG00000(	8.286335	0	3.958241	1.498151	6.443024	9.041614	-0.37233	0.71431	0.8071	RP11-357N	chr16	-	54015141	54015824	547
ENSG00000(	0	2.408575	1.319414	3.745378	11.04518	9.863579	-2.2352	0.032293	0.066284	RP11-390D	chr15	+	72264547	72332606	781
ENSG00000(	0	0	0	0	5.522592	3.28786	-2.1349	0.11377	0.19496	RP11-405F	chr16	-	57655946	57665559	556
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-352D	chr15	-	69570667	69591102	2419
ENSG00000(	1.035792	0	1.319414	0.749076	0	0	0.56083	0.6714	NA	RP11-618N	chr15	+	36905675	36906399	725
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-700H	chr16	-	58881711	58914117	505
ENSG00000(	32.10955	34.92434	19.79121	57.67882	36.81728	53.42772	-0.74783	0.065618	0.12276	RP11-529E	chr4	-	3505324	3506184	861
ENSG00000(	4.143168	1.204288	1.319414	0	0	0	2.1615	0.11037	0.19002	RP11-327F	chr16	-	50769624	50774627	1150
ENSG00000(	0	4.817151	0	0	1.840864	0	0.69806	0.6069	0.72127	DISC1FP1	chr11	+	89984400	90648220	1734
ENSG00000(	7.250543	7.225726	7.916483	0	0	0	4.0928	0.000765	0.002189	RP11-489G	chr4	-	1.74E+08	1.74E+08	2209
ENSG00000(	2.071584	0	0	0	1.840864	0	0.093542	0.94384	NA	GOLGA6L7I	chr15	-	29087381	29093821	1984
ENSG00000(	3.107376	4.817151	2.638828	0.749076	5.522592	4.109825	0.032934	0.97491	0.98535	FLJ27352	chr15	+	55700746	55710962	729
ENSG00000(	7.250543	6.021439	5.277655	3.745378	3.681728	4.93179	0.51831	0.55938	0.67993	RP11-96K1	chr1	-	1.11E+08	1.11E+08	5985
ENSG00000(	3.107376	16.86003	3.958241	0	0	0	4.1077	0.000836	0.002374	CTD-3064M	chr8	-	1.42E+08	1.42E+08	1963
ENSG00000(	0	0	3.958241	0	0.920432	0.821965	0.58423	0.66674	NA	CTD-2258A	chr16	-	66503699	66515133	533
ENSG00000(	9.322127	9.634302	13.19414	7.490755	4.60216	2.465895	1.0261	0.19182	0.29751	RP11-102F	chr8	-	70579284	70582549	3266
ENSG00000(	43.50326	57.80581	44.86007	18.72689	29.45382	29.59074	0.89394	0.026277	0.055383	LA16c-313I	chr16	+	739001	742554	3413
ENSG00000(	54.89697	40.94578	44.86007	14.23244	12.88605	9.863579	1.8734	3.49E-05	0.000121	RP5-1042I8	chr1	-	1.2E+08	1.2E+08	1359
ENSG00000(	11.39371	16.86003	6.597069	37.45378	31.29469	31.23467	-1.4558	0.005441	0.013376	RP11-304L	chr16	+	2290488	2291819	788
ENSG00000(	17.60846	6.021439	3.958241	32.95932	33.13555	29.59074	-1.6746	0.003932	0.009951	RP11-50D9	chr4	-	1.29E+08	1.29E+08	3843
ENSG00000(	7.250543	10.83859	2.638828	0.749076	3.681728	7.397684	0.70624	0.45548	0.58519	CTD-2515A	chr16	-	24814772	24831060	579
ENSG00000(	3.107376	2.408575	0	0	0	0.821965	1.3904	0.30459	0.42988	RP11-1C8.5	chr8	+	1.04E+08	1.04E+08	4597
ENSG00000(	2.071584	1.204288	3.958241	0.749076	2.761296	1.64393	0.36627	0.75755	0.83961	RP11-475B	chr4	+	1.75E+08	1.75E+08	885
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-328J	chr16	-	72258464	72259043	391
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-146F	chr16	-	30635606	30636035	430
ENSG00000(	677.4079	574.4452	629.3604	90.63814	135.3035	92.88204	2.5548	4.04E-42	8.88E-41	RP11-401P	chr16	+	50679720	50683160	3441
ENSG00000(	23.82321	44.55865	35.62417	32.21025	33.13555	28.76877	0.13539	0.74869	0.83301	AC009133.	chr16	-	29829301	29832573	970
ENSG00000(	0	4.817151	0	0.749076	1.840864	0.821965	0.30687	0.81654	0.88106	RP1-168P1	chr16	-	89486483	89488634	415
ENSG00000(	0	0	5.277655	3.745378	2.761296	0.821965	-0.35643	0.77658	0.85305	RP13-467H	chr8	+	1.43E+08	1.43E+08	3377
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-719K	chr16	-	14828542	14840034	579
ENSG00000(	0	0	0	17.22874	17.48821	5.753754	-4.5819	6.65E-05	0.000222	RP11-354P	chr9	-	21394887	21396345	1459
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-178L	chr16	-	87296365	87326044	1718
ENSG00000(	5.17896	10.83859	3.958241	0.749076	4.60216	0	1.5681	0.13881	0.2292	HPR	chr16	+	72088522	72111145	1244
ENSG00000(	87.00652	73.46155	60.69303	67.4168	99.40666	78.90863	-0.14222	0.63294	0.74271	RP11-61A1	chr16	+	66921918	66922834	762
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	RP11-264M	chr16	-	77775365	77776897	800
ENSG00000(	8.286335	15.65574	18.47179	4.494453	0	5.753754	1.8078	0.029233	0.060773	RP11-358L	chr15	+	79705700	79706228	529
ENSG00000(	0	2.408575	1.319414	0.749076	1.840864	0.821965	0.072894	0.9559	0.97381	CTD-2562G	chr15	+	75707590	75708361	466
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-653G	chr18	+	37646250	37679197	1226
ENSG00000(	180.2278	215.5675	215.0644	101.1252	100.3271	93.704	1.0408	1.47E-06	5.98E-06	RP11-196G	chr1	-	1.5E+08	1.5E+08	4527
ENSG00000(	2.071584	6.021439	5.277655	4.494453	6.443024	2.465895	-0.00972	0.99189	0.99508	CTD-2196E	chr16	+	23617162	23635428	627
ENSG00000(	0	0	0	3.745378	0	1.64393	-1.4934	0.26982	NA	GS1-204I17	chr1	+	1.86E+08	1.86E+08	901
ENSG00000(	0	0	0	11.98521	4.60216	2.465895	-3.4359	0.005906	0.01442	RP4-668J24	chr6	-	1384025	1385301	1277
ENSG00000(	6.214751	7.225726	7.916483	2.996302	5.522592	15.61733	-0.16021	0.84543	0.90132	CTD-2358C	chr16	-	31720434	31723305	441

ENSG00000(	10.35792	18.06432	10.55531	4.494453	13.80648	14.79537	0.22626	0.73941	0.82547	LA16c-431I	chr16	+	1682260	1736716	5326
ENSG00000(	1.035792	0	1.319414	0	0	1.64393	0.22525	0.86714	NA	AC002551.	chr16	+	27654520	27655984	592
ENSG00000(	8.286335	4.817151	9.235896	5.992604	9.20432	20.54912	-0.62146	0.40586	0.5367	RP4-612B1	chr1	-	87169185	87170145	961
ENSG00000(	2.071584	1.204288	3.958241	1.498151	9.20432	10.68554	-1.3125	0.18964	0.29482	BOLA2B	chr16	-	29454551	29465972	3103
ENSG00000(	12.4295	8.430014	9.235896	0	1.840864	3.28786	2.2033	0.019863	0.043118	RP11-256I9	chr16	-	65318402	65610203	1760
ENSG00000(	15.53688	28.90291	23.74945	3.745378	14.72691	7.397684	1.331	0.034496	0.070235	RP11-21B2	chr16	-	88579368	88597461	733
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	RP11-506E	chr6	-	52990445	52990944	500
ENSG00000(	0	0	0	10.48706	9.20432	0.821965	-3.4902	0.005321	0.013111	CTC-523E2:	chr19	-	35302493	35305249	2757
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	AC005592.	chr5	+	1.42E+08	1.42E+08	1640
ENSG00000(	3.107376	3.612863	7.916483	2.247227	4.60216	10.68554	-0.23627	0.79836	0.86857	RP11-102N	chr3	+	1.36E+08	1.36E+08	3151
ENSG00000(	0	0	3.958241	2.996302	0.920432	0.821965	-0.19478	0.88228	0.92653	RP11-1223	chr2	+	1.11E+08	1.11E+08	857
ENSG00000(	2.071584	1.204288	2.638828	13.48336	9.20432	13.15144	-2.2809	0.010033	0.023324	RP11-650L	chr15	-	78881465	78883618	2154
ENSG00000(	0	0	1.319414	0	2.761296	0	-0.44505	0.73801	NA	KRT18P18	chr16	+	72762515	72763793	1279
ENSG00000(	3.107376	6.021439	0	0	0	0	2.5044	0.063254	0.11894	RP11-498D	chr16	-	71915456	71916176	426
ENSG00000(	9.322127	12.04288	10.55531	3.745378	7.363456	4.109825	0.982	0.20261	0.31049	RP11-22P6	chr16	-	28873487	28874661	544
ENSG00000(	12.4295	15.65574	23.74945	25.46857	27.61296	24.65895	-0.57388	0.25832	0.37699	CTC-459F4.	chr19	-	28248092	28251757	3666
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	WI2-89031	chrX	-	1.54E+08	1.54E+08	792
ENSG00000(	2.071584	0	5.277655	2.996302	10.12475	3.28786	-0.94629	0.37311	0.50365	RP11-10O1	chr15	+	74781943	74809300	361
ENSG00000(	3.107376	1.204288	7.916483	17.97781	16.56778	20.54912	-2.0184	0.0065	0.015736	RP11-529K	chr16	-	70349543	70380650	1471
ENSG00000(	9.322127	0	3.958241	1.498151	6.443024	2.465895	0.30885	0.77302	0.85085	CTD-2354A	chr18	+	70992176	71017113	1165
ENSG00000(	6.214751	6.021439	1.319414	8.988907	3.681728	6.575719	-0.43197	0.63425	0.74375	RP11-252K	chr16	-	75413716	75415158	374
ENSG00000(	81.82756	98.75159	112.1502	125.8447	98.48622	96.99186	-0.13924	0.59539	0.71116	RP4-555D2	chr3	+	44158791	44163857	5067
ENSG00000(	0	0	2.638828	2.996302	1.840864	0	-0.51791	0.70021	0.79624	TCF24	chr8	-	67858736	67874825	2450
ENSG00000(	0	0	2.638828	1.498151	1.840864	0	-0.19645	0.88476	0.9281	RP11-480G	chr16	-	46737281	46737937	657
ENSG00000(	2.071584	2.408575	0	0	0	0	1.5041	0.26224	NA	RP11-709D	chr16	-	4610002	4611663	1662
ENSG00000(	14.50109	8.430014	6.597069	0	3.681728	8.219649	1.154	0.20713	0.31633	GOLGA8H	chr15	+	30896329	30906764	1899
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-90P1	chr7	-	161765	164972	3208
ENSG00000(	117.0445	136.0845	139.8579	98.87797	102.168	87.95025	0.43815	0.068026	0.12664	RP11-283I:	chr12	-	383120	386289	3170
ENSG00000(	472.3211	440.7693	492.1413	27.7158	13.80648	15.61733	4.5574	1.37E-72	6.26E-71	LOXL1-AS1	chr15	-	74200424	74220589	2358
ENSG00000(	0	0	0	5.243529	4.60216	4.109825	-3.0071	0.018465	0.040385	RP11-44F1	chr16	+	53407405	53418657	721
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-895K	chr16	+	10127541	10131154	488
ENSG00000(	0	0	0	0.749076	3.681728	6.575719	-2.58	0.050272	0.097603	TUBB8P7	chr16	+	90159562	90162762	2115
ENSG00000(	7.250543	4.817151	5.277655	0	5.522592	7.397684	0.37126	0.70745	0.80218	RP11-680G	chr16	-	15082116	15084017	1902
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CTD-2311N	chr15	+	74657776	74659391	785
ENSG00000(	2.071584	0	2.638828	0	0	0.821965	1.2046	0.37464	NA	RP11-48G1	chr15	-	56700681	56702384	839
ENSG00000(	241.3395	220.3847	284.9934	244.1986	188.6886	185.7641	0.26679	0.18251	0.28607	LINC00662	chr19	-	28175488	28284848	2480
ENSG00000(	0	0	0	0	0.920432	4.109825	-1.3831	0.30514	NA	RP11-223I:	chr2	+	2.32E+08	2.32E+08	598
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-533E	chr1	-	1.8E+08	1.8E+08	447
ENSG00000(	2.071584	0	1.319414	0	0	0.821965	0.88094	0.51378	NA	RP11-264L	chr16	+	78568271	78569545	707
ENSG00000(	0	0	1.319414	4.494453	4.60216	6.575719	-2.5228	0.037598	0.075847	RP11-303E	chr16	+	81103459	81110203	408
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP1-265C2	chr6	+	28104627	28107456	2830
ENSG00000(	14.50109	9.634302	22.43003	19.47596	18.40864	31.23467	-0.55276	0.31706	0.44399	RP11-146F	chr16	-	30709030	30710379	1142
ENSG00000(	3.107376	0	0	0	0.920432	0	0.70943	0.5938	NA	RP11-143I:	chr7	+	1.49E+08	1.49E+08	2216
ENSG00000(	0	0	0	6.74168	0.920432	7.397684	-3.0571	0.017201	0.037922	MIA	chr19	+	41277553	41283395	632

ENSG00000(	0	0	0	6.74168	3.681728	4.93179	-3.1499	0.012771	0.028962	RP11-141J:	chr17	+	4513744	4520945	1273
ENSG00000(	2.071584	0	0	0	6.443024	0.821965	-1.0111	0.44809	0.57777	RP11-67A1	chr16	+	68111243	68156174	549
ENSG00000(	0	6.021439	7.916483	2.247227	4.60216	3.28786	0.36249	0.7297	0.81891	RP11-104C	chr17	+	4204667	4205993	1327
ENSG00000(	1.035792	1.204288	1.319414	2.247227	0	0	0.34377	0.79908	NA	RP5-867C2	chr17	+	45247192	45248415	673
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-515E	chr17	-	53545427	53588299	566
ENSG00000(	13.46529	14.45145	9.235896	5.992604	10.12475	7.397684	0.62424	0.36667	0.49673	RP11-333E	chr17	+	5095379	5151364	1715
ENSG00000(	18.64425	12.04288	14.51355	8.988907	23.0108	14.79537	-0.03472	0.95403	0.97262	CTC-479C5	chr16	-	67963517	67969920	5685
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-63A1	chr17	-	44994136	45000400	395
ENSG00000(	98.40023	77.07441	91.03955	8.988907	11.04518	27.94681	2.4163	4.83E-09	2.50E-08	AC144831.	chr17	+	81061205	81063860	2656
ENSG00000(	1.035792	0	2.638828	2.996302	3.681728	4.109825	-1.1696	0.32147	0.44873	RP11-473N	chr16	-	3206737	3207484	748
ENSG00000(	106.6866	116.8159	92.35896	15.73059	38.65814	73.15488	1.283	0.00138	0.003783	RP1-59D14	chr17	-	2292560	2295372	2813
ENSG00000(	5.17896	12.04288	10.55531	2.996302	0.920432	6.575719	1.22	0.16648	0.26538	RP11-235E	chr17	-	3505055	3505566	512
ENSG00000(	11.39371	12.04288	5.277655	4.494453	11.96562	12.32947	0.011129	0.98793	0.99279	CTD-2561B	chr17	-	78940039	78945013	3133
ENSG00000(	11.39371	19.2686	14.51355	2.247227	10.12475	3.28786	1.4206	0.057064	0.10898	PCDHGA9	chr5	+	1.41E+08	1.41E+08	4605
ENSG00000(	0	3.612863	0	0	0	0.821965	0.85103	0.52479	NA	CTC-496I23	chr16	-	19830826	19830950	125
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	CTD-3148I:	chr19	+	49927006	49932075	1876
ENSG00000(	0	0	0	0	2.761296	1.64393	-1.2339	0.35779	NA	RP11-74E2	chr17	-	2627714	2652714	792
ENSG00000(	8.286335	12.04288	7.916483	2.247227	3.681728	7.397684	0.97458	0.23761	0.35235	RP11-342L	chr6	+	80262511	80262877	367
ENSG00000(	49.71801	48.17151	34.30476	50.18806	30.37426	28.76877	0.26718	0.50355	0.6314	RP11-473N	chr16	-	3101992	3109371	2163
ENSG00000(	0	4.817151	3.958241	0	1.840864	0	1.4076	0.28303	0.40585	CTD-2529C	chr17	+	77997693	77999906	415
ENSG00000(	2.071584	0	1.319414	0	0	0.821965	0.88094	0.51378	NA	CTC-281F24	chr17	-	6556783	6558328	879
ENSG00000(	1.035792	1.204288	1.319414	13.48336	6.443024	9.863579	-2.5651	0.009421	0.022034	RP11-212I2	chr16	+	55572112	55575939	3828
ENSG00000(	39.36009	30.10719	39.58241	66.66772	65.35067	89.59418	-1.0061	0.003356	0.008608	DLGAP1-AS	chr18	+	3602998	3608334	2261
ENSG00000(	17.60846	8.430014	31.66593	3.745378	5.522592	4.93179	1.8736	0.008116	0.019256	RP11-676J:	chr17	+	812872	814452	820
ENSG00000(	1.035792	0	0	0	3.681728	0	-0.68494	0.60991	NA	RP11-700H	chr17	-	48986998	48987593	492
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-510N	chr16	-	71476958	71477759	193
ENSG00000(	0	0	0	2.247227	0	5.753754	-2.0123	0.13708	0.22692	RP11-66H6	chr16	-	11160353	11164959	610
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-177N	chr16	+	47563101	47563827	493
ENSG00000(	2.071584	8.430014	0	0	0	2.465895	1.3622	0.28935	0.41306	RP11-81K2	chr17	+	47448102	47554350	382
ENSG00000(	14.50109	20.47289	23.74945	41.94823	24.85166	64.11326	-1.1308	0.017586	0.038674	RP13-1032	chr17	-	79668354	79670330	1977
ENSG00000(	12.4295	1.204288	0	5.243529	7.363456	6.575719	-0.3799	0.70202	0.79743	SNORD3B-2	chr17	-	18966762	18967449	688
ENSG00000(	2.071584	6.021439	17.15238	0.749076	6.443024	0	1.4983	0.1496	0.24345	RP11-510N	chr16	-	71481500	71486552	5053
ENSG00000(	38.3243	25.29004	17.15238	5.992604	13.80648	12.32947	1.2852	0.024648	0.052302	RP11-589P	chr17	-	6897961	6898508	343
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	AC139099.	chr17	-	81168296	81175490	2409
ENSG00000(	4.143168	3.612863	2.638828	1.498151	1.840864	0	1.2206	0.30344	0.42855	PCDHB19P	chr5	+	1.41E+08	1.41E+08	2347
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTD-2135D	chr16	-	14103137	14109873	760
ENSG00000(	5.17896	0	0	0	2.761296	0	0.51241	0.70504	0.79994	CTD-2561B	chr17	-	78997345	78999303	368
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	CTC-524C5	chr17	+	5372412	5373680	398
ENSG00000(	0	0	1.319414	0.749076	0.920432	0.821965	-0.46006	0.7339	NA	RP11-455C	chr17	+	79171193	79174088	805
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	BCAR4	chr16	-	11913686	11922702	1273
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-433P	chr16	-	3417719	3419246	1528
ENSG00000(	2.071584	8.430014	6.597069	2.247227	2.761296	2.465895	0.99661	0.31426	0.44086	RP11-676J:	chr17	+	781142	783333	585
ENSG00000(	2.071584	0	0	0.749076	5.522592	2.465895	-1.2931	0.31406	0.4406	CTD-2033A	chr16	+	69760916	69776466	592
ENSG00000(	5.17896	1.204288	6.597069	2.247227	0	1.64393	1.3037	0.25673	0.37513	RP11-417N	chr16	+	71867690	71869835	881

ENSG00000(	0	9.634302	0	1.498151	3.681728	4.109825	0.039428	0.97328	0.98451	CTC-479C5	chr16	-	67889858	67890014	157
ENSG00000(	8.286335	8.430014	11.87472	14.23244	7.363456	13.9734	-0.30474	0.65537	0.76056	RP13-638C	chr17	-	80545189	80546287	318
ENSG00000(	2.071584	1.204288	0	4.494453	2.761296	16.4393	-2.2237	0.039348	0.078858	LINC00514	chr16	+	3038962	3044510	3385
ENSG00000(	3.107376	9.634302	3.958241	0.749076	4.60216	2.465895	0.92524	0.36065	0.49022	RP11-266L	chr16	+	25078258	25080264	1875
ENSG00000(	17.60846	9.634302	10.55531	4.494453	6.443024	7.397684	0.97453	0.17769	0.27998	RP11-81A2	chr17	-	4704454	4710308	562
ENSG00000(	7.250543	14.45145	6.597069	6.74168	6.443024	4.109825	0.64413	0.41197	0.54267	CTA-972D3	chr16	+	15978886	15980015	536
ENSG00000(	3.107376	7.225726	1.319414	0.749076	3.681728	1.64393	0.75904	0.49316	0.62206	CTD-2529C	chr17	-	77965743	77966640	443
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP1-302G2	chr6	+	44184676	44185973	817
ENSG00000(	17.60846	26.49433	17.15238	9.737982	14.72691	9.863579	0.80102	0.16454	0.26293	OCLM	chr1	+	1.86E+08	1.86E+08	884
ENSG00000(	25.8948	9.634302	27.70769	1.498151	0.920432	1.64393	3.524	1.76E-05	6.32E-05	RP11-462G	chr16	-	3997610	4000445	1394
ENSG00000(	1.035792	2.408575	1.319414	0	0	0	1.6865	0.21314	NA	RP11-353N	chr17	+	77893156	77899261	1540
ENSG00000(	18.64425	12.04288	13.19414	29.21395	6.443024	21.37109	-0.36021	0.56109	0.68128	CTD-3195I5	chr17	-	3705459	3706676	518
ENSG00000(	0	0	0	7.490755	5.522592	5.753754	-3.4627	0.005078	0.012567	RP11-124N	chr13	+	23492730	23498741	585
ENSG00000(	1.035792	6.021439	5.277655	11.23613	0.920432	4.109825	-0.36012	0.71986	0.81143	RP11-160E	chr17	-	19015313	19015949	637
ENSG00000(	0	3.612863	2.638828	0	2.761296	0	0.71299	0.59193	0.7081	PCDHGB3	chr5	+	1.41E+08	1.41E+08	4727
ENSG00000(	21.75163	7.225726	21.11062	6.74168	13.80648	10.68554	0.64874	0.3178	0.44474	RP11-876N	chr16	+	11034576	11036878	2147
ENSG00000(	0	0	1.319414	3.745378	0.920432	4.109825	-1.7244	0.18529	0.28968	RP11-1055	chr17	-	79349801	79359160	702
ENSG00000(	3.107376	4.817151	2.638828	0.749076	0	5.753754	0.52956	0.6465	0.75329	RP5-1050D	chr17	+	4891001	4891741	551
ENSG00000(	40.39588	30.10719	46.17948	99.62705	71.7937	93.704	-1.1704	0.00037	0.00111	CORO7	chr16	-	4404543	4475706	3578
ENSG00000(	6.214751	9.634302	1.319414	3.745378	7.363456	8.219649	-0.13649	0.87721	0.92319	RP11-235E	chr17	-	3522550	3523207	344
ENSG00000(	2.071584	7.225726	0	17.97781	23.93123	9.863579	-2.2089	0.007159	0.017209	RP11-199F	chr17	-	7588578	7589689	1112
ENSG00000(	4.143168	12.04288	5.277655	0.749076	1.840864	1.64393	1.9507	0.054176	0.10423	RP5-867C2	chr17	-	45238441	45239430	401
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-160E	chr17	+	19064102	19065587	1486
ENSG00000(	0	0	0	0.749076	1.840864	0	-0.68825	0.58858	NA	RP11-55L4	chr17	-	9550337	9550977	195
ENSG00000(	0	1.204288	2.638828	2.247227	1.840864	0.821965	-0.25805	0.84102	0.89827	RP5-1107A	chr17	+	55017293	55018636	549
ENSG00000(	0	0	1.319414	0.749076	0.920432	0	-0.15244	0.90808	NA	SHPK	chr17	-	3468738	3539543	4753
ENSG00000(	1.035792	2.408575	0	1.498151	1.840864	0	0.034606	0.97936	0.98794	LA16c-390I	chr16	+	3594431	3595785	480
ENSG00000(	3.107376	0	0	0.749076	0	3.28786	-0.18859	0.88879	0.93099	CTD-2561B	chr17	-	78914218	78915833	494
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	RP11-433P	chr16	-	3373192	3373925	734
ENSG00000(	1.035792	1.204288	0	0.749076	2.761296	0	-0.32983	0.80721	NA	CTC-457L1(	chr17	-	19044330	19047002	2673
ENSG00000(	5.17896	2.408575	15.83297	14.23244	15.64734	19.72716	-1.0237	0.14755	0.24066	HNRNPA1P	chr17	+	2210055	2211009	955
ENSG00000(	0	1.204288	1.319414	0	6.443024	0	-0.77609	0.56239	0.68226	RP11-1197	chr17	+	80936401	80939614	401
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	AP005530.	chr18	+	11103	15928	920
ENSG00000(	3.107376	4.817151	0	5.992604	0.920432	4.93179	-0.45295	0.68257	0.78281	CTD-3195I5	chr17	+	3632655	3633787	398
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	DOC2B	chr17	-	5810	31427	1281
ENSG00000(	0	1.204288	0	16.47966	6.443024	12.32947	-3.6857	0.000772	0.002207	LA16c-380I	chr16	-	3053432	3055102	608
ENSG00000(	4.143168	0	2.638828	0	4.60216	2.465895	-0.02226	0.98558	0.99136	RP11-669E	chr17	+	44112679	44113136	304
ENSG00000(	6.214751	0	0	2.247227	1.840864	4.109825	-0.25617	0.83366	0.89332	CTB-193M1	chr16	+	15777147	15778427	503
ENSG00000(	2.071584	1.204288	7.916483	0	2.761296	0	1.4194	0.25413	0.37219	RP11-667K	chr17	-	2030724	2031198	475
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-670E	chr17	-	54962000	54962180	181
ENSG00000(	4.143168	13.24716	1.319414	1.498151	0.920432	1.64393	1.7662	0.098771	0.17359	RP11-388C	chr17	+	80702944	80703585	642
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-85G1	chr10	+	27532059	27539733	1002
ENSG00000(	4.143168	6.021439	2.638828	1.498151	0	2.465895	1.2904	0.2564	0.37474	RP11-490C	chr16	+	11835766	11838362	2597
ENSG00000(	24.85901	22.88147	29.0271	11.98521	6.443024	4.93179	1.6192	0.005932	0.014477	RP11-676J	chr17	-	692984	693765	486

ENSG00000(	0	2.408575	1.319414	0	1.840864	0	0.51994	0.70155	NA	CTD-2545H	chr17	+	1898908	1906832	737
ENSG00000(	22.78742	39.74149	3.958241	8.988907	10.12475	21.37109	0.67519	0.31064	0.4368	RP11-65J2:	chr16	+	14396145	14420210	651
ENSG00000(	11.39371	14.45145	14.51355	17.97781	11.96562	21.37109	-0.33714	0.56438	0.68398	RP11-95P2	chr16	-	4295826	4303790	2093
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	TVP23CP2	chr16	+	14294214	14294836	623
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	SAMD11P1	chr17	-	2516578	2517238	661
ENSG00000(	2.071584	9.634302	3.958241	0.749076	0.920432	3.28786	1.3244	0.21961	0.33125	LA16c-321I	chr16	-	2989715	3004277	510
ENSG00000(	5.17896	6.021439	0	0	0	1.64393	1.7997	0.16017	0.25746	CTC-360G5	chr19	-	39399620	39402798	1057
ENSG00000(	2.071584	2.408575	0	0	0.920432	0	1.1261	0.40655	NA	RP11-1099	chr17	+	7858186	7858940	430
ENSG00000(	0	0	1.319414	1.498151	0.920432	0.821965	-0.67966	0.61642	NA	AC002128.	chr19	-	35723194	35723906	713
ENSG00000(	1.035792	0	1.319414	4.494453	5.522592	1.64393	-1.6476	0.17297	0.27427	RP11-530N	chr17	-	6830791	6831510	720
ENSG00000(	4.143168	1.204288	7.916483	0.749076	3.681728	4.109825	0.51943	0.62166	0.7338	RP11-96D1	chr16	+	68233698	68234884	1187
ENSG00000(	1.035792	1.204288	2.638828	0	0	2.465895	0.573	0.66733	0.77067	RP11-95J1:	chr16	+	3890529	3891011	483
ENSG00000(	1.035792	0	0	4.494453	0	0	-0.88888	0.51082	NA	CTA-276F8.	chr16	-	14285677	14294134	415
ENSG00000(	0	1.204288	3.958241	8.239831	11.96562	8.219649	-2.1205	0.030415	0.062919	RP11-44F1	chr16	-	53524952	53527880	2929
ENSG00000(	26.93059	16.86003	17.15238	0	9.20432	1.64393	2.2902	0.004215	0.010605	PCDHGA4	chr5	+	1.41E+08	1.41E+08	4602
ENSG00000(	6.214751	30.10719	15.83297	29.96302	34.05598	29.59074	-0.81909	0.1286	0.21535	RP11-334C	chr17	-	78174472	78179748	4399
ENSG00000(	0	0	0	2.247227	6.443024	5.753754	-3.0344	0.017476	0.038472	RP11-77K1	chr16	-	75533686	75550178	637
ENSG00000(	4.143168	0	6.597069	0	1.840864	0	1.6672	0.19525	0.30166	RP11-353N	chr17	-	77889051	77900524	5271
ENSG00000(	2.071584	6.021439	11.87472	0.749076	2.761296	1.64393	1.6144	0.11562	0.1978	RP11-266L	chr16	+	25043202	25069430	574
ENSG00000(	48.68222	44.55865	34.30476	18.72689	35.89685	22.19305	0.72428	0.090357	0.16128	CTC-786C1	chr16	+	85204882	85218969	777
ENSG00000(	0	0	0	3.745378	10.12475	11.50751	-3.8893	0.001228	0.003393	LINC00621	chr13	-	23468795	23490508	1177
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP5-1107A	chr17	+	55029025	55029765	410
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CTD-3088G	chr16	-	11474716	11474975	260
ENSG00000(	4.143168	0	13.19414	0	11.96562	0	0.2282	0.86496	0.91473	RP13-638C	chr17	+	80535899	80536492	594
ENSG00000(	1.035792	2.408575	2.638828	1.498151	0	0.821965	0.87552	0.49825	0.62657	RP11-170L	chr16	+	31923175	31928172	4998
ENSG00000(	1.035792	0	1.319414	2.247227	0	0	0.018495	0.9891	NA	CTD-2561B	chr17	-	78934566	78935513	549
ENSG00000(	1.035792	4.817151	0	0.749076	1.840864	10.68554	-0.88954	0.44422	0.57386	RP11-497H	chr17	+	80876158	80876661	504
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AJ003147.!	chr16	+	3238212	3274779	629
ENSG00000(	1.035792	15.65574	5.277655	1.498151	8.283888	8.219649	0.24848	0.78846	0.86154	RP5-1050D	chr17	+	4889761	4890619	542
ENSG00000(	2.071584	7.225726	2.638828	0.749076	0	2.465895	1.3909	0.23895	0.35393	AC005356.	chr16	-	4374668	4378341	340
ENSG00000(	30.03797	45.76293	25.06886	0.749076	0.920432	4.109825	3.8086	7.78E-08	3.60E-07	CTC-277H1	chr16	+	67295011	67297687	2677
ENSG00000(	14.50109	15.65574	17.15238	17.97781	19.32907	26.30288	-0.41246	0.43988	0.5696	CTD-3195I!	chr17	+	3624922	3625782	291
ENSG00000(	0	6.021439	5.277655	2.247227	0.920432	2.465895	0.74622	0.51649	0.64297	RP11-266L	chr16	+	25104708	25106576	1869
ENSG00000(	0	4.817151	0	3.745378	11.96562	2.465895	-1.4792	0.19029	0.29565	RP11-485G	chr16	-	11442000	11443178	1095
ENSG00000(	0	0	1.319414	1.498151	0	2.465895	-0.80883	0.55106	NA	RP11-411G	chr17	+	519242	519835	594
ENSG00000(	9.322127	8.430014	3.958241	23.97042	23.0108	23.01502	-1.5809	0.009987	0.023229	RP11-295D	chr16	-	4385871	4387819	1949
ENSG00000(	0	0	1.319414	10.48706	22.09037	13.9734	-4.0698	0.000111	0.000359	RP11-44F1	chr16	+	53420856	53422997	2142
ENSG00000(	9.322127	10.83859	2.638828	0.749076	0	3.28786	2.0259	0.053302	0.10272	AC123768.	chr15	-	32898619	32907361	966
ENSG00000(	1.035792	1.204288	0	0.749076	0	0	0.55357	0.6746	NA	CTD-2135D	chr16	-	14024534	14029492	4934
ENSG00000(	0	0	0	2.996302	0.920432	4.109825	-2.1501	0.10895	0.18808	CTD-2377D	chr17	+	46760729	46781844	618
ENSG00000(	200.9436	189.0732	134.5802	270.4163	195.1316	206.3132	-0.35253	0.11283	0.19366	CTD-3195I!	chr17	-	3710042	3712148	2107
ENSG00000(	4.143168	1.204288	0	0.749076	0	4.93179	-0.04035	0.97494	0.98535	MRPS21P9	chr17	-	48527540	48528086	257
ENSG00000(	29.00217	19.2686	14.51355	6.74168	11.04518	18.08323	0.77743	0.19354	0.29943	RP11-196G	chr16	+	31129399	31130068	543
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-353N	chr17	+	77774397	77776326	605

ENSG00000(	2.071584	3.612863	0	0	0	0.821965	1.4184	0.29471	0.41906	RP11-353N	chr17	+	77797251	77801503	1788
ENSG00000(	6.214751	13.24716	11.87472	2.996302	2.761296	2.465895	1.7083	0.044068	0.087069	RP11-818C	chr17	+	1327767	1329778	570
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-214C	chr17	-	14198829	14200917	1885
ENSG00000(	1.035792	0	0	5.992604	0	3.28786	-1.7778	0.17927	0.28197	U91319.1	chr16	+	13340173	13656775	764
ENSG00000(	0	0	0	1.498151	0.920432	3.28786	-1.678	0.21598	NA	RP11-160A	chr6	+	71403542	71404322	781
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-667K	chr17	+	1992975	2004854	528
ENSG00000(	22.78742	18.06432	43.54065	72.66033	58.90765	66.57916	-1.2182	0.001954	0.005214	MRPL12	chr17	+	79670387	79674556	1028
ENSG00000(	1.035792	4.817151	2.638828	0	2.761296	0.821965	0.89446	0.46862	0.59785	RP11-565F	chr17	+	9368059	9370739	513
ENSG00000(	12.4295	12.04288	26.38828	0.749076	4.60216	5.753754	2.0078	0.009289	0.021762	RP11-615I2	chr16	+	68595964	68601032	5069
ENSG00000(	0	0	0	0.749076	2.761296	5.753754	-2.3326	0.08012	0.14563	RP13-580F	chr17	-	4385261	4389648	854
ENSG00000(	11.39371	7.225726	3.958241	0	10.12475	1.64393	0.81849	0.41146	0.54218	RP11-28G8	chr17	-	78775440	78779432	3204
ENSG00000(	12.4295	2.408575	5.277655	8.239831	8.283888	13.15144	-0.49047	0.53485	0.65918	RP11-304F	chr17	+	47911601	47913816	416
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-517A	chr16	-	16383992	16386099	567
ENSG00000(	2.071584	2.408575	2.638828	0	0.920432	0	1.7487	0.1868	0.29146	CYCSP40	chr17	-	75195032	75195625	294
ENSG00000(	1.035792	2.408575	1.319414	0	0	0	1.6865	0.21314	NA	CTD-2561B	chr17	-	78991769	78993811	869
ENSG00000(	12.4295	12.04288	21.11062	29.96302	23.0108	46.852	-1.1003	0.032262	0.066238	RP11-1055	chr17	-	79361930	79364056	1561
ENSG00000(	185.4068	183.0517	211.1062	60.67512	90.20234	72.33291	1.3696	1.08E-08	5.41E-08	RP11-156P	chr17	-	45061411	45177689	1081
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-104H	chr17	+	7323422	7347400	1975
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	CTD-3060P	chr17	-	2865542	2869189	2546
ENSG00000(	8.286335	10.83859	6.597069	0	0	0	4.3067	0.000328	0.000991	RP11-462G	chr16	-	3981218	3996306	774
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-750B	chr17	+	51183095	51183719	625
ENSG00000(	37.28851	49.3758	19.79121	44.94453	35.89685	38.63235	-0.15866	0.70468	0.79966	RP11-235E	chr17	-	3558915	3561386	874
ENSG00000(	0	1.204288	3.958241	17.22874	0.920432	2.465895	-1.5975	0.15329	0.24852	RP11-144N	chr16	+	74701404	74702604	1201
ENSG00000(	2.071584	0	1.319414	0.749076	0	0	0.90441	0.50226	NA	RP5-1029F	chr17	+	455806	456657	592
ENSG00000(	7.250543	1.204288	2.638828	32.95932	56.14635	41.92021	-3.3049	1.30E-07	5.91E-07	ALOX12P2	chr17	+	6757180	6857426	4326
ENSG00000(	309.7018	322.7491	381.3106	229.2171	222.7445	214.5328	0.60048	0.000559	0.001629	RP11-473I1	chr16	+	9198705	9200618	1914
ENSG00000(	1.035792	7.225726	0	2.247227	0	1.64393	0.72552	0.56618	0.68548	RP11-670E	chr17	+	54946308	54946925	618
ENSG00000(	3.107376	1.204288	0	0	0	0	1.4526	0.27741	NA	LA16c-321I	chr16	-	2972663	2973203	541
ENSG00000(	6.214751	6.021439	2.638828	0	0	0.821965	2.8013	0.02289	0.048903	RP11-85B7	chr17	-	9074386	9082435	5671
ENSG00000(	1.035792	0	0	3.745378	0.920432	0.821965	-1.2325	0.36015	0.48975	CTD-2047H	chr17	+	78289451	78290433	653
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	CTD-3088G	chr16	+	11559116	11567030	2279
ENSG00000(	283.807	302.2762	295.5487	146.8188	194.2112	183.2982	0.748	7.47E-05	0.000248	ZNF234	chr19	+	44645710	44663156	3245
ENSG00000(	12.4295	20.47289	15.83297	5.243529	11.04518	13.15144	0.6871	0.28379	0.40671	RP11-166P	chr17	-	55155659	55162385	713
ENSG00000(	0	3.612863	7.916483	8.988907	4.60216	1.64393	-0.35876	0.73063	0.81963	ROCK1P1	chr18	+	112367	118504	560
ENSG00000(	3.107376	2.408575	3.958241	2.247227	6.443024	2.465895	-0.187	0.85661	0.90907	RP11-473N	chr16	+	3156765	3159577	302
ENSG00000(	18.64425	10.83859	31.66593	14.23244	20.2495	20.54912	0.14128	0.79872	0.86884	RP11-876N	chr16	-	11032743	11033901	1159
ENSG00000(	0	1.204288	0	0	2.761296	3.28786	-1.2261	0.36367	0.49341	RP11-356I2	chr17	+	862274	862606	333
ENSG00000(	0	0	2.638828	0.749076	0	2.465895	-0.17101	0.89966	NA	RP11-396B	chr16	+	11290034	11318373	602
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP11-28B2	chr17	-	18889461	18889647	187
ENSG00000(	18.64425	14.45145	5.277655	5.992604	4.60216	10.68554	0.79095	0.28233	0.40499	RP11-667K	chr17	-	1946769	1948262	443
ENSG00000(	0	0	1.319414	0	0	2.465895	-0.38078	0.77353	NA	RP11-565F	chr17	+	9450615	9451858	235
ENSG00000(	35.21692	18.06432	14.51355	45.69361	50.62376	45.20807	-1.0157	0.020317	0.043998	RP11-1055	chr17	+	79369275	79376779	1890
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-388C	chr17	-	80671784	80674131	898
ENSG00000(	20.71584	22.88147	14.51355	5.243529	11.96562	6.575719	1.2298	0.051603	0.099816	CTD-2047H	chr17	-	78325628	78388968	3651

ENSG00000(	166.7625	161.3746	146.4549	214.2356	149.11	194.8057	-0.23335	0.28317	0.40602	RP11-473N	chr16	-	3166043	3184883	1592
ENSG00000(	0	0	2.638828	1.498151	0.920432	6.575719	-1.2045	0.3458	0.47525	RP11-485G	chr16	-	11435666	11439068	714
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	CTD-2034I2	chr16	+	50914120	50918012	2248
ENSG00000(	0	6.021439	1.319414	0	7.363456	5.753754	-0.6291	0.59188	0.7081	RP11-166P	chr17	-	55169506	55173786	4281
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-567C	chr17	-	80753362	80753971	413
ENSG00000(	2.071584	1.204288	0	0	0	2.465895	0.22121	0.87044	NA	RP11-95P2	chr16	-	4230118	4233516	318
ENSG00000(	3.107376	0	0	0	0.920432	0	0.70943	0.5938	NA	RP5-1107A	chr17	+	55060110	55062465	2356
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	CTC-479C5	chr16	+	67916364	67920270	3907
ENSG00000(	199.9078	204.7289	279.7157	63.67142	115.054	58.35951	1.5181	2.45E-08	1.19E-07	RP11-156P	chr17	+	45055847	45131935	4693
ENSG00000(	2.071584	0	0	23.22134	28.53339	27.12484	-4.355	1.44E-06	5.86E-06	RP11-849I2	chr18	-	76736555	76739074	1256
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-1055	chr17	+	79336072	79348014	665
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-462G	chr16	+	4082013	4082937	244
ENSG00000(	1.035792	0	2.638828	0	3.681728	0	0.005155	0.99695	0.99811	RP11-333E	chr17	-	5143803	5144838	498
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-893F	chr17	-	48290294	48292718	578
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-485G	chr16	+	11336510	11337409	900
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CTC-479C5	chr16	-	68047339	68049814	1185
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-26L2	chr16	+	55366267	55366879	613
ENSG00000(	7.250543	7.225726	7.916483	2.247227	1.840864	4.93179	1.1401	0.20781	0.3171	ZNF205-AS	chr16	-	3160461	3165599	1219
ENSG00000(	1.035792	2.408575	7.916483	1.498151	2.761296	5.753754	0.12942	0.90273	0.93977	RYKP1	chr17	+	4125386	4127123	1738
ENSG00000(	3.107376	1.204288	3.958241	0.749076	1.840864	4.93179	0.10643	0.92516	0.95462	RP11-420A	chr17	-	5267610	5274921	512
ENSG00000(	0	7.225726	0	0	0	0	1.9679	0.14595	0.2386	ATP5A1P3	chr16	-	72038936	72040442	1507
ENSG00000(	0	4.817151	3.958241	8.988907	9.20432	2.465895	-1.0549	0.29304	0.41735	RP11-461A	chr16	-	3700637	3701704	1068
ENSG00000(	1271.952	1248.846	1290.387	716.1162	753.8338	729.9048	0.79155	2.02E-11	1.25E-10	RP11-473I2	chr16	+	9201098	9207038	5941
ENSG00000(	0	0	0	0.749076	0.920432	0.821965	-0.73223	0.57364	NA	RP11-65J2	chr16	-	14501896	14512729	580
ENSG00000(	7.250543	4.817151	3.958241	1.498151	5.522592	4.93179	0.38169	0.68578	0.78496	CTB-133G6	chr19	+	7413848	7448271	1558
ENSG00000(	60.07593	103.5687	72.56776	155.0586	126.0992	117.541	-0.7517	0.006563	0.015875	CTC-524C5	chr17	-	5328459	5336196	1938
ENSG00000(	2.071584	0	1.319414	1.498151	7.363456	0.821965	-1.0448	0.39559	0.52667	RP11-96D1	chr16	+	68258616	68261637	3022
ENSG00000(	0	0	0	2.247227	0.920432	0.821965	-1.2297	0.36205	NA	RP11-109N	chr16	+	10785130	10786830	483
ENSG00000(	1.035792	0	1.319414	2.247227	0.920432	2.465895	-0.80323	0.53745	0.66142	LA16c-325I	chr16	-	2916349	2917619	667
ENSG00000(	4.143168	4.817151	0	0	0.920432	2.465895	0.97923	0.43546	0.5651	RP11-290H	chr17	-	45380832	45400979	535
ENSG00000(	0	3.612863	3.958241	0	2.761296	0	0.91283	0.48741	0.61656	RP5-1029F	chr17	+	426380	443816	478
ENSG00000(	6.214751	1.204288	6.597069	4.494453	8.283888	2.465895	-0.09594	0.91977	0.95123	RP11-166B	chr16	+	11945506	11989468	562
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-498D	chr16	-	72038138	72038702	403
ENSG00000(	0	1.204288	3.958241	0	0	0	1.651	0.221	NA	RP11-530N	chr17	-	6857417	6882279	539
ENSG00000(	12.4295	8.430014	11.87472	0.749076	3.681728	7.397684	1.3185	0.11747	0.20038	RP11-498D	chr16	+	71963914	71965102	1189
ENSG00000(	1.035792	0	0	7.490755	2.761296	1.64393	-2.185	0.085803	0.15461	RP11-388C	chr17	-	80687040	80692019	333
ENSG00000(	4.143168	1.204288	3.958241	1.498151	2.761296	1.64393	0.5207	0.64362	0.75092	RP11-266L	chr16	-	25082811	25084048	676
ENSG00000(	10.35792	32.51577	19.79121	13.48336	10.12475	31.23467	0.1743	0.77072	0.84912	TAPT1-AS1	chr4	+	16228286	16321763	2165
ENSG00000(	2.071584	3.612863	9.235896	5.992604	9.20432	4.109825	-0.34155	0.70339	0.79865	AF001548.	chr16	+	15820531	15826850	836
ENSG00000(	0	0	0	1.498151	0	4.109825	-1.5377	0.25628	NA	RP11-235E	chr17	-	3481249	3482147	560
ENSG00000(	25.8948	18.06432	34.30476	24.71949	7.363456	16.4393	0.64648	0.24245	0.35817	RP1-59D14	chr17	-	2278355	2282600	846
ENSG00000(	10.35792	4.817151	9.235896	13.48336	16.56778	33.70056	-1.2959	0.04511	0.088771	RP11-13N1	chr18	+	19210099	19213485	745
ENSG00000(	1.035792	1.204288	0	0.749076	0	1.64393	-0.04349	0.97443	NA	RP11-720N	chr17	-	25853412	25854249	838
ENSG00000(	0	2.408575	2.638828	0	1.840864	3.28786	-0.02515	0.98442	0.99094	RP11-68I3.	chr17	+	27966645	27967843	270

ENSG00000(	2.071584	2.408575	0	0	0	0	1.5041	0.26224	NA	CTC-297N7	chr17	+	10584051	10587305	171
ENSG00000(	1.035792	3.612863	5.277655	5.243529	3.681728	2.465895	-0.18535	0.85764	0.90952	RP11-53I6.	chr18	-	29702363	29704441	553
ENSG00000(	4.143168	16.86003	7.916483	0	4.60216	2.465895	1.7518	0.068369	0.12716	CTC-297N7	chr17	+	10633094	10672323	876
ENSG00000(	17.60846	18.06432	18.47179	29.96302	18.40864	14.79537	-0.21868	0.68197	0.78242	RP5-890E1	chr17	-	46122503	46125435	2910
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	RP11-973F	chr8	-	1.24E+08	1.24E+08	501
ENSG00000(	13.46529	19.2686	3.958241	8.988907	8.283888	13.9734	0.2221	0.7517	0.83545	RP1-56K13	chr17	-	37059957	37060853	437
ENSG00000(	2.071584	0	2.638828	8.239831	9.20432	18.90519	-2.5216	0.007267	0.017439	RP11-160C	chr17	+	63096930	63107176	664
ENSG00000(	7.250543	3.612863	2.638828	1.498151	0.920432	4.93179	0.72244	0.49307	0.62202	RP11-338L	chr17	+	28190420	28193110	893
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC004702.	chr17	+	20088395	20226286	195
ENSG00000(	1.035792	1.204288	3.958241	1.498151	1.840864	5.753754	-0.44258	0.69947	0.79569	RP11-118E	chr17	-	55678217	55685773	1412
ENSG00000(	3.107376	0	0	2.996302	0.920432	0	-0.16689	0.90156	0.93886	CTB-104H1	chr17	-	10034216	10034704	489
ENSG00000(	5.17896	4.817151	6.597069	0	0	0.821965	2.9683	0.014131	0.031773	RP11-269G	chr17	-	61382623	61390882	562
ENSG00000(	0	1.204288	5.277655	1.498151	6.443024	5.753754	-0.87113	0.43577	0.56534	RP13-753N	chr17	-	29190939	29191958	831
ENSG00000(	2.071584	4.817151	2.638828	4.494453	1.840864	3.28786	-0.02337	0.9823	0.98984	AK4P1	chr17	+	29672539	29673205	667
ENSG00000(	0	0	0	0.749076	2.761296	0.821965	-1.3133	0.33155	NA	RP11-78F1	chr18	+	976590	1174824	776
ENSG00000(	2.071584	0	0	2.247227	1.840864	0.821965	-0.69259	0.60374	0.71879	UBBP4	chr17	+	21729601	21731762	1459
ENSG00000(	22.78742	24.08575	26.38828	3.745378	9.20432	14.79537	1.3338	0.026347	0.0555	CTD-2349P	chr17	+	29056487	29058220	789
ENSG00000(	4.143168	0	0	0.749076	0.920432	2.465895	0.029421	0.98221	0.98984	RP11-737C	chr18	-	2945548	2946888	1264
ENSG00000(	1.035792	1.204288	10.55531	0	4.60216	3.28786	0.53317	0.63964	0.74769	RP11-45M2	chr17	-	17071260	17088868	1231
ENSG00000(	3.107376	0	5.277655	1.498151	2.761296	0	0.68303	0.58399	0.70145	RP11-692N	chr18	+	9615262	9619361	379
ENSG00000(	0	0	1.319414	2.996302	0	0	-0.52076	0.6968	NA	RP11-269G	chr17	-	61468552	61508450	591
ENSG00000(	0	0	3.958241	0	0	2.465895	0.32004	0.8135	0.8789	RP11-471L	chr17	+	12018864	12019202	339
ENSG00000(	0	2.408575	5.277655	0	0	0	2.2174	0.10185	0.17806	RP11-25L3	chr18	-	71581640	71701396	493
ENSG00000(	0	2.408575	6.597069	3.745378	6.443024	7.397684	-0.82983	0.41636	0.54699	RP11-82O1	chr17	+	28088121	28114854	576
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	SNORA70D	chr16	-	71732470	71732604	135
ENSG00000(	0	0	1.319414	0	0.920432	0.821965	-0.17431	0.89516	NA	RP11-57A1	chr17	+	70422080	70424796	636
ENSG00000(	0	2.408575	2.638828	0	0	0	1.6365	0.22501	NA	RP4-777O2	chr7	+	30589833	30591185	427
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-408H	chr18	+	28711419	28712457	1039
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-85B7	chr17	+	9186491	9208968	260
ENSG00000(	0	0	0	2.996302	1.840864	1.64393	-1.8657	0.16751	0.26679	RP11-321A	chr17	+	27467501	27482507	323
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-169F	chr18	-	70818476	70931715	3608
ENSG00000(	0	0	0	0	2.761296	2.465895	-1.4428	0.28594	NA	RP11-466A	chr17	-	30839887	30846368	420
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-285E	chr17	-	75253819	75277979	749
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-389J	chr18	+	63532498	63533633	792
ENSG00000(	0	0	0	0	3.681728	3.28786	-1.8162	0.1806	0.28356	DLGAP1-AS	chr18	+	3878180	3897069	1258
ENSG00000(	6.214751	0	3.958241	0.749076	3.681728	6.575719	-0.07579	0.94519	0.96713	RP11-806L	chr18	-	653985	657259	268
ENSG00000(	43.50326	28.90291	23.74945	89.13999	100.3271	74.79881	-1.4206	4.22E-05	0.000145	RP11-498C	chr17	-	79836301	79838982	2682
ENSG00000(	6.214751	0	0	4.494453	0	0	0.27941	0.83441	0.89393	RP11-161I6	chr18	-	1883525	2240847	779
ENSG00000(	222.6953	264.9433	230.8974	214.9847	197.8929	220.2866	0.18031	0.33024	0.45802	LINC00667	chr18	+	5232875	5246507	3979
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	RP11-746B	chr18	+	30413417	30518280	644
ENSG00000(	3.107376	7.225726	0	2.996302	2.761296	2.465895	0.26669	0.80963	0.87662	RP11-580I2	chr17	-	45681226	45726786	733
ENSG00000(	22.78742	33.72006	34.30476	43.44638	64.43024	76.44274	-1.0051	0.009445	0.022085	RP11-649A	chr17	-	73141356	73142641	717
ENSG00000(	0	2.408575	0	1.498151	0	0	0.25968	0.84497	NA	RP11-146G	chr18	-	6873398	6875023	544
ENSG00000(	4.143168	2.408575	6.597069	2.247227	1.840864	3.28786	0.67936	0.51057	0.6379	RPL26	chr17	-	8271956	8286505	3087

ENSG00000(	7.250543	8.430014	5.277655	0	0	0	3.9848	0.001163	0.003229	RP11-111H	chr18	+	74240612	74322925	2242
ENSG00000(	2.071584	3.612863	6.597069	0	0	0.821965	2.504	0.047431	0.092707	CTD-2206N	chr17	+	37213272	37269443	2305
ENSG00000(	3.107376	1.204288	1.319414	9.737982	18.40864	9.863579	-2.372	0.007733	0.018453	RP11-326K	chr18	+	29522538	29524119	1582
ENSG00000(	9.322127	15.65574	11.87472	3.745378	13.80648	8.219649	0.4864	0.49526	0.62397	RP11-573D	chr3	-	1.86E+08	1.87E+08	2400
ENSG00000(	8.286335	3.612863	2.638828	22.47227	17.48821	22.19305	-1.9211	0.005209	0.01287	RP11-649A	chr17	+	73267450	73269976	2527
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CIAPIN1P	chr18	+	24179372	24180302	931
ENSG00000(	12.4295	8.430014	7.916483	6.74168	15.64734	14.79537	-0.33071	0.62959	0.73981	RP11-143J:	chr18	-	9112402	9115875	544
ENSG00000(	34.18113	33.72006	22.43003	12.73428	13.80648	17.26126	1.0129	0.041693	0.083005	LINC00672	chr17	+	37081421	37084310	2365
ENSG00000(	0	0	0	0	8.283888	2.465895	-2.4008	0.07328	0.1349	DLGAP1-AS	chr18	+	3962353	4013943	757
ENSG00000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	RP11-51F1	chr17	+	61713961	61714473	513
ENSG00000(	10.35792	2.408575	0	11.98521	8.283888	4.109825	-0.76902	0.41677	0.54731	RP11-705C	chr18	+	268148	270278	2131
ENSG00000(	2.071584	1.204288	0	0	0	0	1.127	0.38814	NA	RP11-110H	chr18	-	46958114	46973790	332
ENSG00000(	83.89914	75.87013	83.12307	83.14739	70.87326	60.00344	0.17933	0.53281	0.65736	RP11-214C	chr17	-	62116510	62119203	2694
ENSG00000(	12.4295	12.04288	7.916483	12.73428	9.20432	7.397684	0.13533	0.8437	0.90039	RP11-110H	chr18	-	47010906	47012519	483
ENSG00000(	0	0	1.319414	0.749076	0	0.821965	-0.12362	0.92519	NA	RP11-571L	chr4	+	99850048	99916145	622
ENSG00000(	6.214751	1.204288	9.235896	2.247227	0	4.109825	1.0998	0.30756	0.43329	RP11-210K	chr18	+	29424351	29425141	348
ENSG00000(	4.143168	6.021439	9.235896	0	7.363456	1.64393	0.93327	0.36203	0.49166	RP11-180P	chr17	-	61012763	61044171	498
ENSG00000(	1.035792	2.408575	10.55531	3.745378	0.920432	11.50751	-0.1987	0.84478	0.90093	SNORD3A	chr17	+	19091329	19092027	699
ENSG00000(	0	0	2.638828	0	1.840864	0	0.2163	0.87177	NA	RP11-513N	chr18	+	10893615	10908781	506
ENSG00000(	0	2.408575	6.597069	16.47966	20.2495	36.98842	-2.8186	0.000251	0.000772	RP11-676J:	chr18	+	70535623	70548634	457
ENSG00000(	2.071584	1.204288	2.638828	0	0	4.109825	0.33766	0.79426	0.86548	CTB-58E17.	chr17	-	36871581	36876525	563
ENSG00000(	11.39371	4.817151	9.235896	0	0	1.64393	3.0664	0.005085	0.01258	RP11-504I:	chr18	+	74084672	74090230	398
ENSG00000(	11.39371	9.634302	13.19414	4.494453	5.522592	11.50751	0.61571	0.39854	0.52959	CTC-542B2	chr17	+	30200945	30213685	488
ENSG00000(	0	0	0	0	0.920432	3.28786	-1.1769	0.37857	NA	RP11-286N	chr18	+	5567129	5570941	456
ENSG00000(	0	2.408575	0	0.749076	1.840864	0	-0.04757	0.97202	NA	RP11-68I3.	chr17	-	27948635	27949272	638
ENSG00000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	RP11-627G	chr18	-	19755426	19756623	359
ENSG00000(	0	0	0	11.23613	2.761296	8.219649	-3.6843	0.002612	0.006819	RP11-176N	chr18	+	75133575	75272719	562
ENSG00000(	5.17896	0	0	1.498151	0	0	0.88387	0.51475	0.64144	CTC-297N7	chr17	-	10644584	10672333	667
ENSG00000(	24.85901	20.47289	17.15238	33.7084	26.69253	27.94681	-0.47996	0.30452	0.42984	RP11-423G	chr12	-	1.09E+08	1.09E+08	2227
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-192H	chr17	+	26960224	26962968	1316
ENSG00000(	1.035792	3.612863	2.638828	0.749076	4.60216	1.64393	0.049497	0.96597	0.98015	RP11-583F	chr17	+	62923752	62930321	599
ENSG00000(	25.8948	10.83859	17.15238	17.97781	23.0108	12.32947	0.025287	0.96448	0.97949	KRT222	chr17	-	38785049	38821393	2502
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	MIR4732	chr17	-	27188090	27188984	895
ENSG00000(	0	4.817151	3.958241	14.98151	1.840864	2.465895	-0.95278	0.36712	0.49712	DND1P1	chr17	+	43663237	43664295	1059
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-73M7	chr1	+	32110295	32114972	480
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-227G	chr17	+	30757986	30759860	563
ENSG00000(	25.8948	31.31148	14.51355	20.97412	23.0108	21.37109	0.13607	0.7841	0.85786	CTD-2350C	chr17	+	26729128	26731067	1940
ENSG00000(	13.46529	3.612863	0	8.239831	18.40864	10.68554	-0.96649	0.25356	0.37152	RP11-848P	chr17	-	29417805	29422468	492
ENSG00000(	619.4036	646.7025	568.6673	342.3275	448.2504	396.1871	0.62857	4.82E-05	0.000164	RP11-159D	chr17	-	56066400	56072211	4722
ENSG00000(	0	7.225726	2.638828	0	0	0	2.5888	0.054422	0.10464	RP11-321N	chr18	+	73118967	73130995	536
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-20B2	chr17	+	27175878	27176610	417
ENSG00000(	2.071584	2.408575	0	0.749076	3.681728	2.465895	-0.41566	0.73622	0.82347	RP11-848P	chr17	-	29335172	29335337	166
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	RP11-268I9	chr18	-	19451407	19473957	417
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-715F	chr18	+	2568391	2569121	429

ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-739N	chr18	-	24916343	25175128	1352
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-640N	chr17	+	30410198	30424084	431
ENSG0000(	8.286335	10.83859	6.597069	3.745378	0.920432	0	2.0335	0.041226	0.082173	MAGOH2	chr17	-	10619319	10619828	436
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP1-37N7.:	chr17	-	18283169	18292298	4955
ENSG0000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-737C	chr18	+	2990650	2991076	427
ENSG0000(	0	1.204288	2.638828	0	0	0.821965	0.9798	0.46906	NA	FLCN	chr17	-	17105963	17140499	1693
ENSG0000(	0	0	2.638828	2.996302	0	3.28786	-0.77759	0.55851	0.67901	RP11-13N1	chr18	-	19241748	19242356	336
ENSG0000(	0	1.204288	0	0	6.443024	0.821965	-1.3898	0.30147	0.42658	CTB-104H1	chr17	+	10048831	10050277	1447
ENSG0000(	0	0	3.958241	2.996302	5.522592	0	-0.74339	0.5644	0.68398	RP11-171G	chr17	+	70835178	70835857	624
ENSG0000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP11-757C	chr18	+	14244624	14252139	566
ENSG0000(	0	0	1.319414	0	0	4.109825	-0.74763	0.58005	NA	RNU4ATAC	chr2	+	1.22E+08	1.22E+08	127
ENSG0000(	4.143168	0	0	6.74168	4.60216	0.821965	-1.0858	0.36801	0.49823	RP13-270P	chr18	-	3255434	3261848	1035
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-138C	chr18	+	4430945	4431152	208
ENSG0000(	168.8341	157.7617	158.3297	171.5383	154.6326	175.0785	-0.04746	0.81659	0.88106	RP11-231E	chr18	-	72259010	72265744	3463
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-14P2	chr18	-	508568	515294	500
ENSG0000(	1.035792	2.408575	2.638828	0	0	0	2.0265	0.13497	0.22409	RP11-15F1	chr18	+	46550073	46574844	659
ENSG0000(	11.39371	13.24716	5.277655	2.247227	10.12475	0.821965	1.0636	0.2283	0.34159	RP11-474I:	chr17	-	73679623	73680879	566
ENSG0000(	0	1.204288	0	0	0	1.64393	-0.12916	0.91993	NA	CTD-2514K	chr17	-	72253035	72258159	513
ENSG0000(	1.035792	1.204288	0	0	0.920432	1.64393	-0.08406	0.95059	NA	CTD-2145A	chr17	-	18762667	18764779	463
ENSG0000(	25.8948	46.96722	15.83297	48.68991	57.06678	61.64737	-0.89017	0.032562	0.066772	RP11-162A	chr18	-	74506688	74534251	1295
ENSG0000(	39.36009	22.88147	25.06886	20.97412	13.80648	15.61733	0.76653	0.12448	0.20995	CTD-2031P	chr5	+	55240458	55240856	399
ENSG0000(	1.035792	4.817151	2.638828	0	2.761296	4.93179	0.10697	0.92697	0.95607	RP11-68I3.	chr17	+	27896598	27897537	465
ENSG0000(	2.071584	3.612863	0	0	0	0	1.8175	0.17961	NA	RP11-116K	chr18	+	51668503	51668947	445
ENSG0000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-527H	chr18	-	14969000	14970467	764
ENSG0000(	4.143168	3.612863	10.55531	0	9.20432	9.863579	-0.05084	0.95799	0.97513	RP11-20B2	chr17	+	27219487	27220360	562
ENSG0000(	0	0	3.958241	2.247227	1.840864	0	-0.0492	0.9707	0.98292	RP11-287D	chr2	-	74438731	74590504	5059
ENSG0000(	9.322127	22.88147	10.55531	0	0	0	5.0584	9.66E-06	3.59E-05	RP11-958F	chr18	-	22513451	22567646	487
ENSG0000(	0	2.408575	0	3.745378	3.681728	4.109825	-1.5982	0.19136	0.29698	SNRPGP2	chr18	-	51933259	51933484	226
ENSG0000(	254.8048	295.0505	354.9223	310.1173	421.5579	338.6495	-0.24256	0.1973	0.30435	RP11-159D	chr17	+	56168909	56172897	3989
ENSG0000(	1.035792	3.612863	2.638828	6.74168	5.522592	12.32947	-1.5229	0.10594	0.1839	RP11-621L	chr18	+	21944751	21947948	567
ENSG0000(	0	0	1.319414	2.247227	1.840864	4.93179	-1.7681	0.17222	0.27331	RP11-401F	chr17	+	65220419	65221657	380
ENSG0000(	214.4089	233.6318	232.2168	32.21025	19.32907	46.852	2.7508	1.19E-22	1.34E-21	RP11-720L	chr18	-	316740	317366	492
ENSG0000(	0	1.204288	1.319414	2.247227	1.840864	0	-0.41483	0.75721	0.8394	CTD-2006C	chr18	+	22882090	22882920	464
ENSG0000(	10.35792	26.49433	18.47179	173.0365	156.4734	115.0751	-2.97	7.15E-17	6.22E-16	RP4-594I1(	chr1	-	24865292	24882515	1445
ENSG0000(	3.107376	2.408575	7.916483	3.745378	0.920432	0	1.1476	0.31374	0.4402	RP11-945C	chr18	+	5887486	5909121	620
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-433N	chr17	+	46537732	46543402	701
ENSG0000(	9.322127	27.69862	15.83297	19.47596	23.0108	25.48091	-0.3538	0.51687	0.64334	RP11-848P	chr17	+	29298670	29300330	1661
ENSG0000(	0	0	2.638828	0	0.920432	0	0.55591	0.6721	NA	RP11-220C	chr17	+	30954757	31013502	373
ENSG0000(	44.53905	37.33292	36.94359	62.17327	38.65814	24.65895	-0.07827	0.85115	0.90513	RP11-173N	chr17	+	25641669	25642952	1284
ENSG0000(	3.107376	0	5.277655	0	0	0	2.3663	0.080152	0.14563	RP11-861L	chr18	-	66567018	66569492	559
ENSG0000(	3.107376	0	1.319414	5.243529	0	8.219649	-1.1644	0.3288	0.45651	RP11-349A	chr17	-	65016050	65017859	460
ENSG0000(	9.322127	3.612863	5.277655	1.498151	5.522592	0	1.1504	0.27162	0.39236	RP11-556C	chr17	-	61194380	61208308	478
ENSG0000(	428.8178	482.9194	383.9494	77.15478	57.06678	57.53754	2.7355	4.02E-40	8.33E-39	RP11-720L	chr18	+	316737	319165	548
ENSG0000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	CTC-525D6	chr19	-	29777918	30016659	2582

ENSG00000(	12.4295	4.817151	7.916483	5.243529	5.522592	4.109825	0.68953	0.40168	0.53291	RP4-777O2	chr7	+	30565347	30573229	368
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-158I9	chr11	-	1.19E+08	1.19E+08	2576
ENSG00000(	2.071584	3.612863	9.235896	2.247227	1.840864	3.28786	0.82282	0.42186	0.55236	RP11-556C	chr17	+	61259527	61260178	652
ENSG00000(	239.2679	258.9219	224.3003	293.6376	237.4715	308.2368	-0.2161	0.24104	0.35642	SUZ12P	chr17	+	29036317	29117926	1560
ENSG00000(	2.071584	6.021439	11.87472	2.996302	4.60216	4.109825	0.65531	0.47631	0.60562	RP11-464D	chr17	+	60627087	60629482	1707
ENSG00000(	7.250543	4.817151	11.87472	14.98151	10.12475	2.465895	-0.19383	0.8084	0.87564	RP13-516N	chr17	+	80172103	80175228	2368
ENSG00000(	1.035792	8.430014	1.319414	0	0	0	2.8308	0.033032	0.067571	RP13-650J2	chr17	+	79995781	79997256	709
ENSG00000(	23.82321	18.06432	7.916483	16.47966	9.20432	13.15144	0.34532	0.57659	0.69488	LINC00526	chr18	-	5236723	5238597	1875
ENSG00000(	70.43385	55.39724	83.12307	105.6197	110.4518	166.8589	-0.86588	0.002743	0.007136	AC010761.	chr17	-	27048505	27049895	899
ENSG00000(	4.143168	1.204288	1.319414	0	0	0	2.1615	0.11037	0.19002	RP11-678G	chr18	+	7814116	7815728	1613
ENSG00000(	7.250543	1.204288	5.277655	36.7047	21.16994	26.30288	-2.4326	0.000242	0.000745	RP11-192H	chr17	-	26928845	26929302	458
ENSG00000(	0	2.408575	1.319414	0	6.443024	1.64393	-0.74581	0.5591	0.67962	RP11-4F22	chr17	-	64394187	64412972	2113
ENSG00000(	4.143168	2.408575	2.638828	0.749076	3.681728	4.109825	0.10013	0.92671	0.95593	RP11-769C	chr18	-	738058	739662	1605
ENSG00000(	0	0	0	1.498151	0.920432	2.465895	-1.4807	0.27499	NA	RP11-68I3.	chr17	-	27918721	27919259	278
ENSG00000(	1.035792	0	3.958241	3.745378	2.761296	1.64393	-0.53826	0.6546	0.76	CTD-2267D	chr17	+	38524204	38524690	487
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-381P	chr17	+	20841851	20885670	1670
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-63N3	chr18	+	75334508	75336471	661
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-178F	chr18	+	22069339	22071044	459
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	RP11-674P	chr18	+	66879514	66881587	2074
ENSG00000(	1.035792	2.408575	0	0.749076	1.840864	0	0.24318	0.85682	0.90909	RP11-21G1	chr18	+	10724617	10728537	1908
ENSG00000(	0	0	0	9.737982	6.443024	2.465895	-3.4175	0.00611	0.014881	RP11-680C	chr17	+	11191522	11194128	2607
ENSG00000(	0	0	7.916483	1.498151	2.761296	0	0.56322	0.66454	0.76842	DPRXP4	chr17	+	29302405	29302972	568
ENSG00000(	3.107376	4.817151	1.319414	0	0	6.575719	0.35452	0.77167	0.85001	RP11-403A	chr18	-	21574177	21595303	817
ENSG00000(	0	0	0	0	5.522592	0	-1.3606	0.30939	NA	RP11-277J	chr17	+	71637165	71639245	173
ENSG00000(	13.46529	7.225726	11.87472	0.749076	14.72691	7.397684	0.47538	0.56062	0.6811	RP11-498C	chr17	+	79880775	79882387	563
ENSG00000(	0	2.408575	1.319414	2.996302	2.761296	0.821965	-0.57745	0.64645	0.75329	RP11-186B	chr17	+	7476144	7485342	4554
ENSG00000(	0	0	0	2.247227	2.761296	4.109825	-2.3558	0.075912	0.13903	PPIAP14	chr18	-	5002758	5003253	496
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-149I2	chr9	+	21929456	21931072	1617
ENSG00000(	0	0	7.916483	10.48706	3.681728	1.64393	-0.80703	0.47759	0.60662	MIR4523	chr17	-	27696735	27717795	762
ENSG00000(	1.035792	0	3.958241	0	2.761296	0.821965	0.29832	0.82095	0.88423	RP13-20L1	chr17	-	80358579	80359258	680
ENSG00000(	7.250543	9.634302	5.277655	0.749076	3.681728	0.821965	1.7712	0.074081	0.13615	RP11-474I2	chr17	-	73675554	73676047	352
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-465I4	chr18	+	67136753	67138972	347
ENSG00000(	0	0	1.319414	0	3.681728	4.109825	-1.4768	0.26819	0.38855	RP11-16C1	chr17	-	73367028	73369817	2790
ENSG00000(	10.35792	0	5.277655	1.498151	10.12475	7.397684	-0.21827	0.82398	0.88635	RP11-75N4	chr18	-	29122109	29136874	2024
ENSG00000(	2.071584	1.204288	0	2.247227	0.920432	0	0.03728	0.97785	0.98705	RP11-143K	chr17	+	71161116	71192732	588
ENSG00000(	4.143168	4.817151	0	0	0	0	2.4846	0.065461	0.1225	CTB-167B5	chr7	-	87900207	87903065	2859
ENSG00000(	5.17896	0	0	0	0	0	1.5469	0.24589	NA	RP11-138E	chr18	-	10323129	10372377	928
ENSG00000(	149.154	171.0089	167.5656	128.0919	143.5874	97.81383	0.39758	0.085899	0.15473	RP11-815I9	chr17	-	18570942	18572774	1833
ENSG00000(	8.286335	6.021439	5.277655	5.243529	11.04518	6.575719	-0.1871	0.81556	0.88035	RP11-421E	chr17	-	49326940	49329109	2170
ENSG00000(	3.107376	6.021439	13.19414	4.494453	0.920432	2.465895	1.2512	0.19194	0.29761	RP11-343K	chr17	+	55989694	55999942	335
ENSG00000(	81.82756	77.07441	55.41538	23.22134	34.05598	72.33291	0.71324	0.075966	0.13911	RP11-6N17	chr17	-	45968621	45973178	3939
ENSG00000(	8.286335	2.408575	0	0.749076	1.840864	0.821965	1.2212	0.31279	0.43921	RP11-799B	chr18	-	21693601	21700967	507
ENSG00000(	2.071584	6.021439	2.638828	0.749076	0	3.28786	1.0366	0.38124	0.51193	CTD-2104P	chr17	-	19552686	19553248	563
ENSG00000(	13.46529	13.24716	2.638828	6.74168	0.920432	6.575719	0.91882	0.29117	0.41529	AC100830.	chr15	+	64988821	64989060	240

ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	SNORD3C	chr17	-	19092978	19093558	581
ENSG00000(	11.39371	18.06432	5.277655	8.988907	4.60216	7.397684	0.66522	0.37095	0.50149	SH3GL1P2	chr17	+	28951431	28952512	1082
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	ALOX12P1	chr17	+	28856706	28869434	1229
ENSG00000(	20.71584	38.53721	21.11062	15.73059	18.40864	21.37109	0.51476	0.30607	0.43161	RP11-888D	chr18	-	9315192	9334439	466
ENSG00000(	0	0	1.319414	0.749076	2.761296	2.465895	-1.2635	0.34445	0.47364	RP11-387H	chr17	+	38083995	38095854	632
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-110H	chr18	+	46996173	46996593	421
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-344B	chr18	+	29867400	29870303	772
ENSG00000(	0	1.204288	5.277655	0	2.761296	0	0.73444	0.58123	0.69922	RP11-53I6.	chr18	-	29671258	29672082	473
ENSG00000(	4.143168	3.612863	7.916483	5.243529	3.681728	4.109825	0.2179	0.81264	0.87847	RP11-661C	chr17	+	71239232	71240845	321
ENSG00000(	0	1.204288	0	0	4.60216	3.28786	-1.5187	0.2552	0.37339	AC145343.	chr17	-	66092187	66097615	650
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-781P	chr18	+	6954676	6957418	2295
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-835E	chr18	-	5232875	5238525	977
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-178F	chr18	+	22015328	22019602	281
ENSG00000(	0	0	0	2.996302	4.60216	3.28786	-2.6228	0.044937	0.088481	FTLP12	chr17	+	16294748	16295196	449
ENSG00000(	4.143168	2.408575	5.277655	0.749076	0	4.93179	0.80494	0.48193	0.61108	RP11-147L	chr17	-	66242770	66244079	1310
ENSG00000(	0	3.612863	0	1.498151	0	0	0.55191	0.68269	NA	CTD-2370N	chr17	-	29632231	29645849	1008
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-285E	chr17	-	75260262	75260858	597
ENSG00000(	1.035792	1.204288	0	0	0.920432	0.821965	0.18874	0.88919	NA	RP11-15F1	chr18	+	46642671	46652849	502
ENSG00000(	0	0	0	0	0.920432	6.575719	-1.8834	0.16495	0.26344	CTB-58E17.	chr17	+	36757302	36758954	571
ENSG00000(	5.17896	12.04288	11.87472	2.996302	3.681728	3.28786	1.372	0.10397	0.18112	RP13-638C	chr17	-	80534492	80535267	456
ENSG00000(	11.39371	9.634302	2.638828	11.23613	12.88605	9.041614	-0.42977	0.56007	0.6806	RP11-227G	chr17	+	30655460	30656414	271
ENSG00000(	7.250543	1.204288	5.277655	0	1.840864	3.28786	1.1175	0.32222	0.44953	hsa-mir-13	chr18	-	19405448	19411371	4226
ENSG00000(	0	0	0	5.992604	11.96562	12.32947	-4.1736	0.000384	0.00115	BZRAP1-AS	chr17	+	56402811	56493127	2337
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP11-924A	chr17	-	15008554	15009504	467
ENSG00000(	0	0	0	23.97042	34.05598	28.76877	-5.7044	9.64E-08	4.43E-07	CTD-2124B	chr18	+	6557821	6558653	658
ENSG00000(	0	0	0	3.745378	0	0.821965	-1.2809	0.34031	NA	RP11-672L	chr18	-	903145	906668	3524
ENSG00000(	0	1.204288	3.958241	5.243529	6.443024	5.753754	-1.4523	0.17491	0.27673	SNORD3B-1	chr17	+	18965225	18965807	583
ENSG00000(	7.250543	16.86003	31.66593	38.20285	42.33987	32.05663	-0.99637	0.050503	0.097971	RP11-70L8	chr9	-	21858909	21861925	3017
ENSG00000(	1.035792	6.021439	6.597069	0.749076	3.681728	0	1.2466	0.27997	0.40221	RP11-403A	chr18	-	21656758	21679284	564
ENSG00000(	13.46529	2.408575	10.55531	2.996302	7.363456	6.575719	0.58658	0.48375	0.61301	AC010761.	chr17	-	26997072	26999822	499
ENSG00000(	3.107376	16.86003	1.319414	4.494453	2.761296	2.465895	0.95173	0.32997	0.45781	RP11-927P	chr17	+	62888847	62906298	631
ENSG00000(	0	0	1.319414	2.247227	4.60216	0.821965	-1.5451	0.24076	0.35606	RP11-466A	chr17	-	30836972	30850442	927
ENSG00000(	43.50326	37.33292	29.0271	67.4168	55.22592	59.18147	-0.70887	0.045537	0.089527	RP11-649A	chr17	-	73161681	73163344	1664
ENSG00000(	0	0	0	2.247227	9.20432	4.93179	-3.211	0.011063	0.025467	RP11-663N	chr17	-	25564885	25568687	614
ENSG00000(	2.071584	1.204288	3.958241	0	2.761296	5.753754	-0.17839	0.87932	0.92458	RP11-162A	chr18	-	74596891	74600680	2747
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-180P	chr17	-	61028192	61028549	358
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	PGDP1	chr18	+	29542141	29543581	1441
ENSG00000(	1.035792	0	2.638828	0	0.920432	0	0.90832	0.50205	NA	RP11-269G	chr17	-	61507829	61509572	552
ENSG00000(	9.322127	8.430014	7.916483	3.745378	1.840864	12.32947	0.46091	0.58254	0.70022	ARGFXP2	chr17	-	30477452	30478523	949
ENSG00000(	9.322127	15.65574	13.19414	6.74168	3.681728	20.54912	0.27091	0.70721	0.80201	RP13-104F	chr17	+	62746538	62747429	892
ENSG00000(	2.071584	2.408575	0	0.749076	4.60216	0	-0.1409	0.91358	0.94708	RP11-565F	chr17	+	9397314	9398337	692
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-286N	chr18	+	5463626	5480974	578
ENSG00000(	4.143168	1.204288	0	0	1.840864	1.64393	0.41957	0.74861	0.83297	CTD-2349P	chr17	-	29161343	29190046	638
ENSG00000(	1.035792	0	0	2.247227	0	2.465895	-1.0179	0.45303	NA	RP11-16C1	chr17	+	73390204	73391044	372

ENSG00000(	1.035792	0	1.319414	0.749076	1.840864	0	-0.06434	0.96216	NA	RP11-1148	chr17	-	28417384	28444515	385
ENSG00000(	39.36009	9.634302	10.55531	7.490755	13.80648	16.4393	0.63624	0.32902	0.45674	RP13-270P	chr18	+	3190395	3247275	1771
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	RP11-471L	chr17	+	12104917	12118584	718
ENSG00000(	1.035792	8.430014	11.87472	1.498151	3.681728	3.28786	1.123	0.24943	0.36668	RP11-789C	chr18	+	8402845	8405159	2315
ENSG00000(	42.46747	44.55865	60.69303	187.2689	149.11	123.2947	-1.6273	1.31E-08	6.50E-08	CTD-2510F	chr17	-	57280038	57281190	321
ENSG00000(	26.93059	9.634302	9.235896	5.243529	0	8.219649	1.5769	0.056548	0.10811	CTD-2349P	chr17	-	29053323	29054582	460
ENSG00000(	0	6.021439	3.958241	0	0	1.64393	1.6251	0.21109	0.32103	RP11-849N	chr17	+	15164332	15169024	373
ENSG00000(	0	4.817151	1.319414	0	1.840864	0.821965	0.75429	0.56647	0.68571	RP11-204L	chr2	+	1.22E+08	1.22E+08	682
ENSG00000(	9.322127	8.430014	6.597069	8.239831	11.96562	5.753754	-0.07516	0.91993	0.95136	RP13-20L1	chr17	-	80412149	80416397	357
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-690G	chr17	+	37394719	37407071	975
ENSG00000(	4.143168	12.04288	2.638828	6.74168	17.48821	12.32947	-0.86415	0.26711	0.38717	AC010761.	chr17	-	27072587	27074670	521
ENSG00000(	7.250543	14.45145	15.83297	0	0	2.465895	3.2492	0.001048	0.002931	RP11-720L	chr18	-	423744	424416	454
ENSG00000(	11.39371	2.408575	5.277655	0.749076	0	2.465895	2.0194	0.065877	0.12318	CTD-2145A	chr17	-	18713269	18714253	985
ENSG00000(	7.250543	10.83859	3.958241	1.498151	1.840864	3.28786	1.4875	0.11831	0.2015	RP11-806L	chr18	+	706523	707648	326
ENSG00000(	0	1.204288	0	0	4.60216	1.64393	-1.249	0.3546	0.48432	RP11-131K	chr17	+	13812548	13814529	1982
ENSG00000(	1.035792	0	3.958241	6.74168	0	2.465895	-0.64707	0.60138	0.71659	hsa-mir-15	chr18	+	47013709	47018248	582
ENSG00000(	2.071584	0	6.597069	0	7.363456	9.041614	-0.72553	0.51869	0.64498	SENP3-EIF4	chr17	+	7466604	7482033	3520
ENSG00000(	2.071584	7.225726	7.916483	12.73428	3.681728	4.93179	-0.29844	0.73301	0.8214	RP11-524F	chr17	+	17410665	17411622	795
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	CTD-3157E	chr17	-	15691101	15691519	347
ENSG00000(	1.035792	1.204288	1.319414	2.247227	0.920432	0	0.09181	0.94479	0.96694	RP11-60A2	chr17	-	55849307	55912110	505
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	RP11-958F	chr18	+	22635564	22636724	663
ENSG00000(	3.107376	6.021439	3.958241	0	0	0	3.223	0.012626	0.028681	RP11-419J	chr18	+	10125337	10144403	412
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-434D	chr17	+	20336519	20337598	301
ENSG00000(	75.61281	59.0101	48.81831	128.0919	120.5766	78.90863	-0.81947	0.00715	0.017192	RP11-713C	chr18	-	70410991	70413196	2206
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AP000275.	chr21	-	33949158	33984591	929
ENSG00000(	0	0	0	2.247227	2.761296	4.93179	-2.4799	0.060179	0.114	RP11-68I3.	chr17	-	27971814	27972865	1052
ENSG00000(	0	0	2.638828	0	0.920432	0.821965	0.26148	0.84655	NA	RP11-465I4	chr18	-	67150863	67285930	432
ENSG00000(	1.035792	4.817151	2.638828	2.247227	1.840864	1.64393	0.42475	0.71077	0.80446	RP11-13N1	chr18	+	19253589	19262522	447
ENSG00000(	18.64425	16.86003	6.597069	0.749076	2.761296	6.575719	1.861	0.024193	0.051479	CTD-2267D	chr17	-	38497119	38499388	1790
ENSG00000(	7.250543	2.408575	9.235896	7.490755	12.88605	7.397684	-0.50082	0.52905	0.65382	RP11-1376	chr17	+	80111306	80112691	555
ENSG00000(	43.50326	39.74149	29.0271	71.16218	70.87326	73.15488	-0.91692	0.006513	0.015765	RPL17	chr18	-	47014851	47018893	914
ENSG00000(	1.035792	0	0	10.48706	4.60216	10.68554	-3.2707	0.004353	0.010911	RP11-173N	chr17	-	25678884	25679610	727
ENSG00000(	134.6529	83.09585	93.67838	82.39831	86.52061	59.18147	0.44907	0.12564	0.21148	MAFG-AS1	chr17	+	79885705	79888629	1895
ENSG00000(	1.035792	0	0	2.996302	2.761296	2.465895	-1.7351	0.18488	0.28936	RP13-516N	chr17	-	80247922	80250690	1810
ENSG00000(	0	2.408575	2.638828	0.749076	0.920432	4.109825	-0.1537	0.90253	0.93961	RP11-156L	chr17	+	60776605	60815283	3145
ENSG00000(	0	8.430014	6.597069	3.745378	4.60216	2.465895	0.37893	0.71296	0.80601	RP11-82O1	chr17	-	28102765	28103719	955
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-94B1	chr18	-	73966247	73967169	598
ENSG00000(	1.035792	3.612863	1.319414	1.498151	7.363456	7.397684	-1.1685	0.27111	0.39181	RP11-883A	chr18	+	10594587	10604795	855
ENSG00000(	3.107376	6.021439	1.319414	0	4.60216	3.28786	0.33144	0.76966	0.84862	RP11-354P	chr17	-	28449447	28453136	546
ENSG00000(	18.64425	48.17151	23.74945	13.48336	37.73771	35.34449	0.065284	0.89875	0.93723	RP11-849F	chr17	+	8268881	8284646	579
ENSG00000(	17.60846	2.408575	10.55531	12.73428	7.363456	15.61733	-0.19932	0.7853	0.85883	RP11-799B	chr18	-	21739473	21742175	735
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-296E	chr18	-	18960247	19030978	679
ENSG00000(	29.00217	19.2686	26.38828	11.98521	15.64734	3.28786	1.2122	0.044324	0.087472	RP11-17M1	chr18	+	74203608	74205487	813
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-449L	chr17	+	71515985	71517546	1562

ENSG00000(	0	0	0	9.737982	7.363456	11.50751	-4.1032	0.000502	0.001476	CYP4F35P	chr18	+	14337422	14342524	2876
ENSG00000(	0	0	0	2.996302	4.60216	8.219649	-3.1783	0.011945	0.027289	RNASEH1P:	chr17	-	20805252	20805993	742
ENSG00000(	10.35792	10.83859	23.74945	23.22134	22.09037	13.15144	-0.37374	0.52108	0.64676	CTD-2349P	chr17	-	29108511	29109239	308
ENSG00000(	5.17896	0	0	0.749076	3.681728	0.821965	0.023872	0.98526	0.99132	RP11-271K	chr17	-	29365593	29386139	1967
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-387H	chr17	-	38168479	38170958	784
ENSG00000(	42.46747	42.15007	23.74945	37.45378	37.73771	56.71558	-0.27061	0.50218	0.63023	RP11-649A	chr17	-	73134511	73137445	400
ENSG00000(	2.071584	12.04288	1.319414	0	0.920432	2.465895	1.6551	0.15411	0.24959	RP11-720N	chr17	+	25792138	25792567	430
ENSG00000(	2.071584	4.817151	1.319414	0.749076	6.443024	1.64393	-0.06602	0.95326	0.97217	FSBP	chr8	-	95390605	95449180	2472
ENSG00000(	3.107376	6.021439	2.638828	0	1.840864	1.64393	1.3378	0.25177	0.36941	RP11-20B2	chr17	+	27253293	27271767	683
ENSG00000(	3.107376	0	0	0	1.840864	0	0.36193	0.78835	NA	RP11-408H	chr18	+	28681551	28742752	553
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP11-737C	chr18	+	2948236	2960754	673
ENSG00000(	2.071584	6.021439	0	6.74168	3.681728	9.863579	-1.1024	0.27156	0.39231	RP11-20B2	chr17	+	27271814	27272412	599
ENSG00000(	0	4.817151	0	4.494453	4.60216	0	-0.61964	0.62604	0.73734	RP11-583F	chr17	+	62939380	62947172	2474
ENSG00000(	0	1.204288	0	2.996302	4.60216	4.93179	-2.2351	0.073917	0.13594	RP11-434D	chr17	-	20435561	20436194	634
ENSG00000(	1.035792	0	3.958241	0	1.840864	4.109825	-0.17805	0.88954	0.93145	LINC00668	chr18	-	6919495	6929965	2343
ENSG00000(	0	1.204288	5.277655	2.996302	5.522592	1.64393	-0.5184	0.65428	0.75986	UBE2CP2	chr18	-	20480449	20480958	510
ENSG00000(	0	0	1.319414	6.74168	0	0	-1.209	0.37229	0.50277	RP11-739L	chr18	-	20279444	20513727	570
ENSG00000(	0	0	0	9.737982	22.09037	9.863579	-4.634	4.93E-05	0.000168	RP11-865B	chr18	+	6511415	6590652	603
ENSG00000(	0	0	0	0	3.681728	2.465895	-1.6477	0.22446	0.33686	RP11-296E	chr18	+	18896839	18897756	361
ENSG00000(	7.250543	16.86003	5.277655	8.988907	5.522592	5.753754	0.48373	0.532	0.65653	RP11-674N	chr18	-	8695854	8707619	818
ENSG00000(	1.035792	0	0	0	0	1.64393	-0.12526	0.92174	NA	RP11-269G	chr17	+	61532354	61533178	355
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	CTD-2515C	chr18	-	26858474	26941928	471
ENSG00000(	2.071584	2.408575	3.958241	35.95563	14.72691	18.08323	-2.7874	0.000219	0.00068	RP11-927P	chr17	-	62774960	62775055	96
ENSG00000(	0	0	0	5.243529	2.761296	4.109825	-2.7863	0.031556	0.064964	RP11-699A	chr18	-	18820636	18821332	428
ENSG00000(	0	0	0	29.21395	28.53339	36.98842	-5.828	4.25E-08	2.02E-07	ESRG	chr3	-	54666149	54673884	3140
ENSG00000(	2.071584	0	1.319414	1.498151	0	2.465895	-0.13398	0.91971	0.95121	RP11-627G	chr18	-	19746859	19748929	1788
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	MIR3615	chr17	-	72743458	72745051	565
ENSG00000(	5.17896	4.817151	3.958241	2.996302	11.04518	6.575719	-0.4815	0.58569	0.70313	CTB-58E17.	chr17	-	36859733	36862514	486
ENSG00000(	0	0	0	20.22504	26.69253	16.4393	-5.2608	1.54E-06	6.24E-06	RP11-466P	chr5	+	75627662	75629781	2120
ENSG00000(	1.035792	2.408575	1.319414	0	0	0	1.6865	0.21314	NA	RP11-703N	chr18	-	2688562	2833063	690
ENSG00000(	21.75163	24.08575	5.277655	14.23244	23.0108	11.50751	0.07945	0.89813	0.93686	RP11-143J:	chr18	-	9121263	9136643	770
ENSG00000(	0	0	2.638828	2.247227	0	2.465895	-0.50041	0.70994	0.80395	POLRMTP1	chr17	-	60214333	60218000	3668
ENSG00000(	6.214751	7.225726	0	0	0	0	3.1066	0.018476	0.040406	CTD-2535L	chr17	-	63534220	63637151	1616
ENSG00000(	1.035792	4.817151	3.958241	4.494453	0.920432	0	0.61158	0.6064	0.721	RP5-1028K	chr17	+	38673278	38683254	1014
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-118E	chr17	-	55599609	55600958	563
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-243E	chr18	+	10375100	10378111	472
ENSG00000(	0	0	0	1.498151	3.681728	1.64393	-1.9249	0.15383	0.24921	RP11-296K	chr17	+	27679087	27731118	414
ENSG00000(	2.071584	2.408575	1.319414	2.247227	0	0	0.81859	0.53497	0.65921	RP11-354P	chr17	+	28565759	28579255	224
ENSG00000(	1.035792	2.408575	5.277655	4.494453	0	4.109825	-0.01206	0.9916	0.99499	RP11-209D	chr17	-	19832685	19833050	366
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	RP11-474N	chr18	+	9785105	9787802	1166
ENSG00000(	2.071584	3.612863	0	0	0.920432	0.821965	1.0235	0.44213	0.57182	RP11-789C	chr18	-	8360818	8367032	616
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-927P	chr17	-	62932603	62936347	255
ENSG00000(	5.17896	8.430014	5.277655	0.749076	10.12475	5.753754	0.17281	0.85017	0.90462	RP11-769C	chr18	+	735746	737459	1714
ENSG00000(	54.89697	71.05298	47.4989	32.21025	37.73771	26.30288	0.8368	0.023642	0.0504	STRADA	chr17	-	61780192	61819330	3685

ENSG00000(	0	0	0	0	0.920432	8.219649	-2.1461	0.11238	0.19302	RP11-855A	chr17	-	65989996	65992547	414
ENSG00000(	33.14534	25.29004	17.15238	109.365	86.52061	124.1167	-2.0331	5.24E-09	2.70E-08	CTD-2267D	chr17	+	38516907	38520945	2094
ENSG00000(	5.17896	16.86003	9.235896	0	6.443024	3.28786	1.4782	0.10864	0.18771	NARF-IT1	chr17	+	80439974	80441264	769
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-25D3	chr18	+	23845973	23847373	839
ENSG00000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	CTC-525D6	chr19	-	29980682	30017855	543
ENSG00000(	2.071584	0	0	0.749076	0	0	0.47431	0.71145	NA	LINC00683	chr18	+	74327169	74337897	3510
ENSG00000(	5.17896	4.817151	3.958241	2.247227	2.761296	6.575719	0.23262	0.80934	0.87633	RP11-41O4	chr18	+	68002675	68019695	815
ENSG00000(	0	2.408575	1.319414	2.247227	0	5.753754	-0.75918	0.55028	0.67158	RP11-640I2	chr17	+	15554904	15557803	571
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-172F	chr18	-	4775053	5004536	561
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	RP11-41O4	chr18	-	68047376	68051827	2637
ENSG00000(	1.035792	1.204288	0	1.498151	0	0	0.24225	0.85676	NA	UBL5P2	chr17	-	30554909	30555127	219
ENSG00000(	3.107376	0	0	1.498151	0.920432	4.109825	-0.65596	0.61284	0.72623	CTD-3096N	chr18	-	5381640	5385329	463
ENSG00000(	11.39371	12.04288	6.597069	4.494453	0	0	2.2375	0.026211	0.055253	RP11-1C8.(	chr8	-	1.04E+08	1.04E+08	777
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-159D	chr17	-	56154252	56160565	6113
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	hsa-mir-74(	chr17	+	11985216	11985313	98
ENSG00000(	1.035792	3.612863	0	0	0	0.821965	1.1852	0.38234	NA	RP11-484N	chr18	-	68003165	68004546	384
ENSG00000(	0	0	0	2.996302	0	0.821965	-1.0802	0.41594	NA	RP11-173N	chr17	+	25660282	25675517	454
ENSG00000(	0	1.204288	2.638828	0	0	0.821965	0.9798	0.46906	NA	RP11-25O3	chr18	-	49862731	49865395	714
ENSG00000(	3.107376	7.225726	3.958241	4.494453	2.761296	0	0.77868	0.46852	0.59775	RP11-848P	chr17	-	29305628	29307268	668
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-51L5	chr17	-	60308831	60324514	843
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-1096	chr17	-	11857206	11880911	463
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-344E	chr17	+	20759259	20760630	1372
ENSG00000(	3.107376	4.817151	9.235896	8.239831	5.522592	3.28786	-0.01031	0.99069	0.99468	RP11-142C	chr17	+	29460200	29465536	2780
ENSG00000(	23.82321	38.53721	21.11062	3.745378	1.840864	4.93179	2.7861	2.17E-05	7.72E-05	RP11-214C	chr17	+	14230652	14232791	2140
ENSG00000(	3.107376	6.021439	9.235896	0	0	0	3.7446	0.002747	0.007145	RP11-227G	chr17	+	30738236	30739439	552
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	CTB-41I6.1	chr17	+	8869213	8870387	402
ENSG00000(	2.071584	0	2.638828	0	1.840864	0.821965	0.50427	0.70472	0.79966	RP11-737C	chr18	+	2967016	2985408	568
ENSG00000(	0	0	0	3.745378	6.443024	4.109825	-3.0356	0.017217	0.037953	RP11-874J1	chr18	+	3653410	3656282	1455
ENSG00000(	11.39371	40.94578	19.79121	13.48336	30.37426	73.97684	-0.67811	0.23928	0.35432	RP11-329L	chr17	+	62223330	62223836	278
ENSG00000(	13.46529	12.04288	13.19414	5.992604	3.681728	8.219649	1.0232	0.15384	0.24921	CBX3P2	chr18	-	2652169	2655394	1429
ENSG00000(	0	0	5.277655	0	0	7.397684	-0.31329	0.81319	0.87873	RP11-180P	chr17	-	61044178	61045910	912
ENSG00000(	0	6.021439	0	0	1.840864	0	0.90622	0.50342	0.63131	RP11-91I8.	chr18	-	6728820	6729861	491
ENSG00000(	3.107376	13.24716	2.638828	3.745378	2.761296	10.68554	0.12079	0.8951	0.93512	RP13-991F	chr17	-	80434473	80435800	838
ENSG00000(	7.250543	1.204288	3.958241	0	1.840864	0.821965	1.6581	0.16463	0.26301	RP11-149I2	chr9	+	21995481	21996012	435
ENSG00000(	5.17896	15.65574	7.916483	25.46857	15.64734	13.15144	-0.87131	0.18004	0.28289	RP11-806L	chr18	+	650229	652843	2106
ENSG00000(	2.071584	0	5.277655	0	0	0	2.1617	0.11093	0.19077	RP11-822E	chr17	+	21436235	21446049	965
ENSG00000(	210.2658	213.1589	228.2586	278.6561	214.4607	224.3964	-0.14077	0.46153	0.59077	CTB-131K1	chr17	+	37558046	37562486	860
ENSG00000(	33.14534	13.24716	14.51355	5.243529	10.12475	0.821965	1.7791	0.015544	0.034569	RP11-401F	chr17	+	65240953	65241922	689
ENSG00000(	22.78742	9.634302	9.235896	23.97042	5.522592	13.9734	-0.05437	0.93546	0.96116	CTD-2349P	chr17	+	29119390	29119851	462
ENSG00000(	8.286335	1.204288	5.277655	3.745378	1.840864	1.64393	0.84592	0.41574	0.54635	RP11-45M2	chr17	-	17138747	17139432	686
ENSG00000(	1.035792	1.204288	0	0	2.761296	0	-0.12302	0.9277	NA	RP11-766H	chr17	-	71064009	71064427	419
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-629E	chr13	-	30596158	30597937	1780
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	RP11-874J1	chr18	-	3770017	3771430	557
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-138P	chr17	+	26201671	26208263	2266

ENSG00000(	2.071584	0	0	5.243529	0	0	-0.66778	0.6224	0.73431	CTD-2510F	chr17	-	57252344	57259148	798
ENSG00000(	16.57267	34.92434	27.70769	8.988907	10.12475	13.15144	1.2343	0.026372	0.055549	RP11-385D	chr17	-	15434087	15434403	317
ENSG00000(	6.214751	0	3.958241	4.494453	3.681728	4.109825	-0.21267	0.8393	0.89727	RP11-881L	chr18	+	9587384	9590180	534
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-527H	chr18	+	14946266	14973769	1854
ENSG00000(	3.107376	2.408575	3.958241	0.749076	0	0.821965	1.744	0.16284	0.26083	RP11-449D	chr18	+	22305745	22509040	592
ENSG00000(	0	0	0	2.247227	1.840864	0.821965	-1.4859	0.2733	NA	RP11-838N	chr18	+	3284143	3327290	864
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP1-71H19	chr6	+	57358736	57362565	345
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP1-56K13	chr17	-	37159501	37169285	636
ENSG00000(	0	0	0	1.498151	1.840864	1.64393	-1.5124	0.26495	NA	RP11-583F	chr17	+	63048027	63049426	537
ENSG00000(	0	0	1.319414	0	2.761296	4.93179	-1.4604	0.27407	0.39517	RP11-466A	chr17	+	30845971	30858510	408
ENSG00000(	0	3.612863	1.319414	8.239831	6.443024	3.28786	-1.5152	0.15872	0.25553	RP11-6N17	chr17	-	46007048	46010472	335
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-856N	chr18	-	10612301	10626350	860
ENSG00000(	4.143168	7.225726	3.958241	2.996302	8.283888	1.64393	0.22198	0.81607	0.88074	RP11-927P	chr17	+	62895884	62896834	560
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-112H	chr17	-	56553499	56554311	813
ENSG00000(	9.322127	21.67718	9.235896	42.69731	48.7829	70.68898	-1.9497	4.15E-05	0.000143	RP11-138I	chr17	-	16343793	16344266	304
ENSG00000(	2.071584	0	1.319414	0	0	2.465895	0.24177	0.8585	NA	RP11-1376	chr17	+	80117932	80118328	345
ENSG00000(	0	0	2.638828	0	2.761296	0	-0.03456	0.97961	NA	RP11-849N	chr17	-	15283181	15321195	538
ENSG00000(	1.035792	8.430014	1.319414	1.498151	0.920432	0.821965	1.2683	0.28652	0.40995	RP11-258F	chr17	-	18075939	18088067	2158
ENSG00000(	2.071584	2.408575	2.638828	14.23244	16.56778	5.753754	-2.081	0.017159	0.037839	RP5-1148A	chr6	-	64280910	64282313	1404
ENSG00000(	5.17896	0	1.319414	0	0.920432	3.28786	0.43024	0.7384	0.82485	RP11-30L3	chr18	+	46732282	46735151	472
ENSG00000(	1.035792	0	1.319414	0	0	0.821965	0.54471	0.68089	NA	RP11-661C	chr18	-	8635177	8636345	780
ENSG00000(	80.79177	71.05298	106.8725	29.21395	33.13555	35.34449	1.3825	3.03E-05	0.000106	RP11-214C	chr17	+	14207171	14208822	1652
ENSG00000(	7.250543	10.83859	3.958241	0	1.840864	0.821965	2.471	0.021269	0.045853	MYO15B	chr17	+	73584139	73622929	9407
ENSG00000(	4.143168	4.817151	0	2.247227	0	0	1.2555	0.3337	0.46178	RP11-855A	chr17	-	65947001	65947862	709
ENSG00000(	0	1.204288	0	1.498151	4.60216	2.465895	-1.7234	0.18633	0.29091	RP11-466A	chr17	+	30822554	30826351	2480
ENSG00000(	0	0	0	9.737982	0	1.64393	-2.4886	0.062867	0.11835	TBC1D29	chr17	+	28884130	28890511	3018
ENSG00000(	3.107376	1.204288	0	0	0	0	1.4526	0.27741	NA	RP11-94B1	chr18	-	73885259	73889693	464
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-131K	chr17	-	13861065	13870269	511
ENSG00000(	32.10955	68.6444	23.74945	46.44268	32.21512	34.52253	0.13186	0.76351	0.84382	RP11-690G	chr17	-	37408897	37410550	1654
ENSG00000(	1.035792	1.204288	2.638828	0	0	0	1.7123	0.20641	NA	RP11-678G	chr18	-	7741308	7754829	1057
ENSG00000(	4.143168	1.204288	0	0	0	0	1.7302	0.20044	NA	RP11-321N	chr18	-	73144658	73148912	748
ENSG00000(	27.96638	25.29004	29.0271	13.48336	18.40864	13.9734	0.81785	0.10044	0.1761	SH3GL1P1	chr17	+	30366993	30369847	1945
ENSG00000(	7.250543	1.204288	6.597069	6.74168	12.88605	4.93179	-0.61408	0.47898	0.60807	RP11-715F	chr18	-	2561171	2562219	1049
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP1-66C13	chr17	+	26073158	26081980	764
ENSG00000(	0	0	5.277655	2.247227	0.920432	4.93179	-0.46289	0.71039	0.80422	RP11-521L	chr16	+	68967723	68971628	641
ENSG00000(	8.286335	1.204288	7.916483	0	0	0	3.6207	0.00431	0.010819	RP1-77H15	chr17	-	16461299	16462583	689
ENSG00000(	1.035792	2.408575	5.277655	0.749076	0.920432	0	1.5767	0.21443	0.32488	RP11-61L1	chr18	+	9506240	9509724	3485
ENSG00000(	0	1.204288	2.638828	0.749076	0	0	1.0049	0.45751	NA	RP11-6N17	chr17	-	45956838	45959764	2927
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-599B	chr17	+	8080130	8086130	465
ENSG00000(	32.10955	37.33292	19.79121	0.749076	0.920432	0	4.9456	2.18E-08	1.07E-07	RP11-838N	chr18	+	3466248	3478976	643
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-121A	chr17	+	20226371	20226650	280
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-543H	chr18	-	67372214	67392211	483
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	RP11-862L	chr18	+	74686646	74696118	812
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	RP11-793A	chr18	+	6025090	6082454	544

ENSG00000(	0	9.634302	0	0	0	0	2.3734	0.080139	0.14563	ITM2BP1	chr17	-	25939614	25940277	664
ENSG00000(	10.35792	9.634302	14.51355	31.46117	37.73771	42.74218	-1.6444	0.001027	0.002875	RP11-848P	chr17	+	29335515	29420145	739
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	RP6-114E2	chr14	+	72315323	72375147	397
ENSG00000(	3.107376	16.86003	10.55531	0	0	0	4.5038	0.00016	0.000508	RP1-41C23	chr17	+	29910181	29964562	568
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-1090	chr17	+	12721314	12726571	5258
ENSG00000(	4.143168	0	3.958241	2.996302	2.761296	1.64393	0.10255	0.92903	0.95729	RP11-692N	chr18	-	9734879	9735599	368
ENSG00000(	3.107376	3.612863	0	1.498151	1.840864	0.821965	0.50087	0.68635	0.78545	CTC-268N1	chr17	-	35402760	35410075	718
ENSG00000(	16.57267	12.04288	13.19414	16.47966	34.05598	13.9734	-0.58491	0.31134	0.4376	RP1-266L2	chr6	+	1.7E+08	1.7E+08	1630
ENSG00000(	18.64425	3.612863	11.87472	5.992604	16.56778	18.90519	-0.24598	0.7279	0.81771	AC005546.	chr19	+	13242385	13243224	391
ENSG00000(	1.035792	1.204288	1.319414	0	0	3.28786	0.062408	0.96289	0.97847	RP11-173A	chr18	+	59913043	59914645	1603
ENSG00000(	0	0	1.319414	0.749076	2.761296	3.28786	-1.4077	0.28876	0.4124	RP11-567N	chr18	-	77462721	77463651	474
ENSG00000(	5.17896	0	6.597069	0	2.761296	0	1.4388	0.2548	0.373	CTB-171A8	chr19	-	45135500	45222031	829
ENSG00000(	71.46964	33.72006	34.30476	35.95563	31.29469	30.4127	0.51004	0.21989	0.33159	LINC00663	chr19	-	19868175	19887232	2546
ENSG00000(	2.071584	0	1.319414	0	1.840864	0.821965	0.21443	0.87358	0.92056	AC006116.	chr19	-	56831159	56833679	2171
ENSG00000(	0	2.408575	1.319414	2.247227	0	1.64393	-0.05944	0.96425	0.97938	SLC25A6P4	chr18	+	77835609	77836161	553
ENSG00000(	10.35792	18.06432	15.83297	11.98521	12.88605	7.397684	0.42503	0.50217	0.63023	CTC-448F2.	chr19	+	30528330	30529063	734
ENSG00000(	1.035792	16.86003	9.235896	8.239831	4.60216	1.64393	0.77251	0.39627	0.52728	CTC-325H2	chr19	+	9455460	9456574	1115
ENSG00000(	0	0	0	2.996302	0	3.28786	-1.6956	0.21138	0.32124	CTC-548K1	chr19	-	14416270	14481008	573
ENSG00000(	3.107376	8.430014	1.319414	26.21764	18.40864	23.01502	-2.2162	0.001635	0.004422	CTD-3064H	chr19	-	37988063	37997948	670
ENSG00000(	1.035792	6.021439	2.638828	1.498151	1.840864	0	1.106	0.36226	0.49192	RP11-798G	chr17	+	43608943	43611204	2262
ENSG00000(	2.071584	6.021439	3.958241	7.490755	1.840864	5.753754	-0.29338	0.76128	0.84215	RP11-15A1	chr19	-	44501048	44506988	2550
ENSG00000(	0	0	0	0.749076	0.920432	0.821965	-0.73223	0.57364	NA	CTC-499B1	chr19	-	11836776	11841598	491
ENSG00000(	4.143168	2.408575	2.638828	5.992604	5.522592	7.397684	-0.88687	0.34386	0.47307	AC005943.	chr19	-	1581789	1582322	534
ENSG00000(	4.143168	0	0	0.749076	1.840864	0.821965	0.20023	0.88031	0.92524	AC006273.	chr19	+	786650	787037	388
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTB-70G10	chr19	-	28785000	28804407	575
ENSG00000(	124.295	145.7188	93.67838	85.39461	61.66894	127.4046	0.40076	0.17985	0.28273	CTD-2085J	chr19	-	33366831	33369327	495
ENSG00000(	1.035792	0	3.958241	0.749076	1.840864	4.93179	-0.43654	0.72246	0.81346	AC006116.	chr19	-	56853801	56854788	988
ENSG00000(	1.035792	1.204288	5.277655	0	3.681728	3.28786	0.074496	0.95043	0.97025	AC005775.	chr19	-	490046	507813	830
ENSG00000(	9.322127	12.04288	6.597069	1.498151	6.443024	0	1.58	0.096928	0.17092	RP11-332H	chr17	+	59460146	59462041	716
ENSG00000(	15.53688	9.634302	7.916483	9.737982	7.363456	4.93179	0.54682	0.45271	0.58249	CTD-3234P	chr19	+	37119695	37121092	550
ENSG00000(	5.17896	3.612863	6.597069	0	2.761296	6.575719	0.59456	0.5695	0.68867	CTC-215O4	chr19	-	11121593	11126687	366
ENSG00000(	32.10955	24.08575	31.66593	65.16957	44.18074	60.00344	-0.92942	0.014824	0.033143	CTC-479C5	chr16	+	67903863	67906470	2608
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC119403.	chr19	-	2896623	2897220	598
ENSG00000(	0	0	1.319414	5.992604	0	0	-1.0917	0.42098	0.55162	AC104532.	chr19	+	5899906	5901522	341
ENSG00000(	4.143168	4.817151	1.319414	5.243529	4.60216	3.28786	-0.28691	0.77285	0.85079	RP11-378E	chr17	+	35743821	35744861	735
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	AC005262.	chr19	+	3130715	3131396	362
ENSG00000(	2.071584	2.408575	2.638828	11.98521	18.40864	8.219649	-2.1624	0.011447	0.026249	MRPL37P1	chr18	+	56357588	56359385	1337
ENSG00000(	29.00217	13.24716	13.19414	17.97781	20.2495	19.72716	-0.04714	0.93146	0.95881	RP11-799D	chr17	-	33558469	33569982	2658
ENSG00000(	0	2.408575	1.319414	0	0.920432	0.821965	0.58326	0.66656	NA	CTD-2623N	chr19	+	9904297	9912977	408
ENSG00000(	0	0	9.235896	6.74168	0	0	0.14957	0.90725	0.94286	RP11-820I	chr18	-	11993987	11994937	528
ENSG00000(	0	1.204288	1.319414	2.247227	2.761296	0	-0.60198	0.65099	0.75715	RP11-49K2	chr18	-	44603732	44617651	200
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC006126.	chr19	+	45690646	45720191	540
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC005786.	chr19	-	3568118	3568271	154
ENSG00000(	0	0	3.958241	0.749076	0	0	0.94769	0.48013	NA	FAM106DP	chr17	+	58250683	58251183	501

ENSG00000(	8.286335	6.021439	3.958241	2.247227	11.04518	12.32947	-0.41843	0.61807	0.73044	RP11-712P	chr18	+	33175865	33177563	1699
ENSG00000(	17.60846	30.10719	19.79121	22.47227	29.45382	27.94681	-0.23526	0.62282	0.73465	AARSD1	chr17	-	41102543	41116515	1322
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-116C	chr18	+	43226118	43227895	1778
ENSG00000(	1.035792	2.408575	1.319414	2.247227	6.443024	4.109825	-1.1189	0.31219	0.43856	RP11-773H	chr18	-	12984693	12991172	474
ENSG00000(	21.75163	28.90291	21.11062	8.239831	3.681728	10.68554	1.5685	0.009563	0.022343	RP11-806H	chr17	+	76356534	76369992	777
ENSG00000(	0	0	0	2.996302	3.681728	4.93179	-2.721	0.03642	0.073681	AC015849.	chr17	-	34239639	34245014	5376
ENSG00000(	0	0	0	0	0	2.465895	-0.63737	0.61192	NA	CTD-3162L	chr19	+	36868930	36869734	566
ENSG00000(	5.17896	3.612863	6.597069	2.247227	10.12475	4.109825	-0.07617	0.93367	0.9602	CTC-425F1.	chr19	+	13041336	13044110	241
ENSG00000(	1.035792	1.204288	0	7.490755	19.32907	14.79537	-3.4137	0.000618	0.001791	AC079466.	chr19	+	29097595	29106136	4453
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTC-459F4.	chr19	-	28340638	28380130	458
ENSG00000(	5.17896	3.612863	1.319414	0	0.920432	1.64393	1.4296	0.24189	0.3575	RP11-552F	chr17	-	73814896	73816136	890
ENSG00000(	1.035792	2.408575	11.87472	6.74168	4.60216	8.219649	-0.33453	0.71825	0.81024	CTC-232P5	chr19	+	5978414	6020374	639
ENSG00000(	6.214751	3.612863	13.19414	3.745378	0.920432	6.575719	0.87944	0.33925	0.46792	RP11-354P	chr17	-	28471080	28471808	360
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC004528.	chr19	-	999795	1002756	641
ENSG00000(	14.50109	12.04288	18.47179	2.996302	13.80648	17.26126	0.38045	0.57604	0.69439	RP4-657D1	chr1	+	52259637	52264824	1288
ENSG00000(	1.035792	1.204288	2.638828	2.996302	0	1.64393	0.024924	0.98437	0.99094	RP11-127I2	chr16	-	4780116	4802566	556
ENSG00000(	4.143168	0	1.319414	0	0	0	1.7539	0.19459	NA	RP11-703I2	chr18	-	12040100	12040299	200
ENSG00000(	20.71584	22.88147	6.597069	0	0.920432	1.64393	3.6864	7.63E-05	0.000253	RP11-936I5	chr17	-	75369900	75373318	3419
ENSG00000(	0	0	1.319414	4.494453	16.56778	4.109825	-3.1354	0.00676	0.016313	AC015849.	chr17	-	34220711	34238027	5473
ENSG00000(	1.035792	1.204288	2.638828	2.996302	0	0	0.3998	0.76304	0.84358	RP11-27G2	chr18	+	57126304	57132914	487
ENSG00000(	22.78742	9.634302	25.06886	7.490755	22.09037	18.08323	0.26407	0.66041	0.76485	RP11-242D	chr17	-	41316200	41322420	1191
ENSG00000(	11.39371	16.86003	5.277655	5.243529	0.920432	5.753754	1.3221	0.11477	0.19655	CTC-507E2.	chr17	-	34006411	34011922	3329
ENSG00000(	0	0	0	7.490755	0	0	-1.7575	0.1945	0.3007	CTD-2659N	chr19	-	12836331	12836700	97
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC002984.	chr19	-	36664308	36664755	448
ENSG00000(	2.071584	3.612863	3.958241	0.749076	0	0	2.2101	0.088029	0.15784	CTC-448F2.	chr19	-	30519648	30520823	1176
ENSG00000(	5.17896	0	11.87472	0	0	4.109825	1.4844	0.21709	0.32825	RP11-120N	chr17	+	66409783	66489811	773
ENSG00000(	35.21692	44.55865	29.0271	295.8848	166.5982	189.8739	-2.5516	1.34E-17	1.21E-16	RP11-108P	chr18	+	56419380	56421709	2330
ENSG00000(	4.143168	0	2.638828	3.745378	2.761296	6.575719	-0.74361	0.49509	0.62382	CTB-50L17.	chr19	-	4457959	4471490	478
ENSG00000(	64.2191	48.17151	62.01245	0	1.840864	0.821965	5.5401	1.63E-13	1.18E-12	CTD-2171N	chr18	-	52773135	52791537	3067
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-800A	chr18	-	77100258	77103972	502
ENSG00000(	27.96638	21.67718	19.79121	0.749076	5.522592	2.465895	2.7978	0.000103	0.000336	RP11-75C1	chr17	-	75465244	75468852	1132
ENSG00000(	1.035792	0	0	0	4.60216	0.821965	-1.1271	0.40572	0.53658	AC010525.	chr19	+	56207681	56208795	1115
ENSG00000(	170.9057	209.5461	179.4403	220.9773	265.0844	193.9837	-0.27837	0.17271	0.27388	LRRC37A16	chr17	-	66121918	66148609	3725
ENSG00000(	1.035792	0	0	1.498151	0	1.64393	-0.62149	0.64536	NA	CTD-2588C	chr19	-	34917017	34919178	442
ENSG00000(	25.8948	31.31148	32.98534	23.22134	46.0216	36.16646	-0.21716	0.61677	0.72942	AC015849.	chr17	-	34143721	34157297	488
ENSG00000(	0	2.408575	2.638828	0	0	2.465895	0.5704	0.67147	0.77389	RP11-619L	chr18	+	53119764	53150171	396
ENSG00000(	0	1.204288	0	0	0.920432	4.109825	-1.0194	0.45216	0.58187	AC092299.	chr19	+	197955	200775	381
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-807E	chr18	-	13151636	13152688	1053
ENSG00000(	2.071584	2.408575	3.958241	0	0	2.465895	1.1772	0.3551	0.48466	CTD-2562J	chr19	-	16297087	16300269	578
ENSG00000(	2.071584	7.225726	0	8.988907	16.56778	8.219649	-1.6147	0.071739	0.13255	RP11-384C	chr2	-	2.23E+08	2.23E+08	1412
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	AC005559.	chr19	-	590277	591603	1327
ENSG00000(	0	0	0	0	4.60216	1.64393	-1.6592	0.22125	0.33301	RP11-58G1	chr18	-	34481909	34503777	688
ENSG00000(	26.93059	33.72006	19.79121	28.46487	20.2495	32.8786	-0.01991	0.96573	0.98014	RP11-35G9	chr18	+	55297534	55405276	1976
ENSG00000(	72.50543	80.68728	60.69303	244.9477	261.4027	224.3964	-1.7567	8.79E-15	6.85E-14	ZNF850	chr19	-	37205285	37263727	7714

ENSG00000(	5.17896	8.430014	2.638828	0	0	0.821965	2.9195	0.016664	0.036838	CTD-3193K	chr17	+	40831981	40834038	542
ENSG00000(	1.035792	13.24716	0	0	0	9.041614	0.27297	0.83826	0.89652	AC005757.	chr19	-	45639251	45640235	472
ENSG00000(	4.143168	0	0	1.498151	2.761296	1.64393	-0.30081	0.8148	0.87965	AC006126.	chr19	-	45741890	45748628	460
ENSG00000(	2.071584	7.225726	0	0	0	0	2.5144	0.062241	0.11725	RP11-566K	chr16	+	89972565	89984641	559
ENSG00000(	7.250543	4.817151	1.319414	25.46857	12.88605	33.70056	-2.2209	0.001571	0.004259	AC002398.	chr19	-	36260046	36261930	427
ENSG00000(	0	0	1.319414	0.749076	0.920432	0	-0.15244	0.90808	NA	CTB-30L5.1	chr7	-	1.06E+08	1.06E+08	550
ENSG00000(	6.214751	14.45145	2.638828	4.494453	5.522592	9.041614	0.26359	0.75304	0.83667	CTD-3162L	chr19	+	36795482	36803570	2305
ENSG00000(	0	6.021439	0	0	0	3.28786	0.48487	0.71883	0.81058	RP11-486P	chr7	+	20135760	20170098	670
ENSG00000(	52.82539	27.69862	21.11062	8.988907	1.840864	15.61733	1.8315	0.002945	0.007618	RP11-15A1	chr19	-	44395956	44405957	2193
ENSG00000(	3.107376	3.612863	1.319414	12.73428	8.283888	7.397684	-1.5837	0.075642	0.13865	UQCR11	chr19	-	1578011	1605483	1335
ENSG00000(	1.035792	1.204288	2.638828	38.95193	22.09037	20.54912	-3.6838	3.97E-06	1.54E-05	PTGES3L	chr17	-	41120105	41132545	1905
ENSG00000(	0	0	1.319414	0	3.681728	0	-0.65657	0.62582	NA	RP11-760L	chr18	+	57230941	57235847	546
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC006130.	chr19	-	2847225	2858714	555
ENSG00000(	2.071584	0	1.319414	0.749076	0.920432	0.821965	0.26888	0.84077	NA	RP1-212G6	chrX	+	47518232	47519776	1525
ENSG00000(	2.071584	0	1.319414	2.247227	0	0	0.2943	0.82824	NA	CTD-2246P	chr17	+	74795126	74802035	2270
ENSG00000(	0	3.612863	3.958241	2.247227	0	0	1.0403	0.43012	0.56014	CTB-75G16	chr17	+	34990527	34991156	630
ENSG00000(	2.071584	0	0	0.749076	0	0	0.47431	0.71145	NA	RP11-64C1	chr18	+	12288307	12291487	733
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-10K1	chr16	+	5148740	5192596	531
ENSG00000(	0	1.204288	1.319414	0	0	0.821965	0.59385	0.65509	NA	AC005256.	chr19	+	1748055	1748744	415
ENSG00000(	3.107376	0	0	1.498151	0	0	0.45456	0.7352	NA	RP11-820I	chr18	-	11910633	11914343	379
ENSG00000(	81.82756	74.66584	102.9143	225.4717	206.1768	199.7375	-1.2786	2.01E-08	9.87E-08	ASB16-AS1	chr17	-	42253341	42264085	2213
ENSG00000(	2.071584	1.204288	3.958241	0.749076	1.840864	3.28786	0.22093	0.85071	0.9049	CTC-510F1	chr19	+	11314304	11326844	569
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	AC079005.	chr17	+	58887526	58888823	1298
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-15J1(	chr9	-	70116128	70116383	256
ENSG00000(	1.035792	1.204288	1.319414	2.247227	0	0	0.34377	0.79908	NA	RP11-115N	chr18	+	39669276	39669716	441
ENSG00000(	3.107376	0	0	0	0	1.64393	0.41335	0.75876	NA	CTC-499B1	chr19	-	11952056	11953254	442
ENSG00000(	4.143168	6.021439	1.319414	0	2.761296	0	1.4843	0.22803	0.34129	CTBP2P7	chr19	-	36987818	36989061	1244
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTB-25B13	chr19	+	1508381	1508962	450
ENSG00000(	7.250543	2.408575	1.319414	0	6.443024	1.64393	0.3728	0.74422	0.82965	CTD-2105E	chr19	-	55911113	55911787	675
ENSG00000(	1.035792	0	0	0	2.761296	0.821965	-0.71844	0.59551	NA	CTD-2319I	chr17	-	58213123	58217442	542
ENSG00000(	8.286335	1.204288	3.958241	5.243529	3.681728	16.4393	-0.78303	0.388	0.51881	CTD-2537I9	chr19	+	56181998	56183435	802
ENSG00000(	170.9057	186.6646	168.885	331.0914	223.665	300.8392	-0.69862	0.000601	0.001745	ILF3-AS1	chr19	-	10762538	10764520	1983
ENSG00000(	2.071584	3.612863	2.638828	49.43899	25.7721	28.76877	-3.3944	8.29E-07	3.46E-06	RP11-686D	chr17	-	33736621	33737247	627
ENSG00000(	129.474	152.9445	143.8161	119.103	116.8949	106.0335	0.31371	0.16769	0.26706	CTD-3116E	chr19	+	9731967	9756572	2461
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC011526.	chr19	-	41960074	42006559	3472
ENSG00000(	0	1.204288	0	2.247227	0	1.64393	-0.78914	0.56072	NA	RP11-861E	chr18	+	12432896	12437634	168
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	AC008993.	chr19	+	68403	69146	744
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	RP11-839G	chr18	-	52553097	52565314	567
ENSG00000(	7.250543	8.430014	3.958241	1.498151	9.20432	13.9734	-0.28082	0.7425	0.82832	CTB-129P6	chr19	-	45453301	45457264	361
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTD-3064H	chr19	-	37994808	37995367	560
ENSG00000(	1.035792	10.83859	0	0.749076	0.920432	4.93179	0.63267	0.59075	0.70729	AC010525.	chr19	-	56205484	56205924	441
ENSG00000(	2.071584	1.204288	1.319414	1.498151	5.522592	8.219649	-1.355	0.21515	0.32584	RPL10P15	chr19	+	9930817	9931131	315
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	CTD-2020K	chr17	-	43268298	43299589	2238
ENSG00000(	1.035792	7.225726	3.958241	0	4.60216	0.821965	0.90202	0.43825	0.56786	AC004490.	chr19	-	2212028	2215564	2738

ENSG00000(	34.18113	54.19295	50.13772	24.71949	19.32907	17.26126	1.1386	0.007444	0.017825	RP11-795F	chr18	+	77794346	77854968	2218
ENSG00000(	0	0	0	2.996302	2.761296	1.64393	-2.0518	0.12695	0.21323	RNF157-AS	chr17	+	74136637	74150731	1812
ENSG00000(	3.107376	2.408575	3.958241	1.498151	0	1.64393	1.1389	0.34421	0.47343	RP11-332H	chr17	-	59439029	59477604	470
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-146N	chr18	+	61771325	62090836	1722
ENSG00000(	1.035792	0	0	0	0	2.465895	-0.37334	0.77636	NA	RP11-53B2	chr18	-	13514519	13522887	4745
ENSG00000(	0	2.408575	0	0	0	2.465895	-0.0181	0.98928	NA	RP11-15K2	chr17	-	59537585	59540745	552
ENSG00000(	2.071584	0	1.319414	2.247227	0	1.64393	-0.12066	0.92771	0.95653	AC005954.	chr19	-	3754618	3756657	337
ENSG00000(	11.39371	27.69862	14.51355	2.247227	11.04518	14.79537	0.87236	0.20937	0.31902	CTB-31O20	chr19	+	1860249	1862018	607
ENSG00000(	3.107376	0	0	1.498151	0	2.465895	-0.17726	0.89532	0.93521	CTD-3162L	chr19	+	36912438	36913436	999
ENSG00000(	0	0	0	1.498151	0	0.821965	-0.60976	0.62726	NA	AC067968.	chr19	-	44527756	44529414	566
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	CTC-548K1	chr19	+	14444555	14454725	765
ENSG00000(	3.107376	10.83859	1.319414	0	1.840864	1.64393	1.6458	0.15097	0.24533	CTC-550B1	chr19	-	55538961	55565296	1271
ENSG00000(	1.035792	6.021439	0	26.96672	28.53339	13.9734	-2.9698	0.000197	0.000615	RP11-411B	chr18	+	14089934	14091018	1085
ENSG00000(	0	0	5.277655	0	1.840864	0	0.76764	0.57145	0.69031	hsa-mir-21	chr17	+	41522075	41528568	506
ENSG00000(	45.57484	48.17151	31.66593	72.66033	57.06678	38.63235	-0.41403	0.27017	0.39065	CTD-2528L	chr19	-	38219487	38221544	1360
ENSG00000(	3.107376	0	6.597069	2.247227	10.12475	5.753754	-0.75182	0.46039	0.58985	AC005391.	chr19	-	928257	928817	330
ENSG00000(	4.143168	7.225726	3.958241	1.498151	4.60216	4.109825	0.50726	0.60023	0.71569	RP11-1072	chr17	-	42751057	42753625	2569
ENSG00000(	127.4024	81.89156	130.622	136.3317	99.40666	154.5294	-0.1989	0.4583	0.58781	AC005943.	chr19	-	1573595	1575474	1880
ENSG00000(	10.35792	6.021439	6.597069	0	1.840864	3.28786	1.8213	0.070086	0.12986	AC084219.	chr19	-	44598503	44603864	2139
ENSG00000(	3.107376	7.225726	5.277655	0	2.761296	5.753754	0.71632	0.49568	0.6244	RP11-687F	chr18	-	44383187	44383857	671
ENSG00000(	71.46964	56.60152	81.80365	26.96672	52.46462	43.56414	0.7626	0.03216	0.066057	CTB-55O6.	chr19	+	14247991	14282079	2861
ENSG00000(	0	2.408575	0	0.749076	2.761296	1.64393	-0.65401	0.62241	0.73431	CTC-260F2	chr19	+	19615087	19615463	377
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	CTC-510F1	chr19	-	11411453	11435117	655
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	RP11-879F	chr18	-	59259608	59416065	566
ENSG00000(	9.322127	6.021439	10.55531	9.737982	4.60216	4.109825	0.43334	0.58595	0.70335	CTB-179K2	chr19	-	45588587	45593632	618
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTC-260F2	chr19	-	19698901	19699225	325
ENSG00000(	11.39371	16.86003	9.235896	2.247227	7.363456	1.64393	1.5849	0.050652	0.098193	AC010525.	chr19	+	56207251	56209196	537
ENSG00000(	1.035792	0	0	1.498151	0.920432	0	-0.39626	0.76684	NA	PTP4A2P1	chr17	+	40685550	40686027	478
ENSG00000(	2.071584	10.83859	7.916483	2.996302	1.840864	0	1.6979	0.10579	0.18367	RP11-15A1	chr19	+	44406153	44430697	517
ENSG00000(	0	10.83859	1.319414	1.498151	0.920432	2.465895	0.97064	0.41103	0.54181	AC006116.	chr19	+	56898781	56899793	452
ENSG00000(	1.035792	0	7.916483	0	0	0	2.4101	0.074732	0.13721	RP11-116C	chr18	-	43249332	43327180	547
ENSG00000(	44.53905	32.51577	31.66593	58.42789	41.41944	33.70056	-0.28757	0.46829	0.59749	RP1-193H1	chr17	+	67547499	67550002	2504
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	hsa-mir-21	chr17	-	1953565	1953674	110
ENSG00000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	RP11-813F	chr18	-	47496091	47497327	375
ENSG00000(	0	3.612863	5.277655	0.749076	5.522592	2.465895	0.011037	0.99233	0.99518	CTC-429L1	chr19	-	10601015	10601676	357
ENSG00000(	1.035792	0	0	2.247227	1.840864	0	-0.86384	0.52422	NA	RP11-798G	chr17	+	43623170	43640596	630
ENSG00000(	6.214751	6.021439	9.235896	8.988907	7.363456	3.28786	0.10841	0.89439	0.93468	RP11-861E	chr18	+	12438889	12448204	4910
ENSG00000(	3.107376	0	0	0	0	0.821965	0.7418	0.57612	NA	hsa-mir-13	chr17	-	1953202	1953302	101
ENSG00000(	6.214751	6.021439	5.277655	2.247227	10.12475	9.863579	-0.29576	0.72786	0.8177	AC005624.	chr19	-	2458933	2462183	371
ENSG00000(	0	0	2.638828	0	1.840864	2.465895	-0.40543	0.7639	0.84398	SNRPGP4	chr17	+	67314874	67315102	229
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-264B	chr17	-	59111997	59147483	429
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	CTD-2659N	chr19	-	12895353	12895915	388
ENSG00000(	6.214751	4.817151	6.597069	1.498151	0.920432	2.465895	1.5249	0.13538	0.22464	AC007773.	chr19	-	32880956	32896445	951
ENSG00000(	8.286335	15.65574	25.06886	2.247227	11.04518	13.15144	0.82299	0.24877	0.36593	AC010642.	chr19	+	58790332	58826563	4227

ENSG00000(	7.250543	9.634302	1.319414	4.494453	5.522592	1.64393	0.5626	0.55507	0.67581	AC010504.	chr19	-	34839261	34850317	585
ENSG00000(	0	0	0	3.745378	0	2.465895	-1.6796	0.21567	0.32631	CTC-260E6.	chr19	-	20242703	20262717	283
ENSG00000(	0	7.225726	1.319414	6.74168	5.522592	7.397684	-1.0118	0.31909	0.44624	CTD-2132N	chr17	-	40192731	40195135	761
ENSG00000(	1.035792	0	1.319414	2.247227	1.840864	0	-0.4528	0.73609	0.82343	RP11-194N	chr17	+	40647885	40648568	684
ENSG00000(	1.035792	2.408575	7.916483	17.22874	7.363456	9.041614	-1.4249	0.098086	0.17255	RP11-126C	chr18	-	56337712	56339109	738
ENSG00000(	3.107376	0	1.319414	0.749076	0	1.64393	0.51931	0.698	0.79445	IER3IP1	chr18	-	44661027	44702652	561
ENSG00000(	0	2.408575	0	1.498151	4.60216	2.465895	-1.2123	0.34124	0.47009	RP11-376N	chr17	-	41127706	41129292	1587
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC005786.	chr19	+	3558013	3558484	369
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	CTB-184G2	chr19	-	19512788	19513412	488
ENSG00000(	18.64425	24.08575	27.70769	3.745378	1.840864	4.93179	2.5426	0.000166	0.000524	RP11-618P	chr19	+	34873966	34893064	425
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC093074.	chr19	-	28885758	28887335	556
ENSG00000(	29.00217	9.634302	17.15238	23.97042	11.96562	26.30288	-0.14571	0.79827	0.86851	AC069278.	chr19	-	44978645	44979403	759
ENSG00000(	5.17896	3.612863	1.319414	60.67512	61.66894	57.53754	-3.9	1.99E-11	1.24E-10	AC005307.	chr19	-	28926295	29218684	3113
ENSG00000(	22.78742	37.33292	23.74945	20.97412	24.85166	46.852	-0.14046	0.76745	0.8467	CTB-31O20	chr19	+	1822088	1824544	2400
ENSG00000(	0	1.204288	0	0	0.920432	2.465895	-0.65251	0.6297	NA	RP11-798G	chr17	-	43627147	43636104	826
ENSG00000(	0	1.204288	0	2.247227	0	0.821965	-0.5853	0.66478	NA	RP11-64C1	chr18	-	12230410	12231572	485
ENSG00000(	21.75163	15.65574	17.15238	15.73059	9.20432	14.79537	0.43419	0.45047	0.58016	CTD-2319I	chr17	-	58203896	58213005	1023
ENSG00000(	1.035792	8.430014	5.277655	28.46487	23.0108	17.26126	-2.0882	0.002724	0.007089	RP11-973H	chr18	-	12670425	12671144	720
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-118B	chr17	-	66789690	66793963	518
ENSG00000(	25.8948	18.06432	18.47179	3.745378	16.56778	5.753754	1.2048	0.06408	0.12021	AC139100.	chr18	+	77941563	77960875	2035
ENSG00000(	6.214751	22.88147	11.87472	14.98151	5.522592	5.753754	0.57658	0.42563	0.55596	CTD-2162K	chr19	+	37288420	37319017	850
ENSG00000(	0	0	0	1.498151	0	2.465895	-1.1271	0.39798	NA	CTB-50L17.	chr19	-	4429686	4430931	569
ENSG00000(	0	0	2.638828	0	2.761296	0	-0.03456	0.97961	NA	RP11-1151	chr18	+	56202647	56205784	2553
ENSG00000(	0	0	0	2.996302	9.20432	0.821965	-2.8095	0.031155	0.064268	CTD-2008P	chr17	-	26559616	26562307	2692
ENSG00000(	0	0	1.319414	7.490755	10.12475	3.28786	-2.9071	0.013374	0.030222	CTD-2162K	chr19	+	37264055	37267980	1850
ENSG00000(	1.035792	0	1.319414	0	0.920432	0	0.55201	0.67753	NA	CTC-232P5	chr19	+	6067964	6077130	567
ENSG00000(	0	4.817151	3.958241	0	2.761296	0	1.0774	0.40734	0.53818	RP11-75C1	chr17	+	75465150	75467127	768
ENSG00000(	2.071584	0	2.638828	5.992604	3.681728	3.28786	-1.1402	0.30991	0.43609	CTC-459F4.	chr19	+	28294446	28294968	523
ENSG00000(	19.68005	8.430014	21.11062	35.95563	21.16994	34.52253	-0.86581	0.095242	0.16843	CTC-550B1	chr19	+	55517561	55559454	786
ENSG00000(	0	0	1.319414	4.494453	3.681728	0.821965	-1.7466	0.1792	0.28191	AC007204.	chr19	+	20011777	20074273	763
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	RP11-2N1.	chr18	+	57353052	57355632	542
ENSG00000(	53.86118	45.76293	69.92893	23.97042	41.41944	35.34449	0.73908	0.051283	0.099274	AC139100.	chr18	+	77905807	77936315	3333
ENSG00000(	2.071584	0	3.958241	2.247227	0	0.821965	0.59845	0.64635	0.75329	RP5-1052I5	chr1	+	87595448	87634881	3368
ENSG00000(	1.035792	1.204288	0	0	1.840864	0	0.14661	0.91336	NA	CTC-543D1	chr19	+	9609354	9620755	656
ENSG00000(	6.214751	12.04288	10.55531	5.243529	11.04518	13.15144	-0.03095	0.96579	0.98014	CTD-2006C	chr19	+	12050774	12064196	468
ENSG00000(	1.035792	4.817151	0	5.243529	1.840864	1.64393	-0.43204	0.7158	0.8084	CTD-2342J	chr19	-	11478799	11485611	682
ENSG00000(	30.03797	28.90291	27.70769	16.47966	13.80648	18.90519	0.78864	0.10298	0.17965	MAP3K14-/	chr17	+	43325292	43345997	2475
ENSG00000(	19.68005	20.47289	29.0271	42.69731	26.69253	16.4393	-0.30935	0.5358	0.66002	RP11-879F	chr18	-	59252979	59274149	735
ENSG00000(	215.4447	249.2876	221.6615	5.243529	5.522592	18.08323	4.4917	2.39E-37	4.57E-36	RP11-332H	chr17	-	59470817	59488916	861
ENSG00000(	3.107376	8.430014	2.638828	2.247227	0	1.64393	1.4235	0.20653	0.31557	CTB-129P6	chr19	-	45385284	45394133	426
ENSG00000(	8.286335	7.225726	3.958241	10.48706	6.443024	13.9734	-0.60146	0.43034	0.56024	AC005306.	chr19	+	1989400	1990369	661
ENSG00000(	0	0	0	2.996302	2.761296	0.821965	-1.8697	0.16674	0.26571	RP11-397A	chr18	+	53388294	53455992	565
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP5-951N9	chr12	+	1494999	1496153	574
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-567N	chr18	+	77336460	77349010	4167

ENSG0000(	0	3.612863	0	0	1.840864	0	0.45719	0.73538	NA	RP13-890H	chr17	-	43246172	43248951	2048
ENSG0000(	0	3.612863	0	0.749076	0	0	0.87856	0.51086	NA	CTD-2623N	chr19	-	9944755	9945689	750
ENSG0000(	0	0	0	5.992604	2.761296	4.93179	-2.9693	0.020487	0.044305	RP11-8H2.	chr18	+	43608272	43609795	1524
ENSG0000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	CTD-2319I	chr17	-	58191154	58198048	569
ENSG0000(	2.071584	0	0	2.247227	0	3.28786	-0.77521	0.56359	0.68317	CEBPA-AS1	chr19	+	33793763	33795960	2198
ENSG0000(	6.214751	10.83859	1.319414	0	0	1.64393	2.5429	0.03076	0.063527	AC006116.	chr19	-	56823297	56823855	559
ENSG0000(	2.071584	1.204288	0	0	1.840864	0.821965	0.19367	0.88581	0.92875	RP11-178C	chr17	+	58042193	58074333	1603
ENSG0000(	4.143168	20.47289	11.87472	7.490755	2.761296	2.465895	1.3423	0.10433	0.18158	AC004637.	chr19	+	3672580	3674293	482
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-333J	chr17	+	35337466	35337721	256
ENSG0000(	6.214751	16.86003	27.70769	15.73059	24.85166	18.08323	-0.21088	0.7221	0.81311	CTD-2630F	chr19	+	36980551	36981942	1392
ENSG0000(	1.035792	3.612863	5.277655	0	1.840864	0	1.6397	0.19665	0.30342	RP11-99A1	chr18	+	52546688	52548040	1100
ENSG0000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-1094	chr17	-	33786500	33787569	1070
ENSG0000(	83.89914	96.34302	116.1084	16.47966	6.443024	13.15144	2.9521	4.17E-14	3.12E-13	RP11-142I	chr18	-	39047395	39212149	1710
ENSG0000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP11-686D	chr17	-	33704435	33704697	263
ENSG0000(	2.071584	0	0	0.749076	0	1.64393	-0.07972	0.95303	NA	RP11-879F	chr18	-	59238575	59246689	604
ENSG0000(	74.57702	110.7945	60.69303	71.16218	36.81728	52.60575	0.60107	0.082411	0.14919	CTB-25B13	chr19	-	1457664	1462764	927
ENSG0000(	2.071584	1.204288	3.958241	0.749076	0.920432	9.863579	-0.53035	0.63977	0.74777	CTD-2528L	chr19	-	38184181	38184465	285
ENSG0000(	67.32647	78.2787	77.84541	205.9958	138.9852	226.0404	-1.3456	1.85E-07	8.26E-07	RP11-1094	chr17	+	33895139	33901811	1298
ENSG0000(	95.29286	139.6974	141.1773	11.98521	66.2711	43.56414	1.5971	9.24E-05	0.000303	SCARNA17	chr18	+	47340393	47377429	1615
ENSG0000(	0	0	0	1.498151	2.761296	0	-1.199	0.3707	NA	SLC25A1P5	chr19	-	28296331	28297113	783
ENSG0000(	0	0	13.19414	8.239831	5.522592	5.753754	-0.49082	0.64024	0.7481	RP11-397A	chr18	-	53443958	53448952	4071
ENSG0000(	2.071584	0	2.638828	0.749076	0.920432	0	0.84278	0.53072	0.6555	CTD-2008L	chr18	+	53560269	53690753	518
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC131056.	chr17	-	34552690	34554250	247
ENSG0000(	0	4.817151	7.916483	2.247227	16.56778	24.65895	-1.5725	0.080243	0.14573	AC005258.	chr19	-	2329111	2355778	593
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-677C	chr18	+	11745625	11747580	1618
ENSG0000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	CTC-782O7	chr18	-	41903401	42111662	2068
ENSG0000(	1.035792	4.817151	1.319414	4.494453	1.840864	5.753754	-0.61406	0.56983	0.68881	RP11-242D	chr17	-	41321897	41322094	198
ENSG0000(	1.035792	2.408575	3.958241	5.992604	2.761296	4.93179	-0.75207	0.46987	0.59906	RP11-552F	chr17	+	73893141	73896229	1419
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTB-39G8.3	chr17	+	43474298	43474843	457
ENSG0000(	2.071584	1.204288	1.319414	2.996302	0.920432	0	0.14506	0.91071	0.94514	CTD-2293H	chr19	-	37566015	37569507	572
ENSG0000(	2.071584	0	5.277655	0	9.20432	5.753754	-0.78892	0.49142	0.6205	EIF5AP3	chr19	+	45631827	45632288	462
ENSG0000(	7.250543	4.817151	2.638828	2.247227	1.840864	8.219649	0.22719	0.81576	0.88052	AC015849.	chr17	+	34145403	34150717	421
ENSG0000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	CTB-179K2	chr19	-	45579768	45593649	690
ENSG0000(	541.7192	515.4351	444.6424	515.364	565.1452	623.0494	-0.17946	0.23406	0.34807	RP1-178F1	chr17	+	18227536	18231369	2480
ENSG0000(	26.93059	25.29004	22.43003	29.21395	25.7721	32.8786	-0.22694	0.61105	0.72484	SH3GL1P3	chr17	-	66130816	66131745	930
ENSG0000(	2.071584	8.430014	0	5.992604	1.840864	2.465895	0.017127	0.98757	0.99252	RPL9P29	chr17	-	76842035	76842950	593
ENSG0000(	2.071584	9.634302	2.638828	0	2.761296	0	1.7603	0.14218	0.23371	RNU6-2	chr19	+	1021521	1021627	107
ENSG0000(	6.214751	2.408575	0	7.490755	6.443024	4.109825	-0.85507	0.39648	0.5275	KCNJ2-AS1	chr17	-	68163102	68165543	2442
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-53B2	chr18	-	13500640	13501288	487
ENSG0000(	12.4295	7.225726	14.51355	7.490755	2.761296	7.397684	0.8602	0.25696	0.37542	CTD-2623N	chr19	-	9866828	9867539	712
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC005330.	chr19	+	1321224	1322863	1256
ENSG0000(	2.071584	0	6.597069	0	1.840864	4.109825	0.38062	0.7566	0.83898	CTD-2231E	chr19	-	16214571	16215064	367
ENSG0000(	6.214751	0	0	41.19916	34.97642	45.20807	-3.8334	8.43E-08	3.90E-07	LINC00669	chr18	-	36786888	37380282	2306
ENSG0000(	4.143168	13.24716	5.277655	0.749076	4.60216	2.465895	1.3264	0.16633	0.26518	CTB-186G2	chr19	-	39174513	39184246	242

ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-697E	chr17	+	36009162	36010922	607
ENSG00000(	25.8948	37.33292	13.19414	47.19176	19.32907	16.4393	-0.11542	0.82999	0.891	CTD-2086C	chr19	+	37978901	37979554	654
ENSG00000(	7.250543	7.225726	2.638828	107.1178	128.8605	128.2265	-4.2482	1.11E-20	1.15E-19	CTC-260E6.	chr19	-	20236186	20432114	1268
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	CTD-2240E	chr19	-	10199708	10201053	1346
ENSG00000(	1.035792	2.408575	0	0.749076	0	0	0.91766	0.49624	NA	AF038458.	chr19	+	36451414	36454965	600
ENSG00000(	2.071584	0	0	0	4.60216	0	-0.53557	0.69303	0.7906	CTC-459F4.	chr19	-	28303715	28387623	819
ENSG00000(	6.214751	14.45145	3.958241	9.737982	2.761296	0.821965	0.75612	0.41167	0.5424	RP11-635N	chr18	+	61034561	61048862	785
ENSG00000(	9.322127	16.86003	10.55531	2.247227	7.363456	7.397684	1.0249	0.17637	0.27837	CTB-175E5.	chr17	+	42276250	42293933	528
ENSG00000(	10.35792	13.24716	15.83297	3.745378	8.283888	14.79537	0.51538	0.46232	0.59158	AC074212.	chr19	+	46271054	46275762	822
ENSG00000(	18.64425	22.88147	23.74945	4.494453	6.443024	4.109825	1.9953	0.001882	0.005039	RP11-873E	chr18	+	33296334	33297942	1609
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP11-456C	chr18	-	53728340	53730309	552
ENSG00000(	4.143168	0	1.319414	0	0.920432	0.821965	0.97843	0.46421	0.59339	RP11-619L	chr18	+	53159406	53163623	445
ENSG00000(	3.107376	3.612863	6.597069	11.23613	12.88605	4.109825	-0.97737	0.24717	0.36391	CTC-296K1	chr17	-	42872115	42875151	587
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CTB-50L17.	chr19	+	4621206	4622319	486
ENSG00000(	3.107376	2.408575	0	10.48706	2.761296	1.64393	-1.1055	0.32055	0.44775	RP11-973H	chr18	+	12658709	12725739	1011
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	CTC-265F1	chr19	-	2610153	2611860	1708
ENSG00000(	0	0	0	5.243529	6.443024	3.28786	-3.1058	0.014364	0.032236	RP11-636C	chr18	-	37421138	37504804	1115
ENSG00000(	41.43168	43.35436	84.44248	42.69731	21.16994	29.59074	0.82269	0.049092	0.095549	RP11-456K	chr18	-	42256892	42259682	2065
ENSG00000(	5.17896	3.612863	2.638828	0	2.761296	0	1.4955	0.2214	0.33311	CTD-2319I	chr17	+	58156670	58166056	699
ENSG00000(	4.143168	0	3.958241	0	0	0	2.3234	0.08602	0.15487	CTC-239J1(	chr19	-	13124476	13125325	523
ENSG00000(	15.53688	22.88147	17.15238	20.97412	8.283888	18.90519	0.18718	0.74399	0.8295	CTC-559E9.	chr19	+	19887411	19945736	803
ENSG00000(	3.107376	0	0	2.247227	1.840864	1.64393	-0.52913	0.68446	0.78423	AC005498.	chr19	-	57047525	57049944	784
ENSG00000(	2.071584	1.204288	0	3.745378	3.681728	3.28786	-1.2288	0.29956	0.42452	CTD-2554C	chr19	+	38270326	38283505	1094
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	CTD-2265C	chr19	+	12936525	12943797	739
ENSG00000(	1275.06	1252.459	1149.209	1044.96	1096.235	1177.054	0.14835	0.21979	0.33149	CTC-503J8.	chr19	-	6210390	6212492	2103
ENSG00000(	0	0	5.277655	0.749076	0.920432	1.64393	0.3922	0.76619	0.84571	AC006116.	chr19	-	56858450	56859552	1103
ENSG00000(	2.071584	3.612863	3.958241	0.749076	2.761296	1.64393	0.70448	0.53499	0.65921	RP11-635N	chr18	-	61082550	61083702	1153
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-559N	chr17	+	76480964	76495428	932
ENSG00000(	17.60846	20.47289	15.83297	9.737982	23.0108	9.041614	0.35958	0.54697	0.6688	AC002398.	chr19	-	36237958	36244316	1712
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	CTC-501O1	chr17	+	41757641	41783252	549
ENSG00000(	2.071584	4.817151	7.916483	8.988907	6.443024	21.37109	-1.2069	0.13583	0.22513	AC005391.	chr19	+	961827	962424	598
ENSG00000(	0	0	0	0	0	4.93179	-1.2404	0.35057	NA	RP11-1018	chr17	+	49512788	49523163	2845
ENSG00000(	0	0	0	2.247227	1.840864	2.465895	-1.8839	0.16313	0.26107	AC004791.	chr19	-	15962803	15975734	425
ENSG00000(	8.286335	2.408575	6.597069	7.490755	11.04518	14.79537	-0.85167	0.27283	0.39365	ZNF582-AS	chr19	+	56905025	56910541	1606
ENSG00000(	3.107376	4.817151	0	0.749076	0	1.64393	1.1281	0.38026	0.51093	RP5-837J1.	chr17	-	33400850	33401393	544
ENSG00000(	9.322127	25.29004	11.87472	5.243529	2.761296	3.28786	1.8517	0.014734	0.032952	RP11-120N	chr17	+	66553657	66578718	384
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-866E	chr18	+	57677513	57681490	1762
ENSG00000(	0	0	0	0	4.60216	0	-1.1528	0.38283	NA	UBE2V2P2	chr17	-	76062339	76062842	504
ENSG00000(	0	0	1.319414	0.749076	6.443024	0	-1.3497	0.31531	0.44191	RP11-13K1	chr17	-	75559450	75564777	1767
ENSG00000(	12.4295	6.021439	9.235896	0.749076	4.60216	4.109825	1.3806	0.11921	0.20266	CTD-3064H	chr19	+	38039816	38078249	2777
ENSG00000(	0	0	0	2.247227	4.60216	2.465895	-2.3811	0.072509	0.13365	LOC44046:	chr17	+	66195062	66195737	676
ENSG00000(	84.93494	90.32158	85.7619	20.97412	16.56778	32.05663	1.8698	1.41E-07	6.36E-07	AC005789.	chr19	+	38888821	38890521	1701
ENSG00000(	1.035792	1.204288	1.319414	0	0	0.821965	0.9823	0.4689	NA	CTC-548K1	chr19	+	14569213	14570178	889
ENSG00000(	4.143168	6.021439	7.916483	11.23613	11.96562	3.28786	-0.50389	0.53727	0.66123	CTD-2538C	chr19	-	33177995	33182656	568

ENSG00000(	3.107376	0	2.638828	5.243529	13.80648	7.397684	-1.839	0.060208	0.11404	RP11-126C	chr18	-	56339845	56419962	398
ENSG00000(	0	1.204288	1.319414	2.247227	5.522592	3.28786	-1.547	0.20161	0.30921	CTC-268N1	chr17	+	35391965	35400550	411
ENSG00000(	7.250543	6.021439	14.51355	8.239831	5.522592	14.79537	-0.04936	0.94697	0.96794	RP11-703I:	chr18	-	12031177	12032180	527
ENSG00000(	6.214751	12.04288	6.597069	4.494453	10.12475	13.15144	-0.14366	0.84964	0.90434	CTC-559E9.	chr19	-	19899564	19901340	921
ENSG00000(	12.4295	9.634302	14.51355	5.243529	1.840864	2.465895	1.727	0.032505	0.066668	CTD-2373H	chr17	+	76899345	76901106	945
ENSG00000(	14.50109	15.65574	6.597069	2.247227	7.363456	12.32947	0.69312	0.36075	0.4903	CIRBP-AS1	chr19	-	1268165	1270240	642
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	FAM215A	chr17	+	41994576	41995326	751
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CTB-32O4.:	chr19	+	29704142	29706722	709
ENSG00000(	5.17896	2.408575	7.916483	15.73059	19.32907	15.61733	-1.5889	0.025341	0.053616	CTD-2006C	chr19	+	11759179	11763692	1407
ENSG00000(	0	4.817151	0	14.23244	26.69253	15.61733	-3.1107	0.000437	0.001295	RP11-108P	chr18	-	56422091	56425074	740
ENSG00000(	1.035792	1.204288	0	0	0.920432	0	0.54457	0.68095	NA	RP11-845C	chr18	+	56038798	56039898	1101
ENSG00000(	1.035792	2.408575	0	14.98151	3.681728	6.575719	-2.3089	0.028016	0.058541	CTC-296K1	chr17	+	42870567	42871842	562
ENSG00000(	0	0	0	0	6.443024	0.821965	-1.831	0.17712	0.27929	RP11-13K1	chr17	+	75543022	75559325	4902
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	CTD-2587H	chr19	-	55630618	55631751	488
ENSG00000(	110.8297	59.0101	91.03955	32.21025	36.81728	44.38611	1.1863	0.000516	0.001513	ZNF285	chr19	-	44886459	44905774	6013
ENSG00000(	3.107376	0	0	6.74168	0.920432	14.79537	-2.1214	0.061415	0.11586	CTD-2043I:	chr19	+	28556174	28616337	573
ENSG00000(	10.35792	6.021439	9.235896	10.48706	11.04518	11.50751	-0.33732	0.62869	0.73912	CTC-325H2	chr19	+	9402191	9405158	405
ENSG00000(	1.035792	0	0	1.498151	0	1.64393	-0.62149	0.64536	NA	RP11-861E	chr18	+	12450446	12451041	596
ENSG00000(	149.154	113.203	101.5949	70.4131	54.30549	82.19649	0.80728	0.004071	0.010273	CTD-3252C	chr19	-	13945330	13947103	1774
ENSG00000(	41.43168	24.08575	29.0271	7.490755	28.53339	7.397684	1.0886	0.057885	0.11033	RP11-373L	chr2	+	61153044	61155287	2244
ENSG00000(	0	0	3.958241	0.749076	0	0	0.94769	0.48013	NA	CTD-2621I:	chr19	+	56578050	56590167	1661
ENSG00000(	29.00217	15.65574	14.51355	30.7121	34.05598	53.42772	-0.95311	0.044399	0.087597	CTD-2537I9	chr19	-	56173267	56186081	549
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RPSAP57	chr18	+	52411981	52412812	832
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-178C	chr17	-	58140365	58142143	1447
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-53B2	chr18	-	13471011	13472708	1698
ENSG00000(	3.107376	0	0	11.23613	0	17.26126	-2.3769	0.036456	0.073735	AC006273.	chr19	+	782796	785080	829
ENSG00000(	0	0	2.638828	0	0	0.821965	0.55859	0.66971	NA	RP11-815J4	chr18	-	12067172	12068416	1148
ENSG00000(	397.7441	393.8021	328.534	30.7121	45.10117	31.23467	3.3731	5.10E-48	1.33E-46	S1PR2	chr19	-	10334520	10341948	1173
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	LINC00868	chr17	+	74846258	74857918	853
ENSG00000(	0	0	0	4.494453	4.60216	9.041614	-3.3966	0.006325	0.015354	AC005394.	chr19	-	29093286	29139210	185
ENSG00000(	1.035792	0	0	4.494453	2.761296	0	-1.4827	0.26934	0.38973	RP11-380N	chr18	-	45379604	45379828	225
ENSG00000(	3.107376	6.021439	17.15238	2.247227	8.283888	3.28786	0.81338	0.35773	0.48727	RP11-666A	chr17	+	74546033	74546908	570
ENSG00000(	6.214751	15.65574	5.277655	2.247227	5.522592	7.397684	0.75601	0.36696	0.49698	RP11-666A	chr17	-	74541750	74553765	578
ENSG00000(	1.035792	2.408575	1.319414	61.42419	23.93123	32.8786	-4.2112	3.90E-08	1.86E-07	RP11-686D	chr17	-	33730856	33731392	537
ENSG00000(	42.46747	66.23582	40.90183	25.46857	21.16994	26.30288	1.0099	0.012722	0.028866	RP11-229E	chr17	+	40127182	40129749	2568
ENSG00000(	5.17896	6.021439	1.319414	5.243529	2.761296	3.28786	0.12998	0.896	0.93559	AC006116.	chr19	+	56826072	56852656	1550
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	ZNF607	chr19	-	38180766	38210089	704
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	AC008992.	chr19	+	31910835	31912101	549
ENSG00000(	2.071584	0	0	0.749076	0	0.821965	0.18163	0.8922	NA	CTC-379B2	chr19	+	33157204	33164116	573
ENSG00000(	1.035792	0	0	0.749076	1.840864	0	-0.44174	0.74166	NA	RP11-173A	chr18	-	59967269	59968231	637
ENSG00000(	0	2.408575	0	2.996302	3.681728	3.28786	-1.4114	0.25753	0.37612	CTC-421K2	chr17	+	35814273	35815033	443
ENSG00000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	CTC-503J8.	chr19	+	6259168	6259810	523
ENSG00000(	12.4295	6.021439	10.55531	18.72689	10.12475	14.79537	-0.55275	0.40051	0.53172	CTC-559E9.	chr19	-	20003242	20006656	403
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CTD-2538C	chr19	-	33209204	33210501	516

ENSG00000(	1.035792	0	1.319414	2.996302	0	0	-0.1842	0.892	NA	RP11-87G2	chr17	-	74946399	74965238	623
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-773H	chr18	+	12911185	12912022	838
ENSG00000(	2.071584	3.612863	5.277655	3.745378	3.681728	12.32947	-0.7457	0.42815	0.55841	AC104532.	chr19	-	5911589	5913910	589
ENSG00000(	1.035792	1.204288	0	0	0	0	0.74702	0.55047	NA	KRT8P5	chr18	-	41900765	41902222	1458
ENSG00000(	53.86118	55.39724	50.13772	56.92974	75.47542	61.64737	-0.27629	0.38701	0.51778	CTC-459F4.	chr19	+	28284371	28475892	2401
ENSG00000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	CTD-2587H	chr19	+	55670307	55688908	1643
ENSG00000(	0	0	0	0	8.283888	0	-1.8662	0.16883	0.26865	RP11-126C	chr18	+	56224302	56233909	335
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	CTC-559E9.	chr19	-	19871847	19932525	609
ENSG00000(	0	0	0	0.749076	0	1.64393	-0.62797	0.61779	NA	CTD-3252C	chr19	-	13907388	13907747	360
ENSG00000(	0	1.204288	3.958241	0	0	0	1.651	0.221	NA	RP11-322E	chr18	-	33023833	33047052	697
ENSG00000(	3.107376	9.634302	2.638828	0	1.840864	1.64393	1.6749	0.13785	0.22792	RP11-21F1	chr18	+	39739247	40271387	3376
ENSG00000(	2.071584	2.408575	3.958241	0.749076	0	0	2.0292	0.12192	0.20658	RP11-687F	chr18	-	44432595	44433845	621
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	MIR1302-2	chr19	+	71161	72719	712
ENSG00000(	3.107376	6.021439	1.319414	5.992604	0	2.465895	0.22559	0.84109	0.89829	NDUFA3P1	chr19	+	44801257	44801508	252
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-689E	chr18	+	47625112	47625532	421
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	CTC-507E2.	chr17	-	33923923	33924147	225
ENSG00000(	2.071584	0	1.319414	1.498151	3.681728	6.575719	-1.3068	0.26907	0.38945	RP11-242D	chr17	-	41320187	41320266	80
ENSG00000(	1.035792	0	1.319414	0	1.840864	0.821965	-0.08167	0.95197	NA	RPIAP1	chr18	-	59624506	59625247	742
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP5-905N1	chr17	-	41860172	41862050	494
ENSG00000(	3.107376	0	0	1.498151	0	1.64393	0.00723	0.99574	0.99727	CTD-3220F	chr19	-	37756841	37762420	813
ENSG00000(	1.035792	3.612863	2.638828	2.247227	0.920432	0	0.80794	0.52016	0.64606	AC006116.	chr19	-	56865862	56879422	649
ENSG00000(	2.071584	3.612863	3.958241	0	0	0	2.7354	0.039239	0.078686	AC007787.	chr19	-	13180610	13182188	1579
ENSG00000(	0	1.204288	1.319414	2.247227	0	3.28786	-0.71064	0.59122	0.7076	CTD-3116E	chr19	+	9841529	9842619	600
ENSG00000(	0	2.408575	0	0.749076	2.761296	1.64393	-0.65401	0.62241	0.73431	RP11-378E	chr17	-	35768023	35768681	293
ENSG00000(	24.85901	48.17151	22.43003	14.98151	40.49901	55.89361	-0.21137	0.67211	0.77439	AC004152.	chr19	-	2270133	2270945	813
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	AC002115.	chr19	-	36099187	36103568	568
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC138430.	chr19	-	19365557	19384178	5409
ENSG00000(	15.53688	21.67718	25.06886	2.996302	21.16994	12.32947	0.73434	0.25386	0.3719	RP11-400F	chr17	+	40661802	40663537	1736
ENSG00000(	2.071584	0	0	0	7.363456	0	-0.96207	0.47537	0.60462	RP11-619I	chr17	+	57862174	57862396	223
ENSG00000(	2.071584	4.817151	0	0	0.920432	0	1.6018	0.23337	0.34712	RP11-546N	chr17	+	42193280	42197963	359
ENSG00000(	0	0	0	1.498151	0	5.753754	-1.8682	0.16834	0.26796	CTD-2554C	chr19	+	38307999	38317278	1058
ENSG00000(	2.071584	1.204288	1.319414	3.745378	7.363456	0.821965	-1.04	0.36236	0.49202	CTC-260E6.	chr19	-	20285822	20287872	534
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-258B	chr18	-	31132087	31158151	2492
ENSG00000(	1.035792	0	0	0	0.920432	0	0.1572	0.90001	NA	CTD-2008P	chr17	+	26546311	26547031	721
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTC-499B1	chr19	-	11906899	11909413	2515
ENSG00000(	0	0	0	5.243529	6.443024	5.753754	-3.3492	0.007167	0.017225	RP11-686D	chr17	-	33733967	33734837	871
ENSG00000(	0	4.817151	2.638828	0.749076	4.60216	1.64393	0.066537	0.95555	0.97379	CTD-2587H	chr19	+	55728028	55732984	857
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	CTD-2553C	chr19	+	10106673	10107839	1167
ENSG00000(	5.17896	6.021439	0	0.749076	3.681728	0.821965	0.85015	0.46667	0.59593	RP11-95O2	chr18	-	34814082	34816205	2124
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-973H	chr18	-	12739489	12749420	569
ENSG00000(	3.107376	15.65574	2.638828	12.73428	3.681728	9.863579	-0.27341	0.74654	0.83145	CTD-2286N	chr18	+	76877207	76877920	714
ENSG00000(	0	0	0	1.498151	0	2.465895	-1.1271	0.39798	NA	RP11-807E	chr18	-	13139779	13140488	710
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTB-186H2	chr17	-	34290506	34292480	407
ENSG00000(	6.214751	4.817151	6.597069	3.745378	0	1.64393	1.3678	0.19224	0.29798	RP11-358B	chr17	+	40306618	40307990	425

ENSG00000(	24.85901	26.49433	22.43003	1.498151	9.20432	13.15144	1.5427	0.016952	0.037417	RP11-118B	chr17	+	66587937	66760023	2616
ENSG00000(	4.143168	2.408575	2.638828	0	0	0	2.6697	0.044906	0.088441	AC007796.	chr19	+	31839787	31908700	560
ENSG00000(	1.035792	3.612863	1.319414	4.494453	0	0	0.24694	0.84851	0.90347	AC004156.	chr19	+	663482	668063	1882
ENSG00000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	RP11-136H	chr17	-	59208065	59213325	286
ENSG00000(	0	1.204288	0	0	0.920432	1.64393	-0.43846	0.74402	NA	RP11-697E	chr17	+	36002976	36044255	628
ENSG00000(	36.25272	27.69862	36.94359	0	0	0	6.323	2.49E-09	1.32E-08	RP11-824N	chr18	+	57488272	57492493	959
ENSG00000(	0	0	1.319414	1.498151	1.840864	0.821965	-0.90829	0.50213	NA	CTD-2293H	chr19	+	37582243	37583466	1224
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	FDX1L	chr19	-	10416103	10426691	1956
ENSG00000(	0	2.408575	0	0	2.761296	0	-0.08034	0.95255	NA	RP11-1151	chr18	+	56083997	56084860	646
ENSG00000(	8.286335	4.817151	1.319414	1.498151	4.60216	9.041614	-0.03814	0.96861	0.98169	THA1P	chr17	-	76244574	76250497	1145
ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	RP11-27G2	chr18	+	57027932	57053981	417
ENSG00000(	6.214751	22.88147	15.83297	8.988907	14.72691	4.109825	0.63966	0.36421	0.49402	ZNF224	chr19	+	44598492	44612479	2994
ENSG00000(	7.250543	4.817151	6.597069	6.74168	2.761296	2.465895	0.54987	0.54547	0.66762	CTD-3199J	chr17	+	41296973	41297272	300
ENSG00000(	7.250543	8.430014	3.958241	2.996302	1.840864	9.041614	0.4383	0.62881	0.73916	CTD-3220F	chr19	+	37828138	37828645	375
ENSG00000(	2.071584	2.408575	0	1.498151	3.681728	0	-0.11595	0.92857	0.95717	AC010525.	chr19	-	56217344	56217538	195
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	SHC1P2	chr17	-	42306128	42307596	1469
ENSG00000(	0	1.204288	0	1.498151	1.840864	0	-0.64701	0.63267	NA	TAF9P3	chr19	+	30528192	30528318	127
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTB-151G2	chr19	-	28129391	28137391	457
ENSG00000(	1.035792	0	0	2.996302	6.443024	7.397684	-2.6689	0.027903	0.05833	AC002116.	chr19	+	36505410	36536874	643
ENSG00000(	2.071584	6.021439	1.319414	0	0	0	2.6699	0.045268	0.089035	RP11-53B2	chr18	+	13486461	13490675	4215
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTD-2013N	chr19	+	16551757	16554395	401
ENSG00000(	1.035792	1.204288	1.319414	0.749076	0	2.465895	0.080826	0.95137	0.97088	RP11-95O2	chr18	+	34823739	34827179	411
ENSG00000(	0	0	0	0	0	4.109825	-1.0413	0.42586	NA	RP11-147L	chr17	-	66148917	66155184	579
ENSG00000(	53.86118	44.55865	44.86007	22.47227	22.09037	21.37109	1.097	0.006203	0.015084	AC006116.	chr19	+	56784138	56821819	632
ENSG00000(	0	0	0	7.490755	7.363456	2.465895	-3.3108	0.008291	0.019621	RP11-686D	chr17	-	33727897	33730025	394
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-456C	chr18	-	53750587	53804767	2068
ENSG00000(	1.035792	8.430014	0	2.247227	0	0.821965	1.0766	0.39595	0.52694	CTB-25B13	chr19	+	1484535	1485273	412
ENSG00000(	0	1.204288	1.319414	2.247227	3.681728	0	-0.76698	0.561	0.68128	SRSF10P1	chr18	-	48684652	48685753	764
ENSG00000(	0	0	0	2.996302	5.522592	0	-2.0936	0.12126	0.20564	CTD-2189E	chr19	-	14365001	14404017	627
ENSG00000(	3.107376	2.408575	0	0	0	2.465895	0.68066	0.61116	0.72494	RP11-49K2	chr18	+	44632317	44634433	2117
ENSG00000(	3.107376	0	1.319414	2.247227	0.920432	2.465895	-0.22719	0.8567	0.90907	AC010761.	chr17	+	27054276	27054757	197
ENSG00000(	2.071584	0	0	5.243529	1.840864	1.64393	-1.3183	0.30229	0.4274	CTD-2537I9	chr19	-	56088136	56088780	645
ENSG00000(	5.17896	4.817151	1.319414	0	3.681728	5.753754	0.2252	0.83814	0.89651	RP4-604K5	chr1	-	87397882	87400574	746
ENSG00000(	1.035792	0	1.319414	0	0.920432	4.109825	-0.63521	0.6346	0.74391	HMGB2P1	chr19	+	1203208	1203820	613
ENSG00000(	7.250543	4.817151	1.319414	2.247227	0	0	1.8154	0.13415	0.22311	AC061992.	chr17	+	76311810	76343879	799
ENSG00000(	3.107376	6.021439	3.958241	0.749076	4.60216	3.28786	0.50441	0.6248	0.73627	UBE2L4	chr19	+	9885173	9885636	464
ENSG00000(	0	0	0	0.749076	1.840864	3.28786	-1.711	0.20694	NA	FAM60CP	chr18	-	57684010	57684673	664
ENSG00000(	6.214751	8.430014	2.638828	14.98151	15.64734	14.79537	-1.2787	0.072504	0.13365	RP11-686D	chr17	-	33733703	33736787	1212
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-379L	chr18	+	31802929	31804725	507
ENSG00000(	0	0	0	0	3.681728	2.465895	-1.6477	0.22446	0.33686	RP11-392C	chr17	+	41622153	41687706	561
ENSG00000(	4.143168	19.2686	1.319414	3.745378	5.522592	3.28786	0.85055	0.35916	0.48869	AC003102.	chr17	-	42376942	42392683	5203
ENSG00000(	7.250543	8.430014	7.916483	8.239831	11.04518	10.68554	-0.31775	0.65908	0.76362	AC009005.	chr19	-	567212	572215	719
ENSG00000(	17.60846	12.04288	13.19414	0	1.840864	8.219649	1.8588	0.030699	0.063423	CTC-439O9	chr19	-	31827904	31829830	1927
ENSG00000(	5.17896	0	5.277655	0	5.522592	7.397684	-0.22994	0.83787	0.89629	RP11-411B	chr18	-	14074911	14075740	830

ENSG0000(	0	3.612863	1.319414	0	0	0	1.6005	0.2346	NA	RP11-358B	chr17	+	40420605	40421825	496
ENSG0000(	15.53688	14.45145	19.79121	8.239831	34.05598	24.65895	-0.40181	0.49295	0.62189	CTB-25B13	chr19	+	1413900	1414734	230
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTD-2130C	chr18	+	44812096	45120914	704
ENSG0000(	7.250543	0	3.958241	0	0.920432	0	2.229	0.086728	0.15593	RP11-426J!	chr18	-	46199946	46214790	465
ENSG0000(	18.64425	6.021439	27.70769	0	0.920432	0.821965	4.1038	2.54E-05	8.95E-05	RP11-484L	chr18	-	46352422	46361141	877
ENSG0000(	11.39371	3.612863	5.277655	0	1.840864	0.821965	2.349	0.031743	0.065292	CTD-3193K	chr17	-	40835205	40851484	719
ENSG0000(	0	0	0	1.498151	4.60216	0	-1.6319	0.22883	0.34221	CTC-523E2:	chr19	-	35282724	35323773	2077
ENSG0000(	8.286335	3.612863	13.19414	11.98521	12.88605	9.863579	-0.4402	0.53937	0.66301	CTB-50L17.	chr19	+	4454011	4455283	510
ENSG0000(	0	0	0	2.996302	0	2.465895	-1.5141	0.2635	NA	CTC-260E6.	chr19	-	20317653	20317763	111
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-15E1	chr17	+	58641908	58663984	646
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-2N1.:	chr18	+	57363691	57364644	382
ENSG0000(	0	1.204288	1.319414	5.243529	0	0	-0.60871	0.65142	0.75747	AC006116.	chr19	-	56888073	56888653	581
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTC-439O9	chr19	+	31658422	31698569	677
ENSG0000(	4.143168	8.430014	1.319414	1.498151	0	0	2.2044	0.071599	0.13235	AC004221.	chr19	+	1238178	1239521	844
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-154H	chr18	+	77552726	77576365	363
ENSG0000(	2.071584	1.204288	1.319414	1.498151	1.840864	0	0.30509	0.81445	0.87952	AC006116.	chr19	+	56897595	56898059	465
ENSG0000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	CTB-55O6.:	chr19	+	14229918	14230349	315
ENSG0000(	8.286335	7.225726	11.87472	0.749076	4.60216	0.821965	1.8718	0.046804	0.091634	AF038458.	chr19	+	36438017	36450094	500
ENSG0000(	0	0	5.277655	2.247227	0.920432	0	0.40329	0.76319	0.84363	RP11-35G9	chr18	+	55306687	55405276	1976
ENSG0000(	5.17896	3.612863	3.958241	5.243529	2.761296	3.28786	0.14674	0.88	0.92501	RP11-576C	chrY	+	21760074	21760643	570
ENSG0000(	0	0	0	1.498151	0	2.465895	-1.1271	0.39798	NA	RP11-127I:	chr16	+	4838398	4846492	862
ENSG0000(	18.64425	24.08575	22.43003	11.23613	10.12475	26.30288	0.4269	0.4479	0.5776	LIN37	chr19	+	36239262	36245420	1635
ENSG0000(	5.17896	0	5.277655	0	2.761296	2.465895	0.74391	0.53647	0.6605	RP11-333J:	chr17	+	35355897	35357333	710
ENSG0000(	1.035792	0	0	4.494453	3.681728	2.465895	-2.0627	0.10666	0.18493	CTC-478M(	chr19	-	29281719	29283778	1400
ENSG0000(	6.214751	1.204288	5.277655	0.749076	1.840864	0	1.7051	0.15118	0.24562	RP11-49K2	chr18	+	44663389	44663661	273
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-552F	chr17	+	73872453	73875627	3175
ENSG0000(	0	0	0	0	2.761296	2.465895	-1.4428	0.28594	NA	RP11-665N	chr11	-	64658158	64658547	390
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC018755.	chr19	+	52102542	52103723	1182
ENSG0000(	56.96855	57.80581	39.58241	56.92974	59.82808	66.57916	-0.23946	0.46818	0.59745	NDUFV2P1	chr19	-	53727226	53728132	907
ENSG0000(	0	0	1.319414	5.992604	1.840864	0	-1.4833	0.26654	0.38656	RP11-167N	chr9	-	1.32E+08	1.32E+08	497
ENSG0000(	13.46529	14.45145	15.83297	3.745378	0.920432	7.397684	1.6789	0.029654	0.061519	AC008746.	chr19	-	54949847	54950362	516
ENSG0000(	2.071584	0	3.958241	0	0	0	1.8862	0.16413	0.26236	DKFZP434A	chr9	-	1.39E+08	1.39E+08	552
ENSG0000(	15.53688	14.45145	21.11062	2.247227	20.2495	18.90519	0.28985	0.66832	0.77147	AL118506.	chr20	+	62585007	62585495	489
ENSG0000(	0	0	3.958241	0	4.60216	0	-0.12355	0.92718	0.95612	AL133262.	chr6	-	44400472	44400720	249
ENSG0000(	1.035792	1.204288	3.958241	0	0.920432	0.821965	1.143	0.38299	0.51359	CTB-133G6	chr19	-	7455408	7459925	363
ENSG0000(	16.57267	18.06432	11.87472	9.737982	22.09037	13.15144	0.057608	0.92319	0.95355	NDUFA7	chr19	-	8373490	8386280	601
ENSG0000(	1.035792	1.204288	6.597069	0	0	4.109825	0.73644	0.56017	0.68068	PRED58	chr21	-	46520728	46534873	735
ENSG0000(	60.07593	71.05298	43.54065	19.47596	32.21512	44.38611	0.84906	0.033779	0.06896	AC016629.	chr19	+	59070496	59086164	2567
ENSG0000(	1.035792	0	0	3.745378	6.443024	10.68554	-2.9644	0.012145	0.027699	RP11-120K	chr13	-	1.14E+08	1.14E+08	1297
ENSG0000(	3.107376	10.83859	5.277655	15.73059	22.09037	13.15144	-1.3132	0.060287	0.11415	CTC-444N2	chr19	-	57778588	57791702	712
ENSG0000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	CTD-2527I:	chr19	+	35527238	35527964	405
ENSG0000(	3.107376	25.29004	10.55531	2.996302	3.681728	3.28786	1.7474	0.038544	0.077484	AL031666.	chr20	+	45947246	45949467	2222
ENSG0000(	7.250543	2.408575	1.319414	0	0	0	2.9125	0.027401	0.057457	PRED60	chr21	-	47183565	47190005	354
ENSG0000(	3.107376	1.204288	0	0	0	0	1.4526	0.27741	NA	FKSG48	chr1	+	33439268	33439642	375

ENSG00000(	14.50109	4.817151	10.55531	44.19546	57.06678	39.45432	-2.1398	2.28E-05	8.10E-05	CTD-2291D	chr19	+	23258003	23283163	581
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC079354.	chr2	+	2.03E+08	2.03E+08	144
ENSG00000(	0	3.612863	0	0.749076	2.761296	1.64393	-0.31995	0.80712	0.87475	CTD-2540F	chr19	+	39228924	39230503	1580
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	AC007461.	chr17	+	70036164	70036872	709
ENSG00000(	5.17896	3.612863	2.638828	5.243529	3.681728	11.50751	-0.71907	0.43183	0.56165	AC018766.	chr19	-	50363139	50363771	548
ENSG00000(	2.071584	8.430014	1.319414	2.247227	0	4.109825	0.67879	0.55179	0.67278	CTD-2639E	chr19	+	49467232	49468415	819
ENSG00000(	159.512	148.1274	113.4696	71.16218	71.7937	103.5676	0.76776	0.003809	0.009664	CTC-429P9	chr19	-	16750778	16751479	546
ENSG00000(	0	0	0	1.498151	4.60216	0	-1.6319	0.22883	0.34221	CTD-2616J	chr19	+	51843949	51847371	437
ENSG00000(	3.107376	0	3.958241	3.745378	0	1.64393	0.25705	0.83679	0.89561	ZSCAN5D	chr19	+	56751773	56758863	1491
ENSG00000(	4.143168	3.612863	3.958241	0.749076	2.761296	0	1.3269	0.25648	0.37482	AP001055.	chr21	-	45587818	45593580	621
ENSG00000(	1.035792	4.817151	3.958241	6.74168	5.522592	4.93179	-0.70835	0.46146	0.59074	RP11-256I	chr2	+	2.21E+08	2.21E+08	542
ENSG00000(	0	0	1.319414	0	1.840864	0	-0.18532	0.88663	NA	SNX6P1	chr19	-	23309371	23310594	1224
ENSG00000(	0	0	0	5.992604	4.60216	3.28786	-2.9939	0.019181	0.041792	AC007193.	chr19	+	46604380	46699475	332
ENSG00000(	0	0	0	0	3.681728	4.93179	-2.1075	0.1187	0.20199	RP11-255H	chr19	-	24000401	24057503	2291
ENSG00000(	7.250543	0	0	2.996302	4.60216	2.465895	-0.3175	0.78772	0.86102	CTD-2525I	chr19	+	52674411	52680255	578
ENSG00000(	13.46529	8.430014	10.55531	11.98521	11.96562	6.575719	0.087228	0.89856	0.93718	CTB-176F2(	chr19	+	23506770	23511903	5134
ENSG00000(	4.143168	0	2.638828	2.247227	0	4.93179	-0.05658	0.96323	0.97865	AP001421.	chr21	+	38888740	38888973	234
ENSG00000(	2.071584	6.021439	0	0.749076	2.761296	4.109825	0.07601	0.94816	0.96872	AC007292.	chr19	-	4347777	4349058	334
ENSG00000(	2.071584	12.04288	11.87472	8.239831	3.681728	4.93179	0.53545	0.52607	0.65092	CTD-2325N	chr19	+	8073613	8080909	421
ENSG00000(	12.4295	9.634302	6.597069	16.47966	8.283888	9.863579	-0.25047	0.71728	0.80967	RP11-290F	chr11	-	6223131	6224483	1353
ENSG00000(	0	0	3.958241	0.749076	4.60216	0	-0.27078	0.83887	0.89711	AC008267.	chr7	+	65939543	65940709	1167
ENSG00000(	43.50326	32.51577	34.30476	12.73428	17.48821	13.9734	1.2874	0.005919	0.014449	AC090673.	chr12	-	66291518	66317967	204
ENSG00000(	0	0	2.638828	2.247227	16.56778	9.041614	-2.7021	0.013829	0.031171	CTD-2620I2	chr19	+	53510765	53516433	4060
ENSG00000(	34.18113	25.29004	31.66593	56.92974	61.66894	59.18147	-0.94327	0.009601	0.022422	RP11-178G	chr10	-	75880013	75880621	609
ENSG00000(	7.250543	10.83859	2.638828	1.498151	2.761296	2.465895	1.3914	0.15125	0.24572	MIR3188	chr19	+	18392659	18393560	902
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	OR10B1P	chr19	-	15251943	15252849	907
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC013469.	chr2	+	2.41E+08	2.41E+08	51
ENSG00000(	0	0	3.958241	2.247227	0	1.64393	-0.01549	0.99079	0.99468	AC092964.	chr3	-	1.72E+08	1.72E+08	249
ENSG00000(	5.17896	1.204288	1.319414	6.74168	3.681728	9.863579	-1.1529	0.24006	0.35527	AC007292.	chr19	+	4363786	4364637	746
ENSG00000(	4.143168	0	0	2.996302	1.840864	0	-0.11268	0.93239	0.95947	AP003041.	chr11	+	1.3E+08	1.3E+08	348
ENSG00000(	7.250543	1.204288	5.277655	2.247227	7.363456	9.863579	-0.42196	0.64975	0.75611	AC005488.	chr7	+	72459478	72464996	78
ENSG00000(	0	1.204288	1.319414	0	0	0.821965	0.59385	0.65509	NA	AC130469.	chr19	+	8646044	8647599	388
ENSG00000(	0	0	0	0	4.60216	4.93179	-2.2511	0.09436	0.16715	AC096582.	chr7	-	45902684	45906045	498
ENSG00000(	0	2.408575	2.638828	0	0	1.64393	0.85739	0.5258	0.65076	hsa-mir-15(	chr19	+	50003781	50004614	834
ENSG00000(	16.57267	9.634302	19.79121	49.43899	25.7721	22.19305	-1.0462	0.047664	0.0931	CTC-241F2(	chr19	+	48758932	48761456	1969
ENSG00000(	219.5879	226.4061	233.5362	251.6894	206.1768	209.6011	0.023549	0.89983	0.9378	PTOV1-AS1	chr19	-	50341896	50354933	3181
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC016559.	chr5	-	78523714	78523911	198
ENSG00000(	5.17896	9.634302	10.55531	3.745378	10.12475	13.15144	-0.08681	0.90976	0.94462	CTD-2525I	chr19	-	52725478	52734547	595
ENSG00000(	0	0	0	12.73428	15.64734	13.9734	-4.689	3.38E-05	0.000117	AC006129.	chr19	+	42051554	42061832	661
ENSG00000(	43.50326	19.2686	17.15238	10.48706	19.32907	23.83698	0.56561	0.30171	0.42679	AC005253.	chr19	-	18668585	18672370	2001
ENSG00000(	1.035792	0	0	0.749076	0.920432	2.465895	-0.92447	0.49522	NA	CTB-52I2.4	chr19	+	18133212	18142839	1402
ENSG00000(	2.071584	0	3.958241	0	5.522592	6.575719	-0.74765	0.52774	0.65247	AC005795.	chr19	+	42012068	42012814	747
ENSG00000(	61.11172	44.55865	51.45714	0	2.761296	0.821965	5.0883	1.44E-12	9.76E-12	PRED62	chr21	-	47347679	47352477	351
ENSG00000(	6.214751	8.430014	11.87472	0.749076	6.443024	0	1.6095	0.10313	0.17988	CTD-2575K	chr19	-	42412671	42414249	675

ENSG00000(	3.107376	6.021439	0	0	0	0	2.5044	0.063254	0.11894	AP001094.	chr18	-	8336437	8337038	174
ENSG00000(	3.107376	18.06432	2.638828	2.247227	0	9.041614	0.88836	0.38073	0.51141	AC018766.	chr19	-	50356144	50358224	484
ENSG00000(	39.36009	39.74149	36.94359	8.239831	9.20432	15.61733	1.751	0.000369	0.001106	CTD-2619J	chr19	+	58869365	58870969	1154
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTC-244M1	chr19	+	38454493	38455430	607
ENSG00000(	0	0	2.638828	0	0	0.821965	0.55859	0.66971	NA	CTD-3032J	chr19	-	17263398	17278861	467
ENSG00000(	0	0	0	2.996302	0.920432	2.465895	-1.8353	0.17499	0.27674	CTD-2017D	chr19	-	24281227	24281782	556
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	AL441883.	chr6	-	13615728	13621126	704
ENSG00000(	10.35792	18.06432	11.87472	4.494453	3.681728	5.753754	1.4031	0.057678	0.11	NAPA-AS1	chr19	+	47987539	48004854	1753
ENSG00000(	0	2.408575	0	2.996302	0	0.821965	-0.36191	0.78935	0.8622	AC004466.	chr12	+	48178706	48179787	1082
ENSG00000(	3.107376	2.408575	0	8.239831	4.60216	7.397684	-1.52	0.13655	0.22613	AC006539.	chr19	+	20144253	20145141	572
ENSG00000(	1.035792	4.817151	0	1.498151	0	1.64393	0.55933	0.66869	0.77174	AC087239.	chr12	+	25381515	25390840	111
ENSG00000(	4.143168	0	0	0	0	4.109825	0.023332	0.98623	0.99155	AC016885.	chr8	+	94241867	94242388	471
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP11-678G	chr19	-	21737442	21752039	447
ENSG00000(	2.071584	0	0	0	0	4.109825	-0.45547	0.73699	0.82369	AC051642.	chr8	-	23412287	23420651	45
ENSG00000(	68.36227	61.41867	83.12307	41.19916	58.90765	50.13986	0.49715	0.12338	0.20854	CTC-429P9	chr19	+	16721222	16747342	376
ENSG00000(	13.46529	2.408575	13.19414	5.992604	3.681728	4.109825	0.95683	0.25501	0.3732	AC022154.	chr19	-	49122529	49127389	766
ENSG00000(	1.035792	3.612863	0	2.247227	0.920432	0.821965	0.14138	0.91276	0.94661	CTC-429C1	chr19	+	52391278	52403716	579
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	AP000688.	chr21	+	37402368	37417818	114
ENSG00000(	4.143168	0	0	2.247227	4.60216	0.821965	-0.564	0.65543	0.76059	RP11-369G	chr19	+	23308467	23311345	896
ENSG00000(	0	2.408575	0	0	0.920432	1.64393	-0.04249	0.975	NA	CTB-60B18	chr19	+	49563870	49564389	520
ENSG00000(	0	0	0	0	2.761296	5.753754	-2.0874	0.1225	0.20741	AL031663.	chr20	-	44095910	44107452	60
ENSG00000(	8.286335	0	0	4.494453	1.840864	2.465895	-0.04033	0.97298	0.98436	VN1R84P	chr19	-	21902603	21902837	235
ENSG00000(	8.286335	2.408575	2.638828	192.5124	166.5982	193.9837	-5.1442	6.45E-29	9.41E-28	CTD-2561J	chr19	-	21627043	21646710	4690
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC091948.	chr5	+	1.48E+08	1.48E+08	123
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-91G2	chr3	-	1.43E+08	1.43E+08	561
ENSG00000(	0	0	0	0.749076	4.60216	0.821965	-1.7467	0.19759	0.30468	AL606500.	chr1	+	1.55E+08	1.55E+08	21
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AC005176.	chr19	+	40129325	40133041	1831
ENSG00000(	4.143168	3.612863	2.638828	0	2.761296	0	1.374	0.26685	0.38695	FKSG61	chr14	+	77882741	77883115	375
ENSG00000(	10.35792	8.430014	17.15238	0	0.920432	4.93179	2.2581	0.01493	0.033354	AC010524.	chr19	+	49859409	49861026	494
ENSG00000(	1.035792	0	0	2.247227	0.920432	0	-0.62282	0.6445	NA	HBCBP	chr12	+	57390745	57391335	591
ENSG00000(	0	0	1.319414	1.498151	0	0.821965	-0.38347	0.77483	NA	AC004076.	chr19	-	57949338	57988904	664
ENSG00000(	9.322127	22.88147	11.87472	0.749076	1.840864	9.863579	1.6306	0.049543	0.096311	CTC-471F3.	chr19	+	40526292	40526948	657
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	AC068620.	chr4	+	57276682	57277131	450
ENSG00000(	31.07376	19.2686	35.62417	3.745378	6.443024	6.575719	2.2436	0.000191	0.000598	AL590452.	chr1	+	1.45E+08	1.45E+08	2057
ENSG00000(	0	0	3.958241	2.996302	6.443024	0	-0.85195	0.50586	0.63349	CTC-513N1	chr19	+	20599320	20599875	556
ENSG00000(	60.07593	51.78437	48.81831	168.542	219.9832	224.3964	-1.9083	5.67E-14	4.21E-13	AC117395.	chr3	+	1.5E+08	1.5E+08	1470
ENSG00000(	0	1.204288	2.638828	0	0	9.863579	-0.89266	0.49114	0.62021	AL645608.	chr1	-	861264	866445	336
ENSG00000(	4.143168	4.817151	5.277655	4.494453	1.840864	1.64393	0.68333	0.49792	0.62625	SMIM17	chr19	+	57154513	57167134	1076
ENSG00000(	0	0	0	2.247227	0	0.821965	-0.85594	0.51054	NA	CTC-241F2(	chr19	-	48766157	48774540	437
ENSG00000(	20.71584	18.06432	9.235896	20.97412	16.56778	17.26126	-0.17378	0.75755	0.83961	AC005785.	chr19	+	15489887	15492004	1771
ENSG00000(	2.071584	7.225726	0	0	0.920432	7.397684	0.12016	0.92095	0.95207	CTD-3137H	chr19	+	18551920	18555242	1743
ENSG00000(	14.50109	33.72006	13.19414	10.48706	16.56778	5.753754	0.85868	0.17257	0.27368	CTD-3138B	chr19	+	58778001	58779051	550
ENSG00000(	1.035792	0	2.638828	3.745378	0	1.64393	-0.37209	0.77579	0.85283	CTD-3214H	chr19	-	7698652	7701876	843
ENSG00000(	727.1259	779.1742	464.4337	838.2155	593.6786	669.0794	-0.09123	0.63174	0.7417	CTC-444N2	chr19	+	57815673	57819930	4258

ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC061975.	chr17	+	26638667	26642323	141
ENSG00000(	4.143168	1.204288	2.638828	1.498151	0	3.28786	0.53402	0.65884	0.76342	AC008372.	chr14	-	78227711	78228033	33
ENSG00000(	11.39371	15.65574	10.55531	6.74168	4.60216	4.93179	1.1081	0.12857	0.21531	AL359091.	chr9	+	1.31E+08	1.31E+08	1846
ENSG00000(	31.07376	45.76293	27.70769	29.96302	18.40864	36.16646	0.29409	0.50936	0.63666	AC137932.	chr16	+	89334512	89339452	3660
ENSG00000(	76.6486	99.95588	102.9143	62.92235	57.98722	45.20807	0.73748	0.013461	0.030403	RP11-379K	chr3	+	1.7E+08	1.7E+08	1781
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	EEF1A1P7	chr19	+	35873074	35874954	1394
ENSG00000(	14.50109	7.225726	13.19414	26.96672	15.64734	17.26126	-0.73928	0.21365	0.32396	CTD-2331H	chr19	-	53365060	53366119	1060
ENSG00000(	33.14534	59.0101	32.98534	11.23613	18.40864	21.37109	1.2584	0.007561	0.018078	CTD-2619J	chr19	-	58858220	58874117	3322
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	AC018470.	chr2	-	1.75E+08	1.75E+08	1551
ENSG00000(	4.143168	1.204288	1.319414	3.745378	2.761296	0	0.037682	0.97517	0.98553	AIRN	chr6	-	1.6E+08	1.6E+08	4374
ENSG00000(	1.035792	0	3.958241	0	0	0	1.6134	0.2311	NA	CTC-246B1	chr19	-	39805291	39811498	877
ENSG00000(	2.071584	1.204288	3.958241	3.745378	9.20432	8.219649	-1.3212	0.17313	0.27446	AP000304.	chr21	-	34947431	34947645	36
ENSG00000(	1.035792	1.204288	0	0.749076	0.920432	0	0.21038	0.87653	NA	AC003005.	chr19	+	57989017	57994364	539
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AL035588.	chr6	+	41653964	41654127	36
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP11-420K	chr19	+	21820776	21839102	1367
ENSG00000(	14.50109	9.634302	18.47179	10.48706	12.88605	7.397684	0.44145	0.49382	0.62266	RP11-434D	chr3	+	14178644	14189548	787
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	CTD-2620I2	chr19	+	53507293	53508403	1111
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTD-2528A	chr19	+	17162804	17165897	280
ENSG00000(	0	4.817151	3.958241	5.243529	0	0	0.47306	0.71049	0.8043	CTD-2623H	chr19	+	58648080	58648421	342
ENSG00000(	0	0	0	9.737982	7.363456	32.05663	-4.8267	2.32E-05	8.23E-05	CLEC4GP1	chr19	+	7852435	7855507	870
ENSG00000(	2.071584	0	5.277655	0	0	0	2.1617	0.11093	0.19077	CTB-52I2.5	chr19	-	18122108	18142348	367
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AC018630.	chr12	+	11187087	11187275	189
ENSG00000(	2.071584	2.408575	5.277655	1.498151	0	0	1.7425	0.17031	0.27059	CTD-2619J	chr19	+	58911588	58912046	459
ENSG00000(	0	0	0	1.498151	0.920432	1.64393	-1.2565	0.35231	NA	AC087645.	chr17	-	76210462	76220740	1011
ENSG00000(	6.214751	3.612863	0	0	3.681728	2.465895	0.52462	0.66191	0.76629	CTD-3030D	chr19	+	21500963	21501521	559
ENSG00000(	0	0	5.277655	2.247227	0.920432	2.465895	-0.09382	0.94153	0.9649	C15ORF31	chr15	+	59439899	59440054	156
ENSG00000(	2.071584	0	2.638828	2.247227	1.840864	4.109825	-0.58869	0.62344	0.73512	AC019206.	chr2	-	70129482	70129841	192
ENSG00000(	5.17896	14.45145	2.638828	5.992604	11.96562	0.821965	0.22312	0.8069	0.87472	RP4-806M	chr20	-	57408864	57411584	1153
ENSG00000(	6.214751	3.612863	14.51355	5.243529	4.60216	8.219649	0.37286	0.65166	0.75759	RP3-477O4	chr20	+	34106682	34107108	427
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	AC012414.	chr15	+	21004687	21005367	681
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	AC006129.	chr19	+	42037566	42038534	594
ENSG00000(	7.250543	3.612863	9.235896	35.20655	22.09037	22.19305	-1.8817	0.002295	0.006052	VN1R81P	chr19	+	21306620	21306991	372
ENSG00000(	1.035792	0	0	11.23613	16.56778	18.08323	-4.0956	0.000107	0.000346	FLJ11235	chr5	+	1.12E+08	1.12E+08	1031
ENSG00000(	77.68439	52.98866	75.20659	63.67142	60.74851	70.68898	0.077155	0.80191	0.87107	CTD-2017D	chr19	+	24216247	24249711	1966
ENSG00000(	24.85901	36.12863	30.34652	12.73428	12.88605	12.32947	1.2196	0.01519	0.033865	RP11-373A	chr9	-	72808913	72873782	1818
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	AL646016.	chr1	-	2.41E+08	2.41E+08	69
ENSG00000(	8.286335	6.021439	6.597069	2.247227	7.363456	16.4393	-0.27745	0.73698	0.82369	CTC-492K1	chr19	+	40949343	40949994	558
ENSG00000(	4.143168	0	1.319414	0.749076	0.920432	0.821965	0.73295	0.57494	0.69339	AC126614.	chr12	+	57810198	57810536	339
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	CTD-2568A	chr19	-	51295942	51296841	260
ENSG00000(	6.214751	7.225726	9.235896	0	0	0	4.1066	0.000729	0.00209	FENDRR	chr16	-	86508135	86542705	3095
ENSG00000(	4.143168	12.04288	9.235896	5.243529	5.522592	0	1.0623	0.25829	0.37699	AC003682.	chr19	+	58136400	58138318	462
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AC012485.	chr2	+	2.39E+08	2.39E+08	75
ENSG00000(	3.107376	0	0	0	0.920432	0	0.70943	0.5938	NA	CTD-3214H	chr19	+	7694682	7707934	762
ENSG00000(	5.17896	19.2686	1.319414	1.498151	6.443024	9.041614	0.53125	0.56026	0.68074	CTC-344H1	chr19	+	46530912	46533419	544

ENSG00000(	14.50109	14.45145	10.55531	6.74168	6.443024	4.93179	1.0457	0.13842	0.22867	AL031320.	chr6	+	1.44E+08	1.44E+08	48
ENSG00000(	2.071584	2.408575	2.638828	1.498151	1.840864	2.465895	0.22208	0.84796	0.90301	AC132192.	chr11	-	9481747	9482010	264
ENSG00000(	18.64425	14.45145	9.235896	3.745378	9.20432	4.93179	1.1684	0.10452	0.18184	AL138781.	chr9	+	1.39E+08	1.39E+08	1843
ENSG00000(	3.107376	1.204288	2.638828	0.749076	0.920432	1.64393	0.76238	0.53558	0.65984	AC013449.	chr2	-	26251074	26251481	408
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AL355531.	chr10	-	1.31E+08	1.31E+08	642
ENSG00000(	2.071584	0	0	0	4.60216	0.821965	-0.72555	0.59028	0.70695	AC011551.	chr19	-	47050313	47104118	495
ENSG00000(	0	0	7.916483	16.47966	10.12475	9.041614	-1.904	0.046453	0.091068	CTD-2607J	chr19	+	22009315	22010081	412
ENSG00000(	14.50109	6.021439	9.235896	18.72689	4.60216	8.219649	-0.08	0.91391	0.94739	HAVCR1P1	chr19	-	24345172	24346227	1056
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-359H	chr19	+	23778924	23780961	1595
ENSG00000(	2.071584	1.204288	1.319414	2.247227	5.522592	0	-0.52179	0.67163	0.77391	AL160175.	chr20	+	30309001	30309134	51
ENSG00000(	2.071584	3.612863	1.319414	2.247227	0	2.465895	0.39861	0.74465	0.8299	CTC-471J1.	chr19	+	52645879	52647409	332
ENSG00000(	2.071584	1.204288	0	1.498151	0	0.821965	0.27475	0.83886	NA	AC006262.	chr19	+	46706683	46718094	3346
ENSG00000(	3.107376	1.204288	0	12.73428	0	2.465895	-1.3126	0.27127	0.39203	AC007204.	chr19	-	20047769	20048639	237
ENSG00000(	6.214751	12.04288	11.87472	4.494453	5.522592	10.68554	0.48818	0.52049	0.6463	AL132989.	chr14	+	58754751	58755865	1115
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	RP11-15H2	chr19	+	23419110	23419653	544
ENSG00000(	44.53905	54.19295	55.41538	69.66403	45.10117	69.04505	-0.2566	0.44788	0.5776	MIR4453	chr4	+	1.53E+08	1.53E+08	3000
ENSG00000(	0	0	1.319414	0.749076	1.840864	0.821965	-0.71603	0.59765	NA	AP002884.	chr11	+	1.12E+08	1.12E+08	1130
ENSG00000(	3.107376	0	0	1.498151	0	2.465895	-0.17726	0.89532	0.93521	AC087477.	chr15	+	96904487	96904900	414
ENSG00000(	21.75163	13.24716	1.319414	0.749076	0.920432	2.465895	2.6569	0.006218	0.015114	CTD-2587H	chr19	+	54945363	54945845	483
ENSG00000(	2.071584	4.817151	0	0	0.920432	1.64393	0.92304	0.47796	0.60703	CTB-102L5.	chr19	+	38690476	38691574	432
ENSG00000(	1.035792	2.408575	1.319414	0	0	0	1.6865	0.21314	NA	AC007421.	chr17	+	7517264	7517427	164
ENSG00000(	108.7581	67.44011	84.44248	79.40201	75.47542	84.66239	0.12403	0.66463	0.76845	CTD-3138B	chr19	-	58768639	58790174	2705
ENSG00000(	6.214751	14.45145	5.277655	0.749076	1.840864	9.041614	1.0018	0.27967	0.40193	CTD-2545M	chr19	-	50990067	50990895	626
ENSG00000(	9.322127	10.83859	2.638828	5.243529	15.64734	5.753754	-0.18298	0.81988	0.88374	CTD-2616J	chr19	-	51864966	51868798	473
ENSG00000(	10.35792	9.634302	7.916483	20.22504	23.0108	18.90519	-1.09	0.066184	0.12366	VN1R83P	chr19	-	21472356	21472800	445
ENSG00000(	0	0	0	4.494453	9.20432	0.821965	-2.9796	0.020937	0.045203	CYP2T3P	chr19	+	41640627	41643213	817
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	DKFZP547L	chr15	+	22011370	22012050	681
ENSG00000(	1.035792	1.204288	3.958241	6.74168	1.840864	4.93179	-0.92986	0.38946	0.52001	AC004076.	chr19	+	57905551	57949825	521
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RP11-420K	chr19	+	21892324	21892993	670
ENSG00000(	0	0	0	1.498151	0	1.64393	-0.88211	0.49937	NA	AC005523.	chr19	-	4785132	4791219	418
ENSG00000(	4.143168	7.225726	5.277655	0	17.48821	8.219649	-0.53009	0.57576	0.69413	AC109583.	chr3	-	46927699	46930171	69
ENSG00000(	5.17896	2.408575	1.319414	0.749076	6.443024	1.64393	0.040626	0.97095	0.98309	KIAA1658	chr22	-	30814212	30814469	258
ENSG00000(	12.4295	7.225726	18.47179	10.48706	11.04518	10.68554	0.22292	0.73466	0.82247	CTD-2619J	chr19	+	58929927	58930677	495
ENSG00000(	4.143168	1.204288	1.319414	1.498151	7.363456	0.821965	-0.38198	0.73917	0.82532	VN1R107P	chr19	+	57971280	57971488	209
ENSG00000(	10.35792	21.67718	14.51355	7.490755	11.04518	16.4393	0.38671	0.54073	0.66379	RP11-295P	chr10	+	13724521	13726874	1978
ENSG00000(	2.071584	3.612863	0	0	0	0	1.8175	0.17961	NA	AC090427.	chr19	+	14834747	14835121	285
ENSG00000(	0	0	0	2.247227	0.920432	2.465895	-1.668	0.21871	NA	RP11-678G	chr19	-	21753624	21770124	1178
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	CTD-2332E	chr19	+	20794365	20798195	628
ENSG00000(	2.071584	4.817151	1.319414	3.745378	2.761296	2.465895	-0.10379	0.92401	0.95396	AC003956.	chr19	+	15234971	15236985	356
ENSG00000(	0	2.408575	1.319414	0	0.920432	1.64393	0.29993	0.82362	0.8862	AC007228.	chr19	-	57183942	57185269	1328
ENSG00000(	17.60846	15.65574	19.79121	32.21025	11.04518	13.15144	-0.09423	0.87081	0.91876	RP11-158H	chr18	-	32860831	32870165	4382
ENSG00000(	110.8297	118.0202	120.0667	59.17697	63.50981	64.93523	0.88644	0.00072	0.002066	RP1-283E3	chr1	-	1634175	1669127	5079
ENSG00000(	13.46529	0	2.638828	0	8.283888	1.64393	0.56744	0.61862	0.73102	AL354718.	chr9	-	45441273	45441542	270
ENSG00000(	3.107376	0	0	5.243529	0.920432	0.821965	-0.72468	0.5763	0.69458	CTC-453G2	chr19	+	48707340	48716411	566

ENSG00000(	6.214751	4.817151	14.51355	8.988907	10.12475	7.397684	-0.06052	0.93594	0.96146	RP11-464F	chr10	+	75385754	75386548	795
ENSG00000(	15.53688	16.86003	25.06886	6.74168	15.64734	18.90519	0.45314	0.44446	0.57404	AL355312.	chr6	+	1.5E+08	1.5E+08	1740
ENSG00000(	4.143168	4.817151	3.958241	1.498151	1.840864	6.575719	0.31791	0.75367	0.83712	CTD-2611C	chr19	+	56218707	56219330	462
ENSG00000(	3.107376	2.408575	0	0	0	5.753754	-0.02803	0.98288	0.99026	VN1R80P	chr19	+	21246730	21247067	338
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC115522.	chr19	-	44298461	44299810	556
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-316C	chr2	-	2.2E+08	2.2E+08	636
ENSG00000(	5.17896	1.204288	7.916483	10.48706	9.20432	18.90519	-1.3049	0.1003	0.17589	CTD-2620I2	chr19	-	53638190	53638575	386
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	AC006262.	chr19	-	46692423	46706340	1037
ENSG00000(	17.60846	3.612863	6.597069	0.749076	3.681728	2.465895	1.7575	0.061762	0.11645	AC073657.	chr15	-	42073346	42076229	183
ENSG00000(	10.35792	8.430014	5.277655	10.48706	1.840864	12.32947	-0.03271	0.96773	0.98106	hsa-mir-29(	chr20	-	57392187	57392780	594
ENSG00000(	1.035792	2.408575	1.319414	2.996302	1.840864	0	-0.02219	0.98608	0.99155	AC068499.	chr19	+	18315540	18331346	911
ENSG00000(	0	0	0	2.247227	0.920432	0.821965	-1.2297	0.36205	NA	CTB-60B18	chr19	-	49521504	49522741	493
ENSG00000(	7.250543	9.634302	3.958241	3.745378	2.761296	7.397684	0.51689	0.5549	0.67564	AC110084.	chr2	-	27998851	28009186	63
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AL133373.	chr14	-	92038788	92041383	2596
ENSG00000(	0	0	0	29.96302	41.41944	21.37109	-5.7828	6.36E-08	2.97E-07	CTD-2561J2	chr19	+	21666176	21686040	3760
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AL596220.	chr1	-	1.86E+08	1.86E+08	135
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	WBP1LP6	chr1	+	610222	610645	424
ENSG00000(	24.85901	14.45145	29.0271	2.247227	13.80648	12.32947	1.203	0.06323	0.11894	CTD-2622I2	chr19	-	4061613	4062747	684
ENSG00000(	3.107376	1.204288	0	0	0.920432	0	1.0851	0.42378	NA	CTC-444N2	chr19	-	57862216	57863380	1045
ENSG00000(	1.035792	1.204288	0	0	0.920432	0	0.54457	0.68095	NA	CTD-2553L	chr19	-	35129027	35131594	413
ENSG00000(	1.035792	0	1.319414	4.494453	0	0.821965	-0.70271	0.59804	0.71366	AC010524.	chr19	-	49871962	49891338	3263
ENSG00000(	1.035792	4.817151	3.958241	0	0.920432	0	2.143	0.097796	0.1722	AC007382.	chr2	-	37068327	37068530	204
ENSG00000(	1.035792	0	1.319414	5.243529	0	0	-0.6462	0.63176	0.7417	CTD-2561J2	chr19	-	21704145	21704698	554
ENSG00000(	1.035792	0	0	2.996302	0	2.465895	-1.1733	0.38614	0.51699	RP11-247A	chr9	+	1.32E+08	1.32E+08	507
ENSG00000(	68.36227	52.98866	36.94359	59.17697	45.10117	64.11326	-0.08207	0.81589	0.88063	CTC-444N2	chr19	+	57772722	57774106	1385
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-588H	chr12	-	70840240	70841365	1126
ENSG00000(	0	1.204288	1.319414	0	0	1.64393	0.26393	0.84486	NA	AC022819.	chr15	-	99859300	99859828	81
ENSG00000(	0	1.204288	0	2.247227	4.60216	0.821965	-1.5737	0.23296	0.34666	CTD-2561J2	chr19	-	21564022	21564723	394
ENSG00000(	1.035792	4.817151	0	0	0	0.821965	1.43	0.29086	0.41492	AL139080.	chr13	+	24322243	24323901	96
ENSG00000(	19.68005	18.06432	14.51355	3.745378	4.60216	5.753754	1.7653	0.01008	0.023426	CTD-2538G	chr19	+	16954836	16957284	371
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTD-3105H	chr19	-	12490003	12512088	2593
ENSG00000(	16.57267	14.45145	6.597069	3.745378	0	0.821965	2.5811	0.005341	0.013156	CTD-2571L	chr19	+	48110781	48236355	344
ENSG00000(	6.214751	0	0	2.247227	0	0	0.79648	0.55541	0.67608	CTD-3030D	chr19	-	21458825	21459134	310
ENSG00000(	2.071584	1.204288	1.319414	7.490755	5.522592	0.821965	-1.2302	0.27184	0.39249	SCGB1B2P	chr19	-	35067638	35068606	612
ENSG00000(	8.286335	6.021439	13.19414	4.494453	9.20432	4.93179	0.51288	0.51318	0.64014	AC104534.	chr19	+	39310806	39313863	566
ENSG00000(	1.035792	0	0	5.992604	0	0	-1.171	0.38809	0.5189	AC135983.	chr15	+	32774822	32780287	5466
ENSG00000(	6.214751	2.408575	0	2.996302	0	1.64393	0.63282	0.60914	0.72316	CTC-450M9	chr19	-	38599140	38600173	328
ENSG00000(	1.035792	0	3.958241	0	0	0	1.6134	0.2311	NA	RPL7P50	chr19	+	6593340	6594066	727
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	SMIM7	chr19	-	16688453	16770926	956
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	AC093323.	chr4	-	6693782	6694189	408
ENSG00000(	46.61064	48.17151	48.81831	12.73428	11.04518	15.61733	1.8122	3.82E-05	0.000132	AC027307.	chr19	+	1440838	1441937	1100
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-321E	chr5	-	17491470	17491878	409
ENSG00000(	5.17896	2.408575	10.55531	0.749076	1.840864	3.28786	1.3414	0.19095	0.29646	AC112205.	chr5	-	1.63E+08	1.63E+08	99
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	PRED57	chr21	-	46511596	46515493	345

ENSG00000(	31.07376	9.634302	29.0271	0.749076	1.840864	6.575719	2.678	0.000423	0.001259	MGC20647	chr22	+	30641984	30642907	723
ENSG00000(	11.39371	25.29004	14.51355	47.19176	34.05598	34.52253	-1.147	0.016648	0.036807	CTD-3093M	chr19	+	54697731	54698394	664
ENSG00000(	3.107376	1.204288	5.277655	0	0.920432	2.465895	1.0812	0.37406	0.50455	AC068039.	chr2	-	1.73E+08	1.73E+08	66
ENSG00000(	0	1.204288	0	0	7.363456	2.465895	-1.7658	0.18076	0.28372	LA16c-OS1	chr16	-	235747	236293	547
ENSG00000(	2.071584	0	0	1.498151	0	0.821965	-0.06236	0.96323	NA	AC027228.	chr15	+	78830023	78831288	1266
ENSG00000(	0	0	0	8.988907	12.88605	18.90519	-4.6168	5.15E-05	0.000175	CTD-2245F	chr19	+	53665681	53666816	359
ENSG00000(	0	0	0	3.745378	0.920432	0	-1.3029	0.33256	NA	AC018867.	chr2	-	1.87E+08	1.87E+08	138
ENSG00000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	SIGLEC31P	chr19	-	57100863	57101649	551
ENSG00000(	13.46529	26.49433	31.66593	9.737982	18.40864	9.863579	0.8709	0.12816	0.21482	AC132872.	chr17	+	80214131	80216080	1950
ENSG00000(	5.17896	2.408575	5.277655	0.749076	5.522592	0.821965	0.71043	0.51119	0.63835	AP001579.	chr21	-	46492796	46492927	132
ENSG00000(	4.143168	4.817151	7.916483	2.996302	4.60216	8.219649	0.075246	0.93261	0.95966	AC026310.	chr12	+	25055243	25057615	2373
ENSG00000(	0	0	0	0.749076	3.681728	0	-1.2286	0.35939	NA	AC020915.	chr19	+	58735872	58736835	964
ENSG00000(	0	0	0	3.745378	2.761296	0.821965	-2.0174	0.13428	0.22327	ESPNP	chr1	-	17013834	17046652	2015
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	IGFL1P1	chr19	+	46699495	46700580	360
ENSG00000(	1.035792	2.408575	2.638828	0	0	0	2.0265	0.13497	0.22409	CTD-2550C	chr19	+	8411401	8412571	594
ENSG00000(	16.57267	16.86003	21.11062	11.23613	31.29469	41.92021	-0.60303	0.27032	0.39081	AC026740.	chr5	+	667759	668839	744
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	CTD-2616J	chr19	+	51897742	51906904	559
ENSG00000(	11.39371	13.24716	10.55531	5.992604	4.60216	18.08323	0.27115	0.70619	0.80093	AC006014.	chr7	-	74999908	75005425	78
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	CTD-3233P	chr19	-	21404447	21405548	1102
ENSG00000(	2.071584	1.204288	1.319414	1.498151	2.761296	0	0.085559	0.94687	0.96788	PLCE1-AS1	chr10	-	96039034	96046828	1683
ENSG00000(	44.53905	55.39724	60.69303	10.48706	6.443024	27.12484	1.7965	0.000233	0.00072	A1BG-AS1	chr19	+	58859117	58866549	2130
ENSG00000(	6.214751	12.04288	0	0	0	0	3.569	0.005627	0.013802	RP11-256I2	chr2	-	2.2E+08	2.2E+08	448
ENSG00000(	0	1.204288	0	0	0.920432	3.28786	-0.84421	0.53376	NA	RP11-34P1	chr1	-	135141	135895	755
ENSG00000(	17.60846	37.33292	36.94359	2.996302	11.96562	1.64393	2.3333	0.000417	0.001241	CTD-2619J	chr19	-	58939999	58942515	2517
ENSG00000(	10.35792	4.817151	6.597069	13.48336	13.80648	10.68554	-0.73257	0.29973	0.4246	AC026806.	chr19	+	38822274	38822716	443
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	DKFZP434I	chr9	+	98534605	98537013	2409
ENSG00000(	19.68005	18.06432	9.235896	17.97781	9.20432	27.12484	-0.1941	0.74594	0.8309	FLJ00418	chr16	+	70695570	70699739	4170
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-886P	chr19	-	8488239	8492711	511
ENSG00000(	0	4.817151	3.958241	1.498151	1.840864	4.109825	0.16459	0.8864	0.9292	AC005387.	chr19	+	18642228	18643440	421
ENSG00000(	0	2.408575	5.277655	0.749076	0.920432	0	1.3549	0.30069	0.42568	MGC4294	chr20	+	57209828	57210772	945
ENSG00000(	0	6.021439	0	11.23613	8.283888	15.61733	-2.1686	0.024356	0.051785	CKS1B	chr5	-	61808070	61808309	240
ENSG00000(	9.322127	1.204288	3.958241	2.247227	4.60216	10.68554	-0.21797	0.81893	0.88301	CTD-2192J	chr19	-	12793507	12798093	635
ENSG00000(	2.071584	2.408575	1.319414	11.23613	8.283888	8.219649	-1.9356	0.037614	0.075862	AD000684.	chr19	+	35753749	35755707	1016
ENSG00000(	37.28851	26.49433	18.47179	10.48706	15.64734	15.61733	0.95223	0.070872	0.13118	AC004017.	chr19	-	58203868	58204128	261
ENSG00000(	0	1.204288	0	1.498151	0	0.821965	-0.3785	0.77728	NA	AC114494.	chr1	-	31902192	31902614	423
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	LRLE1	chr8	-	8046158	8046331	174
ENSG00000(	0	0	0	9.737982	0	4.93179	-2.891	0.02755	0.057729	ERVV-2	chr19	+	53547991	53554329	2431
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	AC061992.	chr17	+	76422409	76422834	426
ENSG00000(	22.78742	37.33292	19.79121	22.47227	25.7721	60.8254	-0.43317	0.37867	0.50941	CTD-3099C	chr19	-	53100952	53102140	644
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	PIH1	chr16	-	79015647	79015739	93
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTD-2528A	chr19	+	17119999	17124270	405
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	CTC-435M1	chr19	+	41905277	41906270	540
ENSG00000(	3.107376	0	1.319414	2.996302	1.840864	0	-0.07218	0.95577	0.97381	CTB-175P5	chr19	+	23567332	23568095	764
ENSG00000(	10.35792	9.634302	13.19414	59.17697	27.61296	27.94681	-1.7271	0.001184	0.003281	VN1R82P	chr19	+	21371401	21371756	356

ENSG00000(	18.64425	21.67718	14.51355	3.745378	6.443024	13.9734	1.1125	0.09219	0.16396	AL807752.	chr9	-	1.4E+08	1.4E+08	315
ENSG00000(	0	1.204288	0	5.243529	10.12475	4.93179	-2.8957	0.01404	0.031595	ZNF818P	chr19	+	53716241	53716649	409
ENSG00000(	1.035792	0	3.958241	2.247227	0	0	0.61156	0.65008	0.7564	AC005932.	chr19	+	19051131	19057640	957
ENSG00000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	AC003006.	chr19	+	58193403	58264943	612
ENSG00000(	6.214751	3.612863	3.958241	5.243529	4.60216	5.753754	-0.14843	0.87	0.9184	MTRNR2L1	chr3	-	96335981	96337000	1020
ENSG00000(	5.17896	4.817151	3.958241	12.73428	7.363456	6.575719	-0.83798	0.30936	0.43551	AP001462.	chr11	+	64546426	64546877	452
ENSG00000(	0	0	0	2.996302	1.840864	0	-1.3549	0.31496	NA	CTD-2626G	chr19	-	20967402	20967958	557
ENSG00000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	AP001925.	chr11	-	1.08E+08	1.08E+08	51
ENSG00000(	168.8341	179.4389	159.6491	152.8114	123.3379	169.3248	0.18675	0.39073	0.52154	CTC-429P9	chr19	-	16744614	16746080	1467
ENSG00000(	6.214751	15.65574	6.597069	0	0	0	4.4373	0.000198	0.000618	Z98049.1	chr6	+	1.67E+08	1.67E+08	2341
ENSG00000(	0	1.204288	0	0.749076	1.840864	0	-0.44385	0.74106	NA	AC092291.	chr16	+	14564842	14565054	213
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	CTC-360G5	chr19	+	39360799	39364403	504
ENSG00000(	1.035792	0	0	3.745378	0	2.465895	-1.314	0.33021	0.45801	CTD-2245F	chr19	+	53700364	53714268	545
ENSG00000(	3.107376	1.204288	1.319414	4.494453	1.840864	4.93179	-0.77589	0.48383	0.61306	CTD-2619J	chr19	+	58873951	58877958	790
ENSG00000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	CALR3	chr19	-	16589868	16607003	1292
ENSG00000(	7.250543	6.021439	5.277655	0.749076	1.840864	7.397684	0.76286	0.43304	0.56286	CTD-2528A	chr19	-	17206228	17210117	610
ENSG00000(	2.071584	8.430014	0	5.243529	11.96562	8.219649	-1.0854	0.25071	0.36814	RP11-256I	chr2	+	2.2E+08	2.2E+08	544
ENSG00000(	19.68005	33.72006	31.66593	5.992604	4.60216	4.93179	2.315	0.000123	0.000396	CTC-471F3.	chr19	-	40529291	40531409	2039
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	AC099344.	chr2	+	11603927	11606274	36
ENSG00000(	3.107376	2.408575	1.319414	0	4.60216	0.821965	0.26389	0.83042	0.89119	AC009977.	chrY	-	21737895	21738068	99
ENSG00000(	0	0	0	1.498151	2.761296	3.28786	-2.0751	0.1224	0.20728	CTC-523E2	chr19	+	35328793	35346208	5302
ENSG00000(	5.17896	0	10.55531	1.498151	7.363456	12.32947	-0.36922	0.70419	0.79928	AP003733.	chr11	+	61735453	61736755	1303
ENSG00000(	1.035792	1.204288	1.319414	1.498151	0.920432	0.821965	0.079139	0.95167	0.97115	CTD-2126E	chr19	-	50546453	50554319	570
ENSG00000(	0	0	0	0	7.363456	0	-1.7141	0.20548	0.31414	AC003682.	chr19	+	58175648	58176407	760
ENSG00000(	3.107376	9.634302	5.277655	2.247227	6.443024	5.753754	0.28044	0.75641	0.83894	CTD-2525I3	chr19	-	52788033	52801173	447
ENSG00000(	6.214751	0	7.916483	6.74168	0	9.863579	-0.19696	0.85282	0.90612	AC002472.	chr22	-	21358030	21360736	192
ENSG00000(	1.035792	0	0	0	0	1.64393	-0.12526	0.92174	NA	AL035681.	chr22	-	41685388	41685686	39
ENSG00000(	0	0	1.319414	1.498151	0	0.821965	-0.38347	0.77483	NA	FLJ00388	chr1	-	48226979	48227290	312
ENSG00000(	3.107376	14.45145	2.638828	0	0	1.64393	2.6676	0.021785	0.046828	AC007193.	chr19	-	46823454	46843261	472
ENSG00000(	0	3.612863	0	4.494453	0	4.109825	-0.82653	0.52138	0.64701	RP11-98F1	chr13	-	1.14E+08	1.14E+08	182
ENSG00000(	94.25706	115.6116	79.16483	86.89276	66.2711	106.8554	0.15007	0.60069	0.71598	AC004447.	chr19	+	19101702	19104419	2416
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-420K	chr19	+	21983282	21984068	787
ENSG00000(	1.035792	0	2.638828	0	0.920432	0.821965	0.5719	0.67274	NA	CTD-3193C	chr19	+	7990886	7991648	317
ENSG00000(	4.143168	4.817151	5.277655	2.247227	12.88605	9.863579	-0.71211	0.41311	0.54357	AC092301.	chr19	+	46333422	46334366	764
ENSG00000(	1.035792	0	1.319414	0	0	0.821965	0.54471	0.68089	NA	CTD-3193C	chr19	-	7944330	7945005	676
ENSG00000(	13.46529	7.225726	5.277655	14.23244	8.283888	18.08323	-0.58695	0.39845	0.52949	CTD-3131K	chr19	-	17629139	17631374	460
ENSG00000(	6.214751	2.408575	9.235896	4.494453	1.840864	0.821965	1.0832	0.28325	0.4061	AC069547.	chr10	+	52094298	52095876	1579
ENSG00000(	3.107376	6.021439	6.597069	2.247227	1.840864	4.109825	0.78118	0.42862	0.55874	CTC-218B8	chr19	-	39625522	39627103	365
ENSG00000(	13.46529	8.430014	6.597069	14.23244	9.20432	15.61733	-0.41627	0.53617	0.66029	AC093157.	chr1	+	1.01E+08	1.01E+08	1893
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-727F	chr11	-	62553498	62554257	760
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	L34079.3	chr19	+	44057597	44059646	561
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	AC010760.	chr15	+	22456895	22460351	33
ENSG00000(	0	0	5.277655	0	0	0.821965	1.1957	0.37766	0.50836	RP11-573N	chr13	+	98885904	98886954	1051
ENSG00000(	476.4643	452.8122	328.534	115.3576	95.72493	94.52597	2.0293	2.86E-23	3.30E-22	FBXO17	chr19	-	39432044	39466550	2383

ENSG00000(	3.107376	6.021439	2.638828	4.494453	1.840864	5.753754	-0.03908	0.96856	0.98169	AC005387.	chr19	+	18643718	18646998	440
ENSG00000(	5.17896	22.88147	6.597069	1.498151	2.761296	5.753754	1.5839	0.067841	0.12639	RP4-614O4	chr20	-	33789550	33791091	1542
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	AC019171.	chr2	-	39186764	39187483	720
ENSG00000(	6.214751	18.06432	14.51355	5.243529	8.283888	5.753754	0.92732	0.20275	0.31065	RP11-345P	chr1	+	1604714	1605836	502
ENSG00000(	2.071584	2.408575	6.597069	6.74168	10.12475	4.93179	-0.86688	0.34022	0.46898	CTC-429C1	chr19	+	52452387	52484620	698
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	CTD-2619J	chr19	+	58677533	58678512	980
ENSG00000(	12.4295	7.225726	7.916483	5.992604	11.96562	5.753754	0.21485	0.7746	0.852	CTD-2231E	chr19	-	16234471	16250702	2987
ENSG00000(	4.143168	0	0	0	2.761296	0	0.32622	0.80997	0.87669	CTC-246B1	chr19	-	39832413	39832585	173
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC008498.	chr5	-	60411538	60411762	225
ENSG00000(	0	0	2.638828	2.996302	0	5.753754	-1.1267	0.38696	0.51775	CTB-92J24.	chr19	-	24101883	24140732	1585
ENSG00000(	11.39371	6.021439	5.277655	3.745378	4.60216	3.28786	0.8649	0.31991	0.44707	RP11-869B	chr11	-	64552393	64553092	700
ENSG00000(	3.107376	1.204288	1.319414	0.749076	1.840864	3.28786	-0.02826	0.98131	0.98919	AC010877.	chrY	+	15418467	15429181	267
ENSG00000(	94.25706	63.82725	71.24834	26.96672	36.81728	42.74218	1.0945	0.001557	0.004226	RP1-265C2	chr6	-	28089573	28105071	2163
ENSG00000(	0	0	3.958241	0	0	3.28786	0.12119	0.92879	0.95719	AC005614.	chr19	+	40596661	40600313	3653
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTD-2529P	chr19	+	8932177	8934786	537
ENSG00000(	0	1.204288	0	2.996302	0.920432	0	-0.78586	0.56226	NA	AC110771.	chr4	-	1.87E+08	1.87E+08	714
ENSG00000(	3.107376	0	2.638828	0	2.761296	0.821965	0.45594	0.72627	0.81642	CTD-2527I2	chr19	-	35489137	35491074	565
ENSG00000(	5.17896	7.225726	13.19414	0.749076	0	2.465895	2.4326	0.017727	0.038957	AC010522.	chr19	-	58337829	58338146	318
ENSG00000(	3.107376	1.204288	2.638828	2.996302	4.60216	1.64393	-0.31457	0.77662	0.85306	AL158147.	chr9	-	4859120	4859260	141
ENSG00000(	10.35792	16.86003	11.87472	11.98521	19.32907	11.50751	-0.12196	0.84312	0.89993	AC007292.	chr19	-	4356634	4358445	1812
ENSG00000(	1.035792	2.408575	0	0.749076	2.761296	0.821965	-0.1928	0.88273	0.92678	CTC-453G2	chr19	+	48649165	48650670	359
ENSG00000(	6.214751	12.04288	15.83297	1.498151	16.56778	13.15144	0.11693	0.87944	0.9246	AL591479.	chr9	+	70646589	70648956	2368
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC139768.	chr12	+	51619860	51620085	57
ENSG00000(	175.0488	193.8903	167.5656	749.0755	563.3044	604.1442	-1.8299	6.03E-26	7.73E-25	ZNF587B	chr19	+	58331099	58370018	3339
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTD-3099C	chr19	-	53014535	53015595	880
ENSG00000(	22.78742	37.33292	25.06886	14.98151	23.0108	43.56414	0.060613	0.90349	0.94036	AC018766.	chr19	-	50360227	50362546	719
ENSG00000(	3.107376	9.634302	2.638828	0.749076	0	0	2.8459	0.021226	0.045777	AC138393.	chr1	-	2.24E+08	2.24E+08	135
ENSG00000(	5.17896	1.204288	5.277655	6.74168	5.522592	4.109825	-0.41978	0.65734	0.7622	RP11-380N	chr18	-	45404666	45408815	282
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AC020629.	chr12	+	42624050	42628075	135
ENSG00000(	0	0	0	3.745378	8.283888	1.64393	-2.9269	0.023174	0.049468	CTC-513N1	chr19	+	20585356	20585532	177
ENSG00000(	0	0	0	2.247227	0	0.821965	-0.85594	0.51054	NA	CTD-2542C	chr19	-	21021321	21030223	317
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTB-50E14.	chr19	-	42989228	42989866	639
ENSG00000(	0	0	0	2.247227	0	0.821965	-0.85594	0.51054	NA	RP11-120K	chr13	+	1.14E+08	1.14E+08	649
ENSG00000(	31.07376	54.19295	56.73479	41.19916	46.94203	55.89361	-0.02694	0.94211	0.96512	ITGB1P1	chr19	-	14732446	14733054	609
ENSG00000(	13.46529	3.612863	17.15238	5.243529	6.443024	8.219649	0.7141	0.34888	0.4786	RAB11B-AS	chr19	-	8439257	8455569	1013
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-298J	chr6	-	41732030	41732198	169
ENSG00000(	53.86118	73.46155	21.11062	12.73428	19.32907	13.9734	1.6416	0.000828	0.002352	AC018755.	chr19	+	52097814	52109403	929
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	CTB-191K2	chr19	-	50869137	50872588	304
ENSG00000(	10.35792	0	1.319414	0	1.840864	0	1.7478	0.17547	0.27721	AC187652.	chr7	+	302918	304070	501
ENSG00000(	0	3.612863	2.638828	40.45008	42.33987	31.23467	-3.9072	5.88E-08	2.76E-07	CTB-92J24.	chr19	+	24110590	24112089	1500
ENSG00000(	27.96638	16.86003	18.47179	53.93344	34.97642	44.38611	-1.0393	0.01752	0.038559	CTD-3222D	chr19	-	16653434	16655625	1931
ENSG00000(	2.071584	0	3.958241	5.243529	4.60216	1.64393	-0.73199	0.51714	0.64348	AC116407.	chr17	-	30506379	30506885	507
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTD-2616J	chr19	-	51853627	51871353	551
ENSG00000(	0	0	6.597069	0	0	4.93179	0.23285	0.86131	0.91189	SPIB	chr19	+	50922195	50934570	3791

ENSG00000(	2.071584	0	5.277655	0.749076	2.761296	1.64393	0.3665	0.76373	0.84398	AL096677.	chr20	-	23330015	23334066	57
ENSG00000(	0	0	0	151.3133	122.4175	120.8288	-7.7019	8.55E-15	6.66E-14	CTB-175P5	chr19	-	23582035	23598877	2766
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	CTD-2265N	chr19	+	48564628	48568202	568
ENSG00000(	0	0	2.638828	2.996302	0.920432	2.465895	-0.84108	0.51953	0.64558	ZNF92P3	chr19	+	24118022	24118975	954
ENSG00000(	2.071584	3.612863	1.319414	0	1.840864	0.821965	0.95921	0.45056	0.58023	AC092384.	chr16	+	88894366	88894545	48
ENSG00000(	5.17896	3.612863	0	1.498151	0	1.64393	1.0194	0.41671	0.54725	CTC-273B1	chr19	+	48969623	48970237	615
ENSG00000(	0	0	0	5.992604	1.840864	6.575719	-3.0288	0.01792	0.039318	AC007292.	chr19	+	4339574	4343488	279
ENSG00000(	75.61281	87.913	63.33186	65.16957	56.14635	88.77221	0.10954	0.72212	0.81311	CTC-429P9	chr19	+	16741554	16754753	453
ENSG00000(	169.8699	168.6003	133.2608	65.91865	68.11197	87.95025	1.0803	1.70E-05	6.12E-05	LRRC3DN	chr21	+	45879814	45882078	2265
ENSG00000(	0	1.204288	0	0.749076	0	0	0.1572	0.90001	NA	CTB-175P5	chr19	+	23563119	23563678	560
ENSG00000(	68.36227	57.80581	43.54065	20.22504	9.20432	19.72716	1.734	6.58E-05	0.00022	CTD-3131K	chr19	-	17599799	17622698	775
ENSG00000(	4.143168	7.225726	0	5.243529	2.761296	6.575719	-0.29109	0.77422	0.85182	CTB-180A7	chr19	-	6386773	6390411	447
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	AC002451.	chr7	+	95171457	95173854	2398
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CTD-2579N	chr19	+	23108179	23108349	171
ENSG00000(	1.035792	8.430014	7.916483	0.749076	4.60216	1.64393	1.0819	0.29952	0.42451	RP11-727F	chr11	-	62575154	62575535	382
ENSG00000(	0	0	1.319414	4.494453	9.20432	13.15144	-3.2665	0.004043	0.010206	RP11-432N	chr5	-	17655237	17655647	411
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	RP11-15H2	chr19	+	23386812	23387358	547
ENSG00000(	23.82321	13.24716	14.51355	6.74168	11.96562	9.863579	0.81794	0.19236	0.29812	CTD-2619J	chr19	+	58951815	58957216	5402
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTD-3032J	chr19	-	17317947	17318819	629
ENSG00000(	4.143168	8.430014	9.235896	1.498151	5.522592	7.397684	0.52479	0.55109	0.67225	CTD-2521N	chr19	-	17525066	17533133	691
ENSG00000(	3.107376	0	0	0	2.761296	1.64393	-0.25193	0.85132	0.90521	AC006272.	chr19	-	52343177	52346577	423
ENSG00000(	7.250543	9.634302	6.597069	11.98521	11.04518	6.575719	-0.30783	0.67429	0.77634	CTC-360G5	chr19	-	39425976	39429272	3297
ENSG00000(	6.214751	2.408575	1.319414	0.749076	0.920432	1.64393	1.1913	0.3143	0.44089	CTB-174O2	chr19	+	47231860	47235957	562
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-98D1	chr1	+	1.52E+08	1.52E+08	549
ENSG00000(	3.107376	12.04288	13.19414	15.73059	2.761296	7.397684	0.093901	0.90696	0.94268	SBP1	chr6	-	33663196	33663474	279
ENSG00000(	5.17896	2.408575	13.19414	0.749076	1.840864	2.465895	1.6864	0.098032	0.17248	RP11-353N	chr1	+	1.5E+08	1.5E+08	2081
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	AC110792.	chr4	+	54927213	54927377	165
ENSG00000(	0	3.612863	1.319414	11.23613	1.840864	0.821965	-1.1447	0.32754	0.45525	DKFZP779L	chr12	+	48592170	48595814	3645
ENSG00000(	2.071584	1.204288	3.958241	2.996302	0.920432	4.109825	-0.13206	0.9073	0.94286	CTB-83J4.1	chr19	+	54728395	54728753	359
ENSG00000(	0	0	0	4.494453	3.681728	0.821965	-2.3049	0.083929	0.15158	ERVV-1	chr19	+	53517174	53519375	2202
ENSG00000(	1.035792	2.408575	5.277655	1.498151	2.761296	2.465895	0.27957	0.80389	0.87281	AC140061.	chr12	+	50690489	50691718	369
ENSG00000(	0	0	2.638828	1.498151	0	0	0.308	0.81734	NA	ZNF548	chr19	+	57901252	57931362	630
ENSG00000(	12.4295	2.408575	3.958241	2.996302	10.12475	14.79537	-0.48344	0.56981	0.68881	CTC-453G2	chr19	+	48621689	48630963	852
ENSG00000(	1.035792	6.021439	7.916483	5.243529	2.761296	0	0.70285	0.51726	0.64351	CTD-2525I3	chr19	-	52803946	52848482	1905
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	CTD-2126E	chr19	-	50562139	50563489	1351
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	CTD-3138B	chr19	+	58740831	58798173	1463
ENSG00000(	1.035792	0	0	5.243529	5.522592	10.68554	-3.012	0.010351	0.023986	AL031663.	chr20	+	44074071	44077220	3150
ENSG00000(	84.93494	72.25726	36.94359	71.16218	63.50981	55.89361	0.033643	0.92243	0.95302	AL590822.	chr1	+	2121237	2123179	1943
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	AC104057.	chr7	-	65112081	65113280	906
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC093677.	chr4	-	75023327	75024085	759
ENSG00000(	2.071584	0	0	3.745378	0.920432	0.821965	-0.80123	0.54698	0.6688	CTD-2192J	chr19	-	12640582	12643787	533
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	AC138655.	chr2	+	47799601	47801998	2398
ENSG00000(	0	0	1.319414	2.247227	0	2.465895	-0.96287	0.47752	0.6066	AP001350.	chr11	-	58378589	58378759	171
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTD-2611C	chr19	+	56220529	56220899	371

ENSG00000(	5.17896	2.408575	3.958241	0	0.920432	4.109825	0.9191	0.42648	0.55667	CTD-3222D	chr19	-	16697716	16698796	1081
ENSG00000(	0	0	0	1.498151	5.522592	0	-1.8128	0.18144	0.28461	TDGF1P7	chr19	+	40025103	40025661	559
ENSG00000(	19.68005	25.29004	14.51355	8.988907	3.681728	5.753754	1.5748	0.015976	0.035456	AC006128.	chr19	+	15509507	15511167	1661
ENSG00000(	7.250543	8.430014	2.638828	2.247227	2.761296	4.93179	0.76692	0.41602	0.54666	AL354808.	chr13	+	20268547	20269240	694
ENSG00000(	3.107376	4.817151	1.319414	5.243529	0.920432	0	0.42428	0.72006	0.81162	AC016629.	chr19	-	59105263	59110722	890
ENSG00000(	0	0	0	0	2.761296	0.821965	-0.99626	0.45043	NA	Z97053.1	chr20	-	43234346	43248126	72
ENSG00000(	21.75163	7.225726	7.916483	115.3576	97.56579	124.9387	-3.0845	2.86E-14	2.15E-13	RP11-18I14	chr10	+	1.04E+08	1.04E+08	2453
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-277L	chr1	-	1.5E+08	1.5E+08	487
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	AL590560.	chr1	-	1.6E+08	1.6E+08	276
ENSG00000(	0	0	1.319414	0	0	0.821965	0.1572	0.90001	NA	RP11-98D1	chr1	+	1.52E+08	1.52E+08	629
ENSG00000(	2.071584	2.408575	5.277655	2.996302	3.681728	2.465895	0.065788	0.9502	0.97007	AL138847.	chr1	+	63073437	63075249	1813
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC004257.	chr19	-	15331826	15333108	277
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RPL12P41	chr19	+	46722680	46723177	498
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTD-2521N	chr19	+	17516503	17529713	1806
ENSG00000(	0	0	0	0.749076	2.761296	0	-0.97685	0.45852	NA	CTB-167G5	chr19	-	54107656	54111705	766
ENSG00000(	4.143168	4.817151	0	3.745378	7.363456	4.93179	-0.67416	0.50736	0.63489	CTD-2331H	chr19	+	53426635	53427328	486
ENSG00000(	0	2.408575	1.319414	0	4.60216	4.109825	-0.83997	0.50555	0.63323	CTD-2195B	chr19	-	41727331	41727956	286
ENSG00000(	5.17896	7.225726	3.958241	0	1.840864	0	2.3696	0.043519	0.086157	CTB-102L5.	chr19	+	38675016	38676905	1890
ENSG00000(	0	12.04288	11.87472	8.988907	2.761296	2.465895	0.61613	0.52335	0.64862	CTD-2571L	chr19	-	48260293	48272097	540
ENSG00000(	103.5792	137.2888	92.35896	5.992604	10.12475	12.32947	3.484	1.10E-18	1.05E-17	AC079210.	chr17	+	66539369	66542970	3602
ENSG00000(	0	0	0	0.749076	2.761296	1.64393	-1.5386	0.25678	NA	RP11-255H	chr19	-	23981726	23982279	554
ENSG00000(	1.035792	8.430014	5.277655	6.74168	9.20432	12.32947	-0.8524	0.31349	0.43991	CTD-3128G	chr19	-	6748304	6751478	686
ENSG00000(	1.035792	2.408575	0	0	7.363456	0.821965	-0.79662	0.53589	0.66008	AC011755.	chr2	+	1.34E+08	1.34E+08	2049
ENSG00000(	7.250543	16.86003	7.916483	8.988907	15.64734	13.15144	-0.22124	0.74196	0.82779	AC008982.	chr19	-	39335369	39336139	493
ENSG00000(	38.3243	25.29004	31.66593	5.243529	32.21512	18.90519	0.73815	0.18575	0.29022	AC096677.	chr1	+	2.02E+08	2.02E+08	726
ENSG00000(	27.96638	22.88147	11.87472	6.74168	9.20432	11.50751	1.1396	0.061927	0.11674	CTD-2192J	chr19	-	12636534	12691789	5857
ENSG00000(	2.071584	1.204288	0	2.247227	0	3.28786	-0.46532	0.72188	0.813	AC005197.	chr19	+	18992489	18994185	683
ENSG00000(	21.75163	10.83859	25.06886	5.992604	12.88605	11.50751	0.87984	0.15644	0.25249	AC007228.	chr19	-	57056935	57078780	2045
ENSG00000(	6.214751	2.408575	0	0	0	0	2.4198	0.073366	0.13503	RP11-13J1(	chr2	+	1.05E+08	1.06E+08	443
ENSG00000(	215.4447	205.9332	199.2315	286.1469	168.4391	222.7525	-0.12744	0.55821	0.67875	RP11-145N	chr3	-	1.79E+08	1.79E+08	2089
ENSG00000(	2.071584	4.817151	3.958241	0	1.840864	0	1.7818	0.15364	0.24901	AC006262.	chr19	-	46667150	46683904	612
ENSG00000(	22.78742	24.08575	32.98534	8.239831	23.0108	9.041614	0.95224	0.088796	0.15894	RP11-345P	chr1	+	1603429	1604850	1422
ENSG00000(	0	2.408575	0	0.749076	0	0	0.55104	0.6711	NA	AC009060.	chr16	-	70239303	70239683	381
ENSG00000(	1.035792	0	0	0.749076	0	0.821965	-0.11768	0.9281	NA	AL589739.	chr1	+	2258581	2259042	462
ENSG00000(	2.071584	0	0	0	0.920432	0.821965	0.13309	0.92108	NA	CTD-3105H	chr19	-	12543917	12595630	588
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	EXOSC3P2	chr19	-	7878501	7879311	497
ENSG00000(	25.8948	30.10719	21.11062	44.94453	37.73771	43.56414	-0.69326	0.091494	0.163	RP11-178G	chr10	+	75880800	75881121	322
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CTD-2542C	chr19	+	20874142	20880421	2737
ENSG00000(	17.60846	15.65574	14.51355	5.992604	3.681728	14.79537	0.8976	0.18822	0.29316	FLJ20306	chr7	+	6522922	6524873	1952
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	GOLGA7B	chr10	+	99627889	99631294	3406
ENSG00000(	7.250543	4.817151	1.319414	5.992604	0.920432	2.465895	0.4218	0.68481	0.78423	AC010642.	chr19	+	58830643	58831855	1213
ENSG00000(	0	0	0	2.996302	0.920432	1.64393	-1.649	0.22411	NA	AC092782.	chr1	+	2.43E+08	2.43E+08	63
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	AC005795.	chr19	-	42027403	42028349	894
ENSG00000(	2.071584	1.204288	1.319414	2.996302	0	3.28786	-0.31802	0.79862	0.86878	CTD-3001H	chr19	-	48118956	48129652	547

ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	SCGB2B3P	chr19	+	35136567	35136975	409
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTC-273B1	chr19	-	49016464	49016917	454
ENSG00000(	4.143168	6.021439	5.277655	2.996302	12.88605	11.50751	-0.7351	0.37966	0.51038	CTD-2278I:	chr19	-	17407005	17407504	500
ENSG00000(	512.717	659.9497	738.8717	62.92235	202.495	113.4312	2.2644	1.48E-06	6.03E-06	KCNQ1OT1	chr11	-	2629558	2721224	91667
ENSG00000(	93.22127	87.913	65.97069	763.308	821.0253	941.1498	-3.3295	5.78E-73	2.65E-71	CTD-3099C	chr19	-	53153690	53156537	2848
ENSG00000(	2.071584	1.204288	0	0	1.840864	0	0.43378	0.74914	NA	AL669831.	chr1	-	738532	739137	129
ENSG00000(	3.107376	3.612863	1.319414	0.749076	5.522592	0	0.28563	0.81232	0.8783	AL627171.	chr14	+	50291993	50293258	1266
ENSG00000(	8.286335	4.817151	1.319414	15.73059	15.64734	22.19305	-1.7131	0.018121	0.039699	CTD-3018C	chr19	-	52892095	52901019	2732
ENSG00000(	3.107376	10.83859	5.277655	0	2.761296	4.109825	1.2289	0.23478	0.34897	CTD-3032J:	chr19	-	17288320	17289285	125
ENSG00000(	60.07593	38.53721	31.66593	241.2023	209.8585	211.245	-2.3071	9.60E-18	8.74E-17	RP11-15H2	chr19	-	23437855	23440741	2887
ENSG00000(	38.3243	38.53721	18.47179	6.74168	2.761296	7.397684	2.3568	8.81E-05	0.000289	CTC-490E2:	chr19	-	41337126	41343115	482
ENSG00000(	8.286335	4.817151	7.916483	6.74168	11.96562	7.397684	-0.27733	0.71865	0.81049	RP11-420K	chr19	+	21933549	21936240	2692
ENSG00000(	0	0	0	8.988907	1.840864	0.821965	-2.6458	0.044597	0.087944	RBL1	chr20	+	35724188	35725581	1394
ENSG00000(	3.107376	0	0	3.745378	0.920432	0.821965	-0.48423	0.71272	0.80579	AC012313.	chr19	+	58907457	58908407	951
ENSG00000(	180.2278	203.5246	216.3839	98.1289	183.166	193.9837	0.33507	0.18402	0.28813	EGLN2	chr19	+	41304901	41314338	3894
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	FKSG63	chr16	+	70258261	70258641	381
ENSG00000(	95.29286	115.6116	73.88717	90.63814	78.23672	114.2531	0.009264	0.97373	0.98475	CTD-2583A	chr19	-	58378406	58379540	679
ENSG00000(	8.286335	8.430014	0	2.247227	4.60216	1.64393	0.82149	0.43089	0.56079	CTD-2587H	chr19	-	54949192	54949528	337
ENSG00000(	3.107376	7.225726	0	0	4.60216	0	0.81771	0.5177	0.64399	AL353583.	chr10	-	24770273	24770632	360
ENSG00000(	1.035792	0	0	0.749076	0	0	0.1572	0.90001	NA	RP11-266J(	chr3	-	9854446	9854781	336
ENSG00000(	1.035792	3.612863	0	3.745378	1.840864	4.109825	-0.78727	0.50502	0.63277	RP11-477H	chr1	+	1.65E+08	1.65E+08	715
ENSG00000(	8.286335	13.24716	9.235896	1.498151	9.20432	11.50751	0.43366	0.58258	0.70023	RP5-1139B	chr1	-	2.28E+08	2.28E+08	3955
ENSG00000(	1.035792	0	1.319414	0	0	1.64393	0.22525	0.86714	NA	ARHGAP19	chr10	-	98757795	99052413	8956
ENSG00000(	8.286335	7.225726	6.597069	3.745378	3.681728	0	1.3356	0.17091	0.27142	RP4-761J14	chr12	+	6852151	6852807	657
ENSG00000(	823.4546	920.0758	564.7091	674.9171	582.6335	772.647	0.18508	0.30069	0.42568	SNHG8	chr4	+	1.19E+08	1.19E+08	672
ENSG00000(	1.035792	2.408575	9.235896	3.745378	8.283888	5.753754	-0.43784	0.64687	0.75355	RP11-1020	chr3	+	9977390	9977942	553
ENSG00000(	0	0	2.638828	11.23613	15.64734	16.4393	-3.4236	0.000521	0.001528	AP000654.	chr11	+	86544110	86548657	1192
ENSG00000(	20.71584	9.634302	9.235896	28.46487	24.85166	11.50751	-0.66145	0.26922	0.38959	RP4-740C4	chr1	-	2281853	2284259	2407
ENSG00000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	RP11-568J:	chr16	+	85776893	85777831	498
ENSG00000(	31.07376	27.69862	43.54065	9.737982	0.920432	6.575719	2.4008	8.51E-05	0.00028	RP11-589N	chr8	-	11703663	11703900	238
ENSG00000(	433.9968	573.241	905.1179	1.498151	254.0392	258.097	1.4745	0.19059	0.29602	RP11-331F	chr9	-	35657748	35658015	268
ENSG00000(	9.322127	2.408575	2.638828	2.996302	0	1.64393	1.2631	0.25967	0.37846	RP11-178L	chr16	+	87396142	87401082	450
ENSG00000(	14.50109	4.817151	9.235896	2.247227	3.681728	4.93179	1.2519	0.14107	0.23226	RP6-99M1.	chrX	-	45624175	45624702	528
ENSG00000(	5.17896	8.430014	2.638828	5.243529	3.681728	5.753754	0.12939	0.88608	0.92899	RP11-571N	chr12	+	58208277	58208709	433
ENSG00000(	1.035792	0	2.638828	0	0.920432	0.821965	0.5719	0.67274	NA	MAP2K4P1	chrX	-	72744111	72782921	2539
ENSG00000(	16.57267	16.86003	9.235896	26.96672	19.32907	23.83698	-0.68131	0.20843	0.31796	RP11-248J:	chr14	-	51129229	51129896	668
ENSG00000(	2.071584	10.83859	6.597069	2.996302	4.60216	0.821965	1.0219	0.29867	0.42365	RP11-330N	chr9	+	99672358	99672687	330
ENSG00000(	5.17896	12.04288	5.277655	7.490755	17.48821	13.15144	-0.69849	0.33579	0.46405	RP11-73M:	chr14	-	1.04E+08	1.04E+08	535
ENSG00000(	0	0	0	2.996302	0	2.465895	-1.5141	0.2635	NA	FAM226A	chrX	+	71997432	71998921	1490
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTC-1337H	chr11	+	67227339	67227784	446
ENSG00000(	0	0	0	0.749076	3.681728	4.109825	-2.2232	0.096575	0.17043	AP006621.	chr11	-	708564	727047	532
ENSG00000(	0	3.612863	0	0	0.920432	0	0.81649	0.54246	NA	RP11-193N	chr12	+	85657322	85658235	914
ENSG00000(	130.5098	122.8373	85.7619	180.5272	102.168	206.3132	-0.52101	0.063921	0.12001	AF131215.	chr8	-	10962201	10964214	2014
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP1-134E1	chr6	+	1.07E+08	1.07E+08	454

ENSG00000(	0	0	0	0	5.522592	0.821965	-1.658	0.22147	0.33315	RP11-646I(	chr4	+	57253791	57254319	529
ENSG00000(	10.35792	4.817151	5.277655	4.494453	0.920432	0.821965	1.4206	0.15474	0.25026	RP11-214K	chr12	+	1.25E+08	1.25E+08	2835
ENSG00000(	6.214751	9.634302	5.277655	1.498151	7.363456	4.109825	0.63208	0.47921	0.60832	RP11-697N	chr8	+	48439959	48440710	752
ENSG00000(	13.46529	12.04288	5.277655	7.490755	13.80648	10.68554	-0.03468	0.96036	0.97695	RP3-467L1	chr1	+	7836443	7836835	393
ENSG00000(	2.071584	4.817151	6.597069	10.48706	4.60216	8.219649	-0.72117	0.40631	0.53718	RP11-849F	chr17	-	8128139	8128798	660
ENSG00000(	7.250543	2.408575	1.319414	7.490755	3.681728	4.109825	-0.38457	0.6949	0.79211	RP11-2B6.2	chr9	+	96938740	96940174	1435
ENSG00000(	0	3.612863	0	0	0	1.64393	0.50971	0.70603	NA	RP11-932C	chr15	+	30909161	30909952	792
ENSG00000(	46.61064	38.53721	38.263	131.0882	122.4175	157.8173	-1.7128	2.21E-09	1.17E-08	RP5-1086D	chr15	+	31061535	31065196	3662
ENSG00000(	0	0	0	1.498151	2.761296	4.109825	-2.2203	0.096571	0.17043	RP3-333A1	chr1	-	71471537	71472185	649
ENSG00000(	0	4.817151	2.638828	1.498151	0	0	1.3243	0.31937	0.4465	RP5-1139B	chr1	-	2.28E+08	2.28E+08	1483
ENSG00000(	0	0	0	4.494453	1.840864	0.821965	-1.9797	0.14229	0.23373	RP11-482N	chr16	-	87634132	87635796	1665
ENSG00000(	180.2278	202.3203	150.4132	13.48336	12.88605	11.50751	3.7588	5.24E-31	8.24E-30	hsa-mir-14!	chr5	+	1.49E+08	1.49E+08	2549
ENSG00000(	17.60846	14.45145	17.15238	5.243529	9.20432	2.465895	1.4416	0.039667	0.079435	RP11-20I23	chr16	-	2611472	2615097	3626
ENSG00000(	4.143168	6.021439	18.47179	0	0.920432	1.64393	2.8266	0.00666	0.016086	RP11-214K	chr12	-	1.24E+08	1.24E+08	557
ENSG00000(	9.322127	14.45145	10.55531	14.23244	12.88605	15.61733	-0.30225	0.62699	0.73809	RP11-73M2	chr14	+	1.04E+08	1.04E+08	611
ENSG00000(	1.035792	1.204288	0	2.247227	2.761296	4.109825	-1.3748	0.26832	0.38862	RP11-29B2	chr13	+	1.03E+08	1.03E+08	533
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP6-91H8.!	chr14	+	71685817	71689441	3625
ENSG00000(	15.53688	16.86003	9.235896	1.498151	1.840864	8.219649	1.671	0.037602	0.075849	RP11-2B6.3	chr9	+	96928571	96962909	235
ENSG00000(	17.60846	8.430014	11.87472	17.97781	11.04518	15.61733	-0.21879	0.72361	0.81433	RP11-849F	chr17	+	8181081	8181754	674
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-248J2	chr10	+	97709725	97744785	2133
ENSG00000(	4.143168	3.612863	2.638828	7.490755	2.761296	4.109825	-0.39648	0.68463	0.78423	RP11-738E	chr4	-	57827093	57827539	447
ENSG00000(	0	9.634302	1.319414	0	0	0	2.7114	0.043528	0.086161	AP000962.	chr21	-	17947038	17954957	729
ENSG00000(	3.107376	10.83859	9.235896	11.98521	11.04518	12.32947	-0.57767	0.42491	0.55538	RP11-797A	chr15	-	77359996	77360667	672
ENSG00000(	2.071584	3.612863	6.597069	7.490755	1.840864	0.821965	0.19871	0.84992	0.90441	RP11-324I2	chr10	+	35499344	35499678	335
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-148C	chr8	-	11409997	11410500	504
ENSG00000(	13.46529	3.612863	10.55531	5.992604	11.04518	3.28786	0.41302	0.60754	0.72173	MKNK1-AS2	chr1	+	47004368	47035927	2445
ENSG00000(	232.0174	197.5032	189.9956	307.8701	315.7082	467.698	-0.81003	7.90E-05	0.000261	RP11-73M2	chr14	+	1.04E+08	1.04E+08	811
ENSG00000(	20.71584	18.06432	13.19414	2.996302	9.20432	14.79537	0.89446	0.18206	0.28544	hsa-mir-12!	chr19	-	52188616	52196709	3962
ENSG00000(	2.071584	0	1.319414	2.996302	0	2.465895	-0.43488	0.73927	0.82538	CTD-2033C	chr5	-	65220457	65220963	507
ENSG00000(	0	0	0	10.48706	11.96562	17.26126	-4.5875	5.75E-05	0.000194	RP13-238F	chr10	-	1.26E+08	1.26E+08	537
ENSG00000(	14.50109	20.47289	15.83297	60.67512	62.58938	50.13986	-1.7311	3.13E-05	0.000109	RP11-73M2	chr14	+	1.04E+08	1.04E+08	683
ENSG00000(	0	0	2.638828	0	1.840864	0	0.2163	0.87177	NA	RP11-321C	chr6	+	78400375	78636691	4800
ENSG00000(	5.17896	0	0	0.749076	0	0	1.2383	0.36072	NA	RP11-24B1	chr13	-	51935701	51936371	671
ENSG00000(	2.071584	4.817151	9.235896	4.494453	3.681728	1.64393	0.58769	0.54854	0.67015	RP11-84A1	chr1	-	32317514	32387442	587
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP3-426I6.	chr1	+	28100369	28100552	184
ENSG00000(	61.11172	89.11729	68.60952	90.63814	91.12277	79.7306	-0.25608	0.37044	0.50094	RP11-95D1	chr2	+	10076489	10079719	3231
ENSG00000(	19.68005	9.634302	10.55531	25.46857	15.64734	55.07165	-1.2004	0.03713	0.075007	RP11-932C	chr15	+	30941000	30941732	733
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-58B1	chr3	-	9540045	9541253	1209
ENSG00000(	0	0	1.319414	0.749076	0	0.821965	-0.12362	0.92519	NA	RP11-130L	chr2	-	20786008	20786446	439
ENSG00000(	0	0	0	2.247227	0.920432	2.465895	-1.668	0.21871	NA	RP11-338N	chr1	-	7760764	7761030	267
ENSG00000(	27.96638	22.88147	40.90183	29.21395	34.97642	33.70056	-0.09499	0.8247	0.88676	RP11-498E	chr9	+	1.25E+08	1.25E+08	708
ENSG00000(	7.250543	8.430014	2.638828	0.749076	1.840864	0	2.222	0.04577	0.089918	RP11-282C	chr12	+	1.24E+08	1.24E+08	343
ENSG00000(	51.7896	48.17151	47.4989	26.21764	34.97642	40.27628	0.53258	0.15577	0.25169	RP11-1020	chr3	+	10000401	10004223	3823
ENSG00000(	0	4.817151	0	0	0	1.64393	0.75293	0.57891	0.69728	RP11-497H	chr5	+	69745463	69746180	718

ENSG00000(	16.57267	14.45145	15.83297	15.73059	21.16994	18.90519	-0.23757	0.6638	0.76786	RP11-362K	chr3	-	1.69E+08	1.69E+08	3143
ENSG00000(	6.214751	1.204288	2.638828	2.247227	1.840864	0	0.9664	0.41756	0.54825	RP1-232P2	chr6	-	5451916	5458308	1291
ENSG00000(	164.6909	146.9231	149.0938	80.90016	76.39586	74.79881	0.98212	3.35E-05	0.000116	CTD-3074C	chr11	-	66303369	66305407	2039
ENSG00000(	0	0	5.277655	0.749076	0	1.64393	0.6159	0.64721	0.75384	RP11-521C	chr10	-	52102202	52102561	360
ENSG00000(	0	0	0	0	2.761296	3.28786	-1.6293	0.2296	0.34285	AF003625.	chrX	+	1.5E+08	1.5E+08	470
ENSG00000(	6.214751	18.06432	15.83297	20.97412	21.16994	14.79537	-0.49218	0.40832	0.53911	RP11-276H	chr9	-	89623370	89657041	2012
ENSG00000(	221.6595	243.2661	225.6198	455.4379	323.9921	316.4565	-0.66475	0.000533	0.00156	RP11-343N	chr1	+	1.21E+08	1.21E+08	1326
ENSG00000(	5.17896	2.408575	10.55531	2.996302	4.60216	2.465895	0.72549	0.44465	0.57419	RP11-214K	chr12	-	1.24E+08	1.24E+08	553
ENSG00000(	0	1.204288	0	0	0	0.821965	0.1572	0.90001	NA	RP11-272L	chr1	-	98399030	98407302	870
ENSG00000(	3.107376	6.021439	5.277655	8.239831	5.522592	0.821965	-0.02523	0.97911	0.98785	CTD-3185P	chr15	-	66780996	66781427	432
ENSG00000(	7.250543	0	3.958241	5.243529	2.761296	8.219649	-0.43419	0.66707	0.77051	RP3-449M8	chr14	-	74938633	74939063	431
ENSG00000(	6.214751	13.24716	5.277655	0	4.60216	4.109825	1.3006	0.17608	0.27799	RP11-218C	chr20	-	23612463	23612953	491
ENSG00000(	0	0	0	16.47966	13.80648	9.863579	-4.605	5.28E-05	0.000179	RP11-93H1	chr10	+	87403830	87407823	2619
ENSG00000(	9.322127	10.83859	1.319414	8.239831	0.920432	9.863579	0.15408	0.86557	0.91516	RP11-178L	chr16	+	87351115	87351643	395
ENSG00000(	2.071584	1.204288	0	0	5.522592	1.64393	-0.701	0.58725	0.70444	RP1-127C7	chr1	-	1.84E+08	1.84E+08	646
ENSG00000(	0	1.204288	0	0.749076	5.522592	3.28786	-1.835	0.1575	0.2538	CTD-2132N	chr17	-	40190250	40190752	503
ENSG00000(	0	1.204288	1.319414	0	0.920432	3.28786	-0.43245	0.74748	0.83213	ZNF177	chr19	+	9434850	9493293	2470
ENSG00000(	24.85901	34.92434	18.47179	20.22504	34.05598	58.35951	-0.50416	0.2961	0.42053	LL0XNC01-	chrX	+	49129517	49132231	2715
ENSG00000(	62.14751	83.09585	80.48424	50.93714	73.63456	41.92021	0.43374	0.18496	0.28944	RP11-540B	chr15	+	31218717	31220610	1894
ENSG00000(	0	0	1.319414	0.749076	0	0	0.1572	0.90001	NA	RP11-932C	chr15	-	30899898	30900396	499
ENSG00000(	15.53688	27.69862	14.51355	31.46117	29.45382	19.72716	-0.46536	0.35792	0.48749	RP3-462E2	chr12	+	1.12E+08	1.12E+08	571
ENSG00000(	13.46529	10.83859	15.83297	2.996302	11.04518	15.61733	0.41046	0.55825	0.67876	RP11-141B	chr2	-	1.15E+08	1.15E+08	1548
ENSG00000(	9.322127	14.45145	7.916483	10.48706	2.761296	0.821965	1.0236	0.23281	0.34648	RP11-463C	chr16	-	86553989	86557503	3515
ENSG00000(	4.143168	3.612863	1.319414	2.247227	0.920432	0	1.0795	0.3775	0.50821	CTC-203F4.	chr5	+	1.35E+08	1.35E+08	2017
ENSG00000(	2.071584	2.408575	0	0.749076	1.840864	2.465895	-0.10008	0.93698	0.96179	RNU12	chr22	+	43011250	43011913	664
ENSG00000(	0	2.408575	1.319414	0	0	0	1.2548	0.34239	NA	SGKL	chr8	+	67579831	67772707	2949
ENSG00000(	37.28851	30.10719	19.79121	13.48336	5.522592	8.219649	1.5951	0.004919	0.012201	RP11-380L	chr12	-	1.24E+08	1.24E+08	623
ENSG00000(	3.107376	4.817151	0	0	0.920432	0	1.7827	0.18128	0.28443	RP11-326C	chr11	-	325703	326294	592
ENSG00000(	2.071584	0	1.319414	0	0	1.64393	0.51016	0.70682	NA	RP3-426I6.	chr1	+	28146494	28146852	359
ENSG00000(	4.143168	4.817151	3.958241	0	0	0	3.2125	0.01292	0.029275	C12ORF55	chr12	+	97041753	97269333	5096
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	RP11-338N	chr1	-	7758363	7758932	570
ENSG00000(	0	0	0	0	0.920432	4.109825	-1.3831	0.30514	NA	RP11-685G	chr15	+	76635983	76636706	724
ENSG00000(	11.39371	22.88147	14.51355	12.73428	14.72691	13.15144	0.24903	0.67348	0.77563	RP11-571N	chr12	+	58197621	58198198	578
ENSG00000(	1.035792	0	1.319414	1.498151	0	0	0.26794	0.842	NA	RP11-416A	chr1	+	39672184	39672629	446
ENSG00000(	89.0781	74.66584	43.54065	32.95932	26.69253	37.81039	1.0715	0.004116	0.010375	LL22NC03-	chr22	-	24080865	24081476	612
ENSG00000(	5.17896	3.612863	7.916483	0	1.840864	0.821965	2.0756	0.064684	0.12117	RP11-214K	chr12	-	1.24E+08	1.24E+08	263
ENSG00000(	5.17896	10.83859	6.597069	3.745378	14.72691	17.26126	-0.6013	0.42964	0.55973	RP11-297D	chr16	+	67515217	67521153	696
ENSG00000(	2.071584	0	0	2.247227	0	0	-0.04193	0.97501	NA	WI2-80269	chrX	+	1.51E+08	1.51E+08	435
ENSG00000(	99.43602	108.3859	68.60952	44.94453	45.10117	50.96182	0.96147	0.001875	0.005023	CTD-3092A	chr15	+	30780166	30782516	2351
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-88H1	chr3	-	65344943	65345392	450
ENSG00000(	12.4295	9.634302	5.277655	9.737982	11.04518	9.041614	-0.10295	0.88492	0.92814	RP11-390K	chr11	-	47189832	47191114	574
ENSG00000(	4.143168	15.65574	9.235896	10.48706	1.840864	5.753754	0.59155	0.47545	0.60463	RP11-214K	chr12	-	1.24E+08	1.24E+08	355
ENSG00000(	8.286335	7.225726	3.958241	10.48706	12.88605	12.32947	-0.79277	0.27593	0.39743	RP11-248J	chr14	-	51190495	51190990	496
ENSG00000(	20.71584	22.88147	91.03955	3.745378	28.53339	14.79537	1.4357	0.021364	0.046028	SCARNA2	chr1	+	1.1E+08	1.1E+08	427

ENSG00000(	12.4295	24.08575	21.11062	26.96672	11.04518	15.61733	0.084611	0.88131	0.9258	CTC-487M2	chr5	+	1.12E+08	1.12E+08	669
ENSG00000(	0	0	0	2.996302	0	2.465895	-1.5141	0.2635	NA	RP4-761J14	chr12	+	6832399	6832853	455
ENSG00000(	78.72018	92.73015	110.8308	134.8336	68.11197	100.2797	-0.10978	0.71227	0.8055	RP6-99M1.	chrX	-	45604639	45629677	1758
ENSG00000(	0	8.430014	2.638828	0	0	0	2.7587	0.039401	0.078949	AP001172.	chr21	-	17664112	17680454	581
ENSG00000(	2.071584	2.408575	13.19414	1.498151	1.840864	1.64393	1.4666	0.1658	0.26453	RP11-750H	chr11	-	47535157	47536441	430
ENSG00000(	8.286335	3.612863	0	28.46487	16.56778	18.90519	-2.176	0.003549	0.009054	AF131215.	chr8	+	11060474	11061180	707
ENSG00000(	2.071584	0	0	2.247227	0	0.821965	-0.26399	0.84571	NA	KB-1958F4	chr8	+	98156398	98156951	554
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AC004152.	chr19	-	2287163	2287942	780
ENSG00000(	356.3124	399.8235	310.0622	934.8463	721.6187	885.2562	-1.2487	3.99E-15	3.17E-14	RP5-935K1	chr2	-	1.29E+08	1.29E+08	2135
ENSG00000(	14.50109	3.612863	10.55531	7.490755	3.681728	13.15144	0.21718	0.78122	0.85595	RP1-257I2(	chr22	-	42485634	42486032	399
ENSG00000(	21.75163	15.65574	17.15238	17.97781	17.48821	27.94681	-0.2046	0.69727	0.79394	GAS5-AS1	chr1	+	1.74E+08	1.74E+08	694
ENSG00000(	11.39371	1.204288	11.87472	19.47596	11.04518	16.4393	-0.87023	0.2256	0.33832	RP11-78O7	chr17	-	19799903	19800600	681
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-318K	chr9	+	66836662	66836791	130
ENSG00000(	4.143168	2.408575	13.19414	0	0	0	3.815	0.00229	0.00604	AP000473.	chr21	+	18015848	18017384	1537
ENSG00000(	0	1.204288	0	0.749076	3.681728	3.28786	-1.5826	0.22997	0.34327	RP11-214K	chr12	-	1.24E+08	1.24E+08	258
ENSG00000(	0	4.817151	0	2.996302	1.840864	0	-0.00966	0.99417	0.99629	LA16c-380I	chr16	+	3049903	3050390	346
ENSG00000(	23.82321	21.67718	17.15238	38.95193	16.56778	32.8786	-0.48061	0.33238	0.46047	RP11-24B1	chr13	-	51936795	51937579	785
ENSG00000(	8.286335	6.021439	0	10.48706	18.40864	6.575719	-1.1345	0.18072	0.28367	RP11-498E	chr9	+	1.25E+08	1.25E+08	477
ENSG00000(	0	0	1.319414	0	1.840864	1.64393	-0.68367	0.61391	NA	RNU11	chr1	+	28975112	28975242	131
ENSG00000(	1.035792	4.817151	0	0	0	0	1.8349	0.17548	NA	RP11-245P	chr1	-	2.29E+08	2.29E+08	574
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-326C	chr11	-	322186	322727	386
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	TRAX	chr1	+	2.32E+08	2.32E+08	3557
ENSG00000(	44.53905	34.92434	31.66593	17.97781	34.05598	36.98842	0.32081	0.46125	0.59062	RP11-73M1	chr14	+	1.04E+08	1.04E+08	552
ENSG00000(	8.286335	4.817151	6.597069	21.72319	11.04518	14.79537	-1.181	0.087267	0.15678	RP11-393N	chr4	+	57330324	57330745	422
ENSG00000(	6.214751	13.24716	22.43003	0	11.04518	7.397684	1.0619	0.2083	0.3178	RP5-1139B	chr1	-	2.28E+08	2.28E+08	764
ENSG00000(	5.17896	0	0	0.749076	2.761296	0	0.36031	0.78732	0.86067	RP11-742D	chr18	+	44336450	44344371	4685
ENSG00000(	1.035792	6.021439	1.319414	0.749076	7.363456	3.28786	-0.34417	0.75491	0.83789	RP11-415J	chr1	+	33726813	33727281	469
ENSG00000(	7.250543	4.817151	19.79121	8.239831	2.761296	4.109825	0.94268	0.25235	0.37009	AP001429.	chr21	+	38473114	38473643	530
ENSG00000(	10.35792	7.225726	7.916483	1.498151	0.920432	2.465895	2.034	0.031878	0.065541	RP11-118F	chr16	-	85613615	85617177	601
ENSG00000(	0	0	1.319414	0	1.840864	4.109825	-1.1757	0.38375	0.51441	RP11-501C	chr17	-	47082093	47089888	160
ENSG00000(	12.4295	26.49433	6.597069	14.98151	17.48821	9.863579	0.10322	0.87153	0.91931	RP11-526I2	chr15	-	1.01E+08	1.01E+08	2387
ENSG00000(	7.250543	10.83859	7.916483	0	8.283888	1.64393	1.2095	0.20856	0.31805	RP11-214K	chr12	-	1.24E+08	1.24E+08	528
ENSG00000(	0	0	2.638828	8.988907	2.761296	0	-1.4563	0.25377	0.37178	KB-1043D8	chr8	-	97152800	97153172	373
ENSG00000(	0	2.408575	2.638828	0.749076	3.681728	0.821965	-0.04529	0.97142	0.9834	CTC-303L1.	chr5	-	93947611	93953827	409
ENSG00000(	1.035792	0	0	2.996302	0	3.28786	-1.3271	0.32516	0.45269	CTC-137K3	chr8	+	1.34E+08	1.34E+08	725
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	AP001172.	chr21	-	17789459	17791400	467
ENSG00000(	0	7.225726	1.319414	0	2.761296	1.64393	0.66313	0.59817	0.71374	RP5-1021I2	chr14	+	74371970	74372339	370
ENSG00000(	22.78742	26.49433	62.01245	4.494453	12.88605	14.79537	1.7092	0.002688	0.007008	TERC	chr3	-	1.69E+08	1.69E+08	541
ENSG00000(	53.86118	43.35436	47.4989	80.90016	74.55499	79.7306	-0.68929	0.025614	0.054111	AC004257.	chr19	-	15346330	15346819	490
ENSG00000(	4.143168	10.83859	7.916483	92.13629	63.50981	84.66239	-3.3085	1.85E-12	1.24E-11	CTD-2267D	chr17	+	38459457	38460909	1453
ENSG00000(	4.143168	0	0	0	0.920432	0.821965	0.66373	0.62457	NA	RP11-646I(	chr4	+	57262478	57263037	560
ENSG00000(	0	0	0	1.498151	4.60216	4.109825	-2.5071	0.057215	0.10924	F11R	chr1	-	1.61E+08	1.61E+08	2096
ENSG00000(	9.322127	0	5.277655	3.745378	7.363456	5.753754	-0.15975	0.86881	0.91759	RP11-419I1	chr8	+	12333971	12334631	661
ENSG00000(	27.96638	14.45145	11.87472	26.21764	12.88605	21.37109	-0.14137	0.80127	0.87069	RP5-1172N	chrX	+	41095109	41095832	724

ENSG00000(	10.35792	6.021439	6.597069	8.988907	1.840864	1.64393	0.75759	0.40249	0.53363	RP5-894A1	chr7	-	1.41E+08	1.41E+08	925
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP11-568J:	chr16	+	85826021	85826539	408
ENSG00000(	0	2.408575	0	26.21764	22.09037	40.27628	-4.4812	5.13E-07	2.20E-06	AC006129.	chr19	+	42041545	42043266	1718
ENSG00000(	4.143168	15.65574	11.87472	2.996302	0.920432	2.465895	1.9897	0.027424	0.057496	RP11-167P	chr16	-	67772491	67773825	569
ENSG00000(	1.035792	4.817151	2.638828	0	1.840864	6.575719	0.005485	0.99625	0.99765	LA16c-380I	chr16	+	3051301	3052017	491
ENSG00000(	0	2.408575	5.277655	0	0	1.64393	1.3035	0.32586	0.45353	CTC-1337H	chr11	-	67229181	67229791	611
ENSG00000(	395.6725	370.9206	263.8828	576.0391	438.1256	536.7431	-0.58516	0.001406	0.003844	RP11-21N3	chr3	+	1.97E+08	1.97E+08	918
ENSG00000(	35.21692	25.29004	43.54065	65.91865	67.19154	66.57916	-0.92748	0.008641	0.020391	RP5-1024G	chr1	-	53708036	53710212	2177
ENSG00000(	1.035792	0	2.638828	1.498151	0	3.28786	-0.25391	0.84688	0.90246	RP11-382B	chr15	-	30649969	30650976	1008
ENSG00000(	3.107376	0	2.638828	0	1.840864	0	0.94811	0.4804	0.60954	RP1-256G2	chr6	-	5665218	5695505	806
ENSG00000(	0	10.83859	6.597069	23.22134	7.363456	10.68554	-1.1354	0.17431	0.27595	RP11-793H	chr12	-	53893946	53894720	775
ENSG00000(	7.250543	9.634302	2.638828	7.490755	3.681728	4.93179	0.24664	0.77658	0.85305	CTD-2410N	chr5	+	1.34E+08	1.34E+08	1418
ENSG00000(	3.107376	0	2.638828	2.247227	0	4.109825	-0.10344	0.93418	0.96038	RP11-494H	chr3	+	1.8E+08	1.8E+08	304
ENSG00000(	14.50109	2.408575	0	1.498151	6.443024	4.109825	0.43276	0.67771	0.779	RP11-159N	chr11	+	1.13E+08	1.13E+08	640
ENSG00000(	11.39371	6.021439	3.958241	6.74168	15.64734	13.15144	-0.65023	0.38214	0.51287	RP11-568J:	chr16	+	85817988	85821223	689
ENSG00000(	112.9013	140.9017	113.4696	53.93344	57.06678	78.08667	0.94763	0.000598	0.001736	RP11-258C	chrX	+	53198279	53200096	1818
ENSG00000(	2.071584	2.408575	0	0.749076	8.283888	1.64393	-0.8891	0.45715	0.58691	RP11-803D	chr2	-	1.12E+08	1.12E+08	606
ENSG00000(	12.4295	16.86003	13.19414	21.72319	19.32907	22.19305	-0.55286	0.30878	0.43486	RP11-572C	chr4	+	1714548	1715349	802
ENSG00000(	0	0	0	2.247227	1.840864	0.821965	-1.4859	0.2733	NA	RP11-550A	chr7	+	29591137	29591767	631
ENSG00000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP11-172C	chr11	+	1.14E+08	1.14E+08	508
ENSG00000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-157E	chr3	-	7648577	7649584	1008
ENSG00000(	12.4295	15.65574	2.638828	7.490755	0	4.109825	1.2037	0.19294	0.29878	RP11-373D	chr2	+	28648812	28649586	775
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP11-325L	chr15	+	65318426	65319014	589
ENSG00000(	32.10955	37.33292	25.06886	26.96672	30.37426	13.9734	0.3979	0.39765	0.5287	RP13-36G1	chrX	-	73229224	73231303	905
ENSG00000(	10.35792	13.24716	3.958241	16.47966	15.64734	19.72716	-0.84672	0.18862	0.29361	RP11-453E	chr4	-	68584714	68589980	2046
ENSG00000(	5.17896	2.408575	0	0	0	3.28786	0.77394	0.5537	0.67456	RP11-265B	chr9	-	71722842	71723133	292
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP11-381K	chr5	-	1.37E+08	1.37E+08	501
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-123J:	chr4	-	77807182	77807523	342
ENSG00000(	31.07376	16.86003	36.94359	9.737982	45.10117	29.59074	0.014067	0.97917	0.98787	RP11-701H	chr15	+	25287065	25287575	511
ENSG00000(	9.322127	6.021439	3.958241	2.247227	4.60216	1.64393	1.0348	0.2764	0.39794	CTC-471J1.	chr19	-	52613571	52613979	409
ENSG00000(	3.107376	0	0	1.498151	0	0	0.45456	0.7352	NA	RP11-420B	chr8	+	18859137	18859460	324
ENSG00000(	0	4.817151	2.638828	0	2.761296	7.397684	-0.33758	0.77758	0.85348	RP11-17P1	chr4	+	68503895	68504077	183
ENSG00000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	DUXAP4	chr10	+	45551104	45551716	613
ENSG00000(	0	1.204288	3.958241	2.996302	3.681728	9.041614	-1.3021	0.23844	0.35335	NDUFB8P2	chr17	+	57962376	57962913	538
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-731D	chr4	-	1.52E+08	1.52E+08	540
ENSG00000(	3.107376	4.817151	2.638828	2.996302	0	0	1.2575	0.30626	0.43185	RP11-697H	chr11	+	63399705	63400192	488
ENSG00000(	1.035792	1.204288	0	1.498151	5.522592	4.93179	-1.6944	0.16092	0.25835	CTC-559E9.	chr19	-	19981532	19982108	577
ENSG00000(	4.143168	9.634302	2.638828	4.494453	1.840864	7.397684	0.21711	0.81705	0.88148	RP11-65L3	chr2	+	1.79E+08	1.79E+08	1798
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP5-1115A	chr1	+	8572712	8573080	369
ENSG00000(	2.071584	2.408575	2.638828	0	0	0	2.2753	0.091747	0.16332	RP11-1029	chr3	+	48080757	48080980	224
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-453E	chr4	-	68590901	68592113	1213
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-59H1	chr12	-	12924285	12924639	355
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-554D	chr6	-	75239964	75443995	618
ENSG00000(	0	0	2.638828	1.498151	0	0	0.308	0.81734	NA	RP5-850E9	chr20	-	627270	656444	2714

ENSG00000(	0	3.612863	3.958241	2.247227	2.761296	4.93179	-0.32726	0.77107	0.84946	RP11-359E	chr10	-	1.22E+08	1.22E+08	1414
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-461L	chr4	-	1.53E+08	1.53E+08	410
ENSG00000(	1.035792	1.204288	0	1.498151	0	0	0.24225	0.85676	NA	CTC-786C1	chr16	-	85312426	85312641	216
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	GS1-165B1	chr7	-	7775374	7776482	1109
ENSG00000(	0	4.817151	0	0.749076	0	0	1.1462	0.39668	NA	RP11-697E	chr15	-	90825080	90825263	184
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP11-180P	chr17	-	61055855	61056202	348
ENSG00000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	CTC-559E9.	chr19	+	19967784	19968336	553
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP5-874C2	chr6	-	28287437	28287629	193
ENSG00000(	0	0	7.916483	3.745378	0.920432	3.28786	-0.03625	0.97625	0.98632	RP11-82L2	chr9	-	1.07E+08	1.07E+08	7020
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-642D	chr2	-	62576083	62577874	636
ENSG00000(	3.107376	8.430014	1.319414	8.988907	6.443024	7.397684	-0.72607	0.4137	0.54412	CTD-2506P	chr14	-	81725909	81726583	675
ENSG00000(	0	0	6.597069	7.490755	0.920432	0.821965	-0.37645	0.76099	0.84198	RP11-734K	chr12	+	89919431	89934079	338
ENSG00000(	36.25272	37.33292	36.94359	28.46487	10.12475	18.08323	0.92164	0.053534	0.10311	RP1-90J20.	chr6	+	3020388	3022984	2597
ENSG00000(	0	0	0	7.490755	3.681728	4.93179	-3.2203	0.010551	0.024397	RP11-436H	chr2	-	70883916	70885457	1542
ENSG00000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP11-547N	chr2	-	64435632	64435850	219
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	IGHV1OR15	chr15	-	22482836	22483268	348
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-307C	chr1	+	1.55E+08	1.55E+08	690
ENSG00000(	17.60846	15.65574	10.55531	17.22874	34.05598	20.54912	-0.66905	0.22288	0.33501	RP11-46B1	chr6	+	79943435	79946514	2946
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-384L	chr3	-	32285339	32285510	172
ENSG00000(	2.071584	1.204288	1.319414	2.247227	2.761296	0	-0.07498	0.95291	0.97194	RP11-315D	chr4	-	1.49E+08	1.49E+08	858
ENSG00000(	0	0	3.958241	0	0	0.821965	0.91937	0.49384	NA	AC000095.	chr22	-	19005556	19006429	874
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-1407	chr17	+	36333639	36333776	138
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	CTC-412M1	chr19	+	19819774	19821274	617
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-208G	chr7	+	1.52E+08	1.52E+08	253
ENSG00000(	4.143168	0	2.638828	2.996302	0.920432	0	0.52312	0.68295	0.78312	JAG1	chr20	-	10625847	10627014	568
ENSG00000(	4.143168	0	3.958241	0.749076	0.920432	3.28786	0.51514	0.67117	0.77381	RP11-44D5	chr3	+	15773759	15774977	830
ENSG00000(	19.68005	18.06432	17.15238	11.23613	11.04518	18.08323	0.42436	0.45703	0.58686	CAHM	chr6	-	1.64E+08	1.64E+08	896
ENSG00000(	0	0	2.638828	5.992604	0.920432	0	-0.85605	0.51979	0.64576	RP11-351C	chr10	+	65118505	65118864	360
ENSG00000(	0	0	3.958241	0.749076	3.681728	1.64393	-0.42204	0.74435	0.82968	RP11-1348	chr16	-	28761280	28761916	637
ENSG00000(	1.035792	0	1.319414	1.498151	4.60216	4.93179	-1.5742	0.19623	0.30293	RP11-326I2	chr4	-	1.85E+08	1.85E+08	686
ENSG00000(	21.75163	16.86003	6.597069	8.239831	11.04518	9.863579	0.60809	0.35675	0.48624	NRBF2P5	chr10	+	5818034	5818821	788
ENSG00000(	0	1.204288	1.319414	0	0.920432	2.465895	-0.24364	0.85683	NA	RP11-19E1	chr12	-	46274733	46276049	1317
ENSG00000(	1.035792	14.45145	2.638828	0.749076	2.761296	0.821965	1.6429	0.13537	0.22464	RP11-124D	chr14	+	23763061	23765007	1875
ENSG00000(	6.214751	25.29004	14.51355	7.490755	11.96562	6.575719	0.76304	0.26949	0.38988	RP11-694I2	chr3	-	49177519	49198284	1799
ENSG00000(	0	3.612863	0	0.749076	0	0	0.87856	0.51086	NA	RP11-467C	chr1	-	59754975	59755312	338
ENSG00000(	0	0	0	4.494453	1.840864	6.575719	-2.8639	0.026703	0.056165	RP11-796E	chr2	+	1.75E+08	1.75E+08	317
ENSG00000(	3.107376	2.408575	2.638828	9.737982	0.920432	0	-0.30547	0.79153	0.86374	RP11-342K	chr2	+	75924709	75925122	414
ENSG00000(	0	2.408575	0	0	0	4.93179	-0.53136	0.69519	0.79224	RP11-411B	chr18	+	14053950	14054760	811
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-601H	chr2	+	78664976	78666047	1072
ENSG00000(	0	0	0	0.749076	11.96562	4.109825	-3.1714	0.013153	0.029752	RP11-369G	chr19	-	23305990	23306890	901
ENSG00000(	0	0	1.319414	10.48706	2.761296	2.465895	-2.486	0.042873	0.08503	RP11-57B2	chr4	+	83612890	83613621	732
ENSG00000(	3.107376	1.204288	10.55531	2.247227	2.761296	7.397684	0.20393	0.83765	0.89625	RP11-131L	chr12	-	1.19E+08	1.19E+08	611
ENSG00000(	0	1.204288	1.319414	0.749076	0	0.821965	0.30451	0.82223	NA	RP11-230C	chr6	-	1.57E+08	1.57E+08	129
ENSG00000(	0	0	0	0	2.761296	2.465895	-1.4428	0.28594	NA	RP11-622C	chr15	+	67100742	67102898	2157

ENSG00000(	2.071584	1.204288	1.319414	0	0	0	1.6469	0.22376	NA	RP4-743O1	chr11	+	34764453	34764746	294
ENSG00000(	0	1.204288	0	0	2.761296	0	-0.43954	0.74062	NA	RP13-685P	chr3	+	1.29E+08	1.29E+08	489
ENSG00000(	3.107376	9.634302	6.597069	0	0.920432	2.465895	2.0025	0.064828	0.1214	RP1-29OF1	chrX	-	53094235	53094730	496
ENSG00000(	0	1.204288	0	2.996302	0.920432	0	-0.78586	0.56226	NA	RP1-71L16	chrX	-	46420363	46422184	1460
ENSG00000(	126.3666	104.773	105.5531	18.72689	19.32907	24.65895	2.3909	2.50E-13	1.79E-12	RP11-420L	chr6	+	3751345	3754105	2761
ENSG00000(	0	3.612863	2.638828	2.247227	4.60216	3.28786	-0.55198	0.62857	0.73909	RP11-777F	chr11	-	87034751	87035401	651
ENSG00000(	0	0	1.319414	5.992604	0	0	-1.0917	0.42098	0.55162	RP11-145P	chr15	+	25376125	25376484	360
ENSG00000(	3.107376	7.225726	0	0	0	0	2.6875	0.045111	0.088771	RP11-169K	chr3	-	11570962	11571229	268
ENSG00000(	0	0	0	2.247227	1.840864	0	-1.1573	0.3864	NA	PEBP1P2	chr2	-	85568404	85568961	558
ENSG00000(	0	0	0	0	2.761296	1.64393	-1.2339	0.35779	NA	RP11-785G	chr2	+	2.37E+08	2.37E+08	1543
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-293K	chr1	+	62996307	62996544	238
ENSG00000(	4.143168	1.204288	0	0.749076	2.761296	2.465895	-0.07975	0.94867	0.96913	RP11-15E1	chr17	+	58590551	58590911	361
ENSG00000(	1.035792	0	5.277655	0	0	0	1.9229	0.15616	0.25219	RP11-225N	chr3	-	1.83E+08	1.83E+08	1099
ENSG00000(	0	0	0	7.490755	0.920432	13.15144	-3.5673	0.004217	0.010608	RP11-546J	chr2	+	1.59E+08	1.59E+08	883
ENSG00000(	20.71584	28.90291	7.916483	49.43899	20.2495	34.52253	-0.82014	0.11998	0.20374	CTD-2124B	chr5	-	37286551	37287079	529
ENSG00000(	9.322127	13.24716	17.15238	0	0	0	4.9659	1.45E-05	5.29E-05	RP11-154H	chr3	+	71634094	71636560	2467
ENSG00000(	0	3.612863	1.319414	2.247227	0.920432	0.821965	0.18374	0.88647	0.92922	RP11-379K	chr3	-	1.7E+08	1.7E+08	1267
ENSG00000(	1.035792	2.408575	2.638828	5.992604	5.522592	7.397684	-1.3857	0.16541	0.26404	RP11-355F	chr2	+	75381516	75417075	3414
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-171I2	chr2	+	1.79E+08	1.79E+08	2117
ENSG00000(	1.035792	2.408575	0	6.74168	6.443024	11.50751	-2.296	0.026727	0.0562	RP5-1021I2	chr14	-	74307223	74307312	90
ENSG00000(	0	2.408575	0	0.749076	0	0	0.55104	0.6711	NA	RP5-1147A	chr7	+	40155284	40155542	259
ENSG00000(	23.82321	8.430014	7.916483	0.749076	0.920432	8.219649	1.7853	0.042792	0.084891	RP11-712B	chr11	+	94878601	94879168	568
ENSG00000(	22.78742	18.06432	7.916483	9.737982	11.96562	12.32947	0.50288	0.4216	0.55217	RP11-1186	chr16	-	15198580	15225458	2902
ENSG00000(	0	1.204288	2.638828	0	0	0	1.2853	0.33195	NA	RP11-811P	chr13	-	1.03E+08	1.03E+08	459
ENSG00000(	0	8.430014	5.277655	0	0	1.64393	2.0326	0.10662	0.18487	RP11-568G	chr1	+	2.2E+08	2.2E+08	665
ENSG00000(	2.071584	8.430014	15.83297	17.22874	15.64734	8.219649	-0.61406	0.40289	0.53401	RP11-51F1	chr17	-	61688132	61688544	413
ENSG00000(	25.8948	16.86003	21.11062	0.749076	3.681728	4.93179	2.5731	0.000385	0.001152	RP11-348N	chr10	+	1.13E+08	1.13E+08	1649
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-73M1	chr14	+	1.04E+08	1.04E+08	345
ENSG00000(	2.071584	10.83859	0	1.498151	0.920432	0.821965	1.4601	0.22035	0.33206	RP11-324C	chr10	-	1.14E+08	1.14E+08	551
ENSG00000(	0	1.204288	5.277655	0	0	8.219649	-0.24464	0.8489	0.9038	HCG17	chr6	-	30201816	30293911	732
ENSG00000(	54.89697	61.41867	46.17948	65.16957	32.21512	67.40112	-0.02301	0.94984	0.96986	RP5-1092A	chr1	-	28566020	28567964	1945
ENSG00000(	0	0	1.319414	2.996302	0.920432	4.109825	-1.6148	0.21802	0.32937	RP11-713H	chr17	+	8463789	8464280	492
ENSG00000(	0	1.204288	0	8.988907	6.443024	5.753754	-2.9707	0.011032	0.025407	RP11-359E	chr11	-	19732480	19734165	1686
ENSG00000(	1.035792	4.817151	2.638828	0.749076	1.840864	0.821965	0.9595	0.42646	0.55667	CTC-325H2	chr19	-	9458782	9459379	598
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-316N	chr10	-	1.02E+08	1.02E+08	608
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	LOC40191:	chr19	+	35357256	35357823	568
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-340C	chr13	-	1.01E+08	1.01E+08	283
ENSG00000(	0	0	0	0	2.761296	2.465895	-1.4428	0.28594	NA	RP3-466P1	chr6	+	1.46E+08	1.46E+08	1649
ENSG00000(	25.8948	20.47289	22.43003	0.749076	3.681728	18.08323	1.4874	0.041929	0.08341	RP11-373D	chr2	+	28619682	28619977	296
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	DPRXP5	chr21	+	38315567	38316425	539
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP1-20N2.1	chr6	+	1.44E+08	1.44E+08	357
ENSG00000(	1.035792	6.021439	1.319414	8.988907	7.363456	6.575719	-1.2524	0.18607	0.29062	RP11-105N	chr2	+	2.14E+08	2.14E+08	690
ENSG00000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-544H	chr2	+	2.04E+08	2.04E+08	210
ENSG00000(	0	0	1.319414	0	0.920432	0	0.1572	0.90001	NA	XXbac-BPG	chr6	-	27482818	27483053	236

ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	CTB-179I1.	chr4	-	78137569	78138031	463
ENSG00000(	8.286335	7.225726	11.87472	11.23613	15.64734	17.26126	-0.65015	0.3192	0.44629	RP11-16E1	chr8	-	64080284	64081001	718
ENSG00000(	33.14534	54.19295	52.77655	292.1395	318.4695	263.0288	-2.6301	1.17E-26	1.54E-25	RP11-216F	chr3	+	38532215	38534633	2419
ENSG00000(	2.071584	0	1.319414	2.996302	0	1.64393	-0.28027	0.8318	0.89232	CTC-512J1	chr19	+	44794234	44795064	526
ENSG00000(	15.53688	26.49433	15.83297	6.74168	1.840864	5.753754	1.8524	0.007603	0.018166	RP11-372K	chr4	+	1.52E+08	1.52E+08	1113
ENSG00000(	1.035792	2.408575	0	0	0	0	1.176	0.3702	NA	RP11-507D	chr9	+	88843730	88843898	169
ENSG00000(	17.60846	2.408575	19.79121	0	2.761296	3.28786	2.3595	0.011316	0.025993	RP11-712B	chr11	+	94876801	94878289	1489
ENSG00000(	0	0	2.638828	0	0	0.821965	0.55859	0.66971	NA	RP11-349G	chr15	+	65750912	65751872	485
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-403N	chr9	+	82465786	82466413	628
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-89F1	chr3	+	51469985	51470468	484
ENSG00000(	140.8677	144.5145	163.6073	224.7227	148.1896	143.8439	-0.20532	0.38551	0.51636	RP11-342K	chr2	+	75887588	75889334	1747
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-107F	chr15	-	42010568	42010870	303
ENSG00000(	71.46964	24.08575	85.7619	62.92235	97.56579	100.2797	-0.51303	0.17945	0.28219	RP11-701H	chr15	+	25230011	25230320	310
ENSG00000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	RP11-736N	chr14	+	1.04E+08	1.04E+08	42
ENSG00000(	0	0	0	0	2.761296	0	-0.68894	0.58376	NA	CTD-2301A	chr5	-	1.77E+08	1.77E+08	1009
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-568G	chr1	+	2.2E+08	2.2E+08	303
ENSG00000(	2.071584	2.408575	0	2.996302	2.761296	0.821965	-0.37513	0.76168	0.84252	RP11-46A1	chr1	+	1.81E+08	1.81E+08	411
ENSG00000(	0	0	0	5.243529	6.443024	2.465895	-3.0102	0.018538	0.040514	CTC-260E6.	chr19	+	20247742	20248042	301
ENSG00000(	1.035792	0	6.597069	2.996302	1.840864	1.64393	0.14909	0.90077	0.93835	RP11-84C1	chr4	+	90040435	90041022	588
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-401N	chr2	-	70100697	70100951	255
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-383H	chr13	+	98591610	98605793	159
ENSG00000(	21.75163	32.51577	35.62417	31.46117	19.32907	36.16646	0.035866	0.9371	0.96179	RP4-657E1	chr1	+	19623574	19624397	525
ENSG00000(	3.107376	0	0	2.996302	5.522592	0	-0.89445	0.49052	0.61956	RP11-231P	chr1	-	26589532	26589889	358
ENSG00000(	0	0	0	0	1.840864	0.821965	-0.71061	0.57792	NA	RP11-719K	chr16	-	14956237	14956606	370
ENSG00000(	2.071584	0	2.638828	0.749076	2.761296	0	0.27257	0.83627	0.89539	RP11-608C	chr3	-	16316567	16318139	1092
ENSG00000(	2.071584	1.204288	0	6.74168	0	0	-0.62242	0.63869	0.74685	RP11-461L	chr4	-	1.53E+08	1.53E+08	501
ENSG00000(	0	2.408575	3.958241	0	0	0	1.9515	0.15023	0.24432	RP11-461L	chr4	+	1.53E+08	1.53E+08	372
ENSG00000(	3.107376	3.612863	2.638828	0.749076	0	1.64393	1.3794	0.26103	0.38024	RP11-138E	chr9	+	1.33E+08	1.33E+08	369
ENSG00000(	5.17896	12.04288	7.916483	1.498151	4.60216	5.753754	0.96209	0.26909	0.38945	AD001527.	chr19	-	36634983	36639250	379
ENSG00000(	2.071584	7.225726	1.319414	6.74168	13.80648	12.32947	-1.4418	0.092783	0.16483	RP11-385F	chr6	-	47444979	47445308	330
ENSG00000(	2.071584	0	1.319414	0.749076	0	0	0.90441	0.50226	NA	CTB-152G1	chr7	+	1.05E+08	1.05E+08	365
ENSG00000(	0	4.817151	0	0.749076	0	0.821965	0.82903	0.54057	0.66379	RP11-332H	chr3	-	57785783	57787175	1070
ENSG00000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP13-685P	chr3	+	1.29E+08	1.29E+08	754
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RP11-17G1	chr2	-	1.53E+08	1.53E+08	231
ENSG00000(	0	6.021439	0	0	0	0	1.7221	0.20025	0.30776	RP4-590F2	chr1	-	1.15E+08	1.15E+08	565
ENSG00000(	1.035792	7.225726	3.958241	3.745378	7.363456	15.61733	-0.99832	0.26814	0.38853	RP11-501C	chr17	+	46976493	46977110	301
ENSG00000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-58E2	chr14	+	50517086	50518054	969
ENSG00000(	6.214751	0	0	0	0	0	1.7844	0.18526	0.28968	RP5-1173I2	chr7	-	39828566	39828903	338
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-416H	chr2	-	1.23E+08	1.23E+08	204
ENSG00000(	0	6.021439	3.958241	0	0.920432	0	2.0542	0.11822	0.20139	RP11-451F	chr2	+	1.75E+08	1.75E+08	835
ENSG00000(	12.4295	4.817151	3.958241	1.498151	6.443024	3.28786	0.82258	0.37321	0.50374	AC005776.	chr19	+	15449742	15450048	307
ENSG00000(	44.53905	42.15007	54.09597	29.96302	17.48821	25.48091	0.91816	0.024908	0.052797	CTD-2583A	chr19	+	58379253	58380202	891
ENSG00000(	8.286335	6.021439	6.597069	2.996302	0.920432	0	1.9468	0.062694	0.11805	RP11-574K	chr10	-	75500296	75500581	286
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-84N7	chr13	-	42755601	42756057	457

ENSG0000(	1.035792	2.408575	7.916483	10.48706	4.60216	4.93179	-0.7338	0.43895	0.56863	RP11-274B	chr7	+	1.28E+08	1.28E+08	585
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-393K	chr10	+	7196082	7196198	117
ENSG0000(	1.035792	4.817151	1.319414	8.239831	2.761296	1.64393	-0.6655	0.54097	0.66393	NANOGNBF	chrX	-	1.01E+08	1.01E+08	487
ENSG0000(	22.78742	26.49433	46.17948	31.46117	17.48821	17.26126	0.4963	0.30946	0.43563	RP11-355B	chr2	+	61698323	61711265	569
ENSG0000(	2.071584	1.204288	3.958241	0	0.920432	2.465895	0.75399	0.5479	0.66961	RP11-730B	chr7	-	5048795	5048959	165
ENSG0000(	10.35792	14.45145	10.55531	2.996302	3.681728	0	2.1151	0.016917	0.037348	hsa-mir-33!	chr7	-	1.3E+08	1.3E+08	2634
ENSG0000(	0	0	0	3.745378	0	0	-0.95265	0.4619	NA	NF1P1	chr15	-	21122015	21140987	2645
ENSG0000(	5.17896	1.204288	0	0	1.840864	1.64393	0.59635	0.64523	0.75236	RP1-168P1	chr16	+	89525278	89525845	568
ENSG0000(	7.250543	1.204288	2.638828	0.749076	0	0	2.3795	0.06427	0.12054	CTC-571O2	chr5	-	1.75E+08	1.75E+08	598
ENSG0000(	2.071584	7.225726	2.638828	0	0.920432	0	2.4271	0.055325	0.10611	RP11-57B2	chr4	+	83696614	83697254	360
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-674I:	chr2	-	28118983	28120062	1080
ENSG0000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	RP11-757G	chr12	+	12401925	12402361	437
ENSG0000(	1.035792	1.204288	1.319414	0	0	0	1.3148	0.3256	NA	RP11-434C	chr12	+	11665657	11667070	1414
ENSG0000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	GS1-531I17	chr17	+	63651032	63651513	482
ENSG0000(	2.071584	0	1.319414	0	0	2.465895	0.24177	0.8585	NA	RP11-420K	chr10	-	88614453	88615993	1168
ENSG0000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	CTC-523E2:	chr19	-	35414203	35417716	625
ENSG0000(	8.286335	1.204288	7.916483	15.73059	22.09037	10.68554	-1.3516	0.066798	0.12463	CTD-2302E	chr14	-	64060749	64062009	1261
ENSG0000(	0	1.204288	5.277655	0	0	1.64393	1.1002	0.41222	0.54272	RP11-210K	chr18	+	29464821	29465106	286
ENSG0000(	4.143168	0	0	0	0	0	1.2752	0.32937	NA	RP11-461L	chr4	-	1.53E+08	1.53E+08	463
ENSG0000(	16.57267	8.430014	11.87472	6.74168	2.761296	6.575719	1.092	0.1464	0.23919	RP3-468K1	chr6	-	1.44E+08	1.44E+08	628
ENSG0000(	0	0	0	2.247227	0	0	-0.59555	0.63522	NA	AC006077.	chr5	-	1.34E+08	1.34E+08	343
ENSG0000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP11-311B	chr2	+	1.6E+08	1.6E+08	797
ENSG0000(	0	6.021439	10.55531	0	1.840864	0	2.2215	0.07133	0.13192	ASB3	chr2	-	53897430	54087297	2113
ENSG0000(	4.143168	0	0	0	0.920432	0	0.95689	0.47805	NA	NUDT19P4	chr6	+	44866448	44867032	585
ENSG0000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-592P	chr3	+	1.22E+08	1.22E+08	240
ENSG0000(	7.250543	2.408575	6.597069	3.745378	5.522592	7.397684	-0.02546	0.97714	0.98667	RP1-69B10	chr11	-	32613339	32614317	979
ENSG0000(	0	0	0	50.93714	43.2603	36.98842	-6.2674	1.96E-09	1.04E-08	RP11-628E	chr8	+	56449431	56454613	5183
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-24B1	chr9	-	43830636	43835037	1809
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-27M!	chr2	-	2.03E+08	2.03E+08	332
ENSG0000(	8.286335	1.204288	2.638828	2.996302	2.761296	7.397684	-0.07949	0.93689	0.96179	RP11-27I1.	chr9	-	1.24E+08	1.24E+08	371
ENSG0000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	RP11-379K	chr15	-	80872370	80872907	538
ENSG0000(	0	13.24716	5.277655	0	1.840864	3.28786	1.4272	0.20989	0.31961	TAS2R6	chr7	+	1.41E+08	1.41E+08	826
ENSG0000(	0	0	1.319414	0	4.60216	6.575719	-1.9109	0.14226	0.23373	RP11-551L	chr12	-	31258039	31259764	675
ENSG0000(	0	0	0	7.490755	1.840864	7.397684	-3.2487	0.010059	0.023379	CTD-2227E	chr7	-	25988277	25989023	747
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-346C	chr6	+	1.11E+08	1.11E+08	613
ENSG0000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	RP5-879K2	chr1	-	2.11E+08	2.11E+08	668
ENSG0000(	0	1.204288	0	0	0.920432	0	0.1572	0.90001	NA	RP11-45P1	chr14	+	1.04E+08	1.04E+08	643
ENSG0000(	2.071584	0	3.958241	2.247227	2.761296	0.821965	0.029117	0.98103	0.98894	RP5-966M:	chr3	+	52768751	52769029	279
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-144N	chr16	-	74646494	74647119	321
ENSG0000(	4.143168	1.204288	0	4.494453	0.920432	2.465895	-0.38678	0.74877	0.83302	RP11-460N	chr7	-	64402521	64403304	784
ENSG0000(	67.32647	93.93444	101.5949	95.88167	111.3723	92.06007	-0.18968	0.48698	0.61612	RP11-288H	chr6	+	1.61E+08	1.61E+08	3131
ENSG0000(	0	3.612863	0	0	3.681728	0	-0.00497	0.99707	0.99814	RP1-309F2	chr20	-	57451647	57452036	390
ENSG0000(	1.035792	0	3.958241	0	0	0	1.6134	0.2311	NA	RP11-2E11	chr7	+	1.3E+08	1.3E+08	623
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-261B	chr15	+	30574736	30580592	2098

ENSG00000(	2.071584	1.204288	1.319414	5.243529	0	2.465895	-0.53613	0.66251	0.76676	RP11-65L3	chr2	+	1.79E+08	1.79E+08	675
ENSG00000(	51.7896	62.62296	42.22124	33.7084	33.13555	22.19305	0.79977	0.038823	0.07795	LPP-AS2	chr3	-	1.88E+08	1.88E+08	2852
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-403I:	chr1	+	1.49E+08	1.49E+08	296
ENSG00000(	7.250543	3.612863	5.277655	14.23244	5.522592	8.219649	-0.71428	0.3778	0.50853	RP11-502I4	chr15	-	67833410	67834942	1533
ENSG00000(	0	2.408575	0	0	2.761296	0	-0.08034	0.95255	NA	RP11-62H7	chr8	-	8791231	8791516	286
ENSG00000(	0	4.817151	0	0	0	0	1.4375	0.27798	NA	RP11-326C	chr11	+	333192	333688	497
ENSG00000(	0	1.204288	1.319414	2.247227	0	0.821965	-0.17829	0.89512	NA	RP11-723P	chr14	+	69328479	69329242	447
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-550I:	chr3	-	1.57E+08	1.57E+08	889
ENSG00000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-123C	chr15	+	58964495	58965132	638
ENSG00000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP3-467N1	chr6	+	1.01E+08	1.01E+08	736
ENSG00000(	0	0	1.319414	0	2.761296	0	-0.44505	0.73801	NA	RP11-439C	chr8	+	1922984	1923480	497
ENSG00000(	0	0	0	1.498151	0.920432	0	-0.63553	0.61411	NA	RP11-1112	chr17	-	73056586	73056715	130
ENSG00000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP11-293B	chr1	-	1.84E+08	1.84E+08	936
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-29B1	chr9	-	1.03E+08	1.03E+08	466
ENSG00000(	0	2.408575	0	4.494453	0	3.28786	-1.0506	0.42416	0.55468	RP11-342K	chr2	+	75946246	75947144	899
ENSG00000(	1.035792	12.04288	5.277655	1.498151	0.920432	4.93179	1.0731	0.3006	0.42565	RP11-599B	chr17	-	8102441	8102755	315
ENSG00000(	10.35792	6.021439	22.43003	5.243529	5.522592	4.93179	1.1857	0.11833	0.20153	RP11-346C	chr16	+	73094279	73096215	1937
ENSG00000(	0	0	3.958241	0	1.840864	0	0.51729	0.70257	NA	RP11-717A	chr2	-	85587921	85588048	128
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	RP11-60E8	chr12	+	51150675	51151216	193
ENSG00000(	17.60846	10.83859	10.55531	20.22504	18.40864	27.94681	-0.7276	0.19393	0.29994	RP11-10C2	chr3	-	33838641	33839173	533
ENSG00000(	0	0	0	0	0.920432	2.465895	-0.94408	0.47231	NA	RP5-878I13	chrX	-	1.15E+08	1.15E+08	462
ENSG00000(	2.071584	0	0	2.247227	0	4.93179	-1.0365	0.43436	0.5641	RP11-708L	chr11	-	1.12E+08	1.12E+08	237
ENSG00000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	RP11-111A	chr11	-	43085187	43087482	1448
ENSG00000(	17.60846	25.29004	10.55531	2.996302	7.363456	7.397684	1.4928	0.030291	0.062707	CTD-2527I2	chr19	-	35505865	35516239	526
ENSG00000(	8.286335	3.612863	1.319414	4.494453	4.60216	6.575719	-0.18852	0.84167	0.89882	RP5-933K2	chr6	+	1.58E+08	1.58E+08	514
ENSG00000(	0	3.612863	3.958241	5.992604	0.920432	1.64393	-0.16326	0.88893	0.93101	MTRNR2L2	chr5	-	79945819	79946855	1037
ENSG00000(	2.071584	0	1.319414	0	2.761296	3.28786	-0.51789	0.6905	0.78885	CTD-2553L	chr19	+	35125749	35126622	874
ENSG00000(	0	0	0	635.2161	602.883	683.8748	-9.7121	2.52E-26	3.28E-25	RP11-301L	chr3	+	32938576	32939318	743
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	RP11-479I:	chr3	-	1.61E+08	1.61E+08	237
ENSG00000(	12.4295	16.86003	6.597069	2.996302	0.920432	1.64393	2.3438	0.00775	0.018483	RP11-792A	chr7	-	66213825	66214064	240
ENSG00000(	0	0	0	0	1.840864	1.64393	-0.9764	0.45902	NA	RP11-607P	chr12	-	51815740	51818395	347
ENSG00000(	1.035792	0	2.638828	0	0	0	1.2393	0.34779	NA	RP11-465C	chr2	+	1.09E+08	1.09E+08	823
ENSG00000(	1.035792	0	0	0	0	3.28786	-0.59917	0.65385	NA	RP11-1007	chr15	+	72742998	72743815	818
ENSG00000(	10.35792	7.225726	2.638828	0.749076	2.761296	1.64393	1.6664	0.099693	0.17501	RP11-589N	chr14	+	53338176	53338935	760
ENSG00000(	0	0	2.638828	0	0.920432	1.64393	0.005124	0.99699	NA	RP13-395E	chr15	-	32542503	32548326	2059
ENSG00000(	0	0	5.277655	0	0	0	1.5386	0.24869	NA	RP11-465K	chr8	-	30611753	30612056	304
ENSG00000(	0	4.817151	0	3.745378	1.840864	0	-0.14081	0.91466	0.94799	RP11-13B9	chr9	-	1.02E+08	1.02E+08	2133
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP5-1125K	chr7	+	2327550	2328063	224
ENSG00000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	RP11-697H	chr11	-	63466068	63466236	169
ENSG00000(	4.143168	2.408575	1.319414	1.498151	0.920432	0	1.1632	0.35558	0.48517	SCML2P2	chr16	+	25080891	25081430	540
ENSG00000(	0	0	0	15.73059	3.681728	6.575719	-3.913	0.00118	0.003269	CTC-523E23	chr19	-	35340182	35351480	570
ENSG00000(	0	0	1.319414	5.992604	8.283888	8.219649	-3.0361	0.008618	0.020342	CTD-2012J:	chr5	+	1594741	1611582	1661
ENSG00000(	207.1584	197.5032	222.9809	144.5716	189.609	143.0219	0.3948	0.057207	0.10923	RP11-379H	chr7	+	35734824	35739023	4200
ENSG00000(	0	0	3.958241	0	0.920432	0	0.88424	0.51108	NA	LL22NC03-	chr22	-	16179617	16181004	1388

ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-123C	chr16	-	69059763	69060546	479
ENSG0000(	3.107376	2.408575	2.638828	2.247227	3.681728	9.863579	-0.7891	0.43534	0.56503	CTA-293F1	chr7	-	20367922	20371370	737
ENSG0000(	0	2.408575	0	0.749076	0.920432	2.465895	-0.44793	0.73865	0.82493	RP5-966M	chr3	+	52787542	52788706	884
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	IGLVIVOR2	chr22	-	25833273	25833790	397
ENSG0000(	4.143168	4.817151	1.319414	0	0	0	2.8253	0.032791	0.067136	RP11-479F	chr2	+	61476915	61477756	397
ENSG0000(	1.035792	2.408575	10.55531	4.494453	0.920432	8.219649	0.003921	0.99694	0.99811	RP11-394I	chr2	+	1.75E+08	1.75E+08	1068
ENSG0000(	0	2.408575	1.319414	0	3.681728	3.28786	-0.60052	0.64006	0.74803	ABC7-4304	chr2	-	2.43E+08	2.43E+08	454
ENSG0000(	0	0	1.319414	0	8.283888	1.64393	-1.7333	0.18894	0.29404	RP11-435C	chr9	+	98268517	98269918	1402
ENSG0000(	0	1.204288	1.319414	0.749076	3.681728	0	-0.47009	0.72599	0.81626	RP11-642C	chr8	-	89820547	89821137	591
ENSG0000(	18.64425	13.24716	13.19414	12.73428	11.96562	15.61733	0.1581	0.78989	0.86247	RP11-708J	chr3	+	47541331	47541897	567
ENSG0000(	0	7.225726	0	0	0	0.821965	1.5484	0.25303	0.37084	RP11-660N	chr4	+	25222025	25222535	511
ENSG0000(	2.071584	0	0	0	2.761296	0	-0.15346	0.90925	NA	CTA-221G9	chr22	-	25575276	25575521	246
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP11-678G	chr19	-	21817635	21817977	343
ENSG0000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP5-855F1	chr7	+	10980050	10980362	313
ENSG0000(	0	0	3.958241	0	0	0	1.1937	0.35828	NA	RP4-555D2	chr3	+	44038388	44038935	548
ENSG0000(	4.143168	2.408575	5.277655	5.243529	4.60216	5.753754	-0.34871	0.70884	0.80322	RP13-216E	chrX	-	73177894	73189320	347
ENSG0000(	1.035792	0	0	0	0	0.821965	0.1572	0.90001	NA	RP11-430G	chr1	-	62207670	62208096	427
ENSG0000(	0	2.408575	6.597069	0	0	0	2.4461	0.070095	0.12986	RP11-138A	chr7	-	1.31E+08	1.31E+08	1998
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP1-138A5	chrX	-	86978089	86978238	150
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-9M16	chr9	+	1.17E+08	1.17E+08	178
ENSG0000(	0	0	0	0	0.920432	1.64393	-0.68088	0.59209	NA	RP11-180N	chr12	-	12767293	12768841	396
ENSG0000(	23.82321	16.86003	22.43003	0.749076	0	0	4.9596	8.21E-07	3.44E-06	RP11-366C	chr13	-	43384502	43386698	760
ENSG0000(	1.035792	0	1.319414	4.494453	0.920432	0.821965	-0.90203	0.48806	0.61718	RP3-523E1	chr6	-	53783772	53785586	456
ENSG0000(	1.035792	0	1.319414	28.46487	11.04518	8.219649	-3.5818	0.000289	0.000881	RP11-460N	chr9	-	69823283	69823847	565
ENSG0000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP1-152L7	chr6	+	52553459	52553796	338
ENSG0000(	3.107376	0	7.916483	2.996302	0.920432	4.93179	0.23192	0.8351	0.89446	CTC-336P1	chr2	+	32238130	32238437	308
ENSG0000(	0	0	2.638828	0.749076	0	1.64393	0.04452	0.97381	NA	RP5-894D1	chr6	-	1.71E+08	1.71E+08	500
ENSG0000(	0	0	0	0.749076	0	0.821965	-0.42333	0.73521	NA	RP11-140C	chr10	+	50759354	50760698	607
ENSG0000(	2.071584	2.408575	0	0.749076	1.840864	0	0.48665	0.71522	0.80786	RP11-1109	chr12	+	89765597	89766136	540
ENSG0000(	0	0	0	0.749076	0	0	-0.1377	0.91236	NA	RP11-558F	chr1	+	9840880	9841298	246
ENSG0000(	5.17896	2.408575	0	0.749076	7.363456	1.64393	-0.2396	0.83639	0.89542	RP11-230C	chr6	-	1.57E+08	1.57E+08	446
ENSG0000(	5.17896	3.612863	9.235896	9.737982	5.522592	3.28786	-0.05019	0.95374	0.97245	RP11-29H2	chr1	-	1.56E+08	1.56E+08	257
ENSG0000(	110.8297	119.2245	88.40072	58.42789	62.58938	41.09825	0.96552	0.001069	0.002986	AL449209.	chr3	+	1.3E+08	1.3E+08	3496
ENSG0000(	5.17896	0	0	1.498151	0	0	0.88387	0.51475	0.64144	RP13-339P	chr4	+	39934074	39935181	632
ENSG0000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	CTC-412M1	chr19	-	19810012	19810218	207
ENSG0000(	5.17896	7.225726	17.15238	4.494453	2.761296	13.9734	0.41378	0.61187	0.72552	SRXN1	chr20	-	627259	634014	2698
ENSG0000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	DPRXP2	chr6	-	35957292	35958213	557
ENSG0000(	0	0	2.638828	0	2.761296	2.465895	-0.58096	0.66498	0.76874	RP11-435C	chr9	+	98257206	98257661	456
ENSG0000(	0	0	0	0	2.761296	5.753754	-2.0874	0.1225	0.20741	AP000654.	chr11	-	86532185	86532770	586
ENSG0000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-1152	chr2	+	1.59E+08	1.59E+08	660
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	CTAGE6	chr7	-	1.43E+08	1.43E+08	2608
ENSG0000(	2.071584	0	5.277655	8.988907	5.522592	1.64393	-0.93467	0.38264	0.51334	RP11-10C2	chr3	-	33835136	33835637	502
ENSG0000(	23.82321	32.51577	19.79121	12.73428	9.20432	10.68554	1.1671	0.033041	0.067581	RP11-1109	chr12	+	89761584	89763078	1495
ENSG0000(	2.071584	0	0	0	0	0.821965	0.45485	0.72366	NA	RP5-891H2	chr1	-	44653615	44654721	796

ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	CTA-298G8	chr7	-	24713928	24714231	304
ENSG0000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-797J4	chr11	-	28166454	28166751	298
ENSG0000(	31.07376	14.45145	21.11062	4.494453	0.920432	0.821965	3.072	6.79E-05	0.000226	CTD-2078B	chr5	+	39520533	39524810	599
ENSG0000(	39.36009	30.10719	19.79121	58.42789	27.61296	73.97684	-0.81385	0.064407	0.12076	RP11-324I2	chr10	-	35603480	35625329	1107
ENSG0000(	25.8948	19.2686	18.47179	40.45008	15.64734	34.52253	-0.49268	0.32472	0.45221	RP11-474P	chr9	-	1.28E+08	1.28E+08	888
ENSG0000(	4.143168	4.817151	3.958241	10.48706	9.20432	4.93179	-0.82834	0.32919	0.45692	RP11-274B	chr7	+	1.28E+08	1.28E+08	1267
ENSG0000(	14.50109	14.45145	35.62417	11.98521	22.09037	15.61733	0.3555	0.53172	0.65633	RP11-701H	chr15	+	25236633	25236900	268
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-44N1	chr8	-	97139195	97140029	835
ENSG0000(	15.53688	16.86003	26.38828	33.7084	30.37426	18.90519	-0.48901	0.32829	0.45602	RP11-84C1	chr4	+	90032651	90033519	686
ENSG0000(	17.60846	14.45145	19.79121	8.988907	0.920432	0	2.0949	0.012851	0.029124	HTATSF1P2	chr6	-	3023376	3024006	631
ENSG0000(	0	0	0	11.98521	8.283888	14.79537	-4.404	0.000138	0.000441	AC002128.	chr19	-	35742343	35744542	618
ENSG0000(	0	8.430014	0	6.74168	0.920432	3.28786	-0.29293	0.80427	0.87302	RP3-483K1	chr6	+	53214956	53215503	548
ENSG0000(	80.79177	74.66584	77.84541	26.21764	27.61296	42.74218	1.2523	0.000266	0.000814	RP11-350D	chr11	+	34731147	34731708	562
ENSG0000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-253I2	chr12	-	12605037	12605415	379
ENSG0000(	1.035792	4.817151	0	0	0	0.821965	1.43	0.29086	0.41492	CTD-2284C	chr5	+	37130532	37130802	271
ENSG0000(	0	0	0	0	0.920432	0.821965	-0.44415	0.72278	NA	RP11-440G	chr12	-	42463737	42464427	691
ENSG0000(	1.035792	0	1.319414	0	0	0	0.74872	0.54982	NA	RP11-1060	chr12	+	94338817	94341589	2773
ENSG0000(	0	0	2.638828	0	0	3.28786	-0.16812	0.90128	NA	RP11-435C	chr9	-	98169272	98169944	673
ENSG0000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-108N	chr10	-	93224335	93224465	131
ENSG0000(	3.107376	6.021439	0	2.247227	5.522592	3.28786	-0.20464	0.85032	0.9047	RP11-382D	chr1	-	1.84E+08	1.84E+08	952
ENSG0000(	0	0	0	2.996302	0	0	-0.74467	0.55406	NA	RP11-89C3	chr11	-	1.11E+08	1.11E+08	499
ENSG0000(	5.17896	2.408575	3.958241	3.745378	1.840864	0	0.80565	0.47737	0.60647	RP11-697E	chr15	-	90827608	90828812	894
ENSG0000(	3.107376	0	2.638828	0	0	4.109825	0.29909	0.8208	0.88422	RP5-1092A	chr1	+	28573655	28574079	425
ENSG0000(	0	0	0	2.247227	0.920432	0	-0.88346	0.49845	NA	RP11-171I2	chr2	+	1.8E+08	1.8E+08	463
ENSG0000(	2.071584	0	1.319414	0	0	0	1.1599	0.3761	NA	RP11-365F	chr7	+	1.39E+08	1.39E+08	248
ENSG0000(	0	4.817151	0	1.498151	2.761296	0	0.10859	0.93488	0.96073	RP11-506H	chr5	-	54652136	54653351	1216
ENSG0000(	6.214751	1.204288	5.277655	0	2.761296	1.64393	1.1887	0.30151	0.4266	AP000892.	chr11	-	1.17E+08	1.17E+08	376
ENSG0000(	1.035792	1.204288	2.638828	0.749076	0.920432	2.465895	0.1526	0.90364	0.94039	RP11-751K	chr7	+	1.35E+08	1.35E+08	445
ENSG0000(	0	1.204288	0	0.749076	0	0	0.1572	0.90001	NA	RP11-305E	chr1	+	1.01E+08	1.01E+08	236
ENSG0000(	0	3.612863	0	0	0	1.64393	0.50971	0.70603	NA	RP5-1057J	chr1	-	23704873	23705522	650
ENSG0000(	6.214751	0	0	0	0	2.465895	0.74299	0.58201	0.69965	RP11-647C	chr14	-	39839483	39839960	478
ENSG0000(	4.143168	0	2.638828	0.749076	0.920432	4.109825	0.17371	0.88715	0.92967	RP11-188D	chr1	-	1.18E+08	1.18E+08	575
ENSG0000(	1.035792	0	1.319414	5.243529	0	1.64393	-0.97241	0.45812	0.58771	RP1-224A6	chr1	-	22394833	22395320	488
ENSG0000(	172.9772	172.2131	191.315	156.5568	149.11	87.12828	0.44516	0.072073	0.13303	RP3-368A4	chrX	-	73420064	73461983	3897
ENSG0000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	RP13-238F	chr10	+	1.26E+08	1.26E+08	1359
ENSG0000(	0	0	1.319414	0.749076	1.840864	1.64393	-0.92219	0.49549	NA	RP11-295B	chr13	+	99205497	99206034	538
ENSG0000(	0	0	0	0	6.443024	0	-1.5465	0.25144	0.36902	RP11-541E	chr2	-	38762400	38763391	570
ENSG0000(	5.17896	12.04288	6.597069	5.243529	8.283888	2.465895	0.51587	0.53985	0.6633	RP11-342K	chr2	+	75897115	75897580	466
ENSG0000(	0	0	10.55531	1.498151	0	0	1.6054	0.22694	0.33992	RP11-290L	chr9	+	39159068	39160316	1249
ENSG0000(	0	0	2.638828	0	0	2.465895	0.027772	0.98358	NA	FAM22D	chr10	+	89124746	89126248	1018
ENSG0000(	0	1.204288	2.638828	38.20285	49.70333	53.42772	-4.7714	6.86E-10	3.81E-09	RP11-710C	chr4	+	96470280	96473608	3329
ENSG0000(	0	3.612863	0	0	0	0	1.1034	0.39075	NA	CTB-152G1	chr7	+	1.05E+08	1.05E+08	260
ENSG0000(	0	2.408575	0	0	0.920432	0	0.52346	0.68845	NA	RP11-384A	chr3	+	1.94E+08	1.94E+08	163
ENSG0000(	1.035792	4.817151	1.319414	2.247227	0.920432	0	0.78772	0.53336	0.65797	RP11-132J	chr14	+	56013392	56014841	1120

ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-60E8	chr12	-	51200118	51200220	103
ENSG00000(	0	0	0	0	0.920432	0	-0.1377	0.91236	NA	CTC-559E9.	chr19	+	19861427	19863353	1927
ENSG00000(	1.035792	1.204288	3.958241	4.494453	9.20432	0.821965	-0.9879	0.36716	0.49712	RP11-288K	chr12	-	1804996	1807210	1979
ENSG00000(	0	2.408575	0	0	0	0	0.74702	0.55047	NA	RP11-603B	chr15	-	22490343	22490685	343
ENSG00000(	0	1.204288	1.319414	0	1.840864	0	0.21033	0.87627	NA	RP11-712C	chr14	+	64828110	64828355	246
ENSG00000(	0	4.817151	1.319414	92.88537	116.8949	75.62077	-5.2307	2.98E-16	2.52E-15	CTC-260E6.	chr19	+	20332678	20333272	595
ENSG00000(	489.9296	520.2523	461.7948	173.0365	328.5942	318.1004	0.84198	7.39E-05	0.000245	RP11-274B	chr7	-	1.28E+08	1.28E+08	2732
ENSG00000(	0	1.204288	1.319414	2.247227	6.443024	0.821965	-1.33	0.28693	0.41049	RP11-426K	chr2	+	1.02E+08	1.02E+08	279
ENSG00000(	100.4718	163.7831	168.885	95.13259	106.7701	84.66239	0.58677	0.026204	0.055245	RP3-368A4	chrX	-	73429811	73433495	3685
ENSG00000(	2.071584	0	1.319414	8.239831	0.920432	4.93179	-1.5296	0.18949	0.29462	RP11-365F	chr7	-	1.39E+08	1.39E+08	586
ENSG00000(	1.035792	0	1.319414	3.745378	0	0	-0.35742	0.79208	0.86418	RP11-326I1	chr4	-	1.85E+08	1.85E+08	1059
ENSG00000(	2.071584	1.204288	1.319414	0	0.920432	0.821965	0.84259	0.52722	0.65201	RP11-692N	chr11	+	47817721	47817931	211
ENSG00000(	0	0	0	0	3.681728	0	-0.91959	0.47635	NA	AC006499.	chr4	-	10239837	10239859	23
ENSG00000(	2.071584	0	2.638828	0.749076	0	4.109825	-0.0339	0.9792	0.98787	RP11-579D	chr12	-	49194359	49194869	511
ENSG00000(	5.17896	13.24716	6.597069	26.96672	42.33987	30.4127	-1.9074	0.000768	0.002195	RP11-561N	chr7	-	64139332	64147771	563
ENSG00000(	0	2.408575	2.638828	5.992604	9.20432	7.397684	-1.8225	0.072693	0.13395	RP11-230C	chr6	-	1.57E+08	1.57E+08	718
ENSG00000(	14.50109	4.817151	13.19414	10.48706	8.283888	9.863579	0.17094	0.8082	0.87554	RP11-274B	chr7	+	1.28E+08	1.28E+08	1114
ENSG00000(	4.143168	2.408575	1.319414	0.749076	0	4.109825	0.50469	0.67928	0.78006	RP4-665N4	chr1	-	36457710	36479231	385
ENSG00000(	8.286335	2.408575	0	2.247227	1.840864	1.64393	0.70667	0.54032	0.66366	CTD-3214K	chr8	+	53635463	53635701	239
ENSG00000(	1.035792	2.408575	2.638828	0.749076	0.920432	2.465895	0.38529	0.75461	0.83769	RP11-692N	chr11	+	47862876	47863234	359
ENSG00000(	17.60846	43.35436	23.74945	44.94453	18.40864	12.32947	0.14591	0.78974	0.86243	RP11-486G	chr1	-	84542014	84543614	1601
ENSG00000(	3.107376	8.430014	6.597069	2.247227	2.761296	5.753754	0.64159	0.49286	0.62189	RP11-536L	chr1	+	2.05E+08	2.05E+08	784
ENSG00000(	0	0	0	4.494453	2.761296	0	-1.8787	0.16586	0.26454	RP11-89C3	chr11	-	1.11E+08	1.11E+08	508
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-52M1	chr7	+	44640631	44641086	456
ENSG00000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	GS1-531I17	chr17	+	63640426	63640735	310
ENSG00000(	0	3.612863	5.277655	0.749076	1.840864	4.109825	0.29057	0.80453	0.87318	RP11-181E	chr2	-	1.12E+08	1.12E+08	1482
ENSG00000(	0	1.204288	0	0	0	0	0.45211	0.71784	NA	RP11-407N	chr12	-	51342900	51343167	268
ENSG00000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-85D1	chr2	-	69478950	69479496	547
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	CTD-2542C	chr19	-	21208721	21208847	127
ENSG00000(	9.322127	12.04288	9.235896	1.498151	0	0.821965	3.0302	0.002481	0.006501	MILR1	chr17	+	62461569	62464760	631
ENSG00000(	3.107376	3.612863	5.277655	0.749076	0.920432	0.821965	1.7007	0.14347	0.23527	RP3-418A9	chr6	+	1.11E+08	1.11E+08	311
ENSG00000(	0	0	0	0	0	0.821965	-0.1377	0.91236	NA	RP11-697G	chr6	-	1.09E+08	1.09E+08	190
ENSG00000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	KB-1980E6	chr8	+	1.03E+08	1.03E+08	302
ENSG00000(	37.28851	31.31148	26.38828	32.95932	28.53339	44.38611	-0.149	0.72154	0.81281	RP11-591N	chr12	+	90102736	90106367	3632
ENSG00000(	2.071584	3.612863	0	0	0	0	1.8175	0.17961	NA	RP11-435I1	chr16	+	28376021	28376654	634
ENSG00000(	0	0	1.319414	0	0	0	0.45211	0.71784	NA	RP11-651K	chr11	-	1.32E+08	1.32E+08	844
ENSG00000(	0	0	0	0.749076	0	2.465895	-0.89717	0.49245	NA	RP11-3K24	chr17	+	58393195	58393576	382
ENSG00000(	0	0	2.638828	5.992604	1.840864	0.821965	-1.1676	0.36186	0.49152	RP11-408C	chr9	+	1.16E+08	1.16E+08	610
ENSG00000(	0	0	0	0	0	1.64393	-0.44088	0.72472	NA	CTC-575C1	chr19	-	20434801	20435377	577
ENSG00000(	0	0	3.958241	0	0.920432	0	0.88424	0.51108	NA	RP11-289A	chr2	+	2.34E+08	2.34E+08	1551
ENSG00000(	0	1.204288	1.319414	0	0	0	0.77445	0.53994	NA	RP11-66E2	chr12	-	47075854	47076496	643
ENSG00000(	17.60846	13.24716	15.83297	37.45378	38.65814	34.52253	-1.2031	0.009921	0.023097	RP11-10C2	chr3	-	33837180	33838442	1263
ENSG00000(	3.107376	1.204288	1.319414	0.749076	6.443024	3.28786	-0.66271	0.56146	0.6815	RP3-365I15	chr1	-	1.44E+08	1.44E+08	111
ENSG00000(	21.75163	31.31148	13.19414	2.247227	1.840864	15.61733	1.6105	0.027639	0.057895	RP11-326I1	chr4	+	1.85E+08	1.85E+08	2503

ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	AL031601.3	chr10	+	42705438	42705831	394
ENSG0000(	0	0	2.638828	0	0	0	0.74702	0.55047	NA	RP11-259K	chr3	+	37258270	37259479	1210
ENSG0000(	0	1.204288	0	1.498151	0.920432	0	-0.40353	0.76332	NA	RP11-270B	chr2	+	62395997	62398298	395
ENSG0000(	2.071584	4.817151	1.319414	2.996302	1.840864	4.93179	-0.20323	0.85109	0.90513	RP11-435C	chr9	+	98276327	98276802	476
ENSG0000(	0	0	0	1.498151	0	0	-0.41061	0.74286	NA	RP11-141C	chr3	-	1.95E+08	1.95E+08	1070
ENSG0000(	6.214751	7.225726	13.19414	1.498151	2.761296	9.041614	0.87856	0.31324	0.43972	RP4-800G7	chr7	-	1.49E+08	1.49E+08	1095
ENSG0000(	2.071584	0	0	0	0	0	0.74702	0.55047	NA	RP11-1E1.2	chr4	-	78033648	78034611	964
ENSG0000(	3.107376	0	0	0	0	0	0.96659	0.44319	NA	RP11-564A	chr1	+	2.07E+08	2.07E+08	466
ENSG0000(	0	0	0	0	0	3.28786	-0.81922	0.51991	NA	RP11-1259	chr5	+	1.78E+08	1.78E+08	474
ENSG0000(	0	8.430014	0	0	0	0	2.183	0.10757	0.18626	RP11-1012	chr14	+	68201912	68202067	156
ENSG0000(	0	0	0	0	1.840864	0	-0.45113	0.71864	NA	RP11-63N3	chr18	-	75344884	75345316	275
ENSG0000(	0	0	0	0.749076	0.920432	0	-0.42333	0.73521	NA	CTC-575C1	chr19	+	20462311	20462888	578
ENSG0000(	1.035792	0	0	0	0	0	0.45211	0.71784	NA	RP11-114N	chr14	-	81467510	81468130	525
ENSG0000(	4.143168	0	5.277655	0	0	0	2.5467	0.058592	0.11145	RP11-297J2	chr2	-	1.22E+08	1.22E+08	708
ENSG0000(	0	9.634302	3.958241	5.992604	8.283888	3.28786	-0.32253	0.74359	0.82919	RP11-392C	chr3	-	1.5E+08	1.5E+08	616

GeneType	GeneDescri	Skm1M_1_	Skm1M_2_	Skm1M_3_	Skm1WT_1	Skm1WT_2	Skm1WT_3	Skm1M_1_	Skm1M_2_	Skm1M_3_	Skm1WT_1	Skm1WT_2	Skm1WT_3
protein_co	tetraspanin	941	928	774	1844	1300	1453	22.58272	26.2447	24.47723	38.2834	35.04927	34.65468
protein_co	tenomodul	7	17	4	0	0	0	0.276764	0.792077	0.208404	0	0	0
protein_co	dolichyl-ph	640	531	326	1451	996	1149	29.18367	28.53392	19.589	57.23877	51.02327	52.07024
protein_co	SCY1-like_3	92	63	79	142	130	118	1.400797	1.130408	1.585073	1.870418	2.223719	1.785579
protein_co	chromoson	177	170	144	800	634	644	2.151678	2.435342	2.306754	8.413117	8.658492	7.780356
protein_co	complemer	1787	1552	1732	0	0	0	13.5441	13.86196	17.2985	0	0	0
protein_co	fucosidase_	1389	1208	1085	1625	1199	1304	43.51186	44.59431	44.78885	44.03741	42.19623	40.59688
protein_co	glutamate-(	310	210	197	452	388	374	4.304146	3.435988	3.604345	5.429086	6.0521	5.160675
protein_co	nuclear_tra	763	703	763	824	846	711	10.59931	11.50842	13.9673	9.902466	13.203	9.815951
protein_co	sperm-tail_	87	87	51	201	162	159	0.765603	0.902216	0.591411	1.530183	1.601579	1.390564
protein_co	NIPA-like_d	202	209	151	303	264	229	1.951119	2.378952	1.921959	2.53185	2.86474	2.198252
protein_co	LAS1-like_(	672	574	502	1598	1317	1470	6.835033	6.88003	6.72837	14.06084	15.04895	14.8593
protein_co	ectonucleo	7	12	6	45	58	36	0.079679	0.160966	0.089998	0.44312	0.741691	0.407247
protein_co	sema_dom	343	219	198	313	272	314	4.776108	3.593612	3.633122	3.770399	4.254984	4.345295
protein_co	cystic_fibrc	2	0	1	71	58	53	0.017278	0	0.011384	0.530634	0.562925	0.45505
protein_co	ankyrin_rep	921	812	918	705	704	597	8.018197	8.330675	10.53161	5.309691	6.885553	5.165366
protein_co	cytochrom	90	51	79	40	38	31	1.484327	0.991207	1.716916	0.570703	0.704076	0.508111
protein_co	KRIT1_anky	381	387	371	563	524	532	4.235724	5.070149	5.435149	5.414696	6.544599	5.877924
protein_co	RAD52_hor	232	238	151	291	278	318	4.346182	5.254168	3.727621	4.716023	5.85078	5.920477
pseudogen	myosin_he	3	2	3	0	3	8	0.025234	0.019825	0.033252	0	0.028349	0.066875
protein_co	BCL2-assoc	98	40	63	46	47	92	4.484198	2.156879	3.798692	1.820873	2.416048	4.183658
protein_co	leucine_am	1035	776	694	1753	1371	1516	24.76002	21.87658	21.87787	36.27902	36.84658	36.04288
protein_co	CD99_mole	24271	20706	16805	8920	6909	8856	1032.073	1037.591	941.6642	328.1335	330.0555	374.2571
protein_co	heparan_su	5	0	3	22	26	9	0.03296	0	0.02606	0.125461	0.192551	0.058962
protein_co	amiloride_l	0	0	0	0	2	0	0	0	0	0	0.037943	0
protein_co	wingless-ty	159	139	180	11	20	9	2.674807	2.755607	3.990274	0.160085	0.377985	0.150469
protein_co	HECT_C2_a	53	66	71	11	5	4	0.410275	0.602075	0.724257	0.073664	0.043483	0.030773
protein_co	MAD1_mit(	678	506	468	1606	1274	1567	12.00067	10.55439	10.91582	24.59146	25.33344	27.56477
protein_co	LIM_and_SI	9508	8080	7405	11681	12417	13971	122.5025	122.6802	125.7233	130.1964	179.7305	178.8929
protein_co	sorting_nex	256	219	185	415	302	347	4.958981	4.999236	4.722359	6.954462	6.572165	6.680232
protein_co	mannose-6	872	736	776	1390	1411	1496	16.75056	16.66087	19.64307	23.09887	30.45012	28.55973
protein_co	kelch-like_f	0	0	0	210	127	169	0	0	0	1.804121	1.41689	1.667937
protein_co	cytochrom	49	38	56	21	30	36	0.548206	0.501	0.825601	0.20325	0.377066	0.400276
protein_co	islet_cell_a	4	6	1	88	83	107	0.086153	0.152289	0.028382	1.639668	2.008341	2.290359
protein_co	dysbindin_	82	91	56	858	679	732	1.502652	1.965138	1.352282	13.60175	13.97859	13.33108
protein_co	amyotroph	564	502	539	1428	1348	1131	4.494088	4.713823	5.659604	9.843594	12.06706	8.956425
protein_co	caspase_10	3	10	4	26	19	12	0.026792	0.105242	0.047074	0.200872	0.190628	0.106506
protein_co	CASP8_and	260	237	188	643	391	516	3.117703	3.349013	2.970668	6.670146	5.26729	6.14923
protein_co	tissue_fact(	406	387	294	269	168	181	2.795064	3.139669	2.667153	1.602068	1.299344	1.23838
protein_co	NADH_deh	259	238	198	352	287	331	4.61053	4.992697	4.64463	5.420718	5.739606	5.855834
protein_co	RNA_bindi	1592	1401	1434	1498	1198	1204	15.00749	15.56361	17.81349	12.2163	12.68735	11.27979
protein_co	myotubula	25	59	40	73	27	47	0.343773	0.956072	0.724813	0.868395	0.417104	0.642301
protein_co	solute_carr	473	490	547	973	842	716	3.278488	4.002355	4.99614	5.834294	6.556523	4.932137

protein_co	ADP-ribosy	1524	1314	945	2678	1724	1941	53.46725	54.3257	43.68874	81.27864	67.94995	67.67652
protein_co	sterile_alpl	237	181	164	74	82	66	1.717828	1.546027	1.566426	0.464009	0.66772	0.475428
processed_	polymerase	1891	1364	1462	3399	2356	2930	38.68293	32.88132	39.41032	60.15088	54.14423	59.56691
protein_co	plexin_D1	2433	1974	1782	3142	3505	3823	18.13906	17.3431	17.50714	20.26477	29.35686	28.32608
protein_co	adenylate_l	1914	1769	1435	2862	2233	2627	28.25685	30.77632	27.91699	36.55228	37.03562	38.54353
protein_co	CD38_mole	0	2	3	15	11	8	0	0.066229	0.111088	0.364641	0.347259	0.223414
protein_co	FK506_bin	1418	1154	1021	4693	3824	4732	33.11439	31.75802	31.41963	94.81	100.3246	109.8234
protein_co	lysine_(K)-s	2351	1948	1809	4392	3182	3175	40.6879	39.72909	41.25589	65.75639	61.8674	54.60922
protein_co	RNA_bindir	1250	1205	973	1184	1387	1385	15.3044	17.38603	15.69835	12.54068	19.07796	16.85256
protein_co	calcium/ca	333	347	249	27	24	33	4.522666	5.553756	4.456403	0.317232	0.366193	0.445424
protein_co	RecQ_prote	552	469	504	612	541	441	7.893957	7.903794	9.497756	7.571294	8.691645	6.267638
protein_co	coiled-coil_	192	146	182	415	275	293	2.812582	2.520368	3.513259	5.259144	4.525699	4.265611
protein_co	heat_shock	140	97	99	17	6	15	4.535948	3.703556	4.226784	0.476488	0.218394	0.482993
protein_co	Rho_GTPas	208	203	118	235	250	355	2.502097	2.877689	1.870499	2.445522	3.378546	4.244033
protein_co	NADH_dehy	1098	1004	774	2566	1906	2308	65.68272	70.77659	61.01331	132.791	128.0916	137.2127
protein_co	pyruvate_d	91	71	57	51	35	22	1.347212	1.238683	1.111999	0.653172	0.582119	0.323688
protein_co	solute_carr	0	0	0	0	1	3	0	0	0	0	0.029933	0.079437
protein_co	zinc_finger_	16	13	13	3	6	7	0.292492	0.280055	0.313164	0.047444	0.123224	0.127175
protein_co	ATP-bindin	9	3	4	0	0	0	0.081994	0.032208	0.048022	0	0	0
protein_co	solute_carr	247	217	209	2831	2510	2466	4.096625	4.241271	4.567834	40.61927	46.76834	40.64732
protein_co	suppressior	184	131	155	408	303	307	3.360173	2.819176	3.730013	6.445655	6.216351	5.571754
protein_co	cell_divisio	1275	1063	1143	1808	1530	1459	11.63588	11.43219	13.74581	14.27416	15.68663	13.23287
protein_co	calcitonin_	0	0	0	65	27	31	0	0	0	0.805446	0.434483	0.441297
protein_co	holocytoch	270	188	224	891	704	851	6.277588	5.151029	6.862967	17.92131	18.38869	19.66384
protein_co	dishevelled	1346	1184	873	1404	1096	1649	23.61119	24.4755	20.18003	21.30605	21.59894	28.7477
protein_co	protease_se	0	0	0	48	31	44	0	0	0	1.586109	1.330269	1.670287
protein_co	UPF1_regul	2128	1649	1546	3946	4012	4990	21.06553	19.23661	20.16717	33.79254	44.61806	49.09202
protein_co	src_kinase_	244	207	249	164	149	206	3.231016	3.23018	4.344937	1.878694	2.216586	2.710979
protein_co	solute_carr	2256	1842	1509	7140	4324	5572	93.74795	90.20267	82.63171	256.6752	201.8633	230.1142
protein_co	coiled-coil_	299	258	229	1106	638	876	6.973285	7.090764	7.037794	22.31436	16.71614	20.30392
protein_co	homeobox_	483	391	326	2	1	8	11.14183	10.62902	9.90973	0.039912	0.025915	0.183404
protein_co	polymerase	666	544	402	1003	751	1103	37.83123	36.41516	30.09103	49.28788	47.92534	62.26749
protein_co	DEAH_(Asp·	478	405	423	1099	1040	1059	4.504414	4.497513	5.252736	8.959238	11.01014	9.917814
protein_co	mesenchyn	5	5	2	0	4	0	0.097785	0.115234	0.051543	0	0.087885	0
protein_co	thrombosp	19	8	24	30	55	67	0.157538	0.078168	0.262227	0.215187	0.512322	0.552097
protein_co	ligase_III_D	278	302	307	804	648	706	3.155574	4.039686	4.592051	7.895009	8.263378	7.964305
protein_co	RNA_polym	253	221	248	793	549	548	5.743598	5.912388	7.41908	15.57398	14.00183	12.36385
protein_co	acyl-CoA_sy	2	2	0	7	13	7	0.037217	0.043858	0	0.112686	0.27177	0.129455
protein_co	Putative_RI	45	39	29	98	87	95	0.876184	0.894859	0.744073	1.650714	1.903054	1.838299
protein_co	cytokine_ir	571	430	379	2069	1386	1639	13.85394	12.29456	12.11745	43.4271	37.77893	39.52082
processed_	signal_pept	1411	1072	894	1529	1206	1689	19.60109	17.54911	16.36536	18.37484	18.8213	23.31806
protein_co	family_witl	707	581	540	587	516	552	6.485753	6.280934	6.527841	4.658457	5.317895	5.032569
protein_co	coatomer_l	272	264	181	22	16	18	16.16156	18.48525	14.17189	1.130837	1.06803	1.06291
protein_co	protein_kir	95	88	84	362	308	240	1.342962	1.465987	1.564784	4.427024	4.891477	3.371795

protein_co	male-specif	462	355	347	688	447	527	7.097719	6.427059	7.024916	9.143833	7.714955	8.046316
protein_co	CREB_bindi	2487	2150	1980	1958	2488	2242	12.18775	12.41633	12.78638	8.300866	13.69768	10.91925
protein_co	benzodiaza	11	13	10	46	34	43	0.076364	0.106352	0.091481	0.276259	0.265169	0.29667
protein_co	paraoxonas	0	0	0	2	3	0	0	0	0	0.035669	0.069481	0
protein_co	GC-rich_sec	181	172	148	336	240	160	2.15818	2.416822	2.325443	3.465863	3.214914	1.896002
protein_co	WD_repeat	404	297	225	532	342	455	9.078167	7.864667	6.662453	10.34169	8.633601	10.16103
protein_co	carnitine_C	156	154	133	973	817	836	2.601195	3.02605	2.922367	14.03538	15.30451	13.85365
protein_co	ATP-bindin	4	1	4	12	8	12	0.052678	0.015519	0.069416	0.136713	0.11836	0.157057
protein_co	myeloid/ly	1107	917	1045	670	620	535	8.35672	8.157643	10.39536	4.375484	5.258102	4.013763
protein_co	rhomboid_	1128	851	910	988	639	856	31.79842	28.27048	33.80436	24.09442	20.23701	23.9817
protein_co	SRY_(sex_d	23	22	16	126	136	156	0.293196	0.330491	0.268773	1.389517	1.947682	1.976352
protein_co	inhibitor_c	814	678	798	987	834	813	7.118264	6.986931	9.195755	7.466719	8.193412	7.065613
protein_co	zinc_finger_	406	376	317	1226	828	913	7.237052	7.898245	7.446115	18.90554	16.58116	16.17395
protein_co	MYC_bindi	743	675	799	509	548	420	2.617981	2.802777	3.709874	1.551524	2.169238	1.470742
protein_co	F-box_and_	676	535	622	721	554	468	10.21642	9.528243	12.38731	9.426495	9.406126	7.029225
protein_co	integrin_al	0	0	0	0	0	5	0	0	0	0	0	0.050464
protein_co	pyruvate_d	204	173	156	102	34	76	3.139524	3.137522	3.163684	1.357991	0.587843	1.162403
protein_co	integrin_al	951	708	713	2456	1602	2019	9.189065	8.061784	9.078522	20.52968	17.39011	19.38817
protein_co	zinc_finger_	496	389	444	509	474	491	3.474297	3.211012	4.098293	3.084367	3.730032	3.418034
protein_co	lysosomal-a	2688	2333	2408	3155	2476	2603	35.31151	36.11677	41.68486	35.85497	36.54153	33.98372
protein_co	gametogen	1244	1066	1043	1846	1336	1380	18.83288	19.01782	20.80729	24.17637	22.72228	20.76277
protein_co	integrin_al	11	9	12	5	9	14	0.174723	0.168464	0.251173	0.068705	0.160601	0.221001
protein_co	ankyrin_rep	2	0	0	9	2	2	0.027682	0	0	0.107762	0.031099	0.027511
protein_co	glycerophо	1055	930	839	1790	1362	1394	18.9075	19.64136	19.81428	27.75221	27.42255	24.8287
protein_co	chromoson	478	436	230	909	550	831	10.26604	11.03491	6.509353	16.88893	13.27049	17.73723
protein_co	cytokine_re	67	59	56	151	105	124	1.979379	2.05406	2.180103	3.859171	3.484917	3.640704
protein_co	oxysterol_b	194	176	140	134	168	157	2.283868	2.441681	2.171861	1.364699	2.221916	1.83687
protein_co	transmemb	1541	1354	1139	1118	665	740	18.3992	19.05119	17.9207	11.54785	8.920046	8.780874
protein_co	Y_box_binc	3	0	0	2	2	6	0.034883	0	0	0.020118	0.026126	0.069335
protein_co	keratin_33	0	0	0	0	2	0	0	0	0	0	0.092426	0
processed_	mitogen-ac	435	367	293	321	241	227	5.157745	5.12795	4.577971	3.292598	3.210234	2.674891
protein_co	synergin_ga	1046	806	880	884	908	857	6.729406	6.110646	7.460407	4.919946	6.56266	5.479431
protein_co	transmemb	1963	1697	1314	2159	1773	2277	26.10479	26.59432	23.02661	24.83794	26.48852	30.09349
protein_co	adaptor-rel	6412	5110	5218	6418	5207	5185	55.78597	52.39134	59.8233	48.30524	50.89418	44.83219
protein_co	tachykinin_	7	4	2	8	11	6	0.299102	0.201413	0.112612	0.295715	0.528035	0.25479
protein_co	zinc_finger_	734	578	546	565	578	663	10.14587	9.415172	9.945366	6.756235	8.975739	9.107863
protein_co	chemokine_	0	6	0	23	33	49	0	0.064584	0	0.181742	0.338631	0.444805
protein_co	spermatoge	767	675	519	528	444	466	11.47379	11.89933	10.2309	6.832953	7.461799	6.927987
protein_co	calcium_ch	300	298	237	59	34	71	2.023738	2.368953	2.106766	0.344309	0.257668	0.475994
protein_co	tumor_nec	1506	1343	1163	3167	2291	3443	47.51438	49.93249	48.35202	86.43929	81.20341	107.956
protein_co	distal-less_	0	0	0	483	405	379	0	0	0	9.601073	10.45475	8.654829
protein_co	mitogen-ac	106	98	134	354	392	354	0.502439	0.547408	0.836984	1.45159	2.087435	1.667595
protein_co	v-ral_simia	1201	1050	998	1546	1310	1516	22.07713	22.74553	24.17492	24.58511	27.05328	27.69545
protein_co	BAI1-associ	51	30	31	810	555	669	0.745442	0.51674	0.59709	10.24216	9.11351	9.718056

protein_co	jumonji_C_	100	111	106	97	74	69	0.570977	0.746876	0.797553	0.47913	0.474678	0.391541
protein_co	ets_variant	1121	888	1072	130	130	110	8.789522	8.205021	11.07616	0.881792	1.145123	0.85716
protein_co	acylglycero	311	341	278	837	564	633	4.277643	5.527206	5.038761	9.959388	8.715099	8.652817
protein_co	aldehyde_d	343	298	235	10	16	31	3.090327	3.163979	2.790056	0.077942	0.161949	0.277576
protein_co	tetratricop	0	0	0	0	4	1	0	0	0	0	0.071122	0.015729
protein_co	putative_h	580	557	546	874	802	730	6.13502	6.94305	7.61054	7.997651	9.530407	7.673977
protein_co	chemokine_	0	1	1	0	0	0	0	0.088745	0.099237	0	0	0
protein_co	FERM_RhoC	325	266	321	225	238	219	4.247303	4.096553	5.528021	2.543756	3.494265	2.844354
protein_co	Usher_synd	0	0	0	0	5	4	0	0	0	0	0.110141	0.077947
protein_co	gamma-glu	556	471	394	1696	1227	1521	25.09394	25.05083	23.43285	66.21905	62.21394	68.22333
protein_co	DBF4_hom	189	161	184	946	667	780	2.561005	2.570879	3.285499	11.08927	10.15368	10.50396
protein_co	thromboxa	138	138	89	5	6	0	2.801326	3.301191	2.380725	0.087805	0.136831	0
protein_co	interferon-r	650	568	553	2248	1512	1520	15.02692	15.47434	16.84677	44.95893	39.26969	34.92286
protein_co	cytochrom	211	176	167	351	309	304	3.888113	3.821873	4.055158	5.595341	6.396818	5.567237
protein_co	GTF2I_repe	568	432	406	682	530	445	5.124486	4.592962	4.826839	5.322913	5.371888	3.989988
protein_co	Paf1_RNA_	1086	943	859	1700	1559	1835	27.82862	28.4761	29.00613	37.68545	44.88042	46.73126
protein_co	vacuolar_p	1106	915	998	1222	902	824	9.919149	9.670468	11.79464	9.480986	9.088138	7.344397
protein_co	Rho_GTPas	16	20	11	144	168	236	0.191295	0.281787	0.173305	1.489395	2.256539	2.804182
protein_co	elaC_homo	1056	821	758	3663	2478	2492	14.95604	13.7026	14.14675	44.87999	39.42786	35.07603
protein_co	scinderin	4	5	3	258	213	222	0.067505	0.099439	0.066717	3.766694	4.038371	3.723404
protein_co	arylsulfatas	277	209	274	169	202	172	2.842538	2.527435	3.705202	1.500294	2.328772	1.754142
protein_co	patatin-like	172	107	105	346	258	258	2.70043	1.979682	2.172344	4.699413	4.550648	4.02563
protein_co	adiponectii	1171	988	1114	2230	1913	1869	15.42905	15.34074	19.34203	25.41851	28.31693	24.47378
protein_co	cyclin-depe	44	37	29	76	57	44	1.078428	1.068679	0.936637	1.611443	1.569503	1.071768
protein_co	uridine_ph	0	3	2	2	3	1	0	0.076864	0.0573	0.037617	0.073276	0.021607
protein_co	MAP/microt	1831	1784	1188	927	850	1091	18.60913	21.36681	15.91069	8.150429	9.705227	11.01976
protein_co	prominin_1	3	0	2	759	651	535	0.036519	0	0.032082	7.992957	8.902925	6.472411
protein_co	coiled-coil_	1734	1366	998	2369	1667	2599	87.01392	80.7788	65.99408	102.8413	93.97759	129.6151
protein_co	carcinoemb	0	0	0	29	26	43	0	0	0	0.785434	0.914473	1.337909
protein_co	platelet-act	2367	2061	2174	3206	3037	2761	22.79631	23.39114	27.59057	26.71117	32.85944	26.42667
protein_co	nitric_oxid	0	1	5	435	397	423	0	0.01494	0.083529	4.770719	5.6542	5.32944
protein_co	dynein_axo	3	2	3	4	0	7	0.011208	0.008806	0.01477	0.012928	0	0.025991
protein_co	KIAA0100	1602	1262	1543	2012	1939	1948	11.45018	10.62958	14.53284	12.44058	15.56957	13.8372
protein_co	growth_arr	759	625	608	1129	1229	1052	4.911651	4.766206	5.184705	6.320372	8.934837	6.765674
protein_co	trafficking_	172	161	110	252	142	237	11.31162	12.47755	9.532871	14.33705	10.4914	15.4901
protein_co	megakaryo	2	6	2	11	3	27	0.04964	0.175493	0.065413	0.236188	0.083651	0.666001
protein_co	CD79b_mo	0	0	0	12	1	2	0	0	0	0.433087	0.046868	0.082922
protein_co	sodium_ch	0	0	0	4	0	0	0	0	0	0.023472	0	0
protein_co	suppressior	271	228	205	249	154	206	3.168509	3.141432	3.158452	2.518535	2.022812	2.39366
protein_co	paired_box	13	14	14	23	23	15	0.099427	0.126181	0.141099	0.152178	0.197623	0.114015
protein_co	RNA_pseud	893	702	541	1994	1170	1600	21.89732	20.2854	17.48121	42.29876	32.23104	38.99142
protein_co	rhomboid_	901	812	628	586	405	471	15.94246	16.93143	14.64283	8.969973	8.050717	8.282493
protein_co	LUC7-like_(	1118	1028	837	1664	1302	1599	21.62515	23.43244	21.33426	27.84413	28.29289	30.73799
protein_co	calcium_ch	51	53	32	31	23	33	0.490907	0.601191	0.405895	0.258139	0.248717	0.315684

protein_co	BAI1-associ	23	15	7	13	18	14	0.260291	0.200046	0.104391	0.127274	0.228851	0.15746
protein_co	TSR3_20S_	1284	948	704	1812	1253	1655	54.68724	47.58131	39.51195	66.76397	59.9544	70.0533
protein_co	phosphatid	818	698	522	1769	1298	1676	14.40643	14.48657	12.11458	26.95218	25.68188	29.33505
protein_co	Crm_cramp	313	291	217	332	306	423	2.132081	2.335928	1.947843	1.956412	2.341692	2.86358
protein_co	TEA_domai	1563	1370	1063	2476	2032	2565	27.73945	28.65276	24.86033	38.01478	40.5146	45.24138
protein_co	selectin_E	0	0	0	2	1	3	0	0	0	0.023748	0.01542	0.040924
protein_co	DnaJ_(Hsp4	717	543	550	1277	1247	1049	11.46442	10.23151	11.58859	17.66391	22.40002	16.66933
protein_co	myosin_reg	280	218	213	855	970	934	5.301673	4.864279	5.314585	14.00503	20.63363	17.57565
protein_co	NADPH_oxi	7	2	3	14	17	28	0.146535	0.049338	0.082756	0.253533	0.399799	0.58252
protein_co	E2F_transcr	8	6	5	240	201	213	0.081589	0.072111	0.067196	2.11746	2.302959	2.158889
protein_co	proteasom	2779	2266	1869	5004	4062	4964	75.87572	72.90902	67.24475	118.1938	124.5958	134.6963
protein_co	synapsin_I	22	26	23	14	11	25	0.363628	0.506426	0.500954	0.200183	0.204257	0.410662
protein_co	jumonji_AT	459	444	445	838	919	929	4.222401	4.813232	5.394381	6.668894	9.497544	8.493215
protein_co	cyclin-depe	21	18	36	4	22	17	0.321411	0.324654	0.726071	0.052962	0.37828	0.258583
protein_co	calcium/ca	0	0	0	44	51	50	0	0	0	0.771498	1.161283	1.00716
protein_co	cyclin-depe	4	2	4	2	7	6	0.079821	0.047032	0.105184	0.034526	0.156929	0.118991
protein_co	NAD_kinase	1096	854	834	1860	1407	1543	15.84038	14.54521	15.88386	23.25579	22.84538	22.16311
protein_co	transcriptic	2	0	1	792	676	747	0.018265	0	0.012034	6.257156	6.935608	6.779834
protein_co	deleted_in_	13	9	2	0	10	13	0.107101	0.087378	0.021713	0	0.092555	0.10644
protein_co	cytohesin_	1921	1524	1603	512	448	446	22.57484	21.10519	24.82365	5.205114	5.914586	5.208849
protein_co	ADAM_met	51	26	52	50	45	28	0.289264	0.173782	0.388653	0.245334	0.286738	0.157831
protein_co	synaptophy	1046	1036	878	1630	1305	1440	25.74444	30.0482	28.47613	34.70582	36.08372	35.2228
protein_co	cytochrom	179	179	140	1142	1102	1392	2.961387	3.489814	3.052144	16.34448	20.48202	22.88711
protein_co	sperm_assc	1418	1185	1575	1612	1379	1256	9.074136	8.936233	13.28142	8.92395	9.913851	7.987821
protein_co	cadherin_E	119	106	104	168	254	249	0.52627	0.552427	0.60608	0.642738	1.261957	1.094386
protein_co	aminoadipa	333	311	308	215	308	306	5.452939	6.001418	6.646177	3.045705	5.666125	4.979864
protein_co	pleckstrin_	43	35	31	355	312	378	0.731746	0.701887	0.695166	5.226169	5.964798	6.392835
protein_co	synovial_sa	172	142	135	451	337	479	8.697088	8.461373	8.995266	19.72809	19.14363	24.0708
protein_co	MPN_doma	116	128	81	145	110	164	3.812014	4.956939	3.507651	4.122186	4.06105	5.356117
protein_co	microsoma	1483	1158	937	5055	2839	3733	36.48304	33.57109	30.37556	107.5806	78.46289	91.26777
protein_co	cryptochro	224	218	201	637	453	382	3.093058	3.547346	3.657386	7.60926	7.02728	5.242193
protein_co	peptidogly	5	10	3	3	3	7	0.367646	0.866496	0.29068	0.190829	0.247816	0.511525
protein_co	nuclear_fac	9563	7974	6730	5	6	8	91.55058	89.96017	84.90179	0.041409	0.064531	0.076114
protein_co	ST3_beta-ga	813	786	712	1009	1293	1394	6.177842	7.038432	7.129533	6.632854	11.03809	10.52734
protein_co	matrix_met	40	65	34	10	17	9	0.595847	1.141025	0.667403	0.128866	0.284494	0.133238
protein_co	interleukin	41	42	32	111	58	64	1.571746	1.897382	1.616528	3.681157	2.497902	2.438305
protein_co	polycystic_	4479	3828	2994	1101	1358	1713	16.77201	16.89208	14.77375	3.5666	5.712852	6.374867
protein_co	mitogen-ac	162	144	121	92	77	49	1.532876	1.60569	1.508732	0.753083	0.818525	0.460784
protein_co	mediator_c	1284	978	842	2640	1703	1864	17.4477	15.66099	15.07718	31.03417	25.99781	25.17264
protein_co	Rho-relatec	396	290	225	681	720	952	3.846016	3.319105	2.879607	5.721712	7.855927	9.188878
protein_co	HEAT_repea	412	371	440	421	320	343	3.158825	3.352042	4.445452	2.792374	2.756306	2.613558
protein_co	SEC62_hon	2007	1784	1832	2236	1670	1959	16.17731	16.94575	19.45894	15.59171	15.12253	15.69289
protein_co	ribosomal_	15135	13493	9089	18819	12023	16119	438.8072	461.0064	347.25	472.0096	391.6095	464.4501
protein_co	cold_shock	11880	9999	9721	13714	11592	11486	150.9333	149.7036	162.7475	150.7286	165.4535	145.0264

protein_co ubiquitin_	2024	1656	1889	2630	2005	2085	20.49198	19.7579	25.2023	23.03521	22.80536	20.97921
protein_co REV3-like_	1113	848	1125	733	617	591	5.374254	4.825319	7.158308	3.061893	3.347012	2.836091
protein_co teneurin_t	38	53	40	96	157	116	0.156059	0.256501	0.216471	0.341067	0.72436	0.473449
protein_co paired_box	1	1	0	94	116	80	0.00956	0.011265	0	0.777374	1.245794	0.760044
protein_co mannan-bi	72	61	50	187	82	134	1.562834	1.560333	1.430162	3.511437	1.9996	2.890645
protein_co family_with	79	81	74	235	194	146	1.172509	1.41671	1.44729	3.017309	3.234743	2.153533
protein_co TRAF3_inte	34	39	47	85	42	54	0.545122	0.736863	0.992996	1.178954	0.756508	0.860436
protein_co protein-O-r	669	470	497	976	761	974	6.271919	5.192533	6.139959	7.91566	8.015083	9.074922
protein_co Vps20-asso	811	590	695	1866	1265	1299	13.06211	11.19828	14.75068	25.99962	22.88927	20.79271
protein_co MLX_intera	2	5	0	0	1	0	0.032301	0.095161	0	0	0.018144	0
protein_co bromodom	2049	1827	1816	3578	4297	4341	17.77714	18.67951	20.76206	26.85488	41.88266	37.42996
protein_co RAN_bindi	476	467	525	1281	1010	1194	8.095057	9.359161	11.76541	18.84626	19.29672	20.18027
protein_co ets_variant	3	9	3	19	16	24	0.073631	0.26031	0.097028	0.403421	0.441175	0.585414
protein_co SprT-like_N	204	164	166	490	382	424	3.03455	2.874849	3.253921	6.305553	6.38376	6.268153
protein_co methyltran	560	476	434	1473	1044	1182	8.911018	8.925927	9.10047	20.27706	18.66332	18.69246
protein_co dual-specifi	210	190	159	259	202	220	6.122031	6.527351	6.108129	6.531892	6.615713	6.373949
protein_co zinc_finger_	1898	1680	1532	4668	2709	3312	7.291344	7.605499	7.755413	15.51334	11.69148	12.64478
protein_co ubiquinol-c	3437	2696	2366	6040	4301	4619	91.6666	84.73417	83.15361	139.3579	128.8695	122.4304
protein_co STARD3_N-	717	623	546	1521	1018	1216	10.3911	10.6399	10.42725	19.0693	16.57445	17.51401
protein_co CD9_molec	655	493	442	7159	4762	6006	22.31425	19.79225	19.84258	210.9874	182.255	203.3462
protein_co hedgehog_	5	0	0	0	0	0	0.141933	0	0	0	0	0
protein_co non-SMC_c	1038	841	851	4146	3108	3354	9.904966	9.457116	10.70089	34.22535	33.31852	31.80741
protein_co intermedia	1178	944	779	339	306	367	20.11109	18.99194	17.52518	5.006717	5.868955	6.226816
protein_co gastric_inh	3	7	1	8	8	5	0.048289	0.13278	0.021211	0.111399	0.144666	0.079985
protein_co PHD_finger	36	33	12	94	80	87	0.894777	0.96657	0.393033	2.021172	2.233837	2.149025
protein_co sema_dom	0	0	3	2	0	3	0	0	0.042721	0.018697	0	0.032219
protein_co nischarin	3581	2660	2455	2672	2292	2176	35.43583	31.01895	32.01287	22.87377	25.48015	21.39966
protein_co stabilin_1	2	1	0	1	0	3	0.013355	0.007869	0	0.005777	0	0.019909
protein_co fuzzy_plan	200	216	126	214	221	230	6.321313	8.045224	5.247865	5.851323	7.84727	7.224616
protein_co solute_carr	4	1	2	2	0	1	0.096917	0.028553	0.063857	0.041921	0	0.02408
protein_co iduronate_	1565	1307	1283	2168	1662	1657	10.87448	10.70229	11.74777	13.03216	12.97401	11.44264
protein_co protease_se	0	0	0	0	1	3	0	0	0	0	0.061569	0.163398
protein_co zinc_finger_	143	122	120	252	152	228	1.757326	1.766783	1.943267	2.679045	2.0985	2.784588
protein_co CD4_molec	12	16	3	0	3	2	0.204012	0.320554	0.067209	0	0.057299	0.033792
protein_co leucine_ric	94	55	57	49	59	72	3.054913	2.1064	2.441072	1.377622	2.154131	2.325483
protein_co Bruton_aga	0	0	0	5	0	0	0	0	0	0.088792	0	0
protein_co hemochror	182	170	178	134	92	134	1.822789	2.006416	2.349199	1.161001	1.035146	1.333765
protein_co sex_comb_	683	616	467	641	454	478	10.80654	11.48561	9.736836	8.773789	8.069954	7.516293
protein_co FYN_oncog	1152	1128	882	3118	2381	2523	16.81037	19.39729	16.96009	39.3608	39.03312	36.5891
protein_co human_imi	663	509	758	170	166	151	3.609984	3.266004	5.438709	0.800763	1.015428	0.817106
protein_co flavin_cont	5	0	2	1	0	0	0.08457	0	0.044577	0.014632	0	0
protein_co transcriptic	723	588	621	1800	1341	1286	7.426531	7.117576	8.405704	15.99496	15.47482	13.12799
protein_co lysophosph	1481	1140	995	3270	2247	2955	43.31802	39.29393	38.35053	82.74167	73.83557	85.89752
protein_co chloride_ch	820	682	647	605	615	643	7.775679	7.62107	8.084693	4.962984	6.551619	6.059616

protein_co	mannose_r	19259	16587	13335	2174	2444	2935	170.2723	172.8165	155.3596	16.62773	24.27507	25.78862
protein_co	solute_carr	0	0	0	0	0	3	0	0	0	0	0	0.042215
protein_co	tetraspanin	1229	916	928	1214	1377	1811	15.05077	13.21933	14.97579	12.86141	18.94479	22.04119
protein_co	BTB_(POZ)_	943	703	998	870	907	795	5.922106	5.202678	8.259046	4.726577	6.399129	4.961823
protein_co	amyloid_be	282	238	132	560	299	388	3.512791	3.493713	2.166765	6.034679	4.184306	4.803353
protein_co	Meckel_syn	93	139	96	358	233	320	2.058325	3.625374	2.799864	6.854518	5.793432	7.038669
protein_co	abhydrolas	161	102	134	348	219	324	5.043491	3.765413	5.531527	9.430781	7.707234	10.08695
protein_co	Kallmann_s	40	54	28	231	214	158	0.335388	0.533566	0.309372	1.67557	2.015813	1.316601
protein_co	A_kinase_(I	786	552	535	1012	529	704	15.137	12.52747	13.57707	16.86013	11.44517	13.4741
protein_co	mbt_doma	376	356	318	444	415	339	3.69859	4.126725	4.122022	3.778282	4.586121	3.31404
protein_co	UTP18_sma	632	507	467	1402	1124	1289	17.66563	16.70041	17.2014	33.90183	35.29616	35.80756
protein_co	ring_finger_	1313	967	964	1374	1162	1210	12.32692	10.69852	11.92619	11.15937	12.2559	11.28977
protein_co	tetratricop	643	571	563	1484	1122	1244	11.07026	11.58484	12.77292	22.10263	21.70146	21.28516
protein_co	polypyrimi	6430	5239	4581	17769	15308	16911	73.03381	70.12429	68.56589	174.5979	195.3352	190.8938
protein_co	D4_zinc_an	81	60	61	39	39	62	1.83179	1.599002	1.817839	0.762989	0.990842	1.393452
protein_co	synaptotag	15	20	16	956	1180	1128	0.1636	0.257057	0.229957	9.020139	14.4585	12.22675
protein_co	leucyl-tRNA	381	334	278	902	784	806	4.251796	4.392391	4.088152	8.707971	9.829072	8.939065
protein_co	phosphatid	803	689	891	2210	1959	1822	5.167329	5.224887	7.555498	12.30285	14.16231	11.65222
protein_co	plasminoge	1204	1109	879	733	378	503	39.59066	42.97391	38.08815	20.8513	13.96391	16.43781
protein_co	anillin_acti	758	496	653	4505	3422	3181	8.382969	6.464239	9.516487	43.10091	42.51652	34.96246
protein_co	widely_inte	2662	2039	1873	2570	1975	2107	20.91554	18.87928	19.39249	17.46856	17.43321	16.45263
protein_co	RAB_GTPas	1606	1436	1390	1131	1256	1180	17.01486	17.92851	19.40584	10.36593	14.94932	12.42437
protein_co	decorin	9436	8570	6309	4587	2849	3498	170.8452	182.8532	150.5255	71.84664	57.95037	62.94253
protein_co	glutaminyl-	487	430	314	582	437	430	11.16115	11.6133	9.482974	11.53894	11.2515	9.793957
protein_co	protein_ph	1741	1464	1340	2436	1751	2092	19.71557	19.53703	19.99632	23.86441	22.27643	23.54408
protein_co	centrosoma	467	377	345	302	256	257	4.228398	4.022605	4.116356	2.365533	2.604042	2.312607
protein_co	mitogen-ac	362	331	375	1125	887	894	4.393544	4.734145	5.997531	11.81196	12.09425	10.78335
protein_co	zinc_finger_	5	8	9	7	0	7	0.128	0.241345	0.303612	0.155025	0	0.178094
protein_co	transmemb	407	351	268	523	440	467	10.6986	10.87294	9.283297	11.89316	12.99375	12.19998
protein_co	gamma-am	0	2	0	303	199	191	0	0.033614	0	3.738434	3.188499	2.707242
protein_co	breast_can	114	97	119	1000	834	827	0.848366	0.850662	1.166971	6.437856	6.972577	6.116365
protein_co	excision_re	1450	1175	917	1016	747	988	20.05341	19.14984	16.71184	12.15561	11.60619	13.57959
processed_	sema_doma	156	118	87	232	190	253	2.515624	2.242386	1.848738	3.236475	3.442103	4.054631
protein_co	membrane-	422	364	478	377	399	406	5.012587	5.095161	7.481905	3.873948	5.324409	4.792754
protein_co	prickle_hor	188	162	127	392	305	283	3.536925	3.591618	3.148521	6.379947	6.446395	5.291321
protein_co	exostosin-li	3157	2414	2507	2179	1956	1902	20.24158	18.23955	21.18161	12.08621	14.08924	12.11965
protein_co	ELOVL_fatt	3536	3021	3393	2304	1808	1863	60.97699	61.39196	77.1032	34.37156	35.02686	31.92833
protein_co	arachidona	0	0	0	3	2	4	0	0	0	0.054871	0.047505	0.084048
protein_co	lysine_(K)-s	722	497	586	681	539	663	6.851299	5.557753	7.327708	5.590438	5.746105	6.252575
protein_co	calcium_bi	781	733	589	289	260	307	10.63449	11.76188	10.56856	3.404291	3.977299	4.154453
protein_co	ubiquitin_p	234	225	237	1021	683	649	3.353598	3.800011	4.475879	12.65855	10.99677	9.243779
protein_co	mitogen-ac	902	891	969	1070	851	841	9.923686	11.55184	14.04834	10.18388	10.51829	9.195431
protein_co	EH-domain	555	408	450	667	610	692	6.337845	5.490551	6.771673	6.589273	7.825779	7.853521
protein_co	proteasom	1206	1045	929	3454	1939	2561	39.33878	40.16955	39.93228	97.46729	71.05595	83.02192

protein_co mannosida	1701	1366	1355	960	806	850	11.66636	11.0405	12.24631	5.695938	6.210337	5.793748
protein_co solute_carr	127	99	178	7	1	3	1.312672	1.205854	2.424417	0.062591	0.011612	0.030817
protein_co claudin_11	6286	5059	3918	119	75	68	153.4288	145.5138	126.0178	2.512711	2.056567	1.649495
protein_co solute_carr	2708	2375	1727	3870	2512	3360	64.66586	66.83395	54.34424	79.94667	67.38994	79.73983
protein_co major_vaul	6576	5495	4414	413	318	385	121.5148	119.6581	107.4817	6.602076	6.601515	7.0703
protein_co negative_re	495	406	411	701	641	684	8.163798	7.890784	8.932308	10.00157	11.87666	11.21122
protein_co phosphoglu	1045	960	917	841	696	691	9.059004	9.807143	10.47534	6.307005	6.778326	5.953219
protein_co RWD_dom	85	71	51	94	73	75	2.052913	2.02077	1.623142	1.964004	1.980722	1.800207
protein_co CDC-like_ki	696	653	541	804	518	578	11.48595	12.69925	11.76494	11.47828	9.603655	9.479714
protein_co polymerase	180	136	188	355	328	297	2.230138	1.985661	3.069388	3.804964	4.565434	3.657003
protein_co angel_hom	321	267	221	267	293	279	4.135814	4.053912	3.752175	2.975981	4.241043	3.57248
protein_co ring_finger_	621	524	549	902	667	618	7.763012	7.719285	9.043693	9.754572	9.367281	7.6778
protein_co deoxyribon	259	216	238	66	53	74	4.558417	4.47997	5.519834	1.004896	1.047947	1.294362
protein_co DEAD/H_(A	224	208	145	1418	1076	1414	2.835673	3.102976	2.418861	15.52914	15.30275	17.78964
protein_co heme_bind	777	676	560	1356	895	1408	20.00737	20.5127	19.00167	30.20589	25.89054	36.03141
protein_co G_protein-	108	93	92	615	424	404	0.77664	0.788109	0.871804	3.825907	3.425399	2.887269
protein_co mastermin	16	13	22	65	44	53	0.174507	0.167087	0.316191	0.613294	0.539131	0.574484
protein_co CD6_molec	0	0	0	1	2	4	0	0	0	0.014083	0.036578	0.064716
protein_co transformir	544	388	358	3217	2712	2952	10.35595	8.704221	8.980674	52.97917	58.00025	55.84922
protein_co UFM1-spec	548	508	529	727	640	501	6.868292	7.50307	8.736926	7.882529	9.011503	6.240445
protein_co polymerase	234	142	178	1440	1039	1102	3.308812	2.366201	3.316737	17.61496	16.5052	15.48629
protein_co zinc_finger_	628	502	396	1140	872	960	10.13626	9.548366	8.42264	15.91791	15.81189	15.39923
protein_co calpain_1_(	3717	3017	2476	6853	5262	6678	63.76593	60.9928	55.97339	101.7044	101.4136	113.855
protein_co acid_phosp	1	0	3	54	57	42	0.016941	0	0.066973	0.791405	1.084841	0.707133
protein_co malate_deh	1827	1400	1228	4086	2956	3276	58.62012	52.93504	51.92079	113.4147	106.552	104.4628
protein_co solute_carr	863	796	838	1639	1272	1224	13.86588	15.07151	17.74253	22.78131	22.96005	19.54464
protein_co myotubula	317	250	240	239	205	246	5.036703	4.680952	5.024966	3.285096	3.659233	3.884471
protein_co cytochrom	637	550	437	1002	791	875	12.09592	12.30748	10.93492	16.46001	16.87426	16.51266
protein_co coiled-coil_	17	12	21	601	707	654	0.120417	0.100168	0.196017	3.682786	5.6261	4.603905
protein_co YY1_associa	102	92	105	197	134	153	1.059859	1.12653	1.437712	1.770831	1.564234	1.57997
protein_co zinc_finger_	702	633	710	1262	935	914	8.459954	8.989627	11.27519	13.15689	12.65877	10.94679
protein_co Wiskott-Ald	7	8	14	4	19	18	0.200426	0.269931	0.528224	0.099078	0.611164	0.512197
protein_co dipeptidase	0	0	0	2	12	7	0	0	0	0.051692	0.402771	0.207843
protein_co BH3_intera	466	307	300	933	605	657	9.89591	7.682725	8.3951	17.14014	14.43359	13.8658
protein_co matrin_3	4632	3987	4162	8791	6527	6332	33.56456	34.04597	39.74196	55.10788	53.13432	45.5998
protein_co NPC1-like_	1	2	2	0	1	4	0.010488	0.024718	0.02764	0	0.011782	0.041691
protein_co xylosyltran	1071	941	829	591	518	625	16.16761	16.73991	16.49095	7.718036	8.784866	9.376613
protein_co RANBP2-lik	4	7	6	17	9	7	0.029197	0.060212	0.057711	0.107346	0.073802	0.050779
protein_co stathmin-li	0	2	2	1	0	0	0	0.054535	0.060982	0.020017	0	0
protein_co NudC_dom	1564	1297	1227	1722	1412	1502	16.53679	16.16075	17.09598	15.75109	16.77252	15.78316
protein_co ISL_LIM_hc	45	32	24	493	364	424	0.864735	0.724649	0.607738	8.195594	7.858161	8.097407
protein_co choline_de	11	1	9	54	29	86	0.159987	0.017139	0.172492	0.679434	0.473847	1.243079
protein_co interleukin	0	0	0	2	1	3	0	0	0	0.026148	0.016979	0.045059
protein_co chloride_ch	0	0	0	0	0	3	0	0	0	0	0	0.047686

protein_co	glycosyltra	975	910	768	991	599	759	22.24891	24.47105	23.09405	19.56324	15.35607	17.21296
protein_co	ATPase_Ca+	2004	1674	1909	2259	1950	1884	20.93818	20.61122	26.28342	20.41834	22.8889	19.56283
protein_co	SRC_kinase	0	0	1	76	79	83	0	0	0.009884	0.493159	0.665712	0.618726
protein_co	insulin-like	3	8	5	31	15	26	0.02155	0.067721	0.047329	0.192641	0.12105	0.185613
protein_co	solute_carr	85	87	67	114	61	73	1.690452	2.038968	1.755875	1.961336	1.362897	1.442835
protein_co	MAGI_fami	26	11	20	21	6	24	0.460203	0.229443	0.466488	0.321557	0.11931	0.422179
protein_co	ralA_bindir	1749	1380	1293	1985	1475	1749	21.19821	19.71041	20.65108	20.81292	20.08402	21.0673
protein_co	RUN_and_F	970	853	878	660	621	661	12.13153	12.57187	14.47015	7.140864	8.725383	8.215896
protein_co	contactin_	35	31	28	48	53	73	0.333442	0.348033	0.351516	0.3956	0.567253	0.691169
protein_co	solute_carr	1	0	1	0	8	0	0.009172	0	0.012087	0	0.082434	0
protein_co	WW_doma	2686	2329	2524	1908	1753	1567	28.27028	28.88688	35.00647	17.37263	20.72789	16.3909
protein_co	alkylglycer	297	347	325	1493	1522	1403	2.025177	2.788323	2.920282	8.807028	11.65924	9.507665
pseudogen	zinc_finger_	0	3	0	2	1	3	0	0.105503	0	0.051633	0.033526	0.088975
protein_co	chromoson	306	209	203	600	382	462	6.829656	5.497064	5.970466	11.58488	9.578331	10.24776
protein_co	ATPase_Na-	146	109	108	24	53	31	1.425823	1.25443	1.389861	0.202762	0.581484	0.300874
protein_co	tetratricop	404	314	262	781	524	642	7.436774	6.811456	6.355348	12.43705	10.83636	11.74486
protein_co	zinc_finger_	24	51	24	89	64	65	0.449923	1.126691	0.592889	1.443379	1.347896	1.211017
protein_co	V-set_and_i	0	0	0	4	2	0	0	0	0	0.153817	0.099876	0
protein_co	pleckstrin_	4121	3760	3183	768	1039	1115	36.69804	39.45801	37.35181	5.916494	10.39453	9.8679
protein_co	macrophag	0	0	0	0	3	4	0	0	0	0	0.096814	0.114192
protein_co	cytochrom	20	30	13	90	71	60	0.324592	0.573768	0.278027	1.263612	1.29454	0.967763
protein_co	PR_domain	86	56	76	41	63	46	1.463493	1.123019	1.704278	0.603586	1.20443	0.777964
protein_co	synaptotag	7	1	0	20	5	5	0.072043	0.012128	0	0.178067	0.057811	0.051141
protein_co	snail_homo	6758	5895	5414	1448	1223	1202	162.33	166.8674	171.3695	30.0893	33.0032	28.69423
protein_co	CD74_mole	2	4	0	210	162	197	0.06131	0.1445	0	5.569062	5.579096	6.001719
protein_co	hepatocyte	379	314	327	0	0	0	3.350248	3.270955	3.809082	0	0	0
protein_co	zinc_finger_	529	487	476	706	496	508	4.917609	5.335	5.830961	5.677617	5.179992	4.693229
protein_co	neurochon	1083	1001	873	775	677	797	15.5675	16.95632	16.53634	9.637293	10.93272	11.38566
protein_co	G_protein-r	3750	3012	2544	150	177	204	31.66327	29.96999	28.30587	1.095668	1.678985	1.711845
pseudogen	chaperonin	0	0	0	0	1	0	0	0	0	0	0.035529	0
protein_co	ZFP64_zinc	330	283	230	700	507	554	5.35249	5.40923	4.915918	9.822069	9.238447	8.930203
protein_co	menage_a_	161	137	138	369	304	313	3.234725	3.243688	3.653637	6.413585	6.861738	6.24979
protein_co	sterile_alpl	489	382	386	2097	2536	2426	3.943358	3.630177	4.101847	14.62914	22.97501	19.44275
protein_co	runt-relate	61	57	35	326	257	258	0.744102	0.819378	0.562607	3.440194	3.521961	3.127748
protein_co	MRE11_me	162	161	124	463	420	352	3.123249	3.657838	3.150272	7.722102	9.096826	6.744408
protein_co	pleckstrin_	6	3	5	13	7	20	0.133465	0.07864	0.146562	0.250162	0.174929	0.442135
protein_co	serpin_pep	157	104	99	212	170	153	3.17363	2.477405	2.6371	3.707281	3.860598	3.073673
protein_co	cytochrom	0	0	1	0	0	0	0	0	0.037751	0	0	0
protein_co	solute_carr	15	2	9	19	5	13	0.397455	0.06245	0.314249	0.435525	0.148839	0.342334
protein_co	spastin	329	249	264	453	356	338	3.403867	3.03587	3.599278	4.054505	4.137859	3.475386
protein_co	neurexin_3	124	88	91	294	358	318	1.018412	0.85171	0.984868	2.088873	3.303192	2.595605
protein_co	oxysterol_b	964	859	711	501	403	511	13.12294	13.78016	12.75436	5.900039	6.163228	6.913289
protein_co	aquarius_h	404	430	469	1431	1166	1031	3.597672	4.512485	5.503613	11.02409	11.66508	9.124489
protein_co	carbamoyl-	158	132	125	218	191	171	1.436983	1.414736	1.498095	1.715197	1.951538	1.545611

protein_co	four_and_a	5169	4331	4120	622	411	425	94.75485	93.55999	99.5238	9.863892	8.464197	7.742719
protein_co	replication	1234	1074	921	1319	1137	1314	29.78987	30.55377	29.29867	27.54617	30.83635	31.52524
protein_co	gamma-am	0	0	1	2	0	0	0	0	0.016327	0.021436	0	0
protein_co	NLR_family	31	25	20	1628	1128	1227	0.438347	0.416585	0.372667	19.91469	17.91903	17.24291
protein_co	solute_carr	91	67	57	177	172	218	0.64381	0.558597	0.531405	1.08331	1.36708	1.532789
protein_co	ring_finger_	2815	2239	1940	3565	2537	2999	38.9618	36.51925	35.38321	42.68578	39.44847	41.25217
protein_co	zinc_finger_	140	189	104	336	264	265	2.229094	3.54625	2.18207	4.6281	4.722298	4.1933
protein_co	zinc_finger_	468	369	343	858	528	587	11.41769	10.60879	11.0271	18.10851	14.47156	14.23246
protein_co	GRAM_dom	53	41	69	28	20	27	0.363314	0.331205	0.62329	0.166045	0.154023	0.183941
protein_co	ribonuclea	4024	3343	2670	4641	2701	3673	64.92977	63.56665	56.7717	64.78291	48.96204	58.90015
protein_co	NADH_dehy	1047	814	961	1739	1553	1556	10.63696	9.745464	12.86558	15.28388	17.72522	15.71051
protein_co	RB1-induci	393	387	443	492	498	395	3.135766	3.638892	4.657895	3.396091	4.464055	3.132261
protein_co	endoplasm	782	655	651	1931	1362	1564	8.529019	8.418616	9.356386	18.21955	16.68855	16.95269
protein_co	aminolevul	709	579	560	1349	924	1056	15.44657	14.86522	16.07713	25.42499	22.61553	22.86438
protein_co	baculoviral	8	6	6	61	52	56	0.081495	0.072027	0.080543	0.537567	0.595103	0.56694
protein_co	A_kinase_(P	1174	919	1378	884	930	712	6.26982	5.783751	9.697751	4.084155	5.579805	3.778998
protein_co	glutaredoxi	162	146	157	345	237	387	7.58306	8.053588	9.684204	13.97049	12.46312	18.00322
protein_co	small_nucl	194	190	168	311	186	229	3.866925	4.462978	4.412738	5.362748	4.165106	4.536377
protein_co	deoxyribos	294	222	243	1123	754	896	9.107462	8.104199	9.91953	30.09489	26.2404	27.58466
protein_co	serine/thre	3044	2764	2664	6047	4582	5168	86.36248	92.41141	99.59774	148.4169	146.0443	145.7178
protein_co	ATP-bindin	63	46	44	162	155	161	0.627877	0.540255	0.577859	1.396729	1.735461	1.594665
protein_co	differential	30	26	10	76	47	56	0.702135	0.7171	0.308414	1.538778	1.235795	1.302558
protein_co	pleckstrin_	1294	1007	835	1399	1067	1064	18.30234	16.78452	15.56301	17.118	16.95453	14.95628
protein_co	glutamate-(	504	444	474	1365	991	1025	5.493568	5.70314	6.808276	12.87122	12.13519	11.10344
protein_co	ubiquitin_p	489	399	422	578	586	584	3.294915	3.16822	3.746991	3.369195	4.435903	3.91073
protein_co	EH-domain_	10508	8648	7281	874	627	656	155.1754	150.4963	141.6866	11.16548	10.40206	9.627564
protein_co	DEP_domai	196	157	170	1357	1082	1146	1.946433	1.837343	2.224678	11.65806	12.07146	11.31039
protein_co	coiled-coil_	62	46	57	226	145	172	2.194079	1.918339	2.658093	6.918819	5.764711	6.049209
protein_co	Ras-related	8	14	2	106	71	64	0.086434	0.178251	0.028475	0.990752	0.861794	0.687204
protein_co	heat_shock	236	211	222	403	239	274	4.727232	4.980632	5.859799	6.983337	5.378261	5.454502
protein_co	PHD_finger	714	620	629	909	739	688	6.382957	6.531643	7.409845	7.029923	7.421936	6.112541
protein_co	hydroxyste	10	8	4	20	15	16	0.302347	0.285038	0.159368	0.523117	0.509502	0.480768
protein_co	nuclear_rec	69	61	36	296	178	214	1.337579	1.393501	0.919619	4.963924	3.876497	4.122815
protein_co	thymidine_	41	34	24	9	17	16	1.059337	1.035228	0.817139	0.201166	0.493456	0.410847
protein_co	non-SMC_c	551	539	378	1891	1373	1706	14.04453	16.19017	12.69645	41.69751	39.31653	43.21597
protein_co	translocase	1643	1326	1319	1650	994	1207	42.18334	40.11936	44.62549	36.64801	28.67074	30.79785
protein_co	SEC63_hon	2622	2379	2268	2127	1815	1996	21.65205	23.1509	24.67994	15.19486	16.83806	16.38085
protein_co	karyopherii	1247	984	1039	2065	2070	1936	8.947875	8.320619	9.824349	12.81848	16.68679	13.80602
protein_co	vimentin	26752	25197	18674	23839	11840	15072	531.2369	589.6413	488.657	409.5274	264.1391	297.449
protein_co	RTEL1-TNFF	32	23	22	7	32	40	0.294577	0.249508	0.266874	0.055745	0.330939	0.365947
protein_co	Fas_(TNF_re	900	821	771	1145	736	730	18.59028	19.98452	20.98615	20.4603	17.07931	14.98566
protein_co	ribonuclea	235	223	135	191	179	310	5.088398	5.690169	3.85196	3.577747	4.35427	6.670902
protein_co	CD44_mole	10527	9313	8641	2383	1686	1667	121.4447	126.6108	131.3629	23.7827	21.85147	19.11258
protein_co	potassium_	57	59	57	299	411	508	1.364829	1.664801	1.798511	6.19352	11.0559	12.08862

protein_co	1-acylglyce	429	387	363	571	442	475	2.887691	3.069809	3.219844	3.325006	3.342448	3.177581
protein_co	SLAM_fami	0	0	0	13	4	3	0	0	0	0.168093	0.067166	0.044563
protein_co	butyrophili	306	249	201	27	15	14	4.70655	4.513232	4.073916	0.359259	0.259192	0.214003
protein_co	mitochond	323	295	253	651	424	526	7.124975	7.668492	7.354213	12.42295	10.50741	11.53125
protein_co	protein_kir	74	53	44	539	526	457	1.0937	0.923102	0.856947	6.891572	8.733761	6.712624
protein_co	insulin_rec	8	12	5	1	0	2	0.083028	0.146766	0.068382	0.008978	0	0.020629
protein_co	interferon_	417	372	394	1191	824	933	10.3209	10.85004	12.85027	25.50093	22.91171	22.94947
protein_co	xylosylprot	675	535	432	584	396	557	13.46972	12.58102	11.35987	10.08163	8.877672	11.04637
protein_co	SH2_domai	1	4	0	3	6	8	0.031644	0.149164	0	0.082126	0.213303	0.251591
protein_co	vaccinia_re	137	95	109	255	273	250	2.965215	2.423072	3.10883	4.77462	6.638154	5.37756
protein_co	tumor_nec	135	147	102	70	35	35	1.940547	2.490089	1.932081	0.870465	0.565207	0.499998
protein_co	vezatin_adl	1563	1435	1279	1323	1031	955	18.13827	19.62437	19.5588	13.28188	13.4414	11.01412
protein_co	POU_class_	107	101	67	451	243	319	0.82085	0.913079	0.677313	2.993089	2.094283	2.432094
protein_co	bromodom	1125	910	835	1888	1225	1172	12.24226	11.66965	11.97376	17.77355	14.97595	12.67496
protein_co	sorting_nex	2172	1873	1813	1803	1402	1661	14.16281	14.39244	15.57838	10.17064	10.27038	10.76388
protein_co	TBP-like_1	365	298	298	858	465	623	14.92159	14.3564	16.05364	30.34399	21.35622	25.31162
protein_co	aryl_hydro	208	189	218	759	650	624	2.2922	2.454471	3.165778	7.235922	8.047324	6.834131
protein_co	BCL2-assoc	2077	1857	1958	3678	3221	2790	15.13954	15.95126	18.80717	23.19267	26.37642	20.2111
protein_co	solute_carr	1255	1200	1134	1476	1245	1193	12.79679	14.41935	15.2372	13.01987	14.26185	12.08948
protein_co	ankyrin_1_	28	26	17	410	579	453	0.177187	0.19389	0.141761	2.244508	4.116251	2.848932
protein_co	integrin-bi	0	0	0	0	2	0	0	0	0	0	0.115152	0
protein_co	transcriptic	141	108	83	360	233	323	5.242051	4.731654	4.066259	11.57837	9.731663	11.93423
protein_co	rabaptin_R	765	761	748	1285	1057	932	7.518073	8.813266	9.686827	10.92474	11.66995	9.102709
protein_co	high_mobil	817	651	671	2620	2450	2584	12.14966	11.40854	13.1492	33.70594	40.93146	38.18952
protein_co	nucleopori	741	714	703	1712	1814	1779	7.297112	8.28587	9.122691	14.58477	20.0687	17.41079
protein_co	BCL2-antag	503	348	342	1175	1110	1634	12.46691	10.16429	11.16996	25.19369	30.90743	40.24876
protein_co	muscle_ske	22	4	16	0	1	3	0.352619	0.075553	0.337939	0	0.018007	0.047788
protein_co	IKAROS_fan	73	64	104	222	201	203	0.410919	0.424542	0.771439	1.081059	1.271096	1.135636
protein_co	granulin	5880	5011	3938	4442	2753	3106	144.9223	145.5423	127.8994	94.71077	76.22775	76.07972
protein_co	family_witl	471	494	504	646	615	556	4.56271	5.63944	6.433796	5.413741	6.693081	5.352866
protein_co	Rho_GTPas	550	417	433	203	235	189	3.125206	2.792281	3.242192	0.997872	1.500144	1.067302
processed_	nuclear_rec	0	5	1	5	4	9	0	0.148401	0.033189	0.108941	0.11318	0.225274
protein_co	centromere	63	71	49	296	162	234	1.924572	2.555989	1.972534	7.822548	5.55978	7.104263
protein_co	seryl-tRNA_	3750	3083	2859	4616	2905	3421	105.4882	102.2005	105.9794	112.3314	91.80528	95.63904
protein_co	RAN_bindir	1315	1166	914	2651	1850	2344	21.53338	22.50049	19.72275	37.55425	34.03354	38.14641
protein_co	AT_rich_int	359	269	364	203	218	217	3.226246	2.848803	4.310615	1.5782	2.200942	1.938083
protein_co	tumor_sup	441	339	333	900	523	684	7.962817	7.213315	7.92332	14.05833	10.60911	12.27422
protein_co	patatin-like	1764	1439	1078	2168	1623	1972	20.22697	19.44465	16.28868	21.50575	20.90739	22.47236
protein_co	intraflagell	308	261	195	218	195	218	4.14801	4.142253	3.460656	2.539853	2.950344	2.917798
protein_co	ALG1_chitc	657	551	436	582	447	414	13.02218	12.86995	11.38779	9.979395	9.953476	8.155079
protein_co	zinc_finger_	260	283	170	738	495	609	3.133316	4.019059	2.699695	7.693966	6.701702	7.293867
protein_co	ATP-bindin	1499	1216	1107	3109	2074	2354	22.37974	21.3941	21.77889	40.15477	34.78653	34.92766
protein_co	chondroiti	4644	3841	3438	1420	1559	1594	61.8822	60.31494	60.36903	16.3691	23.33827	21.10919
protein_co	leucine_ric	6	9	8	48	19	32	0.048816	0.08629	0.08577	0.337843	0.173666	0.258744

protein_co fucosyltran	423	280	298	1747	1483	1491	4.33489	3.381449	4.024285	15.48794	17.07371	15.18536
protein_co ubiquitin-li	661	564	653	1322	1107	990	5.421223	5.451073	7.057385	9.379729	10.19982	8.06939
protein_co GRB2-assoc	238	199	194	1870	2345	2256	2.068279	2.037945	2.221615	14.05843	22.89413	19.48413
protein_co ATPase_H+_	952	684	727	1173	887	1046	10.83401	9.173088	10.90239	11.54818	11.34031	11.83024
protein_co protein_inh	313	231	301	598	384	410	5.651614	4.915268	7.161919	9.340977	7.789479	7.357354
protein_co solute_carr	987	924	1105	888	790	683	6.736207	7.431515	9.937918	5.242933	6.057235	4.632641
protein_co amyloid_be	672	530	425	562	418	406	8.825688	8.202802	7.355345	6.38526	6.167436	5.299257
processed_ ubiquitin-li	771	631	575	2417	2177	2410	9.474816	9.138036	9.311487	25.69544	30.05549	29.43358
protein_co mitogen-ac	588	564	478	1016	622	770	12.96514	14.65501	13.88873	19.38013	15.40776	16.87331
protein_co EF-hand_ca	75	58	68	15	11	19	1.736909	1.582891	2.075198	0.300518	0.286192	0.4373
protein_co thymosin_b	37399	31996	22976	19962	17247	27239	4024.269	4057.231	3257.889	1858.207	2084.921	2912.915
protein_co asteroid_ho	69	60	77	100	98	98	1.368651	1.402497	2.012654	1.715957	2.183829	1.931876
protein_co ring_finger_	223	172	198	340	263	245	2.726522	2.478219	3.190099	3.596219	3.61251	2.977007
protein_co peroxisoma	123	104	107	236	193	194	3.307132	3.295238	3.791098	5.489356	5.829788	5.183914
protein_co GABA(A)_re	911	788	658	1381	882	1152	21.20899	21.61897	20.18656	27.81367	23.0685	26.65408
protein_co SH3_domai	656	566	548	386	390	380	9.810534	9.974987	10.79951	4.993892	6.552432	5.647836
protein_co family_with	468	461	394	1553	1189	1372	10.3321	11.99364	11.46236	29.66043	29.48994	30.10278
protein_co vinculin	5231	4284	4971	10020	8048	7400	50.51703	48.75393	63.26036	83.71124	87.31525	71.02225
protein_co DEP_domai	80	80	71	827	631	637	1.69479	1.997206	1.98207	15.15634	15.01773	13.41142
protein_co death-assoc	1	2	10	11	2	6	0.01095	0.025807	0.144288	0.104196	0.024602	0.065291
protein_co neutral_sph	414	380	345	828	573	627	6.141096	6.642571	6.743719	10.62524	9.548809	9.243208
protein_co adenylosuc	483	432	475	1176	1057	907	9.198022	9.694784	11.91999	19.37393	22.61369	17.16581
protein_co signal_tran	0	0	0	0	1	0	0	0	0	0	0.039362	0
protein_co TIMP_meta	13142	11331	10239	4161	2971	3157	190.5122	193.5694	195.5932	52.18216	48.38525	45.48263
protein_co replication_	784	682	652	1513	1223	1027	8.49483	8.708234	9.309386	14.1821	14.88724	11.05907
protein_co TBC1_dom	983	895	858	600	492	434	12.83695	13.77331	14.7649	6.778328	7.218094	5.632585
protein_co cullin_3	1294	1002	969	2464	1957	1763	10.16253	9.273476	10.02828	16.74062	17.26663	13.76036
protein_co myomesin_	33	23	31	64	43	52	0.348435	0.286182	0.431325	0.584589	0.510065	0.545658
protein_co cytochrom	41	31	22	4	5	12	0.328428	0.292634	0.232228	0.027719	0.044996	0.095532
protein_co zinc_finger_	669	546	571	970	826	717	7.476784	7.190986	8.409296	9.378285	10.37093	7.963748
protein_co solute_carr	0	0	0	11	6	5	0	0	0	0.170429	0.120722	0.088995
protein_co ubiquitin_s	8	5	7	34	27	13	0.113486	0.083585	0.130853	0.417246	0.430292	0.183275
protein_co tubulin_ga	401	356	224	151	120	150	11.95346	12.50565	8.798973	3.893938	4.018643	4.443754
protein_co ribosomal_	460	418	313	1102	678	1008	32.82056	35.14565	29.42845	68.0194	54.34592	71.47569
protein_co fms-related	2	5	13	74	84	97	0.018078	0.053259	0.154844	0.578644	0.852992	0.871361
protein_co NOP2/Sun_	1181	891	986	3417	2663	2942	17.5726	15.62323	19.33294	43.98394	44.515	43.50493
protein_co F-box_prot	556	507	456	739	551	543	4.746081	5.100061	5.129322	5.457174	5.283978	4.606486
protein_co microfibrill	620	558	736	1136	882	930	6.500974	6.894901	10.16949	10.30453	10.38973	9.691239
protein_co methylthio	176	110	114	183	146	172	3.078168	2.267146	2.627358	2.768814	2.868677	2.989632
protein_co methyltran	133	146	78	277	172	242	3.408109	4.408813	2.633851	6.140512	4.951528	6.162924
protein_co homeobox_	216	87	120	88	31	40	3.392244	1.610125	2.483416	1.195581	0.546946	0.624314
protein_co aspartylglu	152	137	109	260	173	233	3.819189	4.056535	3.609016	5.651502	4.883405	5.81826
protein_co phosphatid	363	334	328	806	795	726	5.428695	5.8863	6.463943	10.42766	13.35688	10.79034
protein_co biorientati	645	435	631	663	685	587	3.232082	2.568733	4.166648	2.874082	3.856224	2.923279

protein_co	methionine	638	555	528	1402	1109	1225	9.907995	10.15699	10.80523	18.83545	19.34843	18.90649
protein_co	tolloid-like	30	40	47	24	11	15	0.236767	0.37202	0.488801	0.16386	0.097531	0.117652
protein_co	enhancer_c	1069	868	724	1129	1299	1128	10.745	10.28148	9.589637	9.817157	14.66854	11.26802
protein_co	trio_Rho_g	5110	3943	4732	2825	3254	2741	24.37194	22.1617	29.74053	11.65603	17.43555	12.99235
protein_co	versican	2867	2224	3056	1348	1297	1009	12.02232	10.99012	16.88686	4.890053	6.11012	4.204957
protein_co	C-type_lect	570	484	440	822	917	812	4.379098	4.381898	4.454483	5.463169	7.914587	6.199769
protein_co	macrophag	24	27	14	0	0	0	0.355707	0.471576	0.273428	0	0	0
protein_co	cadherin_1	1	0	1	6063	5646	5528	0.01086	0	0.01431	56.95975	68.88226	59.66163
protein_co	superkiller_	881	852	809	1601	1150	1017	11.1262	12.67995	13.46338	17.49142	16.31615	12.76443
protein_co	dynein_axo	9	1	6	54	46	60	0.030478	0.003991	0.026775	0.1582	0.175007	0.201935
protein_co	zinc_finger_	522	461	531	946	1024	907	4.080201	4.246382	5.469408	6.396835	8.992077	7.045762
protein_co	family_with	737	609	530	1109	899	1055	9.159041	8.918809	8.679469	11.92277	12.55137	13.03001
protein_co	complemer	11	12	14	3	0	0	0.159069	0.204494	0.266781	0.03753	0	0
protein_co	retinoic_ac	1242	1011	1267	2030	1707	1561	12.91294	12.38688	17.35862	18.2584	19.93821	16.12933
protein_co	SRY_(sex_d	2	8	0	6	3	3	0.032429	0.152864	0	0.084163	0.054649	0.048344
protein_co	polynucleo	836	725	587	931	834	1156	21.0555	21.51813	19.48194	20.28486	23.59796	28.93522
protein_co	bestrophin_	2	0	0	0	0	0	0.048503	0	0	0	0	0
protein_co	PH_domair	246	187	235	435	529	437	1.538146	1.377879	1.936267	2.352961	3.715928	2.715524
protein_co	spindle_ap	307	316	289	1656	1269	1382	6.091786	7.389251	7.556817	28.42691	28.28896	27.2536
protein_co	staufen_RN	248	201	261	710	507	491	3.233038	3.087893	4.483678	8.007196	7.425336	6.361364
protein_co	PQ_loop_re	364	236	154	807	478	620	8.950544	6.838599	4.990035	17.16661	13.20459	15.15128
protein_co	cystinosin_	371	330	248	531	379	398	6.853143	7.183514	6.036739	8.485422	7.865099	7.306487
protein_co	reticulon_4	15	9	11	172	113	110	0.368157	0.26031	0.35577	3.652022	3.115799	2.683146
protein_co	PHD_finger	1120	944	860	1616	1215	1505	29.10845	28.91213	29.45332	36.33335	35.47533	38.87292
protein_co	cadherin_1	34	32	25	543	431	409	0.523558	0.580689	0.507296	7.233509	7.456114	6.259205
protein_co	inositol_pc	443	343	402	518	565	486	3.473469	3.169282	4.15356	3.513601	4.97688	3.78709
protein_co	RAB27B_m	1365	1163	1696	59	55	70	9.925073	9.965242	16.25031	0.371121	0.449276	0.505835
protein_co	proteasom	1574	1235	1086	4248	3299	3778	30.40099	28.10976	27.64061	70.97911	71.58375	72.51948
protein_co	myosin_XV	0	0	2	33	16	16	0	0	0.020298	0.219867	0.138437	0.122465
protein_co	large_subu	419	366	369	1091	745	911	6.210044	6.392472	7.206789	13.98841	12.40469	13.41864
protein_co	poly_(ADP-	95	85	63	17	11	20	2.034545	2.145209	1.777948	0.31496	0.264658	0.42568
protein_co	tenascin_C	4358	3488	3936	13981	15437	13959	30.19459	28.47905	35.93617	83.79983	120.1583	96.11825
protein_co	THAP_dom	297	247	202	341	250	346	7.65878	7.505976	6.86419	7.607125	7.242562	8.867249
protein_co	family_with	258	291	207	14	16	16	3.120579	4.147779	3.299292	0.14649	0.217413	0.192329
protein_co	tyrosyl-DN/	289	238	225	932	698	817	4.139596	4.017392	4.246953	11.54886	11.23219	11.63032
protein_co	apoptosis-i	106	72	80	242	176	226	1.73202	1.386394	1.72255	3.420782	3.230791	3.669992
protein_co	chromoson	1	5	0	0	0	0	0.025379	0.149539	0	0	0	0
protein_co	spermatoge	232	243	198	158	126	97	3.402302	4.199506	3.826352	2.004495	2.075891	1.413729
protein_co	mediator_c	498	530	413	1057	648	664	5.409236	6.784058	5.911415	9.93218	7.907344	7.167774
protein_co	retinol_satu	1162	866	884	630	610	836	19.84433	17.42831	19.89379	9.307519	11.70333	14.18882
protein_co	capping_pr	3330	2517	2069	1187	855	1289	122.2562	108.8973	100.0972	37.69993	35.26485	47.03156
protein_co	adaptor-rel	4497	3834	3057	6416	3788	5407	254.6264	255.8231	228.0924	314.2736	240.957	304.2611
protein_co	Usher_synd	3	0	2	0	0	0	0.008379	0	0.007361	0	0	0
protein_co	thyroglobu	22	33	36	2	7	6	0.137835	0.243644	0.297216	0.01084	0.04927	0.037359

protein_co	ADAM_met	0	1	0	0	2	0	0	0.008847	0	0	0.016868	0
protein_co	BARX_hom	2	0	0	333	229	263	0.049293	0	0	7.10011	6.340775	6.442037
protein_co	DCN1_defe	383	326	344	683	674	656	2.549208	2.557003	3.01717	3.932695	5.039825	4.339303
protein_co	PHD_finger	329	297	267	324	389	351	2.694969	2.866959	2.882067	2.295969	3.579782	2.857424
protein_co	Zic_family_	266	200	196	44	43	47	4.735139	4.195543	4.597715	0.67759	0.859941	0.831493
protein_co	lymphocyt	0	2	0	14	4	10	0	0.026673	0	0.137064	0.050856	0.112471
protein_co	tRNA_isope	286	248	237	493	393	421	7.169093	7.325832	7.82855	10.69075	11.06725	10.48793
protein_co	adrenocept	17	6	5	30	17	27	0.314464	0.130792	0.121879	0.480072	0.353281	0.496359
protein_co	cullin_7	2073	1671	1532	911	914	1008	19.93944	18.94075	19.41812	7.580451	9.876633	9.635713
protein_co	catenin_(ca	5116	4011	4135	8904	6765	6813	72.11026	66.62332	76.80276	108.5712	107.1232	95.43651
protein_co	phosphoryl	210	185	172	247	252	281	1.99993	2.076224	2.158533	2.034958	2.696156	2.65957
protein_co	centlein_ce	231	221	255	214	148	153	2.193215	2.472684	3.190394	1.757705	1.578629	1.443678
protein_co	EPH_recept	390	348	369	3	19	7	3.55431	3.737464	4.431512	0.023652	0.194533	0.063401
protein_co	heat_shock	15010	12968	11404	23372	17470	18057	203.3379	207.0225	203.5774	273.9028	265.8762	243.1044
protein_co	desmoglein	1770	1424	1600	5581	4939	4538	16.07024	15.23583	19.14273	43.83531	50.37756	40.9471
protein_co	gem_(nucle	422	354	260	262	169	194	13.28246	13.13035	10.78386	7.133956	5.97588	6.068446
protein_co	oral-facial-(	255	242	223	516	449	471	3.169747	3.544924	3.652785	5.548776	6.270178	5.818553
protein_co	glycoprotei	43	53	47	235	220	159	0.5753	0.83562	0.828626	2.719925	3.306723	2.114135
protein_co	phosphatid	6	9	10	49	72	29	0.029548	0.052232	0.064896	0.208758	0.39835	0.141936
protein_co	WD_repeat	511	408	438	605	529	529	5.904157	5.555258	6.668773	6.047215	6.8666	6.074385
protein_co	YTH_domai	400	276	369	573	480	476	3.156887	2.566937	3.837605	3.912161	4.25588	3.733496
protein_co	CTP_syntha	268	242	235	599	541	554	3.285063	3.495677	3.795872	6.351828	7.449982	6.748827
protein_co	ATPase_H+_	582	516	479	1536	1071	1213	13.02819	13.61187	14.12965	29.74508	26.93391	26.98556
protein_co	polymerase	2116	1770	1737	3124	2577	2175	27.26951	26.88079	29.49825	34.82857	37.30999	27.85676
protein_co	family_with	270	207	281	116	109	83	3.114176	2.813564	4.270911	1.157445	1.412391	0.951409
protein_co	ArfGAP_wit	14	11	7	146	153	137	0.098639	0.091332	0.064991	0.889891	1.211048	0.959293
protein_co	translocate	1626	1307	1486	3017	3014	2822	11.41975	10.81729	13.75275	18.3305	23.7809	19.69711
protein_co	ceruloplasr	1	6	3	5	1	5	0.011322	0.080053	0.044758	0.048972	0.012719	0.05626
protein_co	KIAA0556	604	509	440	530	462	614	4.833186	4.799781	4.639638	3.668897	4.153246	4.882864
protein_co	dystrobrevi	132	138	94	375	290	310	3.717134	4.579525	3.488164	9.13542	9.174477	8.675721
protein_co	X-linked_K	6	4	6	80	59	45	0.061015	0.047935	0.080403	0.703786	0.674045	0.454789
protein_co	anoctamin_	0	2	1	30	23	15	0	0.033569	0.018769	0.369644	0.368024	0.212325
protein_co	chromoson	343	345	342	625	478	466	4.746148	5.625658	6.236028	7.481525	7.430603	6.408298
protein_co	sex_comb_	184	193	195	270	243	218	2.110757	2.609064	2.947744	2.679459	3.131668	2.485344
protein_co	WWC_fami	791	654	648	1258	1358	1199	6.300034	6.138344	6.801054	8.667824	12.15109	9.490634
protein_co	Rho_GTPas	167	106	127	62	46	76	1.403579	1.049865	1.406562	0.450791	0.434338	0.63481
protein_co	family_with	261	263	202	252	199	271	2.08662	2.477797	2.128086	1.742876	1.787331	2.153187
protein_co	microtubul	10046	8691	7882	8832	9661	10371	59.6239	60.78607	61.64509	45.34708	64.41669	61.17268
protein_co	golgi-associ	903	823	893	1260	1084	971	10.38352	11.15228	13.53141	12.53402	14.00345	11.09649
protein_co	c-ros_onco	0	3	2	0	0	0	0	0.025173	0.018766	0	0	0
protein_co	ubiquitin_s	322	299	328	703	522	587	3.651103	3.995273	4.900912	6.89583	6.649481	6.614788
protein_co	histone_de	166	201	216	184	170	171	1.886286	2.69155	3.234357	1.808757	2.170188	1.931102
protein_co	tetraspanin	1097	986	944	700	678	907	13.06553	13.83899	14.81587	7.212426	9.071917	10.73587
protein_co	NOP16_nu	402	278	194	910	516	667	16.94449	13.80875	10.77554	33.18233	24.43437	27.94074

protein_co	coiled-coil_	549	484	448	465	355	397	5.53717	5.75265	5.954268	4.057247	4.022471	3.979382
protein_co	ribonucleo	1531	1248	1597	1441	1338	1255	16.43737	15.78988	22.59419	13.38394	16.13847	13.39092
protein_co	zinc_finger_	176	177	205	363	298	272	2.138048	2.533875	3.28166	3.814824	4.066963	3.283851
protein_co	tumor_nec	0	1	0	0	0	1	0	0.062764	0	0	0	0.052932
protein_co	sorting_nex	272	255	328	185	218	183	1.762324	1.946992	2.800435	1.036935	1.586801	1.178359
protein_co	LIM_domai	7	9	10	11	11	18	0.098587	0.149372	0.18559	0.134022	0.174045	0.251943
protein_co	mitochond	494	439	377	1193	885	895	12.39472	12.9802	12.46481	25.89483	24.94606	22.31733
protein_co	guanylate_(	2	1	1	29	32	38	0.047417	0.027939	0.031242	0.594791	0.852319	0.895358
protein_co	remodeling	841	758	835	603	795	676	3.854838	4.094364	5.043493	2.39106	4.093797	3.079402
protein_co	vacuolar_p	804	631	744	511	524	447	2.608442	2.412468	3.180775	1.434198	1.909877	1.44126
protein_co	CUGBP_Ela	458	375	412	1116	1071	910	2.626121	2.533889	3.113016	5.53575	6.899026	5.185615
protein_co	family_witl	2060	1854	2044	2230	1835	1667	21.3088	22.60001	27.86169	19.95537	21.32441	17.13709
protein_co	R3H_doma	750	625	638	1290	1049	1071	8.542544	8.389056	9.575941	12.71097	13.42303	12.12342
protein_co	collagen_ty	71	65	64	271	317	356	1.301978	1.404642	1.546536	4.299101	6.530608	6.487912
protein_co	KIT_ligand	1406	1239	1632	842	894	731	14.33925	14.89085	21.9329	7.428757	10.24301	7.409145
protein_co	excision_re	142	107	87	246	166	175	2.195567	1.949617	1.772607	3.290459	2.88347	2.689094
protein_co	ADAM_met	8	19	14	70	67	29	0.05793	0.162135	0.133591	0.438507	0.545054	0.2087
protein_co	hexose-6-pl	2371	2003	1682	879	691	851	13.72437	13.66309	12.82985	4.401622	4.493534	4.895534
protein_co	vesicle-assc	2436	1910	1871	4120	2525	2713	58.48719	54.04107	59.19596	85.57437	68.10734	64.73556
protein_co	period_circ	29	28	47	31	18	31	0.244512	0.278206	0.522197	0.226113	0.1705	0.25976
protein_co	tumor_nec	0	1	1	3	9	3	0	0.032443	0.036278	0.071449	0.278358	0.082081
protein_co	epsin_3	5	3	2	569	511	493	0.065022	0.045975	0.034273	6.401272	7.465535	6.371586
processed_	steroid-5-al	0	0	0	0	0	3	0	0	0	0	0	0.033966
protein_co	latent_tran	14238	11127	12887	1447	1348	1196	119.0232	109.6144	141.9611	10.4644	12.65965	9.936271
protein_co	reticulocall	7179	6479	5835	6475	5403	5179	143.258	152.3596	153.4371	111.7783	121.1264	102.7094
protein_co	elastin	2	11	5	19	8	26	0.028004	0.181504	0.092255	0.230145	0.125842	0.3618
protein_co	replication_	390	313	226	1708	1042	1259	12.18111	11.52057	9.301771	46.15017	36.56278	39.08029
protein_co	AT_rich_int	1190	971	1049	1136	1344	1158	7.640042	7.346409	8.87481	6.30943	9.693868	7.388682
protein_co	CLPTM1-lik	1672	1263	1218	3888	2545	3050	25.0049	22.25867	24.0033	50.30117	42.75882	45.33131
protein_co	neural_pre	277	301	282	1235	876	879	1.738342	2.22602	2.332059	6.704795	6.17602	5.482189
protein_co	forkhead_b	4	18	6	9	8	3	0.088902	0.471444	0.175726	0.173044	0.199751	0.066265
protein_co	protein_ph	202	160	122	99	71	111	3.12601	2.917871	2.487904	1.32537	1.234373	1.70715
protein_co	hexosamini	1888	1482	1476	2853	2000	2192	49.457	45.74894	50.95032	64.65328	58.85791	57.06581
protein_co	pentatricop	104	63	79	212	87	132	2.079254	1.4843	2.081306	3.66668	1.95408	2.622755
protein_co	KIAA2022	0	0	0	13	18	14	0	0	0	0.050632	0.091042	0.062641
protein_co	JNK1/MAPI	626	489	506	745	524	491	14.39664	13.25265	15.33459	14.82197	13.53839	11.2222
protein_co	dickkopf_3	3627	2880	2905	2871	2021	2286	72.45924	67.80251	76.47635	49.61836	45.3588	45.38706
protein_co	Rho_guanir	43	35	52	125	188	201	0.410617	0.393862	0.654345	1.032623	2.01686	1.907544
protein_co	nuclear_fac	65	43	27	1290	776	730	0.933577	0.7278	0.511017	16.02837	12.52125	10.42004
protein_co	mitochond	246	211	184	833	588	643	7.132248	7.209097	7.029816	20.89293	19.15216	18.52729
protein_co	LIM_domai	3002	2561	2674	6831	5459	5090	40.54308	40.75892	47.58852	79.80927	82.82628	68.31773
protein_co	LETM1_dor	718	673	525	861	650	765	12.89404	14.24252	12.42392	13.37614	13.11375	13.65324
protein_co	solute_carr	8	6	8	115	145	125	0.096366	0.085171	0.126987	1.198379	1.962232	1.496418
protein_co	laminin_ga	0	7	0	8	14	8	0	0.071207	0	0.059741	0.135768	0.068631

protein_co prostaglanc	0	0	4	186	201	170	0	0	0.039968	1.22008	1.712211	1.281064
protein_co TNFAIP3_in	2	4	1	6	2	6	0.043591	0.102738	0.028721	0.11313	0.048972	0.129965
protein_co mitogen-ac	517	422	372	1120	798	832	5.684422	5.467834	5.389811	10.65312	9.857068	9.091358
protein_co collagen_ty	24	30	28	157	170	179	0.415088	0.611445	0.638148	2.349045	3.303138	3.076745
protein_co breast_can	4179	3313	2929	7845	5719	6973	47.48667	44.36371	43.85848	77.11792	73.00768	78.74603
protein_co family_with	566	459	441	574	513	520	8.608044	8.226362	8.838152	7.552017	8.765052	7.859611
protein_co homocyste	1174	1017	980	1078	713	778	28.26409	28.85326	31.0905	22.45167	19.28437	18.6147
protein_co homer_hor	718	516	425	260	288	319	19.2075	16.26684	14.98201	6.017037	8.655414	8.480991
protein_co RAD51_hor	62	59	43	946	579	698	1.448518	1.624394	1.32384	19.11993	15.19707	16.2068
protein_co polymerase	105	65	92	507	509	483	0.633482	0.462131	0.731421	2.646159	3.449942	2.896021
protein_co phosphatid	143	178	153	361	367	356	1.59481	2.339376	2.248532	3.482917	4.598201	3.945777
protein_co cytochrom	82	79	48	2326	2092	3099	3.067959	3.483131	2.366528	75.28499	87.93189	115.2303
protein_co THO_comp	469	333	336	765	728	900	13.82479	11.56744	13.05148	19.50789	24.10828	26.36562
protein_co heme_bind	959	700	623	1232	967	1470	51.28325	44.11254	43.90154	56.99419	58.09415	78.12389
protein_co M-phase_pl	243	250	275	559	444	443	2.218428	2.68959	3.308312	4.414828	4.553769	4.019318
protein_co pleckstrin_	372	283	341	623	613	551	3.035926	2.721709	3.667224	4.398446	5.620277	4.468991
protein_co protease_se	6	0	0	1289	984	1198	0.169864	0	0	31.56941	31.29642	33.70676
protein_co suppressor_	564	561	587	1238	985	1009	5.422942	6.356614	7.437531	10.29768	10.63999	9.641768
protein_co ribosomal_	785	607	483	1746	1367	1599	9.447302	8.608627	7.659847	18.17797	18.48229	19.12477
protein_co folliculin_i	226	162	207	579	575	503	1.727749	1.459467	2.085343	3.829251	4.938434	3.821641
protein_co methylster	2817	2421	2448	2996	1974	2274	65.7271	66.56707	75.26686	60.47312	51.74326	52.72999
protein_co tetratricop	1178	875	968	1011	842	798	13.95491	12.2151	15.11095	10.36086	11.2058	9.394946
protein_co ALX_homec	48	20	24	26	92	76	0.441942	0.217001	0.291186	0.207091	0.951615	0.69542
protein_co follistatin-l	13	10	15	0	0	2	0.127004	0.115128	0.193107	0	0	0.019418
protein_co forkhead_b	804	697	770	717	744	631	5.434699	5.552126	6.85875	4.192775	5.649908	4.238951
protein_co methyltran	0	0	1	5	11	4	0	0	0.062344	0.204642	0.58466	0.188075
protein_co aldo-keto_r	1601	1382	947	1391	1181	1323	62.23093	63.30385	48.50648	46.77407	51.572	51.10748
protein_co mRNA_turr	1416	1099	790	5660	3040	3985	32.38205	29.61733	23.80691	111.9749	78.10228	90.56889
protein_co neuronatin	39	20	39	4	23	20	1.595594	0.964262	2.102603	0.141573	1.057145	0.8132
protein_co unconventi	336	275	196	213	106	181	10.01586	9.660262	7.699101	5.492774	3.549801	5.36213
protein_co MCF.2_cell_	26	21	15	11	7	17	0.176176	0.167687	0.133937	0.064481	0.053287	0.114481
protein_co nuclear_rec	94	86	57	61	55	76	1.812255	1.953876	1.448109	1.017383	1.191251	1.456179
protein_co laminin_alp	76	38	61	91	81	92	0.377405	0.222374	0.399171	0.39093	0.451885	0.454037
protein_co adaptor-rel	302	270	281	895	697	549	5.2011	5.479729	6.37719	13.33442	13.48559	9.396589
protein_co anaphase_p	359	309	255	645	437	546	4.992334	5.063779	4.672875	7.759468	6.827154	7.545908
protein_co potassium_	0	0	1	8	0	1	0	0	0.021499	0.112909	0	0.016214
protein_co trafficking_	911	707	641	1715	1230	1607	19.86377	18.16644	18.41774	32.34972	30.12989	34.82322
protein_co thyroid_ho	2825	2594	2422	3223	4051	3952	33.74511	36.51484	38.12425	33.30548	54.36303	46.91578
protein_co phosphohis	2271	1937	1392	1589	1452	2014	91.35942	91.82753	73.79216	55.29974	65.62236	80.52029
protein_co ectonucleo	7	4	5	7	9	19	0.176891	0.119117	0.166499	0.153027	0.255505	0.477168
protein_co lymphocyt	0	2	0	0	1	1	0	0.01812	0	0	0.008637	0.007641
protein_co AT_rich_int	758	589	740	616	550	487	6.614352	6.056762	8.50912	4.650095	5.391751	4.223346
protein_co opsin_3	229	146	211	117	78	85	4.627285	3.476568	5.618341	2.045218	1.770657	1.706944
protein_co serologicall	378	355	300	289	218	251	7.795752	8.627832	8.153091	5.156168	5.050935	5.144576

protein_co	protein_tyr	194	208	86	18	30	17	2.014229	2.54494	1.176631	0.161675	0.349927	0.175415
protein_co	hedgehog_a	107	66	96	155	181	203	1.562241	1.135574	1.847015	1.957758	2.968875	2.945574
protein_co	kinesin_fam	1399	1137	1451	1753	1791	1490	6.942024	6.648688	9.487911	7.525118	9.984194	7.347918
protein_co	forkhead_b	598	440	480	232	133	153	9.184425	7.963621	9.714643	3.082491	2.294835	2.335349
protein_co	TBC1_dom	750	721	518	740	489	643	10.48475	11.87789	9.542482	8.94935	7.679885	8.933413
protein_co	spectrin_re	373	298	375	869	995	990	0.902596	0.849783	1.195778	1.819145	2.704934	2.380835
protein_co	pleckstrin_	13	9	13	291	383	306	0.104215	0.085023	0.137329	2.018092	3.449315	2.437901
protein_co	ATPase_cla	559	445	471	157	172	164	3.650878	3.424937	4.053603	0.88705	1.262011	1.064484
protein_co	chordin-lik	2	0	2	6	5	0	0.05372	0	0.07079	0.139418	0.150878	0
protein_co	family_with	1284	1149	1281	667	701	635	9.316918	9.825041	12.24873	4.186934	5.714449	4.579211
protein_co	RELT_tumo	102	40	35	271	208	283	1.242518	0.574208	0.56183	2.855845	2.846523	3.426087
protein_co	galactosylc	213	147	151	303	282	239	2.904051	2.361833	2.712917	3.573801	4.319394	3.238413
protein_co	NOP58_rib	936	784	667	3454	2153	2689	24.21934	23.90615	22.74297	77.31643	62.58634	69.14916
protein_co	SUZ_RNA_b	4180	3348	3198	2866	2757	3550	60.86176	57.44613	61.35945	36.10002	45.09766	51.3696
protein_co	potassium_	2	2	0	5	12	21	0.022447	0.026452	0	0.048547	0.151306	0.234237
protein_co	cullin_1	826	791	713	3191	2167	2301	14.27195	16.10597	16.23408	47.69723	42.06407	39.51205
protein_co	family_with	326	264	247	279	215	211	3.884484	3.707036	3.878355	2.875961	2.878083	2.498664
protein_co	cytoplasmi	859	703	701	2153	1487	1587	6.696556	6.458338	7.201305	14.51996	13.02322	12.29546
protein_co	TGF-beta_a	1855	1623	1628	1507	1281	1238	21.56941	22.23925	24.94501	15.15901	16.73373	14.30621
protein_co	glycoprotei	611	470	434	497	312	413	15.98169	14.48727	14.95912	11.24608	9.168224	10.73597
protein_co	eukaryotic_	1243	1101	1147	1331	1239	1156	6.553043	6.84016	7.968381	6.070339	7.338246	6.056746
protein_co	ubiquitin_s	1224	930	874	1545	1178	1355	11.01101	9.859063	10.36077	12.02367	11.90529	12.1142
protein_co	myeloid/ly	892	819	987	738	895	697	2.773114	3.000502	4.043476	1.984825	3.1259	2.153502
protein_co	mucolipin_	5	0	9	242	195	258	0.089639	0	0.212621	3.753246	3.927465	4.596825
protein_co	coiled-coil_	61	69	53	99	63	74	0.811	1.081053	0.928542	1.138647	0.94098	0.97776
protein_co	pumilio_ho	1338	1148	1229	2120	1654	1431	11.58003	11.70854	14.01652	15.87276	16.08193	12.30844
protein_co	mitochond	609	612	413	956	530	680	15.10828	17.89189	13.50152	20.51722	14.77143	16.76549
protein_co	inter-alpha	0	3	0	0	2	0	0	0.056104	0	0	0.035657	0
protein_co	inter-alpha	0	0	0	0	1	0	0	0	0	0	0.020431	0
protein_co	chromoson	399	348	305	554	438	505	17.17354	17.65116	17.29903	20.62812	21.17923	21.6017
protein_co	zinc_finger_	1596	1282	1445	2004	1782	1537	17.83323	16.88077	21.27648	19.37126	22.36937	17.06792
protein_co	zinc_finger_	210	145	191	340	221	233	2.399139	1.952141	2.87544	3.360299	2.836465	2.645463
protein_co	neuropepti	0	0	0	2	4	2	0	0	0	0.047658	0.123779	0.054749
protein_co	PHD_finger	10	5	13	79	88	85	0.144214	0.084974	0.247051	0.985593	1.425737	1.21825
protein_co	TNF_recept	32	41	29	27	28	24	0.267886	0.404475	0.319914	0.195536	0.263334	0.199674
protein_co	ring_finger_	984	892	1052	1455	1400	1262	5.632995	6.017502	7.935875	7.205602	9.003707	7.179815
protein_co	polycomb_	840	797	613	1600	1090	1290	14.52333	16.23874	13.96633	23.9315	21.17203	22.16595
protein_co	interleukin	69	36	62	83	60	82	1.294447	0.795875	1.532716	1.347027	1.264548	1.528828
protein_co	TRAF3_inte	603	476	458	571	430	403	6.225316	5.791061	6.230808	5.099683	4.987255	4.134841
protein_co	glycogenin_	98	50	78	385	291	350	1.529094	0.919359	1.603754	5.196752	5.100941	5.427326
protein_co	discoidin_C	4653	3939	4696	2448	1864	1678	40.23758	40.14134	53.51329	18.31358	18.10897	14.42117
protein_co	serpin_pep	0	2	2	0	0	0	0	0.070217	0.078518	0	0	0
protein_co	sterol_O-ac	879	773	814	1026	838	850	6.808359	7.055701	8.308312	6.874861	7.292	6.543079
protein_co	plakophilin	65	62	56	2931	2084	1848	0.799899	0.899126	0.908123	31.2033	28.81167	22.60129

protein_co	mutS_hom	13	5	7	7	4	12	0.210727	0.095511	0.149523	0.098161	0.072843	0.193316
protein_co	coagulatior	0	0	0	0	3	4	0	0	0	0	0.057391	0.067693
protein_co	GDP_dissoc	7186	6110	5569	10388	8691	8666	152.2345	152.5366	155.4669	190.3798	206.8448	182.4543
protein_co	PR_domair	59	53	43	131	99	72	0.604864	0.640308	0.58091	1.161824	1.140224	0.733581
protein_co	autophagy_	333	267	247	1031	617	710	5.481763	5.179578	5.358063	14.68242	11.41065	11.61566
protein_co	transmemb	16	20	11	138	162	154	0.144131	0.212311	0.130576	1.075421	1.639459	1.37869
protein_co	PITH_(C-ter	1818	1445	1334	1430	1044	1303	60.04163	56.23847	58.05628	40.85617	38.73541	42.76738
protein_co	metastasis_	840	790	613	834	722	808	7.625246	8.451013	7.3328	6.549432	7.363102	7.289464
protein_co	ubiquitin_s	572	377	497	582	467	486	3.638381	2.825925	4.165848	3.202567	3.337168	3.072261
protein_co	ATPase_clas	550	421	535	567	544	487	3.975092	3.585697	5.095339	3.545117	4.417051	3.498026
protein_co	laminin_ga	125	104	130	1794	1540	1419	1.285725	1.260603	1.762041	15.96333	17.7954	14.50541
protein_co	cyclin-depe	430	355	349	282	262	168	4.409186	4.289685	4.715744	2.501509	3.018146	1.71202
protein_co	Sec61_alph	14309	11426	10508	9696	8016	9365	208.3996	196.1051	201.6706	122.164	131.1579	135.5517
protein_co	protein_ph	1037	817	971	1437	1219	1152	9.596191	8.909417	11.84061	11.50376	12.67281	10.59454
protein_co	Ras_protein	0	0	0	17	14	15	0	0	0	0.123702	0.132295	0.125391
protein_co	calcium/ca	14	10	12	3	3	1	0.166668	0.140292	0.188253	0.030896	0.040123	0.011831
protein_co	ciliary_root	366	323	248	300	279	372	2.911118	3.02753	2.599353	2.064254	2.493056	2.940569
protein_co	polymerase	436	343	335	1050	827	937	4.808807	4.458123	4.868896	10.01851	10.2472	10.2707
protein_co	ATPase_Ca+	3736	3358	3779	1286	1634	1225	22.05481	23.36061	29.39735	6.567506	10.83671	7.18691
protein_co	zinc_finger_	2750	2341	2406	2180	1964	1829	17.32362	17.37859	19.97269	11.88025	13.89942	11.45063
protein_co	RIO_kinase_	308	378	286	617	376	471	4.157528	6.012892	5.087277	7.204978	5.701924	6.318515
protein_co	Yip1_doma	323	211	209	519	297	425	9.48416	7.30106	8.086814	13.18338	9.797198	12.40209
protein_co	transmemb	413	333	390	2284	1604	1750	4.258791	4.046575	5.299509	20.37489	18.58188	17.93428
protein_co	diacylglyce	5	5	1	6	7	5	0.043724	0.051526	0.011524	0.04539	0.06877	0.043454
protein_co	FLYWCH-ty	1197	847	767	912	726	851	12.32647	10.27862	10.40818	8.124606	8.39905	8.709309
protein_co	unkempt_h	328	233	235	764	787	877	3.419584	2.862611	3.22851	6.89058	9.217713	9.086751
protein_co	thromboxa	100	80	98	5	10	5	2.236628	2.108584	2.888383	0.096745	0.251271	0.111141
protein_co	poly_(ADP-	21	29	23	74	29	28	0.292877	0.476619	0.422696	0.892813	0.454373	0.388091
protein_co	aldehyde_d	2069	1681	1683	2182	1722	1792	32.70675	31.31495	35.05871	29.83972	30.58153	28.15299
protein_co	TAR_(HIV-1	226	210	214	564	397	391	2.332293	2.553884	2.910203	5.035201	4.602717	4.010155
protein_co	PET112_ho	379	318	247	693	445	532	3.062368	3.027976	2.629965	4.844115	4.039497	4.272081
protein_co	MAX_dimer	177	122	176	150	130	146	1.677207	1.362324	2.197662	1.229611	1.383904	1.374915
protein_co	cyclin-depe	1449	1268	1277	548	484	327	18.45357	19.02998	21.43077	6.037479	6.924788	4.138753
protein_co	DnaJ_(Hsp4	171	193	193	307	188	196	3.519794	4.681505	5.234959	5.466666	4.347384	4.009469
protein_co	solute_carr	1693	1525	1321	39855	35450	34719	20.30564	21.55444	20.87841	413.5286	477.6668	413.844
protein_co	pleckstrin_	72	60	51	11	14	10	0.911248	0.894875	0.850568	0.120437	0.199059	0.125781
protein_co	CTD_(carbo	515	480	445	1128	973	1221	7.264751	7.979246	8.271959	13.7653	15.41968	17.11744
protein_co	Y_box_binc	4690	3772	3058	12490	8555	8751	38.8383	36.81003	33.37027	89.47729	79.58962	72.02026
protein_co	serine/thre	0	0	0	56	40	65	0	0	0	0.85634	0.794336	1.141874
protein_co	WNK_lysin	2333	2012	2465	2267	2261	2059	10.99638	11.17558	15.31041	9.243778	11.97249	9.644972
protein_co	cell_divisio	1186	981	974	3192	2297	2660	13.40765	13.06905	14.50981	31.21719	29.17279	29.88541
protein_co	opioid_gro	1193	997	772	1287	1103	1392	14.01656	13.80394	11.95234	13.08105	14.5588	16.25361
protein_co	guanine_nu	0	0	0	1	0	0	0	0	0	0.021472	0	0
protein_co	cAMP_resp	0	0	0	0	0	1	0	0	0	0	0	0.020097

protein_co	phosphatid	157	131	150	206	177	155	3.06367	3.012456	3.857166	3.477543	3.880294	3.005963
protein_co	protein_tyr	336	295	219	1111	1019	1166	3.188416	3.298867	2.738512	9.120377	10.86323	10.99623
protein_co	small_nucl	463	334	310	1918	1321	1565	12.71353	10.80783	11.21713	45.56136	40.75087	42.70798
protein_co	RIMS_bindi	1	0	0	10	3	13	0.008375	0	0	0.072455	0.028228	0.108208
protein_co	collagen_ty	20232	17261	18610	10904	13279	13221	146.1856	146.9735	177.1932	68.15767	107.7905	94.93795
protein_co	glutamine_	761	725	913	1586	1563	1271	4.315811	4.845324	6.823125	7.781153	9.958314	7.163627
protein_co	mitochond	325	215	260	351	234	261	17.88547	13.9432	18.85494	16.71041	14.46712	14.27471
protein_co	acetyl-CoA_	666	597	501	912	664	829	7.470064	7.89099	7.404959	8.84928	8.366951	9.2409
protein_co	branched_c	2672	2296	2394	4840	4455	4070	16.97161	17.18563	20.03759	26.59469	31.78947	25.69156
protein_co	histone_de	3001	2599	2056	2154	1928	2259	24.77018	25.27997	22.36254	15.38055	17.87801	18.53058
protein_co	leucine_zip	1031	815	839	1011	864	880	9.565749	8.910971	10.25787	8.114738	9.005817	8.11433
protein_co	PR_domain	14	19	11	4	4	5	0.242849	0.38839	0.25144	0.060025	0.07795	0.086196
protein_co	wingless-ty	0	0	0	0	1	0	0	0	0	0	0.037242	0
protein_co	sperm_assc	131	145	97	14	22	18	4.77307	6.225892	4.657287	0.441283	0.90053	0.651791
protein_co	NCK-associa	1654	1476	1762	4135	3145	2846	17.55149	18.45746	24.63879	37.9592	37.49284	30.01395
protein_co	mitochond	911	831	736	1759	934	1086	25.54515	27.45985	27.19586	42.66964	29.42294	30.26423
protein_co	guanylate_c	8	20	19	232	224	227	0.135572	0.399409	0.424297	3.401199	4.264598	3.823108
protein_co	splicing_fac	1073	969	852	1317	1142	1250	10.15657	10.80882	10.62727	10.7844	12.14402	11.75891
protein_co	tyrosine_ki	598	475	346	1247	1005	1422	5.32975	4.988918	4.063652	9.614686	10.06284	12.59548
protein_co	MON2_hon	938	875	947	683	654	526	4.783149	5.258068	6.363497	3.01297	3.746605	2.66567
protein_co	cadherin_3	50	45	30	6562	4874	5571	0.715032	0.75836	0.565343	81.1811	78.30514	79.1769
protein_co	GC-rich_pr	843	829	824	1692	1170	1148	9.530057	11.04408	12.27524	16.54746	14.85945	12.89791
protein_co	diacylglyce	1	3	5	0	1	4	0.008934	0.031583	0.058862	0	0.010036	0.035514
protein_co	zinc_finger_	134	89	97	86	111	93	1.94146	1.51957	1.851954	1.077916	1.80674	1.33911
protein_co	citrate_syn	3610	2912	2795	5802	4097	4267	62.51782	59.42855	63.78422	86.92354	79.70979	73.43937
protein_co	leukocyte_	21	7	30	23	12	5	0.322811	0.126804	0.607694	0.305858	0.207233	0.076385
protein_co	mitochond	2	9	1	21	6	4	0.06131	0.325124	0.040396	0.556906	0.206633	0.121862
protein_co	engulfment	676	582	627	963	698	697	8.684327	8.810885	10.61431	10.70234	10.07381	8.898809
protein_co	wings_apar	741	678	691	1376	1291	1156	6.194422	6.679122	7.611942	9.950939	12.12433	9.603954
protein_co	vacuole_m	2453	2134	2018	2362	1477	1833	30.02642	30.78275	32.55082	25.01203	20.3112	22.29863
protein_co	amyloid_be	1095	969	992	1015	794	745	8.962645	9.346585	10.69963	7.187058	7.301156	6.060214
protein_co	polymerase	377	381	250	2381	2027	2615	5.74518	6.842178	5.020386	31.38952	34.70285	39.60442
protein_co	seizure_rela	11	16	5	1	10	2	0.130251	0.223262	0.078018	0.010244	0.133026	0.023536
protein_co	eukaryotic_	15978	14403	12923	8256	7198	7393	203.9275	216.6274	217.3459	91.15616	103.2082	93.77427
protein_co	solute_carr	161	164	151	27	38	28	2.857358	3.429966	3.53143	0.414539	0.757655	0.493863
protein_co	glioma_tun	537	541	384	895	879	910	5.001639	5.93803	4.713072	7.211474	9.19763	8.423432
protein_co	sphingosin	471	414	243	676	528	786	8.064427	8.353338	5.48269	10.01296	10.1563	13.37472
protein_co	ribosomal_	21254	17732	11349	20226	12497	17067	292.718	287.7886	205.9686	240.9804	193.3586	233.6015
protein_co	carbonic_a	69	72	55	4	5	5	1.980981	2.435963	2.080792	0.099347	0.161269	0.142663
protein_co	isochorism	1168	1010	738	739	415	565	27.08501	27.60035	22.5516	14.82496	10.81143	13.021
protein_co	U2_small_r	4205	3432	2976	8193	7050	9542	73.66541	70.85198	68.70137	124.1663	138.7509	166.1295
protein_co	epsin_1	5834	4731	3434	6830	4685	5974	117.8397	112.6121	91.40294	119.3463	106.3124	119.9223
protein_co	mediator_c	958	813	844	1098	939	1008	13.88379	13.88481	16.11832	13.766	15.28823	14.51819
protein_co	aryl-hydroc	2069	1745	1607	40	53	32	19.34904	19.23098	19.80385	0.32361	0.556832	0.297412

protein_co	zinc_finger_	541	447	514	282	252	185	4.462617	4.345172	5.58715	2.012355	2.335296	1.516609
protein_co	myotubula	312	269	299	771	701	771	3.657571	3.716187	4.61896	7.819078	9.232201	8.982602
protein_co	glypican_1	5238	4245	3410	3083	2325	2822	74.72512	71.36511	64.10477	38.04851	37.2626	40.00993
protein_co	aarF_doma	69	60	51	252	139	170	1.026104	1.051479	0.999418	3.241945	2.322234	2.512469
protein_co	hydroxyacy	145	91	89	357	319	378	4.401631	3.255323	3.560167	9.37512	10.87891	11.40373
protein_co	ring_finger_	1218	987	906	2215	1646	1888	15.63961	14.93492	15.32999	24.60455	23.74421	24.09297
protein_co	caspase_8_	371	286	235	395	299	321	6.70345	6.089724	5.595349	6.174255	6.069385	5.764201
protein_co	LIM_and_c	69	57	54	312	230	211	0.592527	0.576821	0.611065	2.317803	2.218891	1.80074
protein_co	asunder_sp	687	593	526	915	684	692	12.22948	12.43979	12.33876	14.09079	13.67906	12.24241
protein_co	transmemb	525	366	464	1995	1752	1725	10.25988	8.428907	11.94912	33.72788	38.46505	33.50286
protein_co	distal-less_	0	0	0	225	241	198	0	0	0	3.96032	5.508723	4.003683
protein_co	sperm_aut	13	12	20	60	29	58	0.139065	0.151274	0.281929	0.55525	0.348515	0.616612
protein_co	tetraspanin	16	19	25	0	3	6	0.254754	0.356501	0.524536	0	0.053662	0.094943
protein_co	WNT1_indu	10	7	9	0	0	0	0.191885	0.158287	0.227571	0	0	0
protein_co	doublesex_	0	0	0	5	5	1	0	0	0	0.104899	0.136225	0.024102
protein_co	ST3_beta-g	57	43	38	86	85	72	0.958589	0.852183	0.842123	1.251177	1.605925	1.203371
protein_co	ATPase_Ca+	8	14	3	27	27	38	0.117647	0.242619	0.058136	0.343492	0.446069	0.555371
protein_co	nerve_grow	9	4	3	36	31	66	0.139441	0.073032	0.06125	0.482517	0.539583	1.01625
protein_co	cell_adhesi	232	296	237	415	533	471	1.344092	2.020876	1.809356	2.079946	3.469103	2.711886
protein_co	TAF2_RNA_	526	488	535	850	687	719	5.516435	6.031143	7.393692	7.711781	8.094286	7.493958
protein_co	homeodom	7034	5580	6768	685	894	716	24.74496	23.13267	31.3747	2.084673	3.533223	2.503267
protein_co	transportin	1171	938	978	1680	1591	1419	16.43965	15.51835	18.09294	20.40365	25.09313	19.79829
protein_co	MEF2BNB-M	0	2	0	0	1	1	0	0.069166	0	0	0.032969	0.029165
protein_co	regulatory_	583	464	380	725	553	697	22.18878	20.81086	19.05827	23.87075	23.64499	26.36376
protein_co	transmemb	880	712	504	607	436	543	24.1389	23.01558	18.21798	14.40411	13.43601	14.80281
protein_co	lysophosph	42	91	49	379	262	315	0.873339	2.229883	1.342655	6.817669	6.12046	6.509594
protein_co	cathepsin_	4958	4221	3519	1593	1036	1242	120.019	120.4109	112.2529	33.3597	28.17423	29.87958
protein_co	SURP_and_	1254	998	991	1154	1307	1280	11.92956	11.18831	12.42325	9.497203	13.96856	12.1017
protein_co	solute_carr	571	403	458	388	450	388	4.390604	3.651744	4.640753	2.58097	3.887315	2.965033
protein_co	sorting_nex	138	108	116	663	453	483	3.385476	3.122277	3.750019	14.07075	12.48498	11.77599
protein_co	eyes_absen	7	8	7	89	87	104	0.137153	0.184716	0.180734	1.50855	1.915028	2.025115
protein_co	calponin_2	9963	8313	6890	18488	13398	16320	207.0059	203.5436	188.6456	332.3117	312.7388	336.9942
protein_co	ATP-bindin	72	62	50	285	268	360	0.559236	0.567494	0.511761	1.915007	2.338548	2.778911
protein_co	synuclein_a	285	240	226	12	5	4	3.02611	3.003019	3.162154	0.110226	0.059643	0.042209
protein_co	DEAD_(Asp-	248	200	214	878	643	603	3.030786	2.88032	3.446293	9.282419	8.828027	7.323701
protein_co	BTB_(POZ)_	1429	1221	1287	1668	1319	1254	22.94591	23.10446	27.23244	23.17033	23.79397	20.01153
protein_co	fatty_acyl_(	155	107	119	415	334	274	3.916875	3.18639	3.962688	9.072337	9.482079	6.881265
protein_co	breast_carc	0	0	1	0	2	0	0	0	0.011414	0	0.019462	0
protein_co	chitinase_3	15	11	17	26	10	29	0.36612	0.316397	0.546785	0.548996	0.274209	0.703461
protein_co	strawberry_	2415	1896	1532	1602	1475	1810	25.97572	24.03233	21.71421	14.90651	17.82344	19.34812
protein_co	PMS1_post	280	227	190	599	435	434	4.596427	4.391322	4.110085	8.506525	8.022333	7.080464
protein_co	high_mobil	1900	1504	1085	1477	1078	1301	41.32617	38.55018	31.09826	27.79169	26.34143	28.12279
protein_co	calcitonin_	165	182	163	29	43	30	1.672461	2.173955	2.177181	0.254292	0.489654	0.302206
protein_co	TAF11_RNA	365	346	243	933	642	754	12.23004	13.66212	10.72942	27.04454	24.1668	25.10822

protein_co ankyrin_rep	786	624	632	8048	8763	8795	6.567491	6.144246	6.958711	58.17386	82.25812	73.03355
protein_co adaptor-rel	6531	5259	4600	6346	5327	6621	68.68447	65.17622	63.74873	57.73537	62.93767	69.20096
protein_co zinc_finger_	373	292	264	429	283	346	4.245752	3.916839	3.959902	4.22441	3.618939	3.914096
protein_co solute_carr	733	664	436	143	121	129	17.68721	18.88125	13.86362	2.98507	3.280121	3.093533
protein_co nth_endon	129	145	85	429	218	315	6.400551	8.478183	5.557525	18.41399	12.15159	15.53273
protein_co UHRF1_bin	151	81	126	537	527	538	0.835328	0.528047	0.918513	2.569907	3.275215	2.957822
protein_co guanine_nu	1874	1627	1561	3470	2599	2581	30.94555	31.6609	33.96771	49.57024	48.21519	42.3571
protein_co importin_5	4509	3636	3684	8339	6309	6375	39.76527	37.78807	42.81325	63.62103	62.50767	55.87449
protein_co ornithine_a	1876	1577	1609	2058	1770	1894	48.49478	48.03977	54.80914	46.02253	51.40253	48.65772
protein_co WD_repeat	559	532	507	1124	880	822	7.670818	8.602974	9.167959	13.34318	13.56631	11.21015
protein_co protein_kir	750	628	745	1204	1233	1033	6.486807	6.400832	8.491038	9.008639	11.98069	8.879319
protein_co WD_repeat	647	510	379	2235	1636	1961	22.12715	20.5541	17.08029	66.12439	62.85698	66.65126
protein_co translocati	6319	5090	5479	1891	2206	2013	48.42706	45.96896	55.33194	12.53702	18.99303	15.3318
protein_co netrin_1	954	821	667	217	255	245	8.482652	8.602675	7.815269	1.669191	2.547255	2.165005
protein_co glucagon-li	0	1	2	0	0	0	0	0.013646	0.030518	0	0	0
protein_co minichrom	74	55	74	1261	1133	1084	0.854073	0.748054	1.12546	12.59046	14.69069	12.43375
protein_co diacylglyce	823	698	551	910	684	833	8.015165	8.010786	7.071297	7.666851	7.483725	8.062455
protein_co v-erb-b2_er	22	6	15	554	652	665	0.196773	0.063241	0.176795	4.286635	6.551495	5.911192
protein_co rhophilin_a	3	0	0	2	7	0	0.077249	0	0	0.044551	0.202496	0
protein_co ankyrin_rep	76	38	80	5	15	18	1.091567	0.643172	1.514124	0.062125	0.242034	0.256932
protein_co lysyl-tRNA_	2850	2388	2016	6591	4164	4231	69.49877	68.62363	64.78249	139.0422	114.0754	102.538
protein_co adenosine_	185	179	179	577	403	428	3.538325	4.034467	4.511426	9.546954	8.659247	8.135409
protein_co protein_dis	1881	1441	1259	1148	932	1105	44.6156	40.2781	39.35124	23.55607	24.83493	26.04773
protein_co TBC1_dom	200	148	159	291	254	300	3.058405	2.667066	3.204033	3.849648	4.363629	4.559276
protein_co NADH_dehy	1363	1192	934	1894	1231	1858	50.60209	52.15019	45.69348	60.82968	51.34281	68.55323
protein_co spen_homo	895	745	992	1324	1528	1219	3.873626	3.799776	5.657715	4.957305	7.429627	5.243339
protein_co myosin_ligl	1715	1496	1684	798	875	691	9.054932	9.308073	11.7165	3.644911	5.190129	3.625841
protein_co zinc_finger_	940	763	697	2168	1404	1699	23.27621	22.26466	22.74322	46.44155	39.05715	41.8107
protein_co mitogen-ac	496	500	449	924	716	719	6.809837	8.089695	8.12337	10.97463	11.04376	9.810556
protein_co transmemb	122	84	81	373	202	262	2.609617	2.117402	2.283162	6.902219	4.854196	5.569649
protein_co synaptoson	1	0	0	7	1	1	0.011202	0	0	0.067836	0.012585	0.011133
protein_co STE20-like_	689	660	814	1287	1250	1157	4.696928	5.302073	7.312299	7.589904	9.573126	7.838586
protein_co cytochrom	188	191	166	351	247	294	4.413706	5.284282	5.135568	7.128787	6.514657	6.859659
protein_co collagen_ty	14	13	19	1042	1097	1048	0.129259	0.141444	0.231165	8.322717	11.37863	9.616241
protein_co glutathione	20	14	18	48	53	33	0.393029	0.324212	0.466124	0.816016	1.17009	0.644493
protein_co Sec61_alph	175	119	141	246	171	243	3.763068	3.015491	3.995379	4.57617	4.130943	5.19302
protein_co protein_kir	7	0	2	108	97	85	0.112812	0	0.042474	1.505717	1.756214	1.361399
protein_co transducin-	8	5	4	26	24	20	0.156572	0.115319	0.103162	0.440211	0.527698	0.389013
protein_co ankyrin_rep	1114	955	917	731	887	887	8.432409	8.518771	9.14683	4.786817	7.542914	6.672671
protein_co family_with	247	166	220	1761	1571	1372	3.454802	2.736159	4.054933	21.30829	24.68604	19.07172
protein_co malic_enzy	448	442	427	1086	807	734	7.035765	8.180177	8.83682	14.75456	14.23823	11.45616
protein_co TBC1_(tre-2	905	776	823	2760	2202	2127	8.405544	8.493487	10.07284	22.17631	22.97649	19.63335
protein_co cyclin-depe	793	665	774	998	803	815	5.752563	5.684823	7.398846	6.262991	6.544144	5.875644
protein_co methylenet	902	835	765	2112	1647	1698	10.71651	11.6907	11.97687	21.7072	21.98313	20.04907

protein_co solute_carr	7	15	11	110	110	101	0.096557	0.243829	0.199947	1.312631	1.704625	1.38458
protein_co forkhead_b	505	485	491	762	766	740	4.840703	5.478553	6.202023	6.318806	8.248878	7.049502
protein_co Y_box_binc	27527	22280	18106	30538	26195	29681	956.238	912.0726	828.8281	917.7211	1022.291	1024.697
protein_co phosphodi	429	366	302	40	50	55	4.934105	4.960658	4.577126	0.397992	0.646056	0.628671
protein_co protein_ph	214	184	183	252	252	235	3.627721	3.675742	4.087954	3.695589	4.799209	3.95911
protein_co catenin_(ca	2	0	3	77	53	70	0.024346	0	0.048124	0.81088	0.724816	0.846858
protein_co ELAV_(emb	1689	1350	1263	4391	3212	3559	14.86573	14.00223	14.64855	33.43358	31.76004	31.13107
protein_co tyrosine_ki	0	4	0	24	16	28	0	0.064284	0	0.283146	0.245135	0.379493
protein_co DIP2_disco	711	557	707	1220	1131	1055	4.380431	4.043985	5.739863	6.502347	7.828146	6.459656
protein_co SWI/SNF_re	1120	904	872	3210	2337	2627	16.20938	15.41785	16.63028	40.18985	37.9976	37.78489
protein_co lysine_(K)-s	1032	895	934	692	644	603	12.21169	12.48033	14.5639	7.083782	8.561129	7.091254
protein_co nuclear_tra	764	688	559	1364	941	1086	17.11677	18.16452	16.50346	26.43661	23.68465	24.18064
protein_co zinc_finger_	0	3	0	7	4	10	0	0.105444	0	0.180615	0.13403	0.296417
protein_co solute_carr	801	791	449	91	123	208	16.41089	19.09779	12.12218	1.612887	2.83109	4.235187
protein_co neuronal_g	80	78	60	19	11	24	1.31735	1.513606	1.301959	0.270662	0.203495	0.392764
protein_co asp_(abnor	396	331	476	1258	1089	885	1.925658	1.896789	3.050181	5.292094	5.949231	4.276976
protein_co ELOVL_fatt	2151	1775	1562	3159	2044	2860	77.09958	74.9751	73.7781	97.95446	82.3079	101.8796
protein_co spleen_focu	0	0	0	0	1	2	0	0	0	0	0.042392	0.075002
protein_co zinc_ribbor	65	56	45	71	57	74	0.937136	0.951447	0.854942	0.885545	0.923237	1.060305
protein_co metallophc	1	2	1	17	3	6	0.009469	0.022317	0.012478	0.139256	0.031913	0.056463
protein_co claudin_18	20	23	26	6	11	8	0.300801	0.407647	0.515297	0.078066	0.185862	0.119577
protein_co zinc_finger_	345	258	269	380	340	280	3.033994	2.67376	3.117329	2.890961	3.359105	2.447165
protein_co ataxin_3	241	203	206	364	298	363	1.835796	1.82226	2.067804	2.398676	2.55019	2.748043
protein_co golgin_A5	699	569	544	794	585	600	12.46405	11.95642	12.78249	12.24801	11.7189	10.63268
protein_co fibroblast_	1027	848	820	659	671	573	12.778	12.43356	13.44439	7.093179	9.379163	7.085276
protein_co leucine_ric	251	287	227	1067	652	752	4.607555	6.208488	5.491077	16.94432	13.44601	13.71906
protein_co isochorism	117	97	71	1132	732	763	3.192833	3.119386	2.553192	26.7239	22.44143	20.69305
protein_co echinodern	641	521	610	250	174	182	7.48295	7.167366	9.383815	2.524747	2.281987	2.111523
protein_co tRNA_meth	164	136	127	537	320	400	3.604119	3.522097	3.677848	10.20922	7.900495	8.736247
protein_co THUMP_do	490	420	456	958	837	681	6.293325	6.356828	7.717627	10.64419	12.07699	8.692423
protein_co Myb/SANT-	322	235	219	680	447	444	8.562029	7.363695	7.673611	15.64202	13.35296	11.73312
protein_co kinesin_fan	122	43	75	431	446	589	0.96199	0.399564	0.779304	2.940025	3.950888	4.61568
protein_co autophagy_	340	329	408	290	242	180	1.547982	1.765184	2.447834	1.142216	1.237803	0.814459
protein_co ADP-ribosy	670	530	703	836	885	795	4.909407	4.576539	6.78804	5.299361	7.285285	5.789366
protein_co acyl-CoA_sy	0	3	0	0	0	2	0	0.063769	0	0	0	0.035853
protein_co zinc_finger_	158	97	156	154	138	146	1.528633	1.105923	1.988865	1.288931	1.499941	1.403811
protein_co mitochond	316	296	239	479	457	399	6.336877	6.994988	6.315691	8.309726	10.29564	7.951896
protein_co stromal_an	33	47	57	28	28	34	0.392596	0.658927	0.893597	0.288173	0.37423	0.401995
protein_co ferrochelat	252	231	231	724	556	605	3.462531	3.740349	4.182538	8.605867	8.582562	8.261485
protein_co myosin_IXA	438	403	552	334	453	265	1.868656	2.026131	3.103339	1.232721	2.171214	1.123598
protein_co DEAD_(Asp	1249	999	1158	1497	1263	1208	14.87588	14.02145	18.17455	15.42429	16.89946	14.29871
protein_co phosphofru	2660	2403	1689	6914	4518	5489	50.857	54.14146	42.55333	114.3567	97.04305	104.297
protein_co isopenteny	1130	909	945	2171	1306	1453	25.99884	24.646	28.65115	43.2114	33.7573	33.22391
protein_co SP100_nuc	687	505	529	60	68	94	9.369001	8.115869	9.50664	0.707866	1.041824	1.274014

protein_co	Kruppel-lik	3549	3108	3344	3059	2652	2522	40.35386	41.64542	50.1049	30.08996	33.87675	28.49928
protein_co	phosphatid	586	605	436	293	239	322	19.42606	23.63468	19.04621	8.40268	8.900904	10.60847
protein_co	neogenin_1	915	766	787	308	364	320	6.597795	6.508989	7.478031	1.921283	2.948683	2.293176
protein_co	translocati	2335	1876	2236	1385	1349	1196	36.42228	34.4842	45.96072	18.6893	23.63966	18.54048
protein_co	phosphoryl	113	99	99	172	111	100	0.969113	1.000548	1.118834	1.276108	1.069468	0.852325
protein_co	tumor_nec	5876	4751	4142	2450	1739	1818	139.9376	133.3352	129.9863	50.47563	46.52659	43.02849
protein_co	calcium_ch	317	250	215	39	37	67	3.161698	2.938382	2.825755	0.336503	0.414583	0.664119
protein_co	ecotropic_	562	488	528	360	372	416	4.019025	4.112551	4.975687	2.227152	2.988659	2.956564
protein_co	stomatin_(	279	208	179	159	85	188	4.826973	4.240735	4.080924	2.379747	1.652109	3.232497
protein_co	pyruvate_k	55786	44688	38333	51193	33783	38694	979.2329	924.3975	886.683	777.3818	666.2052	675.0159
protein_co	DEAH_(Asp-	507	424	526	989	789	656	5.890078	5.804783	8.052554	9.939679	10.29767	7.574022
protein_co	deoxynucle	574	584	438	1967	1210	1525	6.964962	8.350776	7.003511	20.64782	16.49458	18.3902
protein_co	methyltran	419	391	324	376	313	317	13.26691	14.58947	13.51872	10.29928	11.13395	9.975271
protein_co	tumor_pro	1677	1403	1562	1397	1323	1136	13.99024	13.79294	17.17149	10.08211	12.39941	9.418462
protein_co	trophinin	1674	1428	1325	998	784	1015	19.07106	19.17144	19.89162	9.835874	10.03424	11.49199
protein_co	ribosomal_	332	272	266	1203	889	886	2.261795	2.183691	2.387985	7.089961	6.804027	5.998719
protein_co	ras_homolo	10071	8946	7586	17493	11644	13172	262.5154	274.8009	260.5732	394.4659	340.9835	341.2271
protein_co	DEAH_(Asp-	657	528	611	946	893	883	5.596498	5.300196	6.858466	6.971161	8.545775	7.475174
pseudogen	postmeioti	41	45	26	21	38	24	2.06329	2.668677	1.724188	0.914237	2.14837	1.200321
protein_co	protein_kir	13	5	8	435	478	635	0.295887	0.134109	0.239943	8.565144	12.22248	14.36368
protein_co	zinc_finger_	219	244	202	256	230	188	2.213033	2.905632	2.689861	2.237931	2.611082	1.88804
protein_co	isoleucyl-tF	1450	1191	1224	2953	2247	2159	21.58123	20.88945	24.00626	38.02198	37.57166	31.93526
protein_co	synaptotag	416	348	402	466	410	414	4.580585	4.515584	5.832953	4.438912	5.071782	4.530411
protein_co	neuron_na	127	110	150	614	641	529	0.684605	0.698773	1.065522	2.863306	3.881892	2.834012
protein_co	isocitrate_(	1089	922	659	1141	573	680	33.67567	33.599	26.85397	30.52369	19.90637	20.8981
protein_co	rogdi_hom	265	197	200	357	266	399	5.227036	4.579129	5.198456	6.091732	5.894409	7.821537
protein_co	PDZ_domai	146	98	95	97	122	137	2.095252	1.657359	1.796561	1.204254	1.966945	1.953951
protein_co	ATPase_Ca+	9	6	1	4	3	0	0.070672	0.055522	0.010348	0.027172	0.026465	0
protein_co	Rho-associa	939	806	903	984	1141	980	7.475428	7.56158	9.473119	6.776861	10.20482	7.753649
protein_co	core-bindir	757	663	654	1478	1263	1280	12.77944	13.18975	14.54885	21.58507	23.95347	21.47512
protein_co	pyruvate_d	54	57	45	78	60	50	1.48819	1.851172	1.634226	1.859612	1.857655	1.369444
protein_co	hyaluronog	571	481	423	1407	809	1064	7.456662	7.402195	7.279198	15.89518	11.86878	13.80892
protein_co	histone_de	358	288	359	281	328	371	2.111506	2.001745	2.79022	1.433767	2.173362	2.174667
protein_co	Ras_associa	432	329	267	932	612	860	11.10219	9.963866	9.042134	20.72067	17.66954	21.96509
protein_co	fibroblast_	69	54	42	320	306	345	0.850903	0.784751	0.68252	3.413848	4.239374	4.228243
protein_co	interferon-i	181	142	112	17	18	12	7.72145	7.138644	6.296122	0.627382	0.862664	0.508758
protein_co	HEAT_repea	259	226	238	342	257	228	3.487212	3.585866	4.222701	3.983526	3.887414	3.050866
protein_co	CoA_syntha	1031	918	664	2388	1709	2230	22.20593	23.30022	18.84574	44.49462	41.35246	47.73366
protein_co	pleckstrin_	973	734	485	429	349	499	11.87176	10.55372	7.797924	4.52817	4.783843	6.050798
protein_co	myocyte_e	652	523	622	376	379	314	5.926773	5.60247	7.45068	2.956797	3.870428	2.836678
protein_co	OTU_doma	1439	1242	1062	1818	1381	1720	27.80368	28.2794	27.03964	30.38774	29.97673	33.0278
protein_co	transcriptic	1952	1649	1619	1564	1353	1468	30.26086	30.12514	33.07372	20.97496	23.56396	22.61711
protein_co	TBC1_dom	417	335	285	364	281	321	5.46175	5.17068	4.918985	4.124394	4.134768	4.178404
protein_co	acyl-CoA_sy	1000	868	1049	1191	1010	903	9.927057	10.15424	13.72242	10.22811	11.26396	8.908773

protein_co inositol_pc	521	418	431	1088	789	798	9.312038	8.80421	10.15124	16.82283	15.84284	14.17489
protein_co G_patch_d	371	336	257	483	410	525	11.32052	12.082	10.33381	12.74978	14.05483	15.92068
protein_co GRIP1_assc	735	613	510	778	715	900	11.87054	11.66677	10.85396	10.8699	12.97293	14.44559
protein_co FtsJ_RNA_n	846	723	568	1101	879	903	22.5519	22.71215	19.95244	25.39003	26.32393	23.9227
protein_co proline_ric	459	370	383	1863	1476	1621	10.41128	9.890086	11.44787	36.55671	37.61202	36.54129
protein_co receptor_a	7	24	18	149	110	95	0.096082	0.388205	0.325574	1.76926	1.696228	1.295913
protein_co ATPase_cla	179	157	148	613	846	643	1.069817	1.105766	1.165609	3.169421	5.68036	3.819241
protein_co polymerase	2124	1760	1633	3213	3353	3243	8.820039	8.612629	8.935873	11.54223	15.64223	13.38359
protein_co lysosomal_	7000	6050	5428	4753	3415	4310	209.9643	213.8503	214.5468	123.3327	115.0766	128.4796
protein_co tetratricop	289	207	200	842	872	935	2.966831	2.50422	2.705576	7.477735	10.05682	9.539294
protein_co inositol_he	1847	1626	1315	1867	1436	1671	39.26989	40.73994	36.84286	34.33998	34.30017	35.30846
protein_co STON1-GTF	0	0	0	24	18	24	0	0	0	0.287441	0.27996	0.330214
protein_co S1_RNA_bi	215	140	169	490	389	355	3.09218	2.372801	3.202933	6.096567	6.285284	5.074161
protein_co cytoplasmi	2265	1929	1898	3880	3164	3549	17.47215	17.53547	19.29342	25.89243	27.41976	27.20782
protein_co kinesin_hea	480	395	444	1296	1002	871	7.562999	7.334272	9.218719	17.66529	17.73657	13.63894
protein_co RAS_guanyl	1	0	0	4	5	7	0.017748	0	0	0.061413	0.099691	0.123466
protein_co proteasom	965	793	844	2299	2141	1919	7.196515	6.969076	8.294156	14.8319	17.93745	14.22262
protein_co intraflagell	278	230	229	309	201	254	3.417928	3.332368	3.710123	3.286545	2.776279	3.103569
protein_co sirtuin_2	1617	1337	1034	604	388	526	18.08314	17.61986	15.23769	5.843375	4.874663	5.846006
protein_co endoplasm	791	647	606	794	572	654	17.21181	16.59057	17.3763	14.94629	13.98283	14.14286
protein_co protein_ph	514	486	312	157	98	134	9.913177	11.0457	7.929379	2.619464	2.123366	2.568409
protein_co phosphoryl	10	20	6	14	0	11	0.165544	0.390167	0.130888	0.200496	0	0.180974
protein_co paired-like_	821	661	491	224	112	120	13.5151	12.82285	10.65105	3.189974	2.071301	1.963211
protein_co transient_r	0	0	0	0	2	1	0	0	0	0	0.039823	0.017614
protein_co microtubul	189	190	198	170	139	132	0.932251	1.104413	1.286978	0.725409	0.770256	0.647075
protein_co G_protein-r	1	0	0	0	0	0	0.009112	0	0	0	0	0
protein_co sidekick_ce	177	102	166	472	533	463	0.873874	0.593449	1.079987	2.015955	2.956324	2.271781
protein_co nucleopori	667	516	532	1556	1332	1190	8.470051	7.721772	8.902391	17.09357	19.00262	15.01816
protein_co nuclear_ca	4207	3233	4072	4771	5669	4889	34.28614	31.0498	43.73092	33.6371	51.90409	39.59823
protein_co vacuolar_p	2009	1667	1882	4031	3027	3123	15.68709	15.33928	19.36497	27.22941	26.55363	24.23506
protein_co DnaJ_(Hsp4	972	759	787	2106	1621	1804	16.61564	15.28973	17.72803	31.14385	31.13028	30.64764
protein_co B-cell_CLL/	638	486	430	101	67	69	16.57328	14.87754	14.71944	2.26972	1.955293	1.781339
protein_co potassium_	265	230	220	11	10	17	3.283258	3.358104	3.591838	0.1179	0.13919	0.209323
protein_co ATP-bindin	0	0	1	37	42	36	0	0	0.008412	0.204336	0.301217	0.228398
protein_co galanin/GM	26	11	11	398	174	254	1.682721	0.838955	0.938137	22.28357	12.65136	16.33737
protein_co C-type_lect	54	48	52	63	72	66	1.541139	1.614346	1.955628	1.555435	2.308499	1.871982
protein_co FUN14_dor	233	184	141	453	301	457	10.31376	9.598112	8.224601	17.34691	14.96844	20.1042
protein_co monoamin	14	6	13	2	1	0	0.288844	0.145879	0.353438	0.035697	0.023178	0
protein_co RAR-relatec	231	204	272	63	65	44	1.127754	1.173653	1.749872	0.266076	0.356504	0.213484
protein_co dopamine_	18	37	22	14	16	18	0.693046	1.678797	1.116213	0.466316	0.692083	0.688766
protein_co transformir	1094	881	1027	254	279	265	9.027034	8.566644	11.16691	1.813111	2.586312	2.173118
protein_co KIAA1107	27	25	14	4	17	13	0.309262	0.33745	0.211312	0.039636	0.218756	0.147984
protein_co phospholip	1	3	0	7	4	3	0.0531	0.187726	0	0.321557	0.23862	0.158317
protein_co hairy_and_	30	11	17	145	213	210	0.372649	0.161019	0.278267	1.558151	2.9724	2.592433

protein_co	ATPase_Na-	2943	2354	2313	5641	3661	4560	79.85922	75.27458	82.70757	132.4201	111.605	122.9729
protein_co	neural_pre	310	298	286	1105	922	832	2.268377	2.569667	2.757747	6.994857	7.579377	6.050434
protein_co	phosphatid	91	89	87	122	124	111	2.218062	2.556403	2.794386	2.572498	3.395494	2.68884
protein_co	mitogen-ac	1176	1007	1213	2637	1993	1829	14.69056	14.82408	19.96764	28.49734	27.96968	22.70672
protein_co	guanine_nu	262	277	225	308	216	204	4.487396	5.590877	5.078207	4.563592	4.156195	3.472425
protein_co	RAB27A_m	215	203	201	288	241	234	3.290637	3.661379	4.053894	3.813265	4.143884	3.55932
protein_co	cat_eye_syr	861	719	476	950	782	982	12.61267	12.41195	9.188523	12.039	12.86944	14.29635
protein_co	ubiquitin_f	920	769	633	2193	1296	1787	9.667669	9.522859	8.765414	19.93589	15.29988	18.66243
protein_co	low_densit	368	371	394	444	509	463	1.94434	2.309965	2.743187	2.029413	3.021282	2.431168
protein_co	guanylate_(	0	0	0	1	0	0	0	0	0	0.011945	0	0
protein_co	secretin	8	5	11	5	3	14	1.15718	0.852291	2.096711	0.625668	0.487508	2.012559
protein_co	PHD_and_r	2221	1856	1406	2809	3091	3838	21.28951	20.96535	17.75976	23.29334	33.28627	36.56214
protein_co	inhibitor_c	729	559	670	1270	970	987	6.535814	5.905968	7.915563	9.850061	9.769964	8.794254
protein_co	nucleobind	1176	1053	914	683	480	574	18.30059	19.31049	18.74299	9.194783	8.391664	8.877268
protein_co	profilin_2	4463	4118	3557	12062	8530	9118	104.5005	113.6279	109.7514	244.3283	224.3828	212.1782
protein_co	protein_tyr	67	45	47	185	180	154	0.404683	0.320302	0.374087	0.966663	1.221411	0.924423
protein_co	spectrin_be	60	39	22	425	432	496	0.315657	0.241789	0.152518	1.934268	2.553274	2.593319
protein_co	dual_adapt	7	1	2	49	31	17	0.12541	0.021113	0.047217	0.75944	0.623944	0.302687
protein_co	fibroblast_	4	4	3	0	0	0	0.096564	0.113794	0.095435	0	0	0
protein_co	solute_carr	619	534	575	3514	3174	2931	3.117731	3.169541	3.816372	15.31133	17.9599	14.67147
protein_co	transmemb	285	288	324	235	259	252	3.538505	4.213805	5.300962	2.524095	3.612632	3.109461
protein_co	smg-6_hom	1334	1230	1040	1608	1510	1407	11.15515	12.12082	11.46009	11.63239	14.18554	11.69293
protein_co	exocyst_co	923	899	1037	1644	1514	1458	6.697442	7.687304	9.915642	10.31982	12.3419	10.51416
protein_co	clathrin_he	189	187	201	143	114	120	1.814955	2.116181	2.543519	1.187964	1.229867	1.145236
protein_co	fibroblast_	5	4	3	10	9	3	0.154617	0.145766	0.122249	0.267517	0.312665	0.092198
protein_co	follistatin-l	467	414	388	180	108	157	9.885424	10.32728	10.82293	3.296203	2.568332	3.302841
protein_co	DiGeorge_s	2434	2003	1729	2361	2303	2404	26.76742	25.95817	25.05623	22.46182	28.45306	26.27424
protein_co	ring_finger_	873	610	525	2517	1408	1801	22.09249	18.19145	17.50752	55.10318	40.02968	45.29537
protein_co	MNT_MAX_	653	518	460	361	339	433	6.91963	6.468544	6.423361	3.309328	4.035696	4.560025
protein_co	ZXD_family	307	312	247	483	393	558	3.503532	4.195941	3.714492	4.768457	5.038594	6.328657
protein_co	jumonji_do	585	475	385	819	607	717	5.845693	5.593464	5.069623	7.079899	6.814247	7.120475
protein_co	polymerase	243	229	204	576	357	473	9.593334	10.65383	10.61276	19.67201	15.83363	18.55813
protein_co	WD_repeat	740	616	542	490	446	435	20.77218	20.3769	20.04862	11.89897	14.06482	12.13527
protein_co	FERM_and_	0	0	1	14	13	11	0	0	0.012765	0.117326	0.14148	0.105902
protein_co	glucosidase	769	701	586	1801	1372	1562	10.83621	11.64062	10.88136	21.95471	21.71971	21.87467
protein_co	N-deacetyla	2952	2522	2445	5287	7999	8412	19.46224	19.59425	21.24175	30.15427	59.24631	55.11699
protein_co	asparagine_	823	769	548	2290	1256	1330	18.49339	20.3634	16.22677	44.51591	31.70703	29.70148
protein_co	adaptor-rel	319	234	285	542	388	455	4.602937	3.978939	5.419061	6.765606	6.289631	6.524773
protein_co	cyclic_nucl	1	0	0	2	1	0	0.012131	0	0	0.020989	0.013629	0
protein_co	ST6_(alpha-	25	20	12	73	49	55	0.234086	0.220685	0.148065	0.591319	0.515444	0.51181
protein_co	choline_O-a	0	0	0	3	0	3	0	0	0	0.05435	0	0.062438
protein_co	poly(A)_bin	29479	25352	20701	37048	23921	24362	447.8185	453.8461	414.3959	486.8746	408.242	367.8001
protein_co	testis-speci	48	52	33	95	90	78	0.826665	1.055355	0.748923	1.415386	1.741325	1.335034
protein_co	chromosom	317	280	201	850	599	794	10.45626	10.88384	8.73671	24.25487	22.19693	26.02838

protein_co casein_kina	1613	1348	1132	2530	2212	2248	17.15424	16.89407	15.86421	23.27666	26.42843	23.75982
protein_co protein_tyr	468	352	378	524	532	432	4.018227	3.561544	4.276763	3.89209	5.131558	3.686226
protein_co eukaryotic_	377	272	283	710	492	509	12.03059	10.22873	11.90055	19.6005	17.63843	16.14259
protein_co calcium/ca	3	4	8	9	9	3	0.029843	0.04689	0.104868	0.07745	0.100579	0.029658
protein_co Treacher_C	1184	975	864	6564	5598	6453	11.96224	11.6084	11.50295	57.371	63.53935	64.7936
protein_co cell_divisio	5128	4599	4510	8728	7511	8283	120.4443	127.2942	139.5885	177.3438	198.1915	193.3461
protein_co oxysterol_b	768	558	647	1171	865	771	6.014598	5.149756	6.677048	7.933509	7.610454	6.000804
protein_co RAD18_hor	214	191	191	772	602	730	1.9248	2.024474	2.26381	6.006924	6.082994	6.525358
protein_co ATPase_Ca+	1290	1151	1466	3259	3077	2678	9.711872	10.21164	14.54394	21.22563	26.02494	20.03703
protein_co transient_r	3	0	0	0	2	0	0.040392	0	0	0	0.030252	0
protein_co NCK_adapt	2173	1882	1466	1702	1183	1254	42.87767	43.7621	38.11889	29.0532	26.22438	24.59114
protein_co mitogen-ac	6899	5742	5899	4870	5068	4493	52.49208	51.48467	59.14539	32.05528	43.32049	33.97455
protein_co mannosyl_(	5	7	16	42	37	39	0.03158	0.052101	0.133168	0.229486	0.26254	0.244804
protein_co ribosomal_	15943	13741	10671	12079	8383	13439	362.5594	368.243	319.7783	237.631	214.1695	303.7286
protein_co WD_repeat	13423	10695	10247	20823	15454	16746	158.5513	148.8703	159.4967	212.7779	205.0738	196.5807
protein_co sorting_nex	436	296	500	454	408	405	3.386484	2.709326	5.117612	3.050573	3.560178	3.126275
protein_co membrane-	0	0	0	6	3	8	0	0	0	0.23547	0.152894	0.360679
protein_co Rho_GTPas	775	659	626	1484	1105	1230	5.010903	5.021191	5.333636	8.300632	8.026489	7.903674
protein_co ribosomal_	2100	1715	1801	397	454	394	18.55409	17.8563	20.96857	3.034407	4.506353	3.459602
protein_co inhibitor_c	144	160	133	378	227	254	2.018402	2.642848	2.456584	4.583528	3.574539	3.53825
protein_co vasohibin_	276	257	238	98	176	158	2.55271	2.801126	2.900709	0.784118	1.828749	1.45231
protein_co LIM_and_cy	52	52	42	326	193	234	1.487267	1.752654	1.582959	8.06615	6.201433	6.651371
protein_co Williams_B	1229	977	787	2299	1450	2064	16.7433	15.68523	14.12859	27.09513	22.19251	27.94529
protein_co sel-1_suppr	1802	1503	1820	1067	1175	955	12.03781	11.83202	16.02135	6.166237	8.818196	6.340242
protein_co thyroid_ho	263	192	186	2287	1420	1512	5.210884	4.482951	4.856276	39.19989	31.60771	29.77262
protein_co ATPase_H+_	3641	3061	2690	3073	2329	2661	42.69284	42.29653	41.56439	31.17166	30.67983	31.00908
protein_co transcriptic	3826	3284	2595	5761	4630	5115	42.88635	43.37948	38.33066	55.86439	58.30478	56.98092
protein_co tribbles_ho	1800	1348	1457	1145	1007	1022	21.70207	19.15251	23.14851	11.94255	13.63977	12.24586
protein_co DAZ_associ	2673	2323	1938	6396	5227	6931	35.91657	36.78343	34.31504	74.34766	78.90371	92.55533
protein_co methyl-CpG	1472	1139	904	2655	1890	2271	28.01191	25.54264	22.66931	43.70816	40.406	42.94986
protein_co helicase-lik	669	614	628	377	354	361	6.661186	7.204451	8.239861	3.247355	3.959841	3.572254
protein_co family_with	1594	1340	1062	1354	896	1269	57.40676	56.87045	50.40041	42.18484	36.25199	45.41988
protein_co family_with	722	590	516	660	414	628	9.563022	9.209097	9.006218	7.562491	6.160378	8.266606
protein_co cleavage_ar	1924	1482	1330	3052	2655	2821	22.58503	20.5008	20.57321	30.99296	35.01298	32.91003
protein_co myosin_IIIB	19	11	3	0	2	2	0.165332	0.112798	0.0344	0	0.019552	0.017296
protein_co cytochrom	1216	1067	1210	44	52	41	14.74828	15.25033	19.33873	0.461661	0.708533	0.494198
protein_co programme	967	826	672	2243	1420	1698	15.1551	15.25526	13.87831	30.41058	25.00172	26.4472
protein_co solute_carr	65	67	64	382	312	295	0.813706	0.988408	1.05577	4.136955	4.387913	3.670169
protein_co retinol_deh	1324	1144	1151	1922	1533	1685	17.37147	17.68812	19.90026	21.81549	22.59643	21.97142
protein_co protein_kir	1652	1363	1295	1536	1301	1723	28.167	27.3863	29.09612	22.65608	24.92051	29.19614
protein_co latrophilin_	410	346	268	174	294	281	3.836304	3.815156	3.304447	1.40845	3.090477	2.613034
protein_co actinin_alp	10407	8487	8208	36954	29257	30457	117.877	113.283	122.5111	362.0994	372.2907	342.8468
protein_co zinc_finger_	569	525	519	547	632	585	3.113532	3.385381	3.74234	2.589354	3.885145	3.181315
protein_co ribosomal_	33	19	18	45	35	19	0.685926	0.465397	0.493027	0.809168	0.817298	0.392488

protein_co	epsin_2	1109	881	754	562	607	669	12.05329	11.28384	10.79891	5.284127	7.411596	7.226196
protein_co	protein_tyr	458	418	275	680	443	613	6.608606	7.107678	5.228919	8.488214	7.181202	8.790519
protein_co	LIM_and_se	38	22	9	514	346	336	0.418506	0.285527	0.130616	4.897158	4.280979	3.67762
protein_co	acid-sensin	8	5	2	7	0	1	0.126805	0.093395	0.041774	0.095986	0	0.015753
protein_co	SPEG_comp	2954	2623	1998	83	104	155	14.50452	15.17743	12.92775	0.352561	0.573687	0.75637
protein_co	ligand_of_r	36	38	36	131	72	98	0.507287	0.631018	0.66848	1.596927	1.13981	1.372419
protein_co	aldehyde_d	339	256	302	521	461	431	4.568991	4.066003	5.363674	6.074651	6.980244	5.773079
protein_co	transferrin_	3878	3314	3793	3291	2637	2223	40.16928	40.45254	51.77306	29.49016	30.68636	22.88418
protein_co	sterol_regu	1033	791	628	1961	1645	1769	11.75329	10.60578	9.415719	19.30188	21.02684	20.00306
protein_co	transient_r	1	0	3	0	0	0	0.009067	0	0.035843	0	0	0
protein_co	AF4/FMR2_	2408	1922	2517	1948	1966	1565	13.3461	12.55331	18.38298	9.340062	12.24138	8.620288
protein_co	ubiquitin-c	306	308	293	856	617	636	10.45832	12.40505	13.19602	25.30914	23.69054	21.60267
protein_co	membrane_	515	420	448	1026	923	873	4.910773	4.719533	5.629314	8.463559	9.887657	8.273067
protein_co	Rho-relatec	595	530	573	456	405	395	7.042229	7.392242	8.936812	4.66897	5.385143	4.646222
protein_co	N-acylsphir	0	2	0	1	0	1	0	0.060866	0	0.022341	0	0.025665
protein_co	structural_	948	814	937	2786	2763	2350	5.129606	5.190475	6.681132	13.04127	16.79599	12.63727
protein_co	hydroxyste	941	781	572	1655	1229	1768	51.8932	50.75502	41.56729	78.9554	76.14156	96.89754
protein_co	MAP/microc	803	654	557	1685	1629	2003	8.991459	8.629775	8.218728	16.32216	20.49202	22.28975
protein_co	hyaluronan	167	134	138	1551	1056	975	2.851063	2.69589	3.10459	22.90684	20.25365	16.54263
protein_co	checkpoint	477	435	367	795	642	896	7.75103	8.329853	7.85854	11.17561	11.71993	14.46967
protein_co	thyrotropir	34	59	40	492	364	420	0.320398	0.655193	0.496713	4.010869	3.853548	3.933411
protein_co	prolyl_4-hy	2672	2346	1816	293	249	242	42.23898	43.70308	37.82924	4.006891	4.422067	3.801911
protein_co	Fc_fragmen	0	1	0	0	0	0	0	0.013331	0	0	0	0
protein_co	nuclear_fac	162	139	188	287	293	238	1.355316	1.370401	2.072613	2.077163	2.753863	1.978847
protein_co	tRNA_nucle	324	281	262	658	560	571	7.536416	7.702527	8.030747	13.24063	14.63379	13.19975
protein_co	acyl-CoA_d	3313	2925	2083	4902	3689	5669	74.57207	77.58678	61.7844	95.45333	93.28514	126.8151
protein_co	serine/thre	1662	1336	1220	1244	1216	1396	14.51946	13.75413	14.04475	9.401623	11.93444	12.12033
protein_co	F-box_and_	1141	891	997	1107	1031	997	13.30815	12.24663	15.32364	11.16973	13.50951	11.55678
protein_co	ArfGAP_wit	65	69	51	33	28	43	0.702565	0.87888	0.726404	0.308568	0.340001	0.461904
protein_co	collapsin_r	2332	1919	1863	2470	1901	1877	39.24297	38.05533	41.31246	35.95782	35.93888	31.39115
protein_co	Ellis_van_C	1415	1321	1282	305	405	342	10.60619	11.66844	12.66268	1.977724	3.410413	2.547643
protein_co	derlin_2	805	696	577	1193	852	917	10.12533	10.31643	9.563653	12.98125	12.03932	11.46284
protein_co	SID1_transı	3	1	1	3	0	0	0.031264	0.012281	0.013733	0.027047	0	0
protein_co	nudE_nucle	403	290	350	731	493	537	5.420534	4.596657	6.203544	8.505843	7.4496	7.178289
protein_co	murine_ret	333	267	258	69	76	56	2.839779	2.683235	2.899312	0.509041	0.72812	0.474611
protein_co	transmemb	37	17	20	21	29	40	0.739455	0.400374	0.526714	0.363072	0.651114	0.794474
protein_co	adaptor-rel	1685	1264	1106	2556	1702	1943	33.85411	29.92717	29.28205	44.42581	38.4167	38.79662
protein_co	poliovirus_	774	583	599	1171	893	939	12.32371	10.93896	12.56788	16.12948	15.97353	14.85852
protein_co	inhibitor_c	173	119	96	125	125	147	1.6759	1.358489	1.225485	1.04755	1.360382	1.415236
protein_co	X-ray_repai	487	379	300	790	600	761	9.201379	8.438597	7.469302	12.91261	12.73574	14.28954
protein_co	scavenger_I	1561	1290	1127	1529	930	1083	14.95221	14.56128	14.2253	12.6699	10.00771	10.30957
protein_co	cytochrom	13	2	10	8	12	15	0.291501	0.052849	0.295482	0.155185	0.302292	0.33427
protein_co	minichrom	570	424	386	4021	2867	3336	8.338316	7.309311	7.440903	50.88627	47.11729	48.49972
protein_co	Mov10l1_M	14	10	3	0	1	0	0.187165	0.157545	0.052851	0	0.015019	0

protein_co	pannexin_2	45	28	28	13	17	4	0.780841	0.572552	0.64024	0.195144	0.331396	0.068979
protein_co	Selenoprot	587	450	362	682	446	528	13.42392	12.1272	10.90899	13.49238	11.45843	12.00009
protein_co	tumor_pro	2	0	1	0	2	1	0.021569	0	0.014211	0	0.024231	0.010718
protein_co	alpha-kinas	198	154	111	5	4	2	1.860876	1.705612	1.374707	0.040652	0.042234	0.018681
protein_co	lethal_gian	6	1	7	992	754	848	0.090061	0.017689	0.138458	12.88135	12.71473	12.65005
protein_co	phosphodi	499	475	482	440	363	348	5.664142	6.35381	7.20967	4.320651	4.629022	3.925748
protein_co	chloride_cl	114	115	94	60	54	50	0.894115	1.062902	0.971518	0.407101	0.475807	0.389734
protein_co	notchless_h	661	583	420	939	641	693	6.620128	6.880826	5.543053	8.135674	7.212271	6.897756
protein_co	succinate_c	2729	2208	1902	2695	2047	2417	48.14261	45.90207	44.21518	41.12897	40.56888	42.37526
protein_co	SWI/SNF_re	843	761	793	1314	816	856	7.641996	8.129634	9.472994	10.30475	8.310334	7.711922
protein_co	fibronectin	3	5	1	4	12	8	0.114426	0.22474	0.050262	0.131985	0.514201	0.303251
protein_co	gasdermin_	255	274	181	177	193	210	2.900097	3.672232	2.7126	1.741441	2.465919	2.373566
protein_co	lysine_(K)-s	681	575	720	641	720	628	3.3497	3.332987	4.666874	2.727594	3.978692	3.069927
protein_co	ADAM_met	32	13	20	23	42	33	0.370622	0.177432	0.305243	0.230447	0.546486	0.379843
protein_co	protein_ph	374	376	398	477	434	309	2.913897	3.452213	4.086208	3.215022	3.798756	2.392604
protein_co	fermitin_fa	1687	1521	1547	3123	2416	2207	14.88276	15.81265	17.9843	23.83436	23.94498	19.34998
protein_co	ATP-bindin	1	1	2	0	0	0	0.011087	0.013065	0.02922	0	0	0
protein_co	dehydroger	1	6	3	0	0	0	0.018485	0.130701	0.073076	0	0	0
protein_co	prostaglanc	78	92	125	63	66	46	0.914798	1.271527	1.931859	0.639196	0.869608	0.536164
protein_co	insulin-like	1734	1407	1343	3776	3188	3266	24.89145	23.80139	25.40458	46.89172	51.41248	46.59368
protein_co	mitogen-ac	164	145	145	222	220	257	0.879134	0.91598	1.024269	1.029502	1.324899	1.369159
protein_co	ST6_beta-g	172	130	181	305	335	326	1.860995	1.657553	2.580657	2.854827	4.072028	3.505453
protein_co	T-box_21	0	0	0	5	0	0	0	0	0	0.089034	0	0
pseudogen	voltage-dep	2	0	1	4	0	1	0.124861	0	0.082268	0.216033	0	0.062045
protein_co	furry_homo	95	80	99	29	24	10	0.468504	0.46493	0.643369	0.123723	0.132969	0.049012
protein_co	phosphatid	2516	2296	2313	4595	3647	3799	36.86674	39.64634	44.66163	58.24688	60.03561	55.32266
protein_co	N-ethylmal	830	702	710	661	456	484	11.03214	10.99578	12.43583	7.600572	6.809194	6.393472
protein_co	GLI_family_	443	363	334	280	320	291	3.449457	3.330894	3.427112	1.886115	2.799278	2.251903
protein_co	cytoplasmi	1051	990	876	1210	1225	888	6.877748	7.634592	7.554096	6.850022	9.005933	5.775189
protein_co	mitochond	1319	976	785	2519	1703	2488	67.14343	58.54848	52.65786	110.9302	97.39181	125.869
protein_co	notch_3	5034	4264	3436	2505	2955	2911	33.02007	32.96014	29.69974	14.21463	21.77566	18.97652
protein_co	chloride_cl	1001	906	699	2439	1584	1649	17.70596	18.88516	16.29286	37.32159	31.47673	28.98783
protein_co	protein_ph	5	0	0	7	13	15	0.058331	0	0	0.070646	0.170381	0.173912
protein_co	TEA_domai	1175	978	883	1084	932	1001	25.49413	25.00623	25.2463	20.34673	22.71785	21.5847
protein_co	embryonic_	321	377	261	796	583	770	6.141691	8.500244	6.58049	13.17525	12.53143	14.64142
protein_co	cadherin-re	23	32	23	3	4	5	0.270047	0.442761	0.355856	0.030472	0.052762	0.058343
protein_co	synuclein_b	9	11	6	0	3	2	0.344518	0.496215	0.302661	0	0.129015	0.076087
protein_co	tumor_susc	638	567	567	1099	766	902	16.07632	16.83667	18.82712	23.95669	21.68422	22.58823
protein_co	chromoson	601	528	544	856	871	989	7.767953	8.042168	9.265436	9.571256	12.64734	12.70393
protein_co	ATPase_Ca+	32	26	16	18	18	14	0.353014	0.338004	0.232593	0.171782	0.223081	0.15349
protein_co	carbonic_a	4451	3768	3795	1	3	6	36.74417	36.65632	41.28359	0.007142	0.027823	0.049226
protein_co	monoglyce	364	281	395	1345	1159	1426	3.900126	3.548057	5.577109	12.46702	13.95114	15.18471
protein_co	netrin_4	579	421	595	263	218	268	8.479346	7.265625	11.48248	3.331981	3.586653	3.900571
protein_co	BC1_(ubiqu	505	414	313	994	617	817	13.26809	12.81812	10.83668	22.59261	18.21173	21.33284

protein_co	NUAK_fami	788	662	713	1858	2197	1953	6.109769	6.048722	7.284889	12.46256	19.13717	15.0491
protein_co	dipeptidyl-	548	439	489	640	569	558	3.335057	3.148432	3.921628	3.369502	3.890309	3.374944
protein_co	solute_carr	161	173	165	262	269	283	1.477722	1.871199	1.995656	2.080325	2.773756	2.581445
protein_co	zinc_finger_	1585	1386	1557	1634	1472	1325	12.53158	12.91359	16.22184	11.17614	13.07475	10.41123
protein_co	scavenger_I	9	8	9	3	4	16	0.138388	0.144961	0.182361	0.039906	0.069098	0.244503
protein_co	lectin_man	3862	3271	3737	2374	1964	1940	37.03281	36.96255	47.22068	19.69328	21.15753	18.48782
protein_co	protein_tyr	2303	2064	1997	3972	3117	3119	37.80562	39.92815	43.19915	56.40721	57.48417	50.88472
protein_co	interaction	1	0	2	3	1	2	0.007915	0	0.020859	0.020541	0.008892	0.015732
protein_co	zinc_finger_	925	831	924	925	1050	1001	4.274653	4.525507	5.626857	3.697974	5.451267	4.5973
protein_co	NADPH_oxi	0	0	0	10	0	8	0	0	0	0.224285	0	0.206128
protein_co	enolase_1_	56834	47585	36164	65887	46331	52482	1327.824	1310.115	1113.38	1331.665	1216.054	1218.575
protein_co	solute_carr	1	0	0	1	0	1	0.006133	0	0	0.005306	0	0.006095
protein_co	chromoson	6108	5262	4393	2289	1845	2938	317.646	322.4796	301.0512	102.9801	107.7928	151.8468
protein_co	anoctamin_	480	417	273	342	336	501	5.502745	5.633539	4.124161	3.391777	4.327395	5.708021
protein_co	tubulin_ep	151	165	139	277	125	178	2.214429	2.851517	2.686176	3.51421	2.059415	2.594266
protein_co	Rho_guanir	152	160	121	136	143	151	1.755078	2.177107	1.841081	1.358484	1.854974	1.732764
protein_co	TXK_tyrosir	12	4	4	4	3	6	0.218014	0.085639	0.095763	0.062867	0.061231	0.108334
protein_co	WSC_doma	0	0	0	8	0	1	0	0	0	0.07779	0	0.011171
protein_co	potassium_	7	3	7	51	67	70	0.113156	0.057149	0.149112	0.713204	1.216759	1.124575
protein_co	tachykinin_	6	3	6	13	10	27	0.152494	0.089853	0.20095	0.285831	0.28553	0.681987
protein_co	ARP6_actin	245	195	203	392	300	297	5.264019	4.937341	5.747543	7.286189	7.241386	6.341872
protein_co	TIMELESS_i	68	67	84	640	447	569	2.064213	2.396776	3.360158	16.80694	15.24411	17.16594
protein_co	sorcin	837	681	558	1156	689	950	22.04558	21.13734	19.36712	26.34007	20.38752	24.86734
protein_co	eukaryotic_	1989	1633	2091	1657	1730	1442	16.99478	16.44273	23.54342	12.24803	16.60641	12.24491
protein_co	nucleopori	179	169	134	928	683	630	7.368925	8.198698	7.269269	33.04929	31.58791	25.77516
protein_co	sema_dom	169	142	191	969	804	731	1.581026	1.565481	2.354619	7.842223	8.450015	6.796408
protein_co	G-2_and_S-	427	292	280	1642	1347	1465	7.264076	5.853861	6.276902	24.1651	25.74359	24.7685
protein_co	sema_dom	825	733	927	1254	1260	1059	8.4415	8.838463	12.49914	11.10008	14.48389	10.7689
protein_co	tetratricop	669	545	490	636	455	431	13.56993	13.02732	13.09732	11.16019	10.36841	8.688374
protein_co	acetyl-CoA_	863	826	665	995	681	796	20.23387	22.82208	20.54587	20.18154	17.9376	18.54773
protein_co	GRAM_dom	427	402	283	154	218	234	5.041437	5.593191	4.40299	1.572933	2.891559	2.745693
protein_co	cadherin_E	175	176	156	536	637	526	0.813476	0.964109	0.955577	2.155432	3.326557	2.429975
protein_co	wingless-ty	3	5	0	2	0	0	0.0752	0.147698	0	0.04337	0	0
protein_co	zinc_finger_	1111	1022	988	1707	1387	1203	8.622994	9.347641	10.10499	11.46148	12.09399	9.279388
protein_co	solute_carr	93	107	95	282	216	260	1.217185	1.650306	1.638445	3.192903	3.17597	3.381867
protein_co	translocase	524	374	378	1205	800	1025	10.99092	9.244458	10.44791	21.86517	18.85132	21.36664
protein_co	adducin_2_	0	0	0	59	37	33	0	0	0	0.46143	0.375787	0.296493
protein_co	RAS_protei	323	259	411	730	774	610	1.56909	1.482696	2.631007	3.067829	4.224111	2.944996
protein_co	VPS9_dom	346	211	206	146	97	192	6.56309	4.716521	5.149135	2.395787	2.06706	3.619455
protein_co	zinc_finger_	525	465	513	407	344	308	3.955318	4.128404	5.093007	2.652648	2.911586	2.306123
protein_co	MAP/micro	1254	1087	1017	1635	1201	1227	18.52344	18.92172	19.79611	20.89319	19.93041	18.01268
protein_co	solute_carr	11555	9461	8208	14295	10522	12532	189.0399	182.4012	176.9521	202.3162	193.3886	203.7575
protein_co	fibronectin	1700	1448	1685	1530	1465	1340	11.3866	11.42933	14.87236	8.865426	11.02381	8.919892
protein_co	FOS-like_an	14991	13588	12860	3337	3733	3554	118.3122	126.3751	133.7442	22.78339	33.09833	27.87572

protein_co	calcium_ch	35	12	24	1318	1096	1007	0.548206	0.221495	0.495361	17.85886	19.28568	15.67525
protein_co	FRY-like	531	495	608	593	452	524	2.401475	2.638128	3.623447	2.320071	2.296524	2.355182
protein_co	transmemb	1630	1363	1620	1678	1348	1204	11.54741	11.37889	15.12331	10.28376	10.72843	8.476825
protein_co	fascin_hom	19842	15510	12483	26122	20526	23964	378.2698	348.4457	313.5956	430.8099	439.6121	454.0306
protein_co	actin_beta	96453	76281	64830	293215	181604	206696	2274.529	2119.821	2014.59	5981.704	4811.165	4844.149
protein_co	molybdenu	15	2	4	84	86	70	0.128915	0.020256	0.045301	0.624531	0.830346	0.597887
protein_co	phospholip	56	74	79	230	173	132	0.506353	0.788504	0.941298	1.799103	1.757358	1.186175
protein_co	WD_repeat	92	69	50	1220	891	1035	0.815704	0.720943	0.584184	9.357673	8.87507	9.120004
protein_co	discs_large_	1021	957	1078	2257	1804	1723	10.73754	11.86036	14.93938	20.53399	21.31398	18.00834
protein_co	RAB7A_mer	4272	3580	3458	6562	4596	5318	100.7861	99.53123	107.5051	133.9271	121.8143	124.6887
protein_co	B-cell_recep	583	505	443	865	605	747	5.346371	5.45744	5.353392	6.862299	6.232969	6.808019
protein_co	SEC31_hom	200	229	180	63	84	81	2.081423	2.80849	2.468526	0.567197	0.982107	0.83777
protein_co	squamous_	742	609	661	1501	1093	1382	9.810744	9.489043	11.51687	17.16887	16.23556	18.15999
protein_co	Rho_GTPas	0	0	1	0	1	1	0	0	0.023505	0	0.020039	0.017727
protein_co	tubulin_alp	38	31	9	16	25	27	1.301266	1.250983	0.406125	0.473986	0.961771	0.918874
protein_co	paired_box	0	0	0	0	0	5	0	0	0	0	0	0.062502
protein_co	exosome_c	292	255	215	478	367	565	9.386017	9.659302	9.106925	13.29197	13.25298	18.04914
protein_co	kinesin-assc	572	497	504	2132	1705	1948	7.366151	7.542374	8.552832	23.75171	24.6671	24.9312
protein_co	makorin_ri	960	783	771	745	572	554	17.84528	17.15224	18.88606	11.9804	11.9453	10.23462
protein_co	minichrom	434	358	317	2259	1802	1781	6.149998	5.978267	5.919422	27.69265	28.68726	25.0818
protein_co	REX2_RNA_	556	507	455	1372	765	1061	25.35331	27.24425	27.34048	54.12239	39.18956	48.08226
protein_co	RNA_bindir	375	392	323	670	546	597	2.9521	3.636578	3.350712	4.562865	4.828825	4.670719
protein_co	RNA_bindir	511	409	486	548	528	415	8.596393	8.108224	10.77374	7.975151	9.9788	6.9383
protein_co	bromodom	1777	1565	1542	2051	3223	2747	10.63728	11.03989	12.16361	10.62116	21.67468	16.34224
protein_co	protein_tyr	1837	1545	1199	2619	1983	2244	18.5455	18.38082	15.95083	22.87325	22.49061	22.51448
protein_co	mutL_hom	603	506	427	1315	1025	1113	11.60008	11.471	10.82446	21.88429	22.15219	21.27887
protein_co	uracil-DNA_	477	438	383	1925	1511	1882	11.30387	12.23179	11.96031	39.46414	40.22744	44.32392
protein_co	flavin_cont	14	11	24	22	16	26	0.329118	0.304736	0.743481	0.447414	0.422564	0.607445
protein_co	kelch-like_f	343	249	367	363	290	316	5.308027	4.540937	7.484105	4.859691	5.041805	4.859994
protein_co	regulator_c	3	4	3	0	3	2	0.036987	0.058116	0.04874	0	0.041553	0.024506
protein_co	solute_carr	35	28	27	153	122	146	0.285638	0.269286	0.290367	1.080196	1.118554	1.184161
protein_co	plexin_A2	584	516	537	2398	2791	2682	2.701638	2.813008	3.273583	9.5968	14.50518	12.33056
protein_co	sperm_assc	71	59	85	214	335	214	0.930399	0.911108	1.467792	2.425982	4.93179	2.786982
protein_co	ankyrin_rep	974	949	878	539	462	335	12.43118	14.27337	14.76667	5.951208	6.624367	4.249206
protein_co	tumor_pro	3	3	2	1876	1272	1463	0.040537	0.04777	0.035612	21.92924	19.30918	19.64634
protein_co	acetyl-CoA_	63	73	50	30	56	37	0.356334	0.486571	0.372667	0.146791	0.355839	0.207983
protein_co	TNF_recept	1138	975	735	3260	2140	3097	20.62542	20.82439	17.55427	51.11415	43.57359	55.78422
protein_co	phosphopr	37	20	24	96	96	107	0.446505	0.284421	0.381655	1.00221	1.301502	1.28327
protein_co	G_patch_d	149	110	89	255	195	238	2.258937	1.965249	1.778045	3.344422	3.32125	3.585952
protein_co	intercellula	261	275	193	267	268	299	5.547009	6.887445	5.405184	4.908995	6.398854	6.315376
protein_co	5'-nucleoti	955	757	789	2342	1636	1970	9.606432	8.973496	10.45853	20.38021	18.48805	19.69403
protein_co	melanoma_	83	111	67	1110	676	855	0.903207	1.42344	0.960769	10.44949	8.26428	9.246662
protein_co	glypican_4	1660	1474	1356	1511	1329	1287	17.71816	18.54022	19.07238	13.95205	15.93619	13.65207
protein_co	muscleblin	46	32	46	540	585	424	0.215627	0.176767	0.284143	2.189783	3.080699	1.97524

protein_co calmodulin	4	3	2	629	582	622	0.050673	0.044787	0.033388	6.893398	8.283078	7.831046
protein_co RAP1_GTPa	11	9	12	12	8	13	0.13562	0.130761	0.19496	0.127989	0.110807	0.159288
protein_co XPA_bindir	1020	1034	624	1881	1345	1650	11.85506	14.16222	9.557034	18.91279	17.56204	19.05888
protein_co Rho_guanir	1436	1282	1015	2887	1850	2566	22.10621	23.25707	20.59021	38.44764	31.9949	39.25782
protein_co syntaxin_bi	4	2	4	538	330	417	0.107277	0.063209	0.141364	12.48217	9.942783	11.11452
protein_co mitogen-ac	1010	885	657	911	895	1293	15.29036	15.78872	13.1068	11.93103	15.22189	19.45381
protein_co nicotinami	0	0	0	50	43	44	0	0	0	2.033699	2.271283	2.055966
protein_co diacylglyce	692	594	585	1942	2059	2362	5.817876	5.885074	6.481105	14.12442	19.4475	19.73549
protein_co cortactin_b	54	45	49	282	263	225	0.478863	0.470259	0.572596	2.163365	2.620128	1.982942
protein_co retinoic_ac	371	345	345	140	137	123	6.368712	6.979172	7.804258	2.079068	2.642088	2.09842
protein_co topoisomer	2080	1713	1791	2534	2331	2059	20.43371	19.83117	23.18538	21.53543	25.72618	20.10249
protein_co transmemb	3804	3175	3541	4769	4341	4208	32.79393	32.2555	40.22664	35.56668	42.04282	36.05275
protein_co nuclear_fac	849	704	528	729	574	821	14.49433	14.16348	11.87843	10.76666	11.00909	13.92974
protein_co ubiquitin-c	95	87	83	1398	706	875	5.454875	5.886912	6.280209	69.44346	45.5423	49.93199
protein_co protein_ph	392	387	348	212	361	344	1.867777	2.172986	2.185008	0.873852	1.932392	1.628947
protein_co DnaJ_(Hsp4	1605	1345	1507	3195	2378	2253	16.11728	15.91644	19.94182	27.7556	26.82734	22.48472
protein_co general_tra	3135	2425	2592	3281	3002	2894	23.64919	21.55746	25.76609	21.41154	25.44125	21.69636
protein_co interleukin	671	476	562	885	695	820	9.640002	8.058768	10.63961	10.99919	11.2173	11.70788
protein_co ubiquitin_s	756	689	731	1062	747	829	8.890136	9.548011	11.32762	10.80374	9.868616	9.688371
protein_co p21_protei	42	27	34	18	11	26	0.842882	0.63854	0.899148	0.312502	0.248004	0.518562
protein_co calpain_6	6	9	6	744	576	543	0.089026	0.157368	0.117315	9.549996	9.601493	8.007127
protein_co doublecort	0	0	3	7	4	3	0	0	0.022253	0.034087	0.025295	0.016783
protein_co small_nucl	891	761	556	2597	1596	2176	29.09958	29.28875	23.92868	73.37431	58.55865	70.62811
protein_co sperm_assc	0	0	1	0	1	0	0	0	0.024844	0	0.021181	0
protein_co exosome_c	173	151	90	628	471	577	8.192122	8.42625	5.616007	25.72604	25.05649	27.15412
protein_co dynein_cyt	1935	1553	1713	3332	2840	2719	39.32469	37.19315	45.87505	58.5804	64.84131	54.91655
protein_co amyloid_be	1	0	3	38	27	10	0.019105	0	0.075529	0.628061	0.57952	0.189874
protein_co leucine-rich	833	645	466	1399	1078	1397	9.276367	8.464469	6.838387	13.47763	13.48655	15.46105
protein_co family_with	181	141	139	368	330	261	2.424676	2.225878	2.453719	4.264675	4.966359	3.474764
protein_co sirtuin_6	508	411	339	658	451	562	16.3888	15.62545	14.41179	18.36422	16.34591	18.01895
protein_co polymerase	151	151	140	747	628	671	2.092146	2.465466	2.5561	8.95362	9.775157	9.239473
protein_co actinin_alp	15	10	4	5	5	6	0.163297	0.128291	0.057383	0.047089	0.061151	0.064916
protein_co capping_pr	7617	6004	5020	9787	6670	7752	194.9959	181.1296	169.348	216.7475	191.83	197.2264
protein_co G_protein-r	396	311	345	193	183	127	10.28182	9.515735	11.80399	4.335061	5.337956	3.277089
protein_co N-acetylate	30	21	24	39	58	34	0.441175	0.363928	0.465089	0.496155	0.958223	0.49691
protein_co PHD_finger	132	130	85	1188	801	795	1.210919	1.405373	1.027531	9.428019	8.255105	7.247993
protein_co solute_carr	310	243	285	282	164	204	5.897128	5.447437	7.144281	4.64078	3.504869	3.856725
protein_co ubiquitin-c	818	759	694	1609	1140	1197	16.38507	17.91611	18.31847	27.88136	25.65363	23.82861
protein_co fibroblast_g	2714	2314	2024	2354	2167	2320	24.35286	24.46868	23.93235	18.27299	21.8448	20.68891
protein_co FK506_bin	0	4	0	1	0	0	0	0.1291	0	0.023693	0	0
protein_co general_tra	1282	1026	1175	923	959	791	14.92312	14.07428	18.02372	9.294721	12.54121	9.150773
protein_co structural_	3	2	1	5	11	2	0.037806	0.029701	0.016606	0.05451	0.155733	0.025048
protein_co fibulin_1	18661	15530	12970	7837	4884	5359	335.2331	328.7687	307.0342	121.7937	98.56816	95.67652
protein_co integrin_al	41	46	57	154	189	155	0.321329	0.424846	0.588676	1.04412	1.664093	1.20728

protein_co	cystatin_F_	0	0	2	1	1	1	0	0	0.150029	0.049246	0.063953	0.056574
protein_co	microtubul	18	27	36	1018	923	1021	0.09813	0.17346	0.258622	4.80108	5.652999	5.531762
protein_co	protein_inh	535	384	360	477	368	353	4.79327	4.054305	4.250259	3.697085	3.704034	3.143131
protein_co	amphiphys	537	427	409	66	86	72	8.317529	7.793903	8.347918	0.884356	1.496468	1.108312
protein_co	v-raf_murir	815	649	552	1398	986	987	17.55367	16.47259	15.66694	26.04836	23.85812	21.12696
protein_co	methylcrot	219	215	205	299	309	259	4.034126	4.667141	4.976156	4.764743	6.394592	4.741489
protein_co	lysosomal-a	1	0	1	70	26	42	0.015686	0	0.020671	0.949903	0.458185	0.654753
protein_co	fibroblast_a	1271	1100	1029	42	28	13	24.20432	24.68579	25.82245	0.691926	0.599038	0.246037
protein_co	nebulette	777	671	723	1151	1001	912	4.46345	4.542336	5.472966	5.719894	6.460004	5.206599
protein_co	alkaline_ce	287	229	237	994	742	732	2.059375	1.936404	2.240973	6.170251	5.981449	5.220044
protein_co	ubiquitin-c	1173	1062	1050	2581	2333	2334	11.83981	12.63218	13.96596	22.53708	26.45516	23.413
protein_co	phosphatid	884	713	708	856	617	613	4.956035	4.710627	5.230584	4.151632	3.886121	3.415484
protein_co	NEDD4_bin	176	212	225	463	563	482	0.955947	1.356951	1.610417	2.17553	3.43541	2.601823
protein_co	chromoson	310	240	322	1127	1002	1062	12.05857	11.00151	16.50535	37.92459	43.78756	41.0552
protein_co	tubby_like_	1090	975	842	892	599	576	18.75998	19.77504	19.09645	13.28109	11.58195	9.852306
protein_co	synaptojan	544	460	524	505	397	429	3.903483	3.88972	4.954725	3.134785	3.200317	3.059288
protein_co	adenylate_c	383	405	357	8	6	5	2.046468	2.550165	2.513675	0.036979	0.036017	0.026551
protein_co	protein_ph	1622	1372	1409	1806	1423	1675	19.1632	19.10198	21.93628	18.45856	18.88735	19.66716
pseudogen	postmeioti	76	75	56	98	87	97	3.853942	4.481877	3.742092	4.299131	4.956326	4.88847
protein_co	guanine_nu	7828	6707	6055	13161	10128	11742	132.4879	133.7706	135.0437	192.698	192.5742	197.5045
protein_co	homeobox_	248	229	241	43	13	21	6.373479	6.935335	8.161627	0.955997	0.375333	0.536357
protein_co	endothelin_	11	10	20	1000	569	567	0.286449	0.306875	0.686309	22.52774	16.64624	14.67396
protein_co	myeloid/ly	509	475	491	971	797	761	5.256919	5.781149	6.682359	8.675524	9.247426	7.811021
protein_co	zinc_finger_	36	26	20	59	49	43	0.808946	0.688489	0.592218	1.146917	1.236978	0.960273
protein_co	adenylate_c	17	10	3	0	2	1	0.138739	0.096173	0.032263	0	0.018337	0.008111
protein_co	fibroblast_g	0	1	3	12	3	12	0	0.03696	0.123987	0.325585	0.105704	0.374034
protein_co	integral_m	63	42	39	254	200	187	1.964242	1.543159	1.602337	6.850955	7.005408	5.794362
protein_co	nardilysin_	1795	1569	1558	2327	1760	1887	24.39771	25.13128	27.90531	27.36176	26.87487	25.48979
protein_co	voltage-dep	1285	1070	960	3400	2528	2714	47.60614	46.71439	46.86687	108.9687	105.217	99.92619
protein_co	pericentrio	1252	1094	1256	1947	1726	1442	9.718787	10.00765	12.8479	13.07485	15.05212	11.12455
protein_co	trinucleoti	302	250	301	152	199	164	1.641497	1.601328	2.155929	0.714726	1.215165	0.885904
protein_co	core-bindir	506	478	440	503	457	412	3.433057	3.821778	3.933852	2.952307	3.483339	2.778033
protein_co	deleted_in_	0	1	2	26	38	22	0	0.019484	0.043575	0.371884	0.705835	0.361496
protein_co	itchy_E3_u	933	882	974	1107	1098	980	7.716599	8.596466	10.61544	7.920542	10.20224	8.055268
protein_co	polycystic_	7	4	3	4	9	5	0.158846	0.106966	0.089708	0.078524	0.22944	0.112761
protein_co	tumor_pro	624	588	595	195	214	230	7.895598	8.767683	9.920926	2.134509	3.042028	2.892264
protein_co	stromal_ce	8035	6489	4950	5276	3686	4825	120.9843	115.1405	98.21622	68.72441	62.3516	72.20216
protein_co	myosin_he	62	46	21	8	33	26	0.521586	0.456036	0.232803	0.058222	0.311887	0.217379
protein_co	BPI_fold_c	1	3	0	0	1	3	0.027893	0.098611	0	0	0.031336	0.083162
protein_co	tumor_pro	0	3	0	27	16	16	0	0.036076	0	0.238352	0.183426	0.162264
protein_co	toll_interac	1449	1067	938	1192	976	1084	20.92512	18.15813	17.84996	14.89152	15.83429	15.55746
protein_co	ubiquitin-c	12	18	19	29	20	32	0.452165	0.799273	0.943418	0.945315	0.846632	1.198327
protein_co	clusterin-li	40	38	27	13	6	5	0.864696	0.968042	0.769134	0.243114	0.145715	0.107419
protein_co	runt-relate	343	347	274	268	339	250	2.409282	2.872302	2.536173	1.628514	2.675114	1.745192

protein_co	cadherin_1	2	8	11	0	0	2	0.028671	0.135148	0.207797	0	0	0.028494
protein_co	THO_comp	376	332	292	1066	633	670	7.132144	7.421256	7.298774	17.49252	13.48916	12.63039
protein_co	FK506_bin	1515	1247	1038	222	143	152	28.3012	27.45148	25.55197	3.587635	3.001078	2.821925
protein_co	oxysterol_b	128	99	115	509	320	387	0.960517	0.875462	1.137176	3.304273	2.697703	2.886129
protein_co	solute_carr	1230	1154	1045	1856	1621	1580	15.61569	17.26509	17.48265	20.38436	23.12001	19.9353
protein_co	X-ray_repai	4611	3784	3706	13547	9210	9347	64.90586	62.76925	68.74308	164.9662	145.6456	130.7587
protein_co	latexin	173	124	140	134	65	64	8.206803	6.93197	8.751666	5.499152	3.464099	3.017293
protein_co	SP140_nuc	27	14	24	45	38	50	0.440359	0.269078	0.51581	0.63492	0.696268	0.810444
protein_co	MAP_kinas	268	280	240	735	646	561	4.1632	5.125752	4.912907	9.877405	11.2739	8.66094
protein_co	tensin_1	2335	1979	1825	82	176	116	11.96566	11.95096	12.32388	0.363519	1.013238	0.590769
protein_co	REX1_RNA_	697	444	360	1470	1274	1507	8.060261	6.05071	5.485972	14.70607	16.5514	17.31965
protein_co	SAR1_hom	2364	1913	1998	2666	2320	2609	38.78293	36.98411	43.194	37.83696	42.75926	42.53798
protein_co	cell_divisio	59	48	57	281	265	258	0.747075	0.716243	0.95109	3.07809	3.769701	3.246693
protein_co	Rap_guanir	54	37	30	54	67	49	0.497099	0.401382	0.363919	0.430037	0.692903	0.448285
protein_co	carcinoemb	7	12	4	131	94	110	0.10531	0.212746	0.079299	1.704932	1.588729	1.644656
protein_co	SUMO1/ser	169	155	153	567	393	400	1.800569	1.946085	2.148074	5.225997	4.703972	4.235383
protein_co	dual_specif	2	0	0	0	0	0	0.059888	0	0	0	0	0
protein_co	capicua_tra	4789	3753	2882	2055	2186	2623	30.85111	28.49126	24.46554	11.45251	15.82068	16.79322
protein_co	lipase_horr	83	81	88	70	77	110	1.1524	1.32531	1.610063	0.840788	1.201061	1.517846
protein_co	farnesyl-dip	3360	2930	2792	6657	4378	5054	81.74712	84.00554	89.51245	140.1118	119.6625	122.2019
protein_co	platelet-act	410	399	271	620	303	405	19.7685	22.67095	17.21844	25.86095	16.41275	19.40682
protein_co	oligophren	120	118	173	105	154	99	0.80631	0.934351	1.531799	0.610342	1.162494	0.661098
protein_co	afamin	0	0	0	0	2	2	0	0	0	0	0.058539	0.051785
protein_co	kinesin_fam	518	473	396	3254	2315	3002	10.94748	11.7802	11.02845	59.49287	54.96477	63.05285
protein_co	secretagogi	0	0	0	2	0	2	0	0	0	0.063302	0	0.072722
protein_co	leucine_ric	94	79	82	772	766	689	0.916305	0.9075	1.053322	6.510174	8.388612	6.674845
protein_co	phosphoglu	1533	1420	1204	862	650	751	30.54518	33.34233	31.61272	14.85836	14.55	14.87134
protein_co	DEAD_(Asp	2243	1801	1693	3819	3003	3333	42.15359	39.88651	41.92731	62.08946	63.40297	62.25155
protein_co	dynamin_2	2838	2462	2110	4119	3018	4021	26.5876	27.18078	26.04858	33.38271	31.76399	37.43782
protein_co	erythrocyte	773	703	686	1653	1697	1655	9.181824	9.84038	10.73763	16.98577	22.64542	19.53697
protein_co	regulating_	9	8	22	5	3	2	0.067536	0.070744	0.217547	0.032458	0.025291	0.014915
protein_co	monooxyge	1770	1633	1654	100	82	104	30.63274	33.30473	37.72098	1.497186	1.59432	1.788775
protein_co	syntaxin_7	951	819	902	1294	1035	1026	13.64784	13.85079	17.05787	16.065	16.68679	14.63324
protein_co	RAB_memb	599	493	417	1158	798	1009	12.69482	12.31271	11.64583	21.23104	18.99991	21.25203
protein_co	kelch-like_k	1170	915	826	1240	1042	1330	20.96141	19.31803	19.50067	19.21849	20.97256	23.68077
protein_co	DEAD_(Asp	0	0	0	1	3	0	0	0	0	0.018225	0.071002	0
protein_co	protein_tyr	6	14	5	0	0	0	0.081931	0.225285	0.089971	0	0	0
protein_co	dopachrom	0	0	0	0	1	0	0	0	0	0	0.01302	0
protein_co	solute_carr	769	617	492	974	698	1029	16.21977	15.33595	13.67472	17.77216	16.53952	21.56966
protein_co	beta-gamm	307	309	297	231	195	119	3.398763	4.031328	4.332851	2.212369	2.425304	1.3093
protein_co	EPH_recept	6	0	0	15	8	23	0.079991	0	0	0.173	0.119821	0.30474
protein_co	secretin_re	0	1	0	0	0	0	0	0.027423	0	0	0	0
protein_co	regulatory_	274	251	328	314	318	307	1.558594	1.682531	2.458618	1.545166	2.032163	1.735523
protein_co	RAP1_inter	479	407	533	1036	1033	857	2.491035	2.494283	3.652635	4.660871	6.035228	4.429297

protein_co	RAB21_mei	846	773	750	1743	1378	1446	7.247262	7.803514	8.466418	12.91707	13.26178	12.31067
protein_co	solute_carr	17	4	15	8	20	10	0.117801	0.032664	0.13697	0.047957	0.155696	0.068867
protein_co	SWI/SNF_re	1026	901	932	876	1000	852	9.258132	9.580935	11.08222	6.838221	10.13736	7.640561
protein_co	sestrin_1	855	735	752	1000	778	789	12.89956	13.06782	14.95069	13.05184	13.18674	11.83029
protein_co	midline_2	13	5	20	26	28	10	0.239302	0.108463	0.485141	0.414037	0.579042	0.182942
protein_co	collagen_ty	2997	2502	1943	72	90	88	25.69876	25.28249	21.95498	0.534098	0.866996	0.749925
protein_co	Snf2-relate	2801	2137	2018	3028	3847	3599	13.72526	12.34011	13.03057	12.8359	21.1777	17.52665
protein_co	KIAA0020	682	613	536	2530	1725	1908	15.55612	16.47724	16.11078	49.92298	44.20334	43.25188
protein_co	carboxypep	0	3	3	1	2	6	0	0.109006	0.121893	0.026674	0.069279	0.183858
protein_co	cholinergic	8	19	14	3	10	13	0.13227	0.370196	0.305024	0.04291	0.185746	0.213611
protein_co	potassium_	0	0	0	27	10	13	0	0	0	0.384506	0.184938	0.212681
protein_co	CCR4-NOT_	416	338	362	466	404	330	4.744389	4.542665	5.440394	4.59765	5.176275	3.740335
protein_co	presenilin_	823	729	681	1303	1016	1036	7.168549	7.482832	7.816518	9.818357	9.942009	8.968107
protein_co	coproporpl	629	458	574	1078	884	837	11.78757	10.11454	14.17491	17.47654	18.61123	15.58866
protein_co	claudin_do	377	350	315	1478	879	1057	7.082596	7.748653	7.798238	24.02086	18.55193	19.73494
protein_co	MOK_prote	238	149	110	76	80	73	3.307943	2.440476	2.014692	0.913814	1.249166	1.008355
protein_co	heat_shock	10410	8579	8894	34716	25321	26802	157.013	152.4856	176.7734	452.9786	429.0569	401.7555
protein_co	retinoblast	117	88	109	339	278	248	1.089742	0.96589	1.337825	2.731497	2.908921	2.295617
protein_co	discs_large	2763	2165	1978	2962	2800	2755	28.93116	26.71468	27.29268	26.83077	32.93761	28.66925
protein_co	immunoglo	6	6	1	29	69	41	0.04346	0.051214	0.009545	0.181717	0.561477	0.29514
pseudogen	ciliary_roo	270	223	178	76	119	119	2.662829	2.591741	2.313313	0.64842	1.318486	1.16637
protein_co	NDC80_kin	240	183	163	1103	786	956	5.849834	5.256425	5.235458	23.25792	21.52305	23.15793
protein_co	adaptor-rel	175	142	175	328	327	310	1.370919	1.310899	1.806537	2.222853	2.877867	2.413489
protein_co	round_sper	200	240	254	335	274	271	1.599184	2.261449	2.676314	2.317268	2.46132	2.153513
protein_co	membrane_	188	181	209	195	183	131	1.529334	1.735123	2.2404	1.372278	1.672417	1.059072
protein_co	chemokine_	19	6	18	10	7	1	0.825845	0.307329	1.030984	0.376017	0.341816	0.043197
protein_co	alpha-fetop	78	44	0	14	41	72	1.662398	1.105097	0	0.258126	0.981688	1.525045
protein_co	collagen_ty	15	5	5	8	18	9	0.080254	0.031525	0.035252	0.037028	0.108193	0.047855
protein_co	transcriptic	988	777	664	336	332	352	9.795075	9.077765	8.674685	2.881729	3.697754	3.468192
protein_co	osteopetro	250	223	259	663	543	561	2.962894	3.114498	4.044927	6.797554	7.229779	6.607675
protein_co	cadherin_7	0	2	0	63	58	36	0	0.033132	0	0.766153	0.915986	0.502949
protein_co	interphoto	14	6	13	3	9	5	0.178295	0.090047	0.218168	0.033052	0.128767	0.063284
protein_co	PEST_prote	2204	2078	1983	3231	2378	2685	49.8215	55.35512	59.06942	63.18372	60.39015	60.31969
protein_co	exonucleas	370	331	284	439	415	428	5.754456	6.066492	5.820438	5.906498	7.25103	6.615398
protein_co	arginase_ty	108	83	102	275	219	201	2.795906	2.532118	3.479636	6.158777	6.369304	5.171357
protein_co	myocyte_en	246	252	221	484	391	288	2.016644	2.434455	2.387378	3.432436	3.600973	2.346368
protein_co	protein_tyr	0	1	0	0	0	3	0	0.011725	0	0	0	0.029664
protein_co	plakophilin	0	0	0	0	0	2	0	0	0	0	0	0.019319
protein_co	ubiquitin-li	555	485	446	882	746	675	7.530049	7.754497	7.973968	10.35229	11.37084	9.10161
protein_co	serine/thre	585	546	433	568	435	415	5.857855	6.442917	5.713543	4.920329	4.893517	4.129909
protein_co	cell_divisio	508	405	444	718	682	633	4.811957	4.52085	5.542118	5.883631	7.257573	5.958972
protein_co	zinc_finger_	174	132	127	135	173	119	1.640266	1.466378	1.577624	1.100935	1.832146	1.114863
protein_co	low_densit	0	0	0	1333	1581	1194	0	0	0	3.861965	5.948344	3.974012
protein_co	zinc_finger_	80	88	60	64	48	77	1.023014	1.326116	1.011062	0.708002	0.689576	0.97857

protein_co jumonji_dc	66	45	38	86	63	115	0.93201	0.748852	0.707123	1.050602	0.999462	1.613928
protein_co dual_specif	267	237	183	707	490	603	11.13011	11.64243	10.0525	25.49593	22.9474	24.98132
protein_co acetoacetyl	852	645	522	965	680	749	6.793031	6.060254	5.484403	6.656016	6.090907	5.934928
protein_co KIAA0141	1067	1016	867	1110	803	860	11.3658	12.75371	12.16997	10.22873	9.609489	9.104242
protein_co Ca++-depen	78	53	59	100	71	28	0.68311	0.546989	0.680899	0.757633	0.698559	0.243704
protein_co protocadhe	43	32	42	27	11	8	0.628683	0.551341	0.809185	0.3415	0.180678	0.116242
protein_co protocadhe	9	6	12	15	7	3	0.088662	0.069655	0.15578	0.127835	0.077471	0.029371
protein_co protocadhe	5	7	4	0	2	0	0.057482	0.094835	0.060598	0	0.025831	0
protein_co heat_shock	291	252	210	546	421	585	16.83697	17.18219	16.01125	27.32918	27.36542	33.63849
protein_co PH_domair	84	68	60	502	483	394	0.694742	0.662766	0.653929	3.59179	4.487872	3.238546
protein_co ATPase_am	127	111	143	247	217	201	1.132857	1.166813	1.680901	1.906037	2.174604	1.781874
protein_co interleukin	5	2	2	19	13	26	0.065521	0.030885	0.034536	0.215391	0.191383	0.338605
protein_co SWI/SNF_re	1143	918	704	123	115	99	25.05654	23.71509	20.33679	2.332615	2.832187	2.156849
protein_co WD_repeat	431	303	337	869	599	675	3.991877	3.307117	4.113056	6.96278	6.232693	6.213171
protein_co FYN_bindin	1	0	3	18	14	13	0.011145	0	0.044061	0.173554	0.175297	0.143996
protein_co membrane_	46	38	30	22	20	17	0.989149	0.96293	0.850081	0.409251	0.483151	0.363298
protein_co STE20-relat	480	461	451	1260	735	721	11.08228	12.54284	13.72143	25.16643	19.06446	16.54371
protein_co basic_leuci	2297	1761	1951	6959	5099	5386	35.94604	32.47555	40.23298	94.21064	89.64461	83.76567
protein_co C1q_and_t	1813	1467	1231	37	27	43	28.03213	26.72979	25.08137	0.494906	0.468998	0.660749
protein_co malic_enzy	381	360	300	1173	748	779	6.375006	7.098477	6.614723	16.97918	14.06068	12.95396
protein_co chromoson	212	168	207	639	425	471	2.954328	2.75892	3.801263	7.703475	6.653663	6.52309
protein_co cyclin_T2	556	570	593	862	654	653	4.255485	5.141102	5.980863	5.707482	5.623428	4.967034
protein_co family_with	124	139	136	265	209	206	1.023333	1.351815	1.479003	1.891927	1.937719	1.689555
protein_co collagen_ty	38	29	22	42	42	47	0.322811	0.290315	0.246276	0.308658	0.400833	0.3968
protein_co erythrocyte	1093	965	1061	2134	2137	1954	11.78983	12.26654	15.08126	19.91338	25.8965	20.947
protein_co cordon-ble	260	241	263	332	345	257	1.469484	1.60515	1.958764	1.623277	2.190583	1.443558
protein_co discs_large_	418	305	332	768	646	773	3.622415	3.114791	3.791359	5.757662	6.289318	6.657499
protein_co potassium_	98	80	103	22	8	6	1.53543	1.47707	2.126552	0.298188	0.140813	0.093425
protein_co SERTA_dom	77	36	75	597	469	448	0.78108	0.430343	1.002538	5.238924	5.344741	4.516401
protein_co TNF_recept	145	136	99	513	431	390	1.548294	1.711321	1.393014	4.738773	5.170254	4.138661
protein_co mitochond	381	379	277	771	614	749	6.350919	7.444883	6.084518	11.11806	11.49818	12.40804
protein_co gem_(nucle	736	551	603	1147	891	793	7.219672	6.369398	7.794563	9.733434	9.818981	7.730766
protein_co opioid_rec	0	0	0	58	47	43	0	0	0	0.529784	0.557513	0.451217
protein_co nuclear_fac	6094	5178	4840	3133	3687	4154	67.57906	67.66729	70.72775	30.05613	45.93375	45.78106
protein_co sema_dom	2	4	6	13	25	34	0.021913	0.051645	0.086627	0.123217	0.307719	0.370215
protein_co glycogen_s	1582	1371	1762	2402	2356	1910	10.86145	11.09241	15.94124	14.2665	18.17213	13.0324
protein_co integrin_be	2910	2420	2262	5190	4241	4635	35.23749	34.53301	36.09436	54.36787	57.69382	55.77908
protein_co ELKS/RAB6	1135	942	1091	1009	1253	1207	6.357849	6.218309	8.0533	4.889546	7.885232	6.719412
protein_co exportin_1_	2052	1715	1940	5080	4198	4131	16.03231	15.79028	19.97355	34.33566	36.84768	32.07625
protein_co chromoson	1	0	3	0	5	1	0.060643	0	0.239736	0	0.340641	0.060268
protein_co ring_finger_	317	285	293	495	316	320	5.855651	6.203944	7.132115	7.910139	6.557708	5.874562
protein_co transient_r	7	0	5	73	67	59	0.059114	0	0.055641	0.53331	0.635649	0.495171
protein_co partner_an	121	120	134	268	242	213	1.600265	1.870229	2.335318	3.066227	3.595596	2.799598
protein_co dopey_fam	207	126	215	181	199	130	1.334809	0.957473	1.826931	1.009696	1.441621	0.833109

protein_co	LYR_motif_	703	660	515	1093	825	948	6.952647	7.692117	6.711767	9.35143	9.16638	9.317788
protein_co	branched_(	402	409	368	703	615	647	5.649663	6.773714	6.815208	8.547022	9.710032	9.036711
protein_co	K(lysine)_ac	927	687	944	659	1155	907	5.285547	4.616087	7.092788	3.250563	7.398458	5.139574
protein_co	zinc_finger_	734	626	758	341	372	267	6.78873	6.822977	9.238394	2.728411	3.865311	2.454219
protein_co	unc-51-like	274	194	201	345	253	258	2.413616	2.013847	2.333181	2.629055	2.503728	2.25864
protein_co	grainyhead	4	1	0	1277	1302	1239	0.040421	0.011908	0	11.16343	14.781	12.44299
protein_co	transportin	4811	3987	5290	4843	4266	3935	22.77556	22.24268	33.00078	19.83404	22.68839	18.51348
protein_co	procollagen	11089	9443	7714	4067	2858	3186	199.6812	200.3834	183.0456	63.35515	57.81707	57.01645
protein_co	purinergic_	5	2	9	12	11	2	0.114641	0.054039	0.271923	0.238019	0.283341	0.045573
protein_co	integrin_al	179	189	133	460	320	452	2.456308	3.05632	2.405007	5.46073	4.933202	6.164217
protein_co	DIS3_mitot	799	770	868	1460	1055	1095	5.738686	6.517237	8.215239	9.071551	8.512697	7.816088
protein_co	progestero	232	170	205	281	168	233	3.904104	3.371238	4.545923	4.090748	3.176082	3.896718
protein_co	tudor_dom	145	152	148	278	180	225	2.542711	3.141085	3.419995	4.217322	3.546096	3.921219
protein_co	nuclear_fra	211	145	168	446	301	334	3.198897	2.590556	3.356309	5.849459	5.126647	5.032386
protein_co	PDS5_regul	914	675	824	976	969	885	6.454324	5.617143	7.667726	5.962349	7.687363	6.210942
protein_co	3-oxoacid_	1033	920	912	856	786	853	16.14169	16.94118	18.77925	11.57139	13.79813	13.24669
protein_co	Ras-related	379	415	360	197	173	151	9.735389	12.5623	12.18573	4.377673	4.992399	3.85479
protein_co	cylindroma	294	328	303	120	106	120	1.786371	2.34858	2.426062	0.630767	0.723568	0.724628
protein_co	solute_carr	39	33	19	45	41	86	0.410314	0.409141	0.263415	0.409569	0.484601	0.899207
protein_co	zinc_finger_	240	268	205	291	302	305	3.348047	4.405774	3.768504	3.511853	4.732998	4.228534
protein_co	zinc_finger_	139	114	106	107	122	155	2.534894	2.449949	2.547333	1.688075	2.499505	2.809224
protein_co	zinc_finger_	102	66	43	128	54	87	2.108544	1.607806	1.171348	2.289051	1.25408	1.787357
protein_co	zinc_finger_	117	113	142	178	137	199	2.7347	3.1125	4.37368	3.599208	3.59744	4.622603
protein_co	zinc_finger_	123	148	100	80	104	104	1.660312	2.354254	1.778768	0.934195	1.577128	1.395171
protein_co	zinc_finger_	9	28	16	17	14	26	0.215499	0.790075	0.504845	0.35214	0.3766	0.618709
protein_co	zinc_finger_	160	142	156	95	110	94	3.168933	3.314275	4.071482	1.62772	2.447569	1.850251
protein_co	ribosomal_	18244	14953	10192	24166	13462	16752	552.8652	533.9918	406.9991	633.5297	458.3084	504.5166
protein_co	FAT_tumor	6439	5052	7178	4763	4287	3557	23.05472	21.3163	33.86723	14.75316	17.24423	12.65712
protein_co	YTH_domai	1025	841	810	1635	1324	1268	8.7074	8.41914	9.067436	12.0156	12.63577	10.70517
protein_co	charged_m	419	294	297	929	691	706	8.512002	7.03837	7.950765	16.32662	15.77048	14.25384
protein_co	small_ArfG	1577	1257	1229	598	440	528	28.40692	26.68301	29.17287	9.318729	8.904186	9.452269
protein_co	peptidylpro	687	579	415	1130	825	904	7.819923	7.766608	6.224847	11.12723	10.54991	10.22642
protein_co	zinc_metall	1236	1011	1172	1899	1497	1502	21.05375	20.29408	26.30713	27.98331	28.64718	25.42674
protein_co	StAR-relate	1804	1408	1530	4480	3424	3541	28.35676	26.08133	31.69175	60.92016	60.46483	55.31661
protein_co	nitric_oxid	1011	971	747	915	694	688	15.67301	17.73894	15.26008	12.27116	12.08676	10.59984
protein_co	RE1-silenci	774	619	791	917	959	813	5.613196	5.290138	7.559282	5.753095	7.813343	5.85962
protein_co	histidine_a	2	1	3	9	7	3	0.027059	0.015944	0.053486	0.105339	0.106397	0.040338
protein_co	slingshot_p	1475	1043	1363	1788	1946	1710	9.145932	7.62127	11.13696	9.591057	13.55588	10.5376
protein_co	glutathione	9488	7871	6019	16694	11052	13255	298.8127	292.1201	249.7949	454.8286	391.0338	414.8716
protein_co	amyloid_be	9204	7819	7836	19870	14687	14344	130.9863	131.1316	146.953	244.6302	234.818	202.8753
protein_co	KIAA1467	125	109	68	281	223	258	1.376378	1.414364	0.986669	2.676683	2.758554	2.8233
protein_co	solute_carr	0	1	0	28	19	15	0	0.008121	0	0.166932	0.147103	0.102735
protein_co	WW_doma	1084	900	814	3213	2332	2187	20.87597	20.42523	20.65744	53.52924	50.45392	41.85774
protein_co	eukaryotic_	4062	3382	2650	6670	4129	5375	147.494	144.7156	126.7988	209.519	168.4335	193.9647

protein_co	Na+/K+_tra	66	57	39	177	120	160	1.349597	1.373542	1.050895	3.131095	2.756705	3.251544
protein_co	collagen_ty	5391	4679	3384	154	237	268	49.75678	50.89125	41.15742	1.229608	2.457425	2.458258
protein_co	taxilin_alpl	2304	1953	1836	2524	2724	2451	24.3368	24.3103	25.55574	23.06393	32.3249	25.72966
protein_co	apolipopro	27	20	1	0	9	21	0.101226	0.088362	0.00494	0	0.037907	0.078245
protein_co	nuclear_rec	335	317	375	178	214	156	2.395035	2.670751	3.532914	1.100905	1.718818	1.108412
protein_co	ATP/GTP_b	662	573	496	1129	829	970	10.7473	10.96233	10.61104	15.85617	15.11976	15.6503
protein_co	EFR3_homc	32	21	8	41	68	48	0.328189	0.253805	0.108118	0.363765	0.783487	0.489243
protein_co	kinesin_fan	1538	1243	1259	632	725	711	14.90722	14.19772	16.08055	5.299324	7.894551	6.848881
protein_co	RAB10_mel	2565	2138	2222	3245	2458	2745	38.41405	37.73266	43.85121	42.04171	41.35553	40.85589
protein_co	glucokinase	0	1	0	0	0	0	0	0.02854	0	0	0	0
protein_co	hydroxyacy	5275	4497	4068	4315	3370	3609	91.95382	92.37985	93.4465	65.07154	65.99731	62.52358
protein_co	microtubul	930	715	652	180	180	255	26.02279	23.57676	24.04105	4.35719	5.658385	7.091217
protein_co	carbamoyl-	2463	1938	1891	3855	3094	3633	17.9482	16.64245	18.15862	24.3021	25.32945	26.31065
protein_co	CD59_mole	5502	4333	4213	3581	2455	2658	78.38572	72.74651	79.09384	44.13506	39.29316	37.63405
protein_co	CD82_mole	507	385	351	39	52	52	11.72612	10.49335	10.69765	0.780322	1.351135	1.195251
protein_co	BCL6_corep	385	375	368	789	1052	1037	2.859868	3.282643	3.602201	5.070203	8.779103	7.655503
protein_co	alpha_thal	1491	1248	1729	944	1083	837	7.005238	6.909823	10.70471	3.836898	5.716402	3.908232
protein_co	TAF9_RNA_	844	760	585	2120	1168	1447	27.11298	28.77104	24.76427	58.91607	42.15283	46.19692
protein_co	myoneurin	229	177	167	251	227	235	2.425183	2.208967	2.33056	2.299565	2.700747	2.473355
protein_co	MDS1_and_	128	171	170	84	71	72	1.182213	1.861183	2.069044	0.671163	0.736704	0.660888
processed_	secretory_c	649	622	617	481	421	391	5.501794	6.213798	6.892545	3.527506	4.009505	3.29417
protein_co	prolyl_end	782	647	577	1551	1236	1209	14.25124	13.89496	13.8566	24.45236	25.30542	21.89686
protein_co	HECT_dom	265	206	247	387	342	319	2.63809	2.416674	3.240228	3.332865	3.82489	3.156052
protein_co	SEH1-like_(	378	393	431	1515	1226	1103	3.843968	4.709638	5.775639	13.32796	14.00643	11.14739
protein_co	WD_repeat	318	305	375	396	316	357	3.948226	4.462537	6.135373	4.253369	4.40769	4.405069
protein_co	WD_repeat	1114	1032	1224	731	794	667	12.65585	13.81634	18.32409	7.184335	10.13388	7.530809
protein_co	oviductal_g	67	49	55	41	33	38	1.581385	1.362906	1.710647	0.837162	0.875036	0.891366
protein_co	solute_carr	876	749	812	2184	1852	1666	10.85842	10.94086	13.26335	23.41953	25.79007	20.5233
protein_co	mitogen-ac	251	188	205	511	378	419	2.420435	2.13641	2.605004	4.262885	4.095063	4.015535
protein_co	paired_imn	16	14	1	23	9	10	0.64513	0.665216	0.053133	0.802266	0.40768	0.400716
protein_co	immunoglc	24	36	32	696	612	696	0.30216	0.534116	0.530898	7.580508	8.656186	8.708532
protein_co	ATP-bindin	2	1	0	11	2	12	0.022795	0.013431	0	0.108458	0.025609	0.135924
protein_co	zinc_finger_	350	276	213	518	362	324	3.146434	2.923928	2.523277	4.028499	3.656017	2.894711
protein_co	aldo-keto_r	1180	1003	865	2816	1710	2084	32.36807	32.42222	31.26696	66.82369	52.69628	56.81227
protein_co	copine_III	1397	1205	1461	1469	1270	1220	15.2053	15.45584	20.9548	13.83195	15.52928	13.19678
protein_co	RRN3_RNA_	650	505	590	1319	1019	1001	9.147168	8.374748	10.94108	16.05762	16.11004	13.99964
protein_co	cortactin	6212	5389	5005	6801	6599	7539	100.5102	102.7529	106.7131	95.1951	119.9516	121.2278
protein_co	wingless-ty	99	109	95	30	29	52	2.715626	3.523452	3.433944	0.7119	0.89368	1.417581
protein_co	mitochond	474	358	341	811	560	608	8.515111	7.578828	8.072372	12.60363	11.30184	10.85488
protein_co	DDHD_dom	750	650	719	1023	932	977	8.068634	8.240606	10.19301	9.520886	11.26429	10.44583
protein_co	tetratricop	12	5	13	25	20	14	0.101049	0.049616	0.144254	0.182117	0.189203	0.117162
protein_co	epidermal_	829	665	769	1428	1313	1122	8.399633	7.940256	10.26755	12.51691	14.94581	11.29817
protein_co	origin_recc	97	60	66	1128	725	782	1.626632	1.185703	1.458466	16.36401	13.65855	13.03269
protein_co	microsoma	93	54	41	117	87	153	2.766018	1.892661	1.606907	3.010377	2.906969	4.522444

protein_co	calcium_ho	732	603	502	1273	1332	1349	9.286558	9.015049	8.392324	13.97125	18.9844	17.00847
protein_co	autophagy_	384	276	309	1291	883	1024	4.831117	4.091971	5.122827	14.05095	12.48033	12.80342
protein_co	ubiquitin_s	624	488	486	833	645	632	5.803791	5.348772	5.956598	6.702475	6.739629	5.841897
protein_co	protein_O-l	1026	761	750	1133	876	1054	15.60847	13.64283	15.03519	14.91097	14.97152	15.9354
protein_co	RAD54-like_	112	67	68	791	566	586	1.907784	1.344909	1.526352	11.65603	10.8312	9.920152
protein_co	microtubul	1382	1285	1102	2530	2362	2211	12.75086	13.97146	13.39825	20.19366	24.48277	20.27356
protein_co	DnaJ_(Hsp4	2570	2147	2030	7930	5472	6360	57.14337	56.25639	59.47898	152.5348	136.6872	140.5398
protein_co	UDP-Gal:be	2001	1656	1682	2833	2276	2306	25.2166	24.59274	27.93188	30.8851	32.22261	28.88074
protein_co	charged_m	750	646	560	1318	917	1119	23.26054	23.61012	22.88661	35.36201	31.95045	34.49041
protein_co	nuclear_tra	761	699	587	1149	815	987	8.750673	9.471986	8.894667	11.42983	10.52843	11.27934
protein_co	aquaporin_	1	0	0	0	1	2	0.010322	0	0	0	0.011596	0.020516
protein_co	DIM1_dime	556	585	523	1444	870	1045	10.29563	12.76559	12.76187	23.13173	18.09865	19.23109
protein_co	importin_1	229	238	243	1006	779	730	2.78317	3.408696	3.891753	10.57707	10.6363	8.817322
protein_co	folate_hydr	0	0	0	4	3	4	0	0	0	0.067926	0.066158	0.078033
protein_co	eukaryotic_	1680	1462	1282	3543	2429	2447	19.92849	20.43712	20.03955	36.35795	32.36993	28.84754
protein_co	NME/NM23	0	0	0	5	2	1	0	0	0	0.099046	0.05145	0.022757
protein_co	ependymin	545	470	519	663	515	570	11.10152	11.28212	13.93118	11.68321	11.78534	11.53906
protein_co	sorting_nex	0	0	1	110	90	85	0	0	0.027401	1.978743	2.102448	1.756557
protein_co	selenophos	798	629	631	2972	2008	2106	12.9077	11.98958	13.44963	41.58703	36.48874	33.85432
protein_co	mitochond	1065	919	800	1804	1349	2105	25.29482	25.72199	25.03841	37.0665	35.99507	49.68711
protein_co	hemoglobi	4	1	2	13	6	18	0.395082	0.116395	0.260311	1.110794	0.665775	1.76689
protein_co	inositol-tris	404	367	260	763	570	712	6.318512	6.764046	5.35848	10.32336	10.01515	11.06683
protein_co	FAT_tumor	29	9	27	24	21	14	0.105634	0.038633	0.1296	0.075628	0.085936	0.050681
protein_co	RNA_bindir	633	605	494	1493	991	1110	14.30899	16.11639	14.71523	29.19631	25.1668	24.93663
protein_co	transmemb	4539	3804	3673	4880	3603	4228	94.16112	92.99488	100.4077	87.57784	83.97011	87.16779
protein_co	ERO1-like_l	77	77	75	41	16	28	0.89259	1.051862	1.145664	0.411157	0.208368	0.322574
protein_co	zinc_finger_	753	681	681	1521	1044	1242	15.36799	16.37858	18.31488	26.85433	23.93711	25.19146
protein_co	hydroxyste	15	17	8	5	0	0	0.188626	0.251922	0.132567	0.054393	0	0
protein_co	taxilin_gam	156	155	121	533	466	396	1.876572	2.19725	1.918054	5.546652	6.297609	4.734189
protein_co	protein_ph	4	0	0	0	0	1	0.073275	0	0	0	0	0.018206
protein_co	linker_for_	25	25	18	88	39	65	0.523753	0.617211	0.496929	1.594897	0.917911	1.353349
protein_co	HECT_UBA_	6392	5326	5009	5633	9318	7068	22.87097	22.45722	23.61748	17.43615	37.45584	25.13356
protein_co	zw10_kinet	336	296	293	1045	784	775	5.945245	6.172048	6.831765	15.99594	15.5846	13.62831
protein_co	ALG9_alpha	174	113	107	207	190	195	2.053898	1.571865	1.664364	2.113796	2.519604	2.287567
protein_co	myosin_bir	1	0	0	2	0	1	0.014734	0	0	0.025493	0	0.014643
protein_co	NADPH_oxi	16	23	32	59	45	45	0.193569	0.327906	0.510152	0.61749	0.611612	0.541049
protein_co	acyl-CoA_o	494	364	335	368	248	250	9.144354	7.940256	8.171573	5.893006	5.157352	4.59913
protein_co	myotubula	708	645	677	1939	1468	1398	7.830003	8.406118	9.866251	18.55109	18.23912	15.36546
protein_co	protein_ph	1201	1116	960	1138	835	1060	26.73765	29.27868	28.16348	21.91722	20.8841	23.45286
protein_co	hydroxyste	190	134	131	116	53	129	8.125031	6.752791	7.38206	4.291335	2.546223	5.482401
protein_co	thyroid_ho	4211	3740	2771	3529	2989	4058	114.7964	120.1494	99.5438	83.22571	91.54146	109.9422
protein_co	acetylcholi	120	149	90	329	269	217	2.149161	3.144713	2.124051	5.097375	5.412389	3.862398
protein_co	ferritin_ligl	35764	29260	21024	35044	19596	22221	2156.471	2079.117	1670.505	1827.992	1327.437	1331.591
protein_co	serrate_RN	2029	1618	1435	4744	3547	4298	36.25288	34.06795	33.78681	73.32771	71.19847	76.31967

protein_co	BCL2-assoc	2719	2244	1787	4560	3370	5085	105.9989	103.0914	91.8019	153.7872	147.5949	197.0121
protein_co	nemo-like_	286	221	209	483	553	498	3.741321	3.406891	3.602799	5.465992	8.127053	6.474375
protein_co	phosphatid	1397	1054	987	1482	1169	1251	23.95031	21.29426	22.29804	21.97992	22.51533	21.31482
protein_co	ADAM_met	154	66	81	76	72	77	1.207124	0.609652	0.836664	0.515356	0.634034	0.599834
protein_co	transmemb	0	0	0	1	4	3	0	0	0	0.021441	0.111378	0.073896
protein_co	ataxin_7-lik	2056	1783	1658	2479	2270	2807	28.56119	29.18849	30.35096	29.79152	35.42648	38.75299
protein_co	phosphatid	521	431	469	646	523	646	9.007922	8.781552	10.68549	9.662343	10.15869	11.10016
protein_co	proteasom	1451	1075	851	2992	1963	2409	29.7051	25.93457	22.95768	52.9893	45.14742	49.01286
protein_co	ubiquitin_i	464	391	332	682	496	541	9.433418	9.367743	8.894551	11.99495	11.32875	10.93095
protein_co	cholesteryl	0	2	0	0	0	0	0	0.069668	0	0	0	0
protein_co	matrix_met	21367	17925	15607	7007	5218	5676	302.3764	298.9308	291.044	85.78266	82.95786	79.82821
protein_co	metallothic	1	0	0	0	0	0	0.034155	0	0	0	0	0
protein_co	lysophosph	136	90	118	1173	773	1057	1.335555	1.041531	1.527002	9.965149	8.528081	10.31591
protein_co	guanine_nu	5	23	12	120	108	168	0.047489	0.257431	0.15019	0.985983	1.152386	1.585784
protein_co	2-oxoglutar	673	586	547	1368	950	1148	7.667159	7.867271	8.21186	13.48244	12.15884	12.99783
protein_co	SH3-domai	1880	1738	1421	592	525	587	10.80546	11.77178	10.76253	2.943541	3.389953	3.352996
protein_co	NOP14_nu	569	444	459	1203	845	1080	8.514253	7.829325	9.050691	15.57266	14.20496	16.06082
protein_co	adducin_1_	4434	3613	3264	5262	4134	4259	45.32542	43.52324	43.96744	46.53289	47.47508	43.26767
protein_co	L-2-hydrox	63	75	95	223	270	277	0.967871	1.357829	1.923248	2.963771	4.66004	4.229278
protein_co	thioredoxir	81	78	83	93	96	93	0.939575	1.066223	1.268701	0.933238	1.251027	1.072109
protein_co	chromoson	1914	1726	1397	3939	2288	2794	93.82321	99.70483	90.2401	167.0388	126.0008	136.1145
protein_co	nidogen_2_	4438	3250	3835	903	746	656	48.83644	42.14511	55.61051	8.596219	9.222414	7.174146
protein_co	germ_cell-l	283	269	264	471	456	432	3.574875	4.004366	4.394537	5.147049	6.471252	5.423352
protein_co	splicing_fa	5335	4280	4027	6039	5411	5906	71.83118	67.90933	71.44881	70.34069	81.84745	79.02812
protein_co	kelch-like_f	531	446	516	1103	980	892	4.193893	4.151116	5.370409	7.536356	8.695569	7.001601
protein_co	GNAS_com	23332	20006	15779	28940	15187	17317	306.5821	309.7863	273.2179	328.97	224.1898	226.1399
protein_co	dynamin_1	1099	962	912	1948	1502	1418	13.10704	13.52039	14.33298	20.09828	20.12454	16.8071
protein_co	parathyroic	86	98	86	683	486	552	2.407681	3.233209	3.172735	16.54186	15.28572	15.35852
protein_co	phosphatas	19	16	29	7	15	20	0.368724	0.36591	0.741618	0.117519	0.32703	0.385734
protein_co	ERGIC_and_	655	569	587	1000	617	744	6.915906	7.0799	8.167341	9.134205	7.318835	7.807111
protein_co	transcriptic	56	41	34	570	648	582	1.034437	0.892497	0.827617	9.108645	13.44745	10.68436
protein_co	aurora_kina	470	314	317	2951	2072	2252	9.769245	7.691302	8.682748	53.06344	48.38402	46.52016
protein_co	Cas_scaffol	106	71	78	17	11	12	1.778683	1.403971	1.724734	0.246777	0.207365	0.200117
protein_co	pirin_(iron-	16	16	21	205	164	186	0.550394	0.648605	0.951936	6.100569	6.337915	6.358813
protein_co	adipogenes	88	81	71	40	53	60	6.41709	6.960614	6.82258	2.523356	4.341906	4.348269
protein_co	regulatory_	117	64	72	81	41	40	1.551239	0.999954	1.25794	0.929054	0.610697	0.527063
protein_co	methyltran	309	299	228	858	532	691	6.448075	7.352752	6.269621	15.48895	12.47189	14.33043
protein_co	sulfotransfe	0	0	0	9	2	1	0	0	0	0.284858	0.082206	0.036361
protein_co	ALG6_alpha	127	94	109	311	252	312	1.994514	1.739676	2.255769	4.225292	4.446138	4.869648
protein_co	CCR4-NOT_	1079	871	797	2462	1745	1783	12.6463	12.03004	12.30935	24.96279	22.97664	20.7684
protein_co	glycoprotei	1	0	0	3	0	7	0.023343	0	0	0.060581	0	0.162389
protein_co	protein_tyr	142	137	157	345	305	248	0.729866	0.829817	1.063382	1.534041	1.76118	1.266824
protein_co	DEAD_(Asp-	877	812	776	3319	2529	2723	8.182808	8.92824	9.541119	26.79002	26.50945	25.24992
protein_co	KH-type_sp	7034	5846	4519	13563	12941	15535	124.4193	121.8572	105.3325	207.5411	257.1593	273.0903

protein_co	guanine_nu	1347	1062	893	1902	1548	2088	17.19593	15.97679	15.02257	21.00543	22.20128	26.49099
protein_co	ArfGAP_wit	534	468	347	347	325	404	6.980368	7.209249	5.977249	3.924005	4.772759	5.248414
protein_co	ER_degrada	656	530	576	606	408	482	14.42246	13.73152	16.68756	11.5258	10.07731	10.53155
protein_co	DNA_(cytos	103	85	101	1055	1222	958	1.257593	1.223007	1.625021	11.14341	16.76189	11.6246
protein_co	TPX2_micr	1065	852	950	6195	4390	4450	15.63999	14.74462	18.38422	78.70297	72.42698	64.94661
pseudogen	fer-1-like_4	300	298	166	25	14	7	2.649257	3.101175	1.931727	0.190988	0.138893	0.061434
protein_co	p53_and_D	226	203	149	605	483	689	8.638747	9.144194	7.50522	20.00602	20.74142	26.17407
protein_co	erythrocyte	827	692	704	474	413	537	6.987265	6.889931	7.838071	3.46452	3.920133	4.509056
protein_co	solute_carr	5	1	1	148	106	118	0.085224	0.020086	0.022461	2.182305	2.029764	1.99886
protein_co	dedicator_	102	63	109	930	1118	951	0.715324	0.520655	1.007312	5.642202	8.808329	6.628158
protein_co	ankyrin_rep	1323	1142	1069	2194	1670	1628	27.06373	27.52967	28.81644	38.82643	38.37897	33.09725
protein_co	TDP-glucos	144	99	133	297	230	275	4.008151	3.247311	4.878295	7.151564	7.192146	7.607184
protein_co	dedicator_	10	3	11	242	280	282	0.060469	0.021378	0.087652	1.265943	1.902142	1.694707
protein_co	chromoson	175	139	106	21	11	12	3.489519	3.26625	2.785276	0.362251	0.246416	0.237804
protein_co	coenzyme_	460	369	307	588	348	413	13.32942	12.60048	11.72268	14.73988	11.32875	11.8936
protein_co	transmemb	0	0	0	95	49	65	0	0	0	1.885137	1.262704	1.481765
protein_co	kinesin_fam	76	82	63	81	66	113	1.198545	1.523918	1.30923	1.105067	1.169321	1.771042
protein_co	Rho_GTPas	584	553	550	1160	1122	1042	5.629559	6.28194	6.98649	9.673476	12.15076	9.982491
protein_co	cardiolipin	618	559	436	2303	1690	1635	8.266178	8.811203	7.684889	26.64853	25.39522	21.7342
protein_co	protein_ph	71	88	68	252	273	292	0.75813	1.107326	0.956818	2.327819	3.274894	3.09869
protein_co	attractin	1357	1099	1272	914	918	811	8.321664	7.942096	10.27903	4.848859	6.32444	4.942661
protein_co	spermine_c	914	714	655	573	376	404	21.66953	19.94843	20.46348	11.75225	10.01475	9.519067
protein_co	sialic_acid_	4	2	0	0	0	0	0.031512	0.018568	0	0	0	0
protein_co	FK506_bin	10155	8403	7498	12551	8842	9899	331.4524	323.2084	322.4939	354.3909	324.2208	321.1014
protein_co	NSFL1_(p97	485	440	382	1273	800	920	6.758721	7.225744	7.014892	15.34667	12.52454	12.74149
protein_co	solute_carr	30	23	22	175	104	136	0.491864	0.444385	0.475315	2.482133	1.915607	2.216015
protein_co	chromoson	625	576	578	297	399	355	4.817022	5.231523	5.870313	1.980241	3.454781	2.719171
protein_co	zinc_finger_	176	180	115	141	182	172	2.565423	3.091903	2.208914	1.777986	2.980346	2.491635
protein_co	early_B-cell	70	69	42	15	0	5	1.273495	1.479297	1.006893	0.236077	0	0.090402
protein_co	carboxypep	7093	5905	5033	732	596	731	157.0516	154.0776	146.8501	14.02125	14.82545	16.08568
protein_co	mitochond	2552	2138	1749	1912	1845	2176	31.88705	31.48099	28.79773	20.66734	25.89877	27.02105
protein_co	ProSAP-int	181	110	107	335	326	363	1.822773	1.305431	1.419949	2.918515	3.688254	3.633042
protein_co	coagulation	2	0	5	0	7	1	0.033915	0	0.111729	0	0.133354	0.016853
protein_co	5'-3'_exorib	2151	1646	1849	2694	2510	2392	33.1517	29.89526	37.55235	35.91914	43.45984	36.63837
processed_	polo-like_k	171	170	146	52	44	49	2.348355	2.75121	2.642137	0.61778	0.678843	0.668765
protein_co	dynein_ligh	2266	1989	1529	6213	4029	5325	87.18335	90.1811	77.52039	206.794	174.1486	203.6118
protein_co	tescalcin	0	0	0	15	8	6	0	0	0	0.649937	0.450149	0.298661
protein_co	sorting_nex	2019	1685	1475	4136	2826	3135	34.62516	34.05355	33.33361	61.36193	54.44734	53.43215
protein_co	ribosomal_	35295	30879	22057	33421	23139	28314	930.554	959.3978	766.3191	762.2735	685.3652	741.8895
protein_co	mitogen-ac	334	272	292	892	610	590	6.997345	6.71526	8.061289	16.16645	14.35707	12.28425
protein_co	purinergic_	4	3	1	0	0	0	0.070517	0.062325	0.023231	0	0	0
protein_co	ESF1_nucle	340	244	303	660	520	556	5.596996	4.733397	6.572847	9.399029	9.616753	9.09621
protein_co	retinoblast	481	454	408	467	328	388	6.595343	7.335931	7.372033	5.539521	5.052603	5.287296
protein_co	anaphase_p	2270	1795	1598	3299	2129	2480	19.544	18.21206	18.13006	24.57157	20.59265	21.22017

protein_co solute_carr	535	477	511	288	214	242	4.06829	4.274482	5.120517	1.894583	1.828188	1.828871
protein_co solute_carr	271	239	234	179	133	169	4.362119	4.533496	4.963396	2.492552	2.405077	2.703489
protein_co transmemb	2230	1866	1752	2840	1785	2091	68.0452	67.09827	70.44684	74.96766	61.18992	63.40979
protein_co double_zin	83	86	65	104	60	89	1.175208	1.434968	1.212788	1.273893	0.954414	1.25238
protein_co lysine_(K)-s	476	369	371	855	855	835	3.774702	3.448333	3.876899	5.865498	7.617122	6.580697
protein_co chromoson	4	0	4	2	1	0	0.051878	0	0.068362	0.022439	0.01457	0
protein_co LIM_homec	0	0	0	0	0	3	0	0	0	0	0	0.053688
protein_co taspase_thr	95	89	81	210	171	240	2.138348	2.36076	2.402562	4.089188	4.324142	5.368781
protein_co GCN1_gene	2774	2087	2246	4028	3804	4195	16.92891	15.00901	18.06206	21.26547	26.08028	25.44276
protein_co ribosomal_	54524	47017	35210	63298	40577	51292	1114.07	1132.105	948.0375	1118.865	931.4374	1041.559
protein_co paxillin	1581	1207	1403	3600	3648	3993	15.33804	13.79916	17.93621	30.21368	39.7596	38.49879
protein_co sirtuin_4	28	19	19	17	29	29	1.218034	0.974007	1.089156	0.639755	1.417257	1.253745
protein_co rabphilin_3	2	0	0	3	0	1	0.020409	0	0	0.026484	0	0.010141
protein_co kinesin_fan	166	128	121	206	244	186	1.670444	1.517892	1.604516	1.793304	2.758434	1.860143
protein_co tRNA_meth	184	172	174	982	735	805	3.220213	3.547335	4.01283	14.86761	14.45117	14.00142
protein_co chromogra	12	8	6	38	47	54	0.249134	0.195726	0.164149	0.682493	1.096223	1.11418
protein_co phosphatid	8533	7485	6154	8548	6730	8064	266.2024	275.1751	252.9895	230.6948	235.8709	250.0175
protein_co T-box_5	4	1	1	0	1	0	0.055363	0.016311	0.018239	0	0.015549	0
protein_co BRCA1_assc	345	285	264	668	491	489	4.536672	4.416419	4.574641	7.599024	7.253521	6.390529
protein_co endoplasm	2971	2554	1800	4585	3941	5814	90.65573	91.83761	72.37689	121.0305	135.0977	176.3101
protein_co nitric_oxid	4	0	0	3	1	0	0.017418	0	0	0.011301	0.004892	0
protein_co fused_in_sa	4848	4441	3542	6982	7862	11192	52.16625	56.3138	50.22389	64.99349	95.04058	119.6863
protein_co immunoglc	1017	814	577	637	421	526	28.91568	27.27369	21.61837	15.66805	13.44756	14.86305
protein_co FXYD_doma	891	720	567	3483	1746	2286	29.8547	28.42985	25.0353	100.9605	65.72465	76.12387
protein_co zinc_finger_	356	328	297	487	443	442	4.90935	5.33034	5.397159	5.809864	6.863202	6.057674
protein_co GRAM_dom	2705	2139	1735	1510	884	1116	50.69217	47.238	42.84577	24.48012	18.61123	20.78488
protein_co FXYD_doma	0	0	0	29	11	28	0	0	0	0.905364	0.445968	1.004222
protein_co hephaestin	13	3	12	679	636	587	0.114457	0.031126	0.139225	5.171704	6.290817	5.136279
protein_co cell_death-	554	482	434	410	327	365	9.747195	9.993648	10.06223	6.240462	6.463485	6.382229
protein_co CKLF-like_M	25	26	32	12	18	24	1.243914	1.524512	2.098144	0.516529	1.006172	1.186783
protein_co potassium_	1	2	1	4	3	4	0.013505	0.03183	0.017797	0.046734	0.045517	0.053688
protein_co glucosidase	20642	17744	14642	12276	11412	12376	279.7768	283.4122	261.5141	143.9394	173.7683	166.7054
protein_co GEM_intera	326	254	232	268	267	317	4.878113	4.478938	4.574641	3.469222	4.488431	4.714148
protein_co RNA_bindir	164	128	152	258	239	194	2.619102	2.408938	3.198799	3.56444	4.288007	3.079073
protein_co baculoviral	215	201	211	1144	751	885	4.198566	4.625575	5.42975	19.32643	16.47599	17.17574
protein_co lymphocyt	21	8	4	2	8	21	0.429749	0.192927	0.107867	0.035407	0.183922	0.427095
protein_co myeloid_le	5316	4411	3588	6240	4448	5726	143.7356	140.5476	127.84	145.9577	135.1118	153.8652
protein_co OTU_doma	75	71	57	34	17	15	1.012385	1.129406	1.013898	0.397033	0.2578	0.201227
protein_co DEAD_(Asp	1736	1488	1469	2855	1919	2014	16.49122	16.65762	18.38907	23.46239	20.47986	19.01394
protein_co zinc_finger_	49	72	44	141	90	99	1.238829	2.145137	1.465895	3.08388	2.556272	2.487484
protein_co NECAP_end	530	430	463	683	470	661	8.967314	8.573577	10.32291	9.997013	8.933743	11.1147
protein_co Rho_GTPas	9	17	15	25	27	30	0.141302	0.314529	0.310335	0.339553	0.476231	0.468097
protein_co ankyrin_rep	37	29	21	6	8	10	0.486542	0.44939	0.363892	0.068255	0.118184	0.130686
protein_co DEAH_(Asp	319	318	344	728	533	487	5.501035	6.462312	7.817123	10.86046	10.32595	8.346268

protein_co	REST_corep	597	517	600	768	763	610	5.492835	5.605571	7.274586	6.112888	7.886709	5.577784
protein_co	G_patch_d	916	776	1056	831	875	713	3.462123	3.456335	5.259515	2.717134	3.715387	2.678219
protein_co	latent_tran	1335	1130	779	20	14	37	13.74489	13.71026	10.56896	0.178137	0.161934	0.378592
protein_co	biliverdin_	593	596	374	407	280	444	22.55317	26.71199	18.74387	13.39092	11.96355	16.78207
protein_co	solute_carr	650	532	528	1671	1429	1783	7.619939	7.349485	8.156557	16.94641	18.81999	20.773
protein_co	serine_paln	1134	1037	1010	1346	1102	998	31.69751	34.15843	37.20217	32.54769	34.60531	27.72377
protein_co	poly(A)_pol	2413	1986	2131	4986	3815	3871	28.26878	27.41802	32.89789	50.53183	50.21036	45.06948
protein_co	cyclin_K	1174	926	866	2041	1430	1720	11.04545	10.26676	10.73663	16.61197	15.11473	16.08249
protein_co	poly(rC)_bi	1315	1179	899	1642	1123	1438	26.78623	28.30132	24.13128	28.9349	25.69891	29.11081
protein_co	regulator_c	0	0	0	1	0	2	0	0	0	0.017263	0	0.039664
protein_co	yippee-like_	476	412	301	154	135	142	12.98295	13.24253	10.81852	3.63371	4.136656	3.849147
protein_co	mitochond	348	286	247	839	573	792	21.59844	20.91781	20.20109	45.04722	39.95276	48.8515
protein_co	NADH_deh	393	288	268	539	311	451	12.48848	10.78491	11.22242	14.81729	11.10265	14.24306
protein_co	nuclear_dis	2117	1682	1386	4375	3447	4660	62.26449	58.29787	53.71773	111.3168	113.8964	136.2119
protein_co	macrophag	1351	1060	978	2746	1855	2141	13.31657	12.3126	12.70313	23.41534	20.54139	20.97313
protein_co	intercellula	210	139	142	46	33	26	3.418699	2.666634	3.046244	0.647832	0.603538	0.420654
protein_co	striatin_cal	1836	1604	1227	3522	2442	3065	26.79153	27.58267	23.59414	44.46079	40.03313	44.4493
protein_co	interleukin	25	32	20	8	2	10	0.152779	0.230452	0.16106	0.042294	0.013731	0.060734
protein_co	lysozyme	5	5	0	0	2	6	0.17301	0.203881	0	0	0.077746	0.20633
protein_co	mitochond	591	472	436	896	616	669	12.84406	12.08826	12.48637	16.84557	15.03989	14.44943
protein_co	transcriptic	133	117	89	502	434	514	1.084756	1.124536	0.956545	3.541989	3.976667	4.166326
protein_co	programme	517	443	425	710	644	723	9.600314	9.69406	10.39965	11.40555	13.43476	13.34267
protein_co	spastic_par	1887	1590	1345	1768	1170	1237	48.51853	48.17702	45.57145	39.32611	33.79642	31.60932
protein_co	fetuin_B	2	2	2	1	3	4	0.064562	0.076083	0.085077	0.027926	0.108797	0.128327
protein_co	DnaJ_(Hsp4	1561	1518	1210	2860	2190	2569	20.26009	23.2176	20.69467	32.11201	31.9324	33.13692
protein_co	leprecan-lik	1782	1455	1342	1952	1524	1690	26.8854	25.86895	26.68063	25.47719	25.83109	25.33991
protein_co	thrombopo	2	1	2	0	1	5	0.057079	0.033632	0.075216	0	0.032062	0.141817
protein_co	chordin	97	80	80	167	154	213	1.088213	1.057643	1.182679	1.620771	1.940939	2.374824
protein_co	fms-related	3	12	4	6	4	17	0.111768	0.526849	0.196378	0.19338	0.16742	0.629443
protein_co	RAB11_fam	954	959	775	827	830	842	10.4545	12.38456	11.19158	7.840136	10.21838	9.170157
protein_co	N-acetylglu	1505	1199	941	748	530	703	33.19841	31.16787	27.35302	14.27399	13.13427	15.41153
protein_co	zinc_finger_	209	156	210	332	277	294	1.922284	1.690842	2.545221	2.641632	2.862201	2.687375
protein_co	golgin_A3	3955	3408	2800	2169	2445	2472	22.63096	22.98069	21.11297	10.7369	15.71753	14.05771
protein_co	poly(A)_bin	5411	4630	4036	8111	5327	6214	79.75048	80.41625	78.38658	103.4173	88.20384	91.01996
protein_co	ceramide_s	64	63	31	371	291	374	1.411172	1.636996	0.900734	7.076799	7.208451	8.195608
protein_co	mucolipin_	559	500	475	482	324	373	13.13538	13.84548	14.70819	9.798079	8.553128	8.710626
protein_co	ubiquitin_s	1093	1010	971	1470	1226	1336	12.59293	13.71308	14.74214	14.65166	15.86887	15.29758
protein_co	ephrin-B1	1044	765	659	1951	1819	2224	16.67785	14.40151	13.87266	26.96248	32.64535	35.30889
protein_co	pyruvate_d	323	293	369	264	409	275	2.13776	2.285236	3.218234	1.511553	3.041086	1.808834
protein_co	alanyl-tRNA	3382	2898	2491	4297	3458	3636	51.49452	51.99875	49.97996	56.59991	59.15091	55.02004
protein_co	golgi_glyco	4934	3931	4482	2141	2385	2259	55.01493	51.65252	65.85489	20.65195	29.87575	25.03267
protein_co	kinesin_fam	399	301	310	1254	1155	1125	4.858201	4.31893	4.973923	13.20879	15.79915	13.61334
protein_co	trinucleoti	1255	1172	1161	1075	1355	1104	7.874016	8.665373	9.598859	5.834774	9.550826	6.883848
protein_co	Fc_fragmen	44	18	20	7	9	10	0.142123	0.068516	0.085129	0.01956	0.032659	0.032101

protein_co	pleckstrin_	1253	1061	1051	1575	1379	1551	8.822326	8.803482	9.751458	9.593467	10.90801	10.85309
protein_co	delta-like_3	45	38	22	28	8	24	1.021589	1.01661	0.658144	0.549901	0.204034	0.541483
protein_co	N-acetyltra	790	631	502	585	510	851	27.22877	25.62933	22.80024	17.44294	19.74786	29.1501
protein_co	phosphatid	481	472	366	358	399	384	3.753076	4.340016	3.763207	2.416508	3.497552	2.977715
protein_co	exocyst_co	697	607	629	805	458	474	10.3914	10.66442	12.35739	10.38246	7.67107	7.023109
protein_co	RNA_bindir	442	392	475	792	779	706	3.627332	3.791039	5.13681	5.622808	7.182102	5.758103
protein_co	POU_class_	0	0	2	0	0	0	0	0	0.118043	0	0	0
protein_co	oxysterol_b	1315	1215	1693	1485	1336	1191	9.616992	10.47121	16.31568	9.395134	10.97663	8.656352
protein_co	deltex_hon	179	162	111	692	480	563	3.422332	3.649986	2.796578	11.44559	10.31002	10.69762
protein_co	NLR_family	16	10	10	16	15	27	0.236542	0.174219	0.194815	0.204631	0.249131	0.396699
protein_co	pseudourid	411	323	383	1235	813	915	6.252514	5.790585	7.67797	16.25335	13.8948	13.83387
protein_co	laminin_be	35	38	22	11	5	16	0.316308	0.4047	0.261999	0.086	0.050765	0.143705
protein_co	neuronal_c	9	15	11	636	653	473	0.071553	0.140534	0.115242	4.374246	5.832373	3.737265
protein_co	laminin_be	14018	11836	11881	8790	8875	8352	128.7074	128.0647	143.7491	69.81831	91.54505	76.21099
protein_co	solute_carr	2	3	4	3	9	5	0.021477	0.037964	0.056603	0.02787	0.108577	0.053361
protein_co	solute_carr	1	2	0	0	0	0	0.018491	0.043582	0	0	0	0
protein_co	dihydrolipc	1225	892	999	2277	1644	1681	17.27103	14.8202	18.56019	27.77207	26.03952	23.55372
protein_co	WD_repeat	157	134	150	163	211	197	0.915995	0.921309	1.153239	0.822705	1.383008	1.142271
protein_co	thioredoxir	1494	1525	1218	1955	1467	1777	11.47285	13.80059	12.32545	12.98765	12.6561	13.56182
protein_co	interleukin	0	0	0	0	0	2	0	0	0	0	0	0.041857
protein_co	ATP-bindin	19	15	15	6	10	14	0.175027	0.162836	0.182086	0.047815	0.10349	0.128171
protein_co	CKLF-like_M	871	630	841	1517	1279	1278	11.93673	10.17455	15.18792	17.98523	19.69187	17.40636
protein_co	integrin_al	50	59	62	3499	3281	2936	0.446609	0.621035	0.729766	27.03735	32.92399	26.06291
protein_co	Rap_guanir	9	10	7	9	9	10	0.109836	0.143817	0.112573	0.095018	0.123394	0.121286
protein_co	Mitogen-ac	630	481	622	1635	1366	1336	4.645887	4.180039	6.044402	10.43059	11.31691	9.791388
protein_co	small_musc	0	2	1	7	3	1	0	0.133023	0.074375	0.341783	0.190221	0.056092
protein_co	fumarate_h	713	549	546	2964	1574	1966	21.00553	19.06002	21.19686	75.54143	52.09521	57.56217
protein_co	sel-1_suppr	1101	919	962	1013	984	922	12.91272	12.70145	14.86758	10.27787	12.96506	10.7466
protein_co	transferrin	35	25	7	4	12	18	0.402637	0.338916	0.106115	0.039808	0.155087	0.205792
protein_co	CDV3_hom	4020	3481	3377	11474	10077	9836	58.77459	59.97561	65.0623	145.1247	165.5175	142.9196
protein_co	myosin_XV	7	15	8	1	1	3	0.031239	0.078885	0.047046	0.003861	0.005014	0.013305
protein_co	alkB_alkyla	2077	1697	1376	2361	1643	1883	40.01399	38.52692	34.93241	39.34906	35.56002	36.0525
protein_co	apolipopro	27	9	0	0	4	8	1.215482	0.477457	0	0	0.202299	0.357919
protein_co	NLR_family	781	675	567	186	196	206	7.545058	7.68462	7.218208	1.554488	2.127241	1.977827
protein_co	PITPNM_fa	77	50	48	6	23	31	0.575283	0.440218	0.472571	0.03878	0.193049	0.230177
protein_co	sperm_assc	1211	1087	797	1388	982	1295	38.43618	40.65675	33.33413	38.11084	35.0152	40.84844
protein_co	origin_recc	144	148	116	2034	1323	1682	4.159031	5.037307	4.414916	50.82104	42.92779	48.27978
protein_co	zinc_finger_	1452	1205	1569	177	281	212	5.483296	5.362523	7.807874	0.578244	1.192149	0.795647
protein_co	carboxypep	0	6	1	0	0	0	0	0.193851	0.036128	0	0	0
protein_co	zinc_finger_	265	249	226	615	434	450	7.114282	7.877558	7.995183	14.28313	13.08953	12.00625
protein_co	estrogen_re	7	10	7	0	1	0	0.057313	0.096486	0.075525	0	0.009198	0
protein_co	regulator_c	91	71	84	14	23	30	2.944762	2.707536	3.581978	0.391922	0.836153	0.964805
protein_co	angiopoieti	157	133	161	377	257	291	1.534663	1.532047	2.073835	3.187996	2.822251	2.826937
protein_co	transmemb	804	683	495	638	475	559	23.25932	23.2846	18.8704	15.96705	15.43774	16.07172

protein_co	CD200_mo	0	1	0	134	81	71	0	0.029304	0	2.882599	2.262823	1.754625
protein_co	coiled-coil_	22760	19964	17516	715	624	599	258.3484	267.0473	262.0012	7.021059	7.957327	6.75725
protein_co	chymase_1	0	0	1	0	0	0	0	0	0.074454	0	0	0
protein_co	proteasom	1117	930	739	903	608	802	52.05554	51.07446	45.38298	36.40529	31.83218	37.14478
protein_co	protein_ph	227	214	188	307	119	182	6.510079	7.23238	7.10482	7.616611	3.834038	5.187301
protein_co	HAUS_augn	54	54	35	144	87	125	1.741056	2.051728	1.487037	4.016469	3.151282	4.005333
protein_co	junctophili	1	2	3	0	1	0	0.01207	0.028449	0.047718	0	0.01356	0
protein_co	CCAAT/enh	1	1	0	0	0	1	0.034068	0.040147	0	0	0	0.033857
protein_co	solute_carr	4104	3469	3305	1500	1526	1568	51.53459	51.33374	54.68872	16.29468	21.52757	19.56803
protein_co	O-sialoglyc	403	386	242	1005	684	860	6.548564	7.391548	5.181926	14.12765	12.48666	13.8883
protein_co	solute_carr	1537	1337	900	261	189	236	33.77763	34.62532	26.06349	4.962023	4.66623	5.154386
protein_co	ring_finger_	351	272	249	357	320	351	5.123322	4.67865	4.789373	4.507915	5.247393	5.091682
protein_co	sec1_family	922	883	822	1225	880	952	20.69165	23.35242	24.30921	23.78281	22.18686	21.23297
protein_co	G2/M-phas	277	310	249	854	690	731	2.526646	3.332218	2.992946	6.738847	7.070707	6.626615
protein_co	HECT_dom	1203	979	1118	1772	1667	1376	6.972631	6.686839	8.539013	8.885008	10.85465	7.926093
protein_co	heterogene	8500	7058	6297	16506	14116	15547	99.97744	97.82995	97.6004	167.9531	186.5279	181.7353
protein_co	retinitis_pi	6	0	3	15	19	2	0.080539	0	0.053065	0.174184	0.286522	0.026681
protein_co	suppressor_	2085	1728	1803	5894	4836	4917	23.56575	23.0158	26.8538	57.62996	61.40596	55.23127
protein_co	TOX_high_r	1266	902	822	1586	1142	1354	14.26938	11.98078	12.20895	15.46457	14.46061	15.16701
protein_co	gem_(nucle	128	107	75	400	277	367	4.591089	4.522688	3.544882	12.41163	11.16181	13.08222
protein_co	transglutan	17	18	23	95	80	100	0.32409	0.404386	0.577802	1.566761	1.713386	1.894636
protein_co	TERF1_(TRF	484	345	313	560	348	395	11.81893	9.927937	10.07191	11.82998	9.546872	9.586047
protein_co	deleted_in_	1	5	3	0	0	1	0.017056	0.100496	0.067426	0	0	0.01695
protein_co	transducin_	0	0	0	38	34	30	0	0	0	0.72304	0.840125	0.655763
protein_co	sema_dom	158	138	161	4670	5275	4618	1.21615	1.251746	1.633017	31.09638	45.61434	35.32592
protein_co	transient_r	600	539	640	1377	1301	1179	4.373482	4.629903	6.147391	8.683064	10.65375	8.540819
protein_co	TYRO3_pro	441	336	269	2320	2147	2392	5.912124	5.308249	4.752171	26.90642	32.33598	31.86954
protein_co	WD_repeat	65	74	70	481	341	385	0.865049	1.160556	1.227609	5.537776	5.098363	5.092109
protein_co	calpain_3_	4	3	0	5	6	5	0.065602	0.057981	0	0.07094	0.11055	0.081496
protein_co	synaptoson	420	393	398	548	573	501	8.275109	9.124815	10.33338	9.340454	12.68318	9.810063
protein_co	T-box_15	1123	995	940	146	125	111	16.96711	17.71569	18.71504	1.908288	2.121715	1.666712
protein_co	phosphogly	3459	2987	2155	6618	4771	5437	57.58582	58.6013	47.27669	95.31357	89.23258	89.95679
protein_co	collagen_ty	108	70	88	397	349	521	2.300856	1.757401	2.47049	7.316767	8.352956	11.03095
protein_co	ezrin	410	298	389	19079	15526	16223	7.01092	6.00502	8.765477	282.2343	298.2633	275.6969
protein_co	myosin_ligl	6846	5873	4647	10808	6690	11365	231.7353	234.2731	207.2826	316.4927	254.4079	382.3265
protein_co	argonaute_	1111	999	962	1293	1333	1249	4.598706	4.872974	5.247246	4.630022	6.198702	5.137994
protein_co	tektin_2_(t	12	8	0	16	5	4	0.36553	0.28717	0	0.421624	0.171104	0.121091
protein_co	claspin	60	38	62	561	659	583	0.666064	0.497113	0.906967	5.387542	8.218626	6.431955
protein_co	ring_finger_	136	110	96	174	146	125	0.987245	0.940991	0.918316	1.092693	1.19066	0.90179
protein_co	unc-13_hor	16	4	7	10	7	22	0.192819	0.056806	0.111164	0.104254	0.094772	0.263489
protein_co	major_facil	267	242	220	543	281	386	3.913412	4.179909	4.249148	6.885051	4.627002	5.622653
protein_co	dihydropyr	3778	3211	3056	2260	2118	2141	43.45233	43.52096	46.31688	22.48654	27.36693	24.47245
protein_co	transformir	17652	16008	15684	2450	1949	1806	184.9425	197.6455	216.5382	22.20608	22.94054	18.80486
protein_co	G_patch_d	171	140	179	253	208	196	1.547241	1.492785	2.134272	1.980366	2.114338	1.762494

protein_co	nucleopori	783	599	745	2540	2248	2100	7.927481	7.14673	9.9395	22.24693	25.5693	21.13014
protein_co	cell_divisio	90	78	55	1051	694	851	2.279756	2.328346	1.835876	23.03093	19.74942	21.42323
protein_co	catechol-O-	21	10	6	689	476	576	0.456201	0.256002	0.17176	12.94848	11.61696	12.43566
protein_co	cat_eye_syr	1	2	0	87	82	65	0.013282	0.031303	0	0.999625	1.223539	0.857981
processed_	-	10	1	7	5	2	2	0.122322	0.014415	0.112833	0.05291	0.027484	0.024313
protein_co	enoyl_CoA_	998	856	860	1546	1136	1295	20.43911	20.65915	23.20945	27.39076	26.13719	26.35791
protein_co	leucine_ric	706	642	535	1501	1204	1261	9.799775	10.50155	9.785883	18.02416	18.7753	17.39547
protein_co	SEC22_vesi	631	496	521	952	731	741	5.609701	5.196358	6.103555	7.321672	7.300906	6.546937
protein_co	xylulokinas	120	84	85	135	161	157	1.733875	1.430286	1.618417	1.68746	2.613434	2.254478
protein_co	histone_de	877	840	583	1127	856	1124	9.608703	10.84555	8.417217	10.68199	10.5363	12.23886
protein_co	gamma-am	0	0	0	5456	3874	4337	0	0	0	69.87663	64.43224	63.81072
protein_co	keratin_31	1	0	0	0	0	0	0.033171	0	0	0	0	0
protein_co	cell_divisio	211	180	177	2668	2041	2290	3.636247	3.655531	4.019564	39.77587	39.51509	39.22076
protein_co	uracil_phos	153	106	142	227	168	136	3.625771	2.960206	4.434372	4.653694	4.472674	3.203004
protein_co	cell_divisio	522	464	412	1145	971	961	8.764732	9.181068	9.115913	16.6317	18.31624	16.03619
protein_co	achalasia_a	808	700	561	1681	1113	1653	21.21841	21.66241	19.41329	38.18847	32.83566	43.14039
protein_co	chromobox	4129	3536	2886	8004	8301	7472	18.96195	19.13628	17.46503	31.79862	42.82699	34.10238
protein_co	flavin_cont	1	0	0	0	0	3	0.010218	0	0	0	0	0.030466
protein_co	SUN_doma	755	656	822	5303	5095	4812	6.755189	6.91674	9.691637	41.04641	51.21342	42.78837
protein_co	mutS_hom	389	332	374	1980	1613	1391	5.676419	5.709131	7.191694	24.99499	26.44285	20.17259
protein_co	mitogen-ac	201	162	203	653	661	649	1.517778	1.441565	2.019961	4.26568	5.607414	4.870421
protein_co	deoxyhypu	889	718	578	1056	812	1029	34.53011	32.86456	29.58414	35.48323	35.43246	39.7211
protein_co	hook_hom	518	439	324	768	527	897	10.53532	10.52179	8.683559	13.5127	12.04142	18.13093
protein_co	neurexophi	5	4	2	0	2	1	0.115642	0.109022	0.060955	0	0.051967	0.022986
protein_co	archain_1	3985	3334	3229	5054	3942	3734	52.24613	51.51082	55.78644	57.32235	58.06193	48.65301
protein_co	erythrocyte	14	14	23	803	671	708	0.127789	0.150591	0.276647	6.340779	6.880748	6.422543
protein_co	transmemb	138	115	162	380	247	224	1.846779	1.813597	2.856838	4.399288	3.713486	2.979158
protein_co	proteasom	898	831	820	1634	1216	1185	13.80802	15.05786	16.61513	21.73552	21.00573	18.10852
protein_co	prostaglanc	9	2	4	0	0	3	0.095985	0.025136	0.056215	0	0	0.031797
protein_co	nucleopori	931	780	675	3140	2113	2021	8.663749	8.553776	8.277415	25.27836	22.09046	18.69098
protein_co	carnitine_C	959	840	681	227	122	162	18.3751	18.96695	17.19464	3.762704	2.626153	3.084863
protein_co	SH2_domai	29	22	19	23	8	18	0.49145	0.43935	0.424297	0.337188	0.152307	0.303154
protein_co	N-acetylneu	540	507	408	598	388	467	9.44438	10.44948	9.403178	9.047818	7.623606	8.117199
protein_co	TBC1_dom	354	276	283	358	318	286	5.86026	5.384307	6.173549	5.126957	5.914116	4.705322
protein_co	deafness_au	77	46	62	221	253	213	1.143145	0.804777	1.212934	2.838351	4.219688	3.142679
protein_co	phosphodi	13	1	7	2	2	6	0.208114	0.018865	0.147669	0.027698	0.03597	0.095459
protein_co	CWF19-like	272	260	206	733	615	719	5.345193	6.021087	5.334535	12.46125	13.57746	14.04213
protein_co	sema_dom	232	154	136	55	56	69	2.637953	2.063512	2.037759	0.541009	0.715346	0.779719
protein_co	BTAF1_RNA	598	465	736	678	721	596	4.366719	4.00142	7.082176	4.282987	5.914777	4.325238
protein_co	IKAROS_fan	139	159	136	238	145	153	1.615543	2.177749	2.082943	2.393005	1.893306	1.767278
protein_co	B-cell_linke	1	0	0	3	0	2	0.029675	0	0	0.077016	0	0.058984
protein_co	tolloid-like	68	56	52	26	6	18	0.532858	0.517127	0.536958	0.176254	0.052821	0.14018
protein_co	cytochrom	2	4	1	81	96	79	0.047163	0.111159	0.031075	1.652433	2.543291	1.851452
protein_co	tudor_dom	0	0	0	1	0	3	0	0	0	0.010155	0	0.034998

protein_co	sorbin_and	34	39	32	686	700	699	0.244764	0.330857	0.303566	4.272239	5.661292	5.000982
protein_co	cartilage_a	2	0	2	8	10	12	0.036637	0	0.048279	0.126779	0.205799	0.218467
protein_co	BMP_and_a	90	74	54	3731	2918	3334	2.529028	2.450473	1.999585	90.69836	92.11822	93.10788
protein_co	interleukin	128	64	61	31	19	33	2.970823	1.750467	1.865656	0.622431	0.495415	0.761185
protein_co	myosin_IIIA	0	0	0	62	32	42	0	0	0	0.508786	0.341019	0.395949
protein_co	WW_doma	1642	1378	1551	2543	2000	1838	19.20661	18.99476	23.90695	25.73279	26.28189	21.36647
protein_co	cAMP_resp	288	242	248	727	484	667	5.73627	5.680147	6.50914	12.52664	10.83008	13.203
protein_co	nucleotide_	1112	845	676	1844	1227	1632	26.34022	23.58731	21.10066	37.78666	32.65188	38.41885
protein_co	chromoson	1	1	1	0	5	2	0.058305	0.068709	0.076832	0	0.327511	0.11589
protein_co	human_imi	159	120	156	377	284	215	0.932493	0.829348	1.205613	1.912727	1.871182	1.253132
protein_co	triggering_	0	2	0	1	0	2	0	0.119517	0	0.043869	0	0.100793
protein_co	cysteine-ric	0	0	0	8	5	8	0	0	0	0.166164	0.134866	0.19089
protein_co	FK506_bin	6002	5245	5238	413	350	350	43.03248	44.31523	49.48809	2.561613	2.819146	2.493895
protein_co	SRSF_prote	703	517	651	2050	2078	1776	7.815523	6.7733	9.537148	19.71603	25.95358	19.62254
protein_co	bromodom	1078	975	856	1399	1457	1218	9.430005	10.0509	9.867378	10.58702	14.31864	10.58888
protein_co	mitochond	194	197	112	340	267	371	9.670954	11.57287	7.357333	14.66255	14.95298	18.38024
protein_co	progastrics	1	0	0	1	0	2	0.038615	0	0	0.033405	0	0.076753
protein_co	transmemb	299	302	239	581	411	509	15.95701	18.99304	16.80789	26.82375	24.64174	26.99652
protein_co	EF-hand_dc	395	359	329	467	315	336	3.840531	4.113351	4.215265	3.928024	3.440756	3.246707
protein_co	natural_cyt	0	0	0	5	0	1	0	0	0	0.198435	0	0.045593
protein_co	heat_shock	22064	18582	16265	66370	48213	49430	436.8325	433.5411	424.3455	1136.751	1072.368	972.5926
protein_co	motilin	1	2	1	0	2	3	0.093535	0.220451	0.123257	0	0.210162	0.278873
protein_co	cell_divisio	914	794	723	1566	1281	1236	7.533562	7.712262	7.85285	11.16629	11.86185	10.1247
protein_co	inositol_14	85	66	84	1455	1562	1428	0.465451	0.425899	0.606135	6.892574	9.609162	7.771293
protein_co	zinc_finger_	146	138	134	126	99	122	2.492546	2.776365	3.014602	1.860904	1.89878	2.06995
protein_co	desmoplaki	276	218	281	14816	17079	13545	1.4916	1.388375	2.001172	69.26874	103.6943	72.74983
protein_co	sirtuin_1	321	275	287	462	488	436	4.150967	4.190676	4.890587	5.168318	7.08946	5.603255
protein_co	heterogene	1462	1292	1156	2611	2528	3232	23.06309	24.01816	24.0305	35.63199	44.80188	50.67003
protein_co	intraflagell	189	172	150	398	256	258	4.625912	4.961021	4.837953	8.427168	7.039221	6.27574
protein_co	Janus_kina	219	163	210	143	118	119	2.193771	1.924163	2.772051	1.239214	1.327939	1.184687
protein_co	interleukin	0	0	0	0	0	2	0	0	0	0	0	0.036211
protein_co	c-abl_onco	5071	3989	3673	1984	2254	2078	46.5598	43.16071	44.43991	15.75876	23.24986	18.9615
protein_co	acyl-CoA_th	630	466	419	4091	2408	2901	13.73109	11.96899	12.03409	77.13599	58.96172	62.83794
protein_co	SH3-domai	1287	1067	1090	1235	851	906	10.69456	10.44855	11.93564	8.877986	7.944437	7.48208
protein_co	cell_divisio	133	86	106	535	466	445	2.12531	1.619482	2.232088	7.395839	8.365764	7.067085
protein_co	synapse_de	3	3	6	175	157	156	0.028814	0.033956	0.07594	1.454065	1.694071	1.489077
protein_co	proprotein	2703	2297	2350	960	889	701	15.00309	15.0246	17.18848	4.609661	5.54352	3.866895
protein_co	stearoyl-Co	7468	6321	7806	6743	7191	5979	73.7343	73.54585	101.5614	57.59456	79.76339	58.6683
protein_co	transmemb	180	195	152	165	138	161	7.111477	9.078811	7.913447	5.639417	6.125132	6.321539
protein_co	actin_bindi	314	252	309	1474	1426	1232	2.185574	2.067014	2.834191	8.87557	11.15076	8.522286
protein_co	endoplasm	304	252	317	692	566	629	2.993687	2.924425	4.113646	5.895246	6.261787	6.155922
protein_co	RAB18_mer	1120	1075	1118	1877	1282	1502	12.13547	13.72632	15.96303	17.59405	15.60543	16.17403
protein_co	neuropilin_	3438	2981	3221	671	626	496	30.94375	31.61813	38.20257	5.224595	6.329807	4.436683
pseudogen	hydroxyste	0	0	0	1	2	1	0	0	0	0.03269	0.084905	0.037555

protein_co	phosphorib	166	196	150	246	215	238	4.520682	6.290121	5.382969	5.79554	6.577841	6.441432
protein_co	palmdelphi	76	75	47	4	0	3	0.760014	0.883846	0.619357	0.034604	0	0.029815
protein_co	tetraspanin	0	1	0	1070	759	907	0	0.036742	0	28.86032	26.58552	28.10421
protein_co	H2A_histor	255	200	175	1571	1255	1478	6.818158	6.301791	6.165947	36.33842	37.69812	39.27453
protein_co	family_with	465	389	400	477	394	341	5.303223	5.228097	6.011485	4.706178	5.04815	3.865013
protein_co	microtubul	268	210	190	45	43	77	2.409678	2.225106	2.251193	0.350026	0.434352	0.688057
protein_co	myeloid_zi	472	429	280	558	353	418	7.662726	8.207401	5.990101	7.836795	6.438209	6.74415
protein_co	occludin/El	190	105	96	91	93	98	6.773595	4.411254	4.50995	2.806532	3.724754	3.472173
protein_co	myosin_IXE	2057	1882	1559	1820	1968	2143	14.28567	15.40256	14.26747	10.93454	15.35466	14.79102
protein_co	potassium_	52	62	45	111	105	108	1.032608	1.450877	1.17755	1.906856	2.34245	2.131402
protein_co	catsper_ch	4	10	8	8	20	30	0.055948	0.164829	0.147452	0.096801	0.314272	0.41702
protein_co	proteasom	3314	2867	2169	5352	3124	4151	110.9718	113.1345	95.7094	155.0384	117.5223	138.141
protein_co	F-box_and_	1553	1207	1129	2616	2445	3208	20.73578	18.99167	19.8645	30.21688	36.67557	42.56895
protein_co	syntaxin_1	128	89	77	18	6	13	1.452926	1.190503	1.151752	0.176754	0.076513	0.146652
protein_co	hydroxy-de	100	113	59	73	37	40	2.406409	3.204461	1.870924	1.519691	1.000277	0.956619
protein_co	SET_domai	866	761	691	1416	1295	1529	6.641591	6.877743	6.983403	9.394647	11.15766	11.6539
protein_co	B-cell_CLL/	766	657	483	573	439	797	16.83387	17.01484	13.98741	10.89364	10.83849	17.40697
protein_co	melanoma_	0	0	0	0	4	2	0	0	0	0	0.147766	0.065359
protein_co	ephrin-A2	34	31	17	67	38	43	0.839941	0.902482	0.553418	1.431884	1.054636	1.055718
protein_co	cold_induc	5185	4905	3814	3012	2931	5104	77.80585	86.73804	75.4187	39.10043	49.41154	76.11738
protein_co	ATP_synth	2051	1697	1078	2545	1622	2081	68.41965	66.71202	47.38804	73.44563	60.78761	68.99171
protein_co	chromoson	439	329	218	300	240	205	5.454376	4.817077	3.569208	3.224518	3.34997	2.531303
protein_co	protocadhe	0	0	1	8	18	9	0	0	0.008466	0.044465	0.129923	0.057467
pseudogen	protein_kir	830	778	642	550	356	514	6.087701	6.724529	6.205047	3.489803	2.93342	3.746692
protein_co	insulin-like	0	3	0	0	3	6	0	0.087623	0	0	0.083534	0.147792
protein_co	heterogene	4265	3538	3090	14179	10746	12756	87.92576	85.95319	83.94414	252.8749	248.8817	261.3492
protein_co	membrane-	146	78	69	354	224	276	4.636704	2.919162	2.887622	9.725742	7.991965	8.711144
protein_co	NADH_deh	1277	1070	749	1885	1159	1809	127.3176	125.7154	98.40433	162.5818	129.8166	179.2445
protein_co	trans-23-en	2105	1662	1179	4325	2319	2566	38.44111	35.76696	28.37217	68.3271	47.57663	46.57042
protein_co	translocase	1543	1215	825	2983	2006	3190	41.40292	38.4192	29.17116	69.24386	60.4707	85.06783
protein_co	cell_divisio	1315	1037	866	3132	2405	3087	47.55287	44.19131	41.26708	97.97963	97.70463	110.9423
protein_co	methylthio	567	451	466	1309	1142	1256	4.903225	4.596025	5.310305	9.792677	11.09466	10.79439
protein_co	chromoson	2	1	0	2	3	6	0.03688	0.02173	0	0.031904	0.062148	0.109956
protein_co	centrosom	1335	1085	939	2588	2765	3724	10.41808	9.97799	9.656209	17.47163	24.241	28.88189
protein_co	polymerase	3607	2817	2220	6510	4641	5856	78.22948	71.99764	63.44715	122.1429	113.0798	126.222
protein_co	polymerase	1330	1065	920	2010	1451	1650	18.52935	17.48498	16.89006	24.22521	22.71041	22.84557
protein_co	hyperpolar	1090	857	697	61	41	76	16.93242	15.68846	14.2679	0.819757	0.715526	1.173318
protein_co	cadherin-re	52	72	35	9	28	66	0.75734	1.23574	0.671723	0.113395	0.458136	0.955303
protein_co	IZUMO_fam	18	24	17	17	11	27	0.444467	0.69837	0.55316	0.363144	0.305147	0.662584
protein_co	Ras_associa	57	47	34	614	462	724	1.565164	1.520863	1.230265	14.58534	14.25201	19.75756
protein_co	growth_arr	691	598	430	518	347	466	18.22732	18.58887	14.94679	11.82054	10.28308	12.21632
protein_co	paralemmi	1930	1613	1169	145	157	209	37.29055	36.72679	29.76397	2.423665	3.407927	4.013261
protein_co	mucosal_va	31	20	15	14	10	26	0.952508	0.724176	0.607341	0.372133	0.345188	0.793944
antisense	IGF2_antise	6	3	9	0	0	3	0.154122	0.090812	0.304643	0	0	0.076585

protein_co MAP_kinas	2451	1907	1727	3682	2993	3205	31.70251	29.06753	29.43591	41.19999	43.49167	41.19913
protein_co armadillo_	141	119	113	804	747	833	1.847236	1.837204	1.950817	9.11218	10.99443	10.84571
protein_co tRNA_meth	383	328	255	770	554	734	6.840891	6.903905	6.001902	11.89783	11.11662	13.02926
protein_co RAN_bindi	1513	1179	1025	7541	5353	7012	36.79363	33.78738	32.84675	158.6447	146.2446	169.467
protein_co zinc_finger_	1449	1220	874	1035	791	920	15.20244	15.08383	12.08345	9.393949	9.323316	9.592732
protein_co kelch-like_f	532	463	386	417	369	382	10.76629	11.04186	10.29382	7.300514	8.389378	7.682939
protein_co mediator_c	2660	2051	1557	3706	2776	3408	29.95598	27.21915	23.10603	36.10524	35.12128	38.14267
protein_co serpin_pep	5	3	2	1	6	2	0.108619	0.076801	0.057253	0.018793	0.146432	0.043179
protein_co synaptosom	454	395	340	637	452	471	5.61177	5.753713	5.538061	6.811558	6.276702	5.785949
protein_co v-crk_sarco	1305	985	1122	2482	2193	2070	12.97427	11.54027	14.69942	21.34702	24.49403	20.45279
protein_co leucine-zip	1649	1191	1157	938	861	1162	19.09442	16.25192	17.65444	9.396188	11.20052	13.37216
protein_co matrix_met	1379	1181	964	96	74	70	19.09642	19.2728	17.59137	1.150064	1.151247	0.963375
protein_co cat_eye_syn	0	0	0	82	150	138	0	0	0	0.666225	1.582648	1.28805
protein_co SWI/SNF_re	2465	2141	1772	3716	2307	2907	75.52057	77.29869	71.53966	98.48885	79.40448	88.51218
protein_co purinergic_	24	10	9	0	3	21	0.344612	0.16921	0.170293	0	0.048394	0.299673
protein_co derlin_3	21	30	20	40	26	30	0.315393	0.530959	0.39582	0.519704	0.438688	0.447779
protein_co solute_carr	0	0	0	19	17	20	0	0	0	0.376212	0.437134	0.454942
protein_co BCL2-like_1	820	666	720	1187	1011	1054	9.737913	9.320374	11.26729	12.19455	13.48815	12.43948
protein_co D-dopachro	17	10	5	37	24	28	0.582522	0.403804	0.225771	1.096802	0.923898	0.953523
protein_co D-dopachro	9	7	8	9	4	13	0.454646	0.416712	0.532544	0.393311	0.227007	0.652655
protein_co glutathione	0	0	0	2	0	4	0	0	0	0.083727	0	0.192373
protein_co oncostatin_	1	0	0	0	0	0	0.028555	0	0	0	0	0
protein_co calcineurin	2920	2552	2260	2273	2224	2337	20.66681	21.28523	21.07821	13.91723	17.68375	16.43837
protein_co TBC1_dom	444	433	308	125	133	142	4.226142	4.856866	3.863195	1.029281	1.422204	1.343257
protein_co sushi_dom	228	185	127	85	80	44	2.44442	2.337329	1.794236	0.788357	0.963563	0.468817
protein_co splicing_fac	2087	1626	1607	3745	3046	3058	22.4432	20.60582	22.77262	34.83991	36.79944	32.68206
protein_co gamma-glu	394	388	277	8	4	3	8.363573	9.70587	7.748368	0.146909	0.09539	0.063289
protein_co ring_finger_	289	265	165	186	109	148	7.680696	8.299572	5.778585	4.276404	3.254455	3.909076
protein_co SEC14-like_	342	282	211	80	92	111	4.132805	4.015827	3.359975	0.836319	1.248981	1.333065
protein_co SEC14-like_	1	2	0	0	2	2	0.021399	0.050435	0	0	0.048081	0.042534
protein_co sperm_anti	725	565	524	1222	926	1122	5.681205	5.217446	5.410888	8.283935	8.151969	8.737857
protein_co peptidylpro	807	690	585	923	718	764	10.14085	10.21779	9.687045	10.0338	10.13618	9.541214
protein_co ureidoprop	4	0	0	0	1	1	0.061956	0	0	0	0.017401	0.015393
protein_co yippee-like_	26	23	29	35	33	40	0.317964	0.331466	0.467345	0.370285	0.453385	0.486154
protein_co small_nucl	1679	1439	1258	4752	3257	4621	50.41856	50.92226	49.78004	123.4466	109.8769	137.9067
protein_co pescadillo_	3315	2956	2049	4231	3629	4653	63.58674	66.81816	51.79165	70.20839	78.20221	88.70043
protein_co mitogen-ac	1612	1343	1489	3100	2600	2235	7.742776	7.601771	9.424562	12.8812	14.02988	10.66888
protein_co gamma-glu	11	4	11	20	22	31	0.221258	0.094814	0.291564	0.348016	0.497139	0.619694
protein_co proline_del	4	5	2	68	100	102	0.045287	0.066711	0.029839	0.666023	1.27194	1.147697
protein_co protein_ph	1194	862	792	1203	1088	1297	11.31404	9.625599	9.889479	9.861479	11.58221	12.21414
protein_co solute_carr	348	305	222	66	48	55	6.788307	7.011149	5.706503	1.113754	1.051895	1.066239
protein_co topoisomer	442	398	329	988	649	743	5.620927	5.964525	5.513361	10.8694	9.272128	9.390401
protein_co crystallin_b	0	0	0	1	5	6	0	0	0	0.052825	0.342998	0.364111
protein_co cytohesin_	2	0	4	0	0	0	0.028874	0	0.076098	0	0	0

protein_co	DiGeorge_s	469	393	326	500	423	553	4.604845	4.547177	4.217884	4.246931	4.665859	5.396063
pseudogen	crystallin_b	392	320	251	516	384	530	13.30312	12.79748	11.22473	15.14887	14.64023	17.87529
protein_co	MFNG_O-fu	1	6	1	4	1	0	0.025355	0.179275	0.033412	0.087737	0.028485	0
protein_co	caspase_rec	144	128	133	279	278	348	1.853514	1.941558	2.2559	3.106709	4.020011	4.451663
protein_co	low_densit	96	80	70	96	74	99	1.409802	1.384471	1.354627	1.21961	1.220865	1.44488
protein_co	solute_carr	4097	3350	2526	3325	2342	2903	132.175	127.3607	107.387	92.7979	84.88275	93.07653
protein_co	adrenergic_	225	195	169	402	327	283	1.308837	1.336733	1.295461	2.022982	2.136977	1.636059
protein_co	phospholip	4	3	2	1	5	6	0.078518	0.069397	0.051734	0.016981	0.110263	0.11705
protein_co	lectin_gala	18	14	17	4	9	8	1.617891	1.4829	2.013541	0.311028	0.9088	0.714622
protein_co	golgi-associ	958	844	655	1419	1040	1446	15.82448	16.42909	14.25739	20.27727	19.29952	23.73788
protein_co	HIR_histon	169	183	131	599	337	443	2.207508	2.816915	2.25487	6.768701	4.945321	5.750808
protein_co	SH3-domai	67	80	47	379	304	416	1.135782	1.598149	1.049912	5.558048	5.789523	7.008468
protein_co	seizure_rela	2	0	0	43	48	42	0.01621	0	0	0.301493	0.437055	0.338302
protein_co	lectin_gala	41382	35776	24811	562	404	668	3439.253	3503.899	2717.263	40.40657	37.72099	55.17455
protein_co	Hermansky	530	421	368	701	626	638	4.572804	4.280514	4.183978	5.232241	6.067784	5.470626
protein_co	phosphoin	149	128	126	22	27	18	2.603369	2.635521	2.901047	0.332533	0.529983	0.312559
protein_co	SRR1_doma	84	71	69	206	165	154	3.43401	3.420486	3.717117	7.285386	7.578013	6.256806
protein_co	POZ_(BTB)_	433	330	315	1537	1453	1394	6.062801	5.445107	5.812069	18.61754	22.85599	19.39804
protein_co	TRIO_and_F	512	389	377	340	224	290	2.676058	2.395975	2.59658	1.537331	1.315293	1.506375
protein_co	tuftelin_int	717	586	510	1113	829	945	10.58525	10.19498	9.921716	14.21477	13.74945	13.86511
protein_co	glycine_C-a	651	593	405	544	299	399	20.81195	22.34053	17.06167	15.04505	10.73871	12.67694
protein_co	gamma-glu	0	0	0	2	0	0	0	0	0	0.096216	0	0
protein_co	crystallin_b	23	12	13	0	0	0	1.104939	0.679358	0.822979	0	0	0
protein_co	ankyrin_rep	499	443	357	663	450	479	10.99357	11.50136	10.36433	12.63615	11.13781	10.48778
protein_co	eukaryotic_	119	78	60	107	96	142	1.956515	1.511256	1.299937	1.521889	1.773195	2.320247
protein_co	NHP2_non-	2197	1917	1419	3933	2509	3205	69.64752	71.61514	59.2779	107.8605	89.35633	100.9749
protein_co	MICAL-like_	1749	1347	1223	6462	5264	5227	19.65898	17.8421	18.11475	62.83493	66.4716	58.38931
protein_co	polymerase	1095	863	689	1503	1185	1680	27.5263	25.56534	22.82379	32.68554	33.46579	41.97132
protein_co	SRY_(sex_d	5	3	6	0	4	22	0.091943	0.06501	0.145391	0	0.082634	0.402052
protein_co	coiled-coil_	44	44	35	85	71	100	1.834176	2.161465	1.92261	3.065281	3.325032	4.142839
protein_co	DEP_domai	249	191	180	378	285	309	2.436656	2.202598	2.321144	3.199997	3.133205	3.005128
protein_co	protein_int	179	128	126	900	557	782	3.744148	3.155128	3.473004	16.28566	13.08893	16.2561
protein_co	tetratricop	758	762	787	718	734	639	3.402804	4.031158	4.655618	2.788401	3.7018	2.850876
protein_co	solute_carr	6	6	0	16	29	30	0.169141	0.199322	0	0.390193	0.918425	0.84048
protein_co	centromere	108	79	73	433	223	316	5.706215	4.918793	5.082554	19.79134	13.23666	16.59285
protein_co	septin_3	25	23	20	5	6	6	0.28469	0.308651	0.300122	0.049257	0.07676	0.067904
lincRNA	transmemb	0	1	0	4	0	0	0	0.010897	0	0.031999	0	0
protein_co	solute_carr	5	3	2	0	0	0	0.130525	0.09229	0.0688	0	0	0
protein_co	KDEL_(Lys-/	1606	1429	1267	91	84	125	49.20326	51.59263	51.15167	2.411864	2.89119	3.805993
protein_co	cytochrom	4	17	1	5	2	4	0.093825	0.469912	0.03091	0.10146	0.052704	0.093246
protein_co	DEAD_(Asp-	8938	7824	8706	7210	7364	6944	73.46477	75.78351	94.29578	51.2669	67.99886	56.72286
protein_co	DMC1_dosa	0	1	1	76	50	47	0	0.026313	0.029424	1.468037	1.254237	1.042961
protein_co	transcriptic	573	600	561	853	1405	1173	4.093818	5.051638	5.281674	5.272128	11.27715	8.328783
protein_co	HscB_iron-s	119	106	91	131	76	109	5.655277	5.936355	5.698796	5.385688	4.057603	5.148053

protein_co chibby_hor	213	178	164	368	270	301	8.886077	8.750998	9.015901	13.28132	12.65445	12.47977
protein_co translocase	1712	1376	1356	2867	2363	3081	63.29258	59.94799	66.06076	91.69376	98.14357	113.201
protein_co rhabdoid_t	1	0	1	1	1	0	0.041008	0	0.054038	0.035476	0.04607	0
protein_co X-box_bind	2019	1689	1330	2881	1867	2293	49.18908	48.49189	42.69911	60.72096	51.10057	55.51957
protein_co chromoson	1416	1225	1068	3107	2373	2926	36.98295	37.70349	36.75737	70.20089	69.6282	75.94904
protein_co Josephin_d	994	910	833	1667	1327	1408	14.42526	15.56273	15.93005	20.92839	21.63502	20.30718
protein_co F-box_prot	1734	1387	1200	2727	2042	2027	13.33522	12.56999	12.16094	18.14259	17.64233	15.49225
protein_co GTP_bindir	499	407	418	655	707	801	5.153639	4.953532	5.688851	5.852182	8.203175	8.221587
protein_co polymerase	1857	1586	1449	3010	2525	2856	28.5706	28.75529	29.37721	40.0624	43.64333	43.6692
protein_co RAB36_mer	160	200	135	253	183	222	2.21279	3.259547	2.460304	3.026939	2.843284	3.051285
protein_co TIMP_meta	1416	1257	1308	12007	9567	10215	16.286	17.03701	19.82411	119.4672	123.6164	116.7614
protein_co protein_ph	1487	1232	912	1823	1422	1732	19.53431	19.07238	15.78762	20.71747	20.98629	22.61229
protein_co SET_bindin	4040	3069	2821	3444	3339	3940	34.20464	30.62017	31.47325	25.22492	31.75917	33.15198
protein_co Sad1_and_	390	364	309	753	715	902	5.091736	5.60028	5.316117	8.504704	10.48712	11.70354
protein_co cytochrom	9696	8043	6191	5745	3666	4410	130.3494	127.4212	109.6761	66.8143	55.36788	58.92025
protein_co dynein_axo	319	315	253	420	318	426	11.22884	13.06658	11.73545	12.78959	12.57536	14.90265
protein_co chromoson	3	1	0	0	0	0	0.159621	0.062701	0	0	0	0
protein_co myo-inosit	9	7	0	2	3	4	0.287376	0.263398	0	0.055246	0.107616	0.126934
protein_co lipase_mat	4773	3653	3022	3345	2182	2707	95.06673	85.74205	79.31702	57.63632	48.82485	53.58399
protein_co rhomboid_	412	338	268	1011	739	960	12.15813	11.75421	10.42172	25.80975	24.49983	28.15468
protein_co protein_kir	1023	989	985	2690	2472	2853	16.66932	18.99091	21.15015	37.91907	45.25222	46.20126
protein_co tubulin_tyr	153	135	110	127	74	108	4.804254	4.995459	4.551578	3.449858	2.61045	3.370295
protein_co RAS-like_fa	4	2	2	2	2	17	0.123119	0.072544	0.08112	0.053255	0.069158	0.520023
protein_co adaptor-rel	2086	1833	1480	4026	3010	3150	26.44514	27.38427	24.72453	44.15383	42.86938	39.68732
protein_co HMG_box_	435	327	390	762	659	557	5.462365	4.838896	6.453435	8.277696	9.296639	6.951145
protein_co target_of_r	895	793	574	484	349	425	18.07101	18.8686	15.27236	8.454108	7.916512	8.528212
protein_co neurofilam	97	69	66	77	78	70	1.357461	1.137921	1.217123	0.932201	1.226308	0.973562
protein_co choline_kir	0	0	3	6	0	3	0	0	0.099002	0.129987	0	0.074665
protein_co BCL2-intera	3	1	1	316	280	364	0.166656	0.065465	0.073204	15.18621	17.47456	20.09603
protein_co heme_oxyg	2460	1973	1709	378	222	362	71.47906	67.55817	65.43658	9.501639	7.246791	10.45351
protein_co malonyl_Co	299	212	147	597	357	509	11.47887	9.591152	7.436695	19.82737	15.39732	19.42027
protein_co THO_comp	999	906	692	1357	998	1078	11.1273	11.89213	10.15699	13.07577	12.48832	11.93308
protein_co minichrom	304	245	219	3392	2429	2878	3.49947	3.323547	3.322061	33.77906	31.4127	32.92525
protein_co apolipopro	0	0	0	6	5	3	0	0	0	0.262458	0.28403	0.150757
protein_co arylsulfatas	640	573	396	485	416	483	16.50377	17.41265	13.45653	10.81952	12.05162	12.37827
protein_co translocatc	4931	3882	2943	539	301	434	273.3529	253.6012	214.9878	25.84881	18.74581	23.91047
protein_co RASD_famil	0	1	0	3	6	3	0	0.018285	0	0.040269	0.104588	0.046261
protein_co tubulin_tyr	1475	1265	1069	2695	1880	2269	23.06882	23.31476	22.03159	36.46323	33.03241	35.26773
protein_co chromobox	15	5	19	23	35	55	0.194588	0.076437	0.324798	0.258117	0.510085	0.709084
protein_co platelet-der	0	0	0	1868	1281	1625	0	0	0	24.4645	21.78686	24.44891
protein_co acrosin	0	0	0	3	0	0	0	0	0	0.09588	0	0
protein_co calcium_bi	2	5	3	11	8	5	0.032489	0.095716	0.064219	0.154584	0.145998	0.080721
protein_co ribosomal_	68873	58591	42797	56231	39146	46859	1729.699	1734.041	1416.347	1221.688	1104.48	1169.564
protein_co zinc_finger_	222	217	176	130	105	151	4.762115	5.485469	4.975015	2.412422	2.530377	3.219093

protein_co	RNA_bindi	6615	6234	5988	3543	3927	3793	50.52001	56.10576	60.26292	23.40818	33.6933	28.78896
protein_co	synaptogyr	628	567	413	307	217	249	7.571611	8.055988	6.561657	3.202064	2.939256	2.98358
protein_co	TGF-beta_a	679	542	474	682	588	636	11.10502	10.44614	10.21557	9.649321	10.80378	10.33751
protein_co	activating_	1147	985	817	1953	1409	1636	21.51021	21.7683	20.19008	31.68447	29.68529	30.49117
protein_co	myotubula	656	542	560	496	558	552	3.899539	3.796783	4.386642	2.550669	3.726427	3.261055
protein_co	Smith-Mag	938	686	787	1627	1483	1529	8.828205	7.60853	9.760658	13.24708	15.6805	14.30167
protein_co	apolipopro	15	24	6	2	1	4	0.232605	0.438578	0.122607	0.02683	0.017421	0.061645
protein_co	apolipopro	27	30	21	12	1	4	0.476469	0.623877	0.488343	0.183196	0.019825	0.070152
protein_co	patatin-like	538	498	399	153	161	186	10.1541	11.07632	9.923547	2.498122	3.413769	3.488846
protein_co	myosin_he	31515	25960	25236	43724	57331	57006	222.4284	215.9159	234.7082	266.9659	454.5812	399.8556
protein_co	calcium_ch	5	13	5	0	0	0	0.026431	0.080983	0.034829	0	0	0
protein_co	sorting_an	937	685	592	1819	1181	1414	15.27269	13.15751	12.71548	25.64908	21.62594	22.90525
protein_co	thioredoxi	2046	1819	1433	1932	1416	1644	62.39474	65.37055	57.58686	50.96975	48.51261	49.82575
protein_co	FAD-depen	537	423	399	439	258	289	5.723639	5.313068	5.604097	4.04786	3.089347	3.061297
protein_co	GRB2-relat	3	0	0	0	2	0	0.040797	0	0	0	0.030555	0
protein_co	eukaryotic_	5764	5042	3874	6949	4633	4840	141.6018	145.967	125.412	147.6829	127.8663	118.168
protein_co	trinucleoti	901	735	774	1063	1388	1087	2.609543	2.508615	2.954034	2.663397	4.516252	3.128808
protein_co	small_G_pr	1124	898	765	1355	888	1425	14.10756	13.28217	12.65266	14.71255	12.52125	17.77502
protein_co	intraflagell	382	269	327	385	321	308	3.123314	2.591861	3.52318	2.723178	2.948536	2.502722
protein_co	KIAA0930	1015	803	801	1553	1333	1456	8.633533	8.04906	8.978212	11.42765	12.73801	12.30817
protein_co	neutrophil_	0	0	0	1	3	5	0	0	0	0.027909	0.108731	0.160311
protein_co	colony_stir	0	0	0	1	16	12	0	0	0	0.009412	0.195564	0.129751
protein_co	solute_carr	329	331	263	1232	891	1088	6.884422	8.162189	7.252072	22.30208	20.94587	22.62612
protein_co	family_with	412	343	289	388	310	386	6.307603	6.188257	5.830419	5.138801	5.331849	5.873055
protein_co	potassium_	670	481	407	313	185	324	20.11938	17.02127	16.10531	8.131059	6.241092	9.669287
protein_co	suppressior	7344	6725	5843	9357	6743	7669	108.1498	116.7058	113.3872	119.2046	111.5566	112.2384
protein_co	interleukin	10	0	3	82	61	86	0.128716	0	0.050885	0.913083	0.882089	1.100124
protein_co	ring-box_1_	41	65	32	83	34	64	1.160118	2.167398	1.193172	2.031699	1.080802	1.799732
protein_co	E1A_bindin	1430	1101	1273	1529	2046	1674	7.898343	7.16629	9.265379	7.305845	12.69564	9.188933
protein_co	l(3)mbt-like	319	295	261	612	525	489	2.874583	3.13266	3.099271	4.770882	5.314869	4.37928
protein_co	chondroad	1	5	1	20	11	13	0.020901	0.12315	0.027542	0.361618	0.258285	0.270029
protein_co	Ran_GTPas	1851	1433	1381	7988	6244	8490	23.21027	21.17518	22.8193	86.65127	87.96012	105.8013
protein_co	zinc_finger_	2719	2437	2043	3381	4256	5048	24.36056	25.73006	24.12022	26.20513	42.83796	44.94766
protein_co	PHD_finger	432	362	300	1819	1474	1921	21.0594	20.79591	19.27162	76.71106	80.72514	93.06776
protein_co	aconitase_2	1155	990	848	1316	1060	1041	21.7527	21.9722	21.04563	21.44125	22.42777	19.48461
protein_co	polymerase	1072	1087	831	1464	1125	1380	12.85162	15.35676	13.12801	15.18333	15.15181	16.44189
protein_co	tRNA_5-me	517	530	336	1957	1213	1521	9.331911	11.27361	7.991975	30.55863	24.59744	27.28468
protein_co	phosphom	760	589	395	459	285	379	15.8531	14.47848	10.85756	8.282781	6.678738	7.856866
protein_co	desumoylat	1097	853	824	1760	1384	1774	15.15165	13.88383	14.99738	21.0295	21.47526	24.35098
protein_co	ceramide_k	1801	1552	1418	1058	1231	1201	21.42623	21.7586	22.23019	10.88882	16.45278	14.19988
protein_co	bromodom	761	636	707	1131	1175	1145	8.731707	8.599609	10.68978	11.22639	15.14612	13.05659
protein_co	zinc_finger_	681	559	558	1071	1215	944	6.858059	6.633962	7.404967	9.330536	13.7461	9.44791
protein_co	histone_de	8	6	5	9	1	7	0.157621	0.13931	0.129816	0.153402	0.022135	0.137067
protein_co	potassium_	0	2	0	1	3	0	0	0.025807	0	0.009472	0.036903	0

protein_co	abhydrolas	450	379	352	1258	832	942	9.491413	9.420299	9.783536	22.95419	19.71473	19.74599
protein_co	KH_and_NY	793	731	654	405	597	618	6.74413	7.326174	7.329347	2.979688	5.703955	5.223371
protein_co	FK506_bin	698	642	522	1363	1096	1304	21.94348	23.7844	21.62496	37.06883	38.70879	40.74152
protein_co	short_chai	115	84	89	129	84	111	2.606256	2.243394	2.657933	2.529135	2.138689	2.500068
protein_co	granzyme_I	0	0	0	0	2	0	0	0	0	0	0.122884	0
protein_co	RNA_bindi	1011	763	711	1985	1252	1464	12.62343	11.22685	11.69851	21.44123	17.56223	18.16674
protein_co	protein_arg	303	194	275	515	449	550	6.337859	4.781991	7.579969	9.319019	10.55104	11.43332
protein_co	coagulatio	22	24	25	24	19	34	0.433297	0.557033	0.64884	0.408919	0.420403	0.665505
protein_co	adaptor-rel	64	74	67	220	135	197	1.501872	2.046406	2.071871	4.466205	3.559064	4.594401
protein_co	polymerase	55	54	34	375	273	315	1.624863	1.879987	1.323634	9.584034	9.060784	9.248564
protein_co	methyltran	138	126	115	178	171	150	3.951248	4.251408	4.338982	4.408981	5.500477	4.268311
protein_co	son_of_sev	308	289	314	478	466	432	2.970637	3.284761	3.990831	3.988318	5.049331	4.140876
protein_co	cyclin-depe	88	70	58	77	56	70	1.56231	1.464501	1.356898	1.182601	1.116919	1.235072
protein_co	ninein_(GS	872	651	989	1018	1009	996	4.485043	3.945828	6.703185	4.529611	5.830292	5.091188
protein_co	phosphoryl	1410	1202	865	1954	1578	1496	24.49042	24.60304	19.79831	29.36058	30.79167	25.82369
protein_co	tripartite_r	39	14	27	252	286	185	0.390745	0.165297	0.356474	2.184202	3.219173	1.842089
protein_co	proteasom	946	800	751	2174	1555	1822	17.04055	16.98203	17.82655	33.87779	31.4682	32.61749
protein_co	glucosamin	352	356	346	577	537	472	4.82778	5.753894	6.253393	6.846106	8.27424	6.433635
protein_co	DDHD_dom	191	126	201	289	259	227	1.804699	1.402972	2.502663	2.362285	2.749288	2.131606
protein_co	cyclin-depe	119	111	85	622	396	452	5.88783	6.471998	5.541943	26.62329	22.01165	22.22575
protein_co	cornichon_	1804	1436	1342	1735	1314	1433	67.39983	63.22426	66.0708	56.07699	55.15269	53.20814
protein_co	cell_growth	83	112	97	157	87	129	1.903033	3.02617	2.930723	3.114088	2.240972	2.93946
protein_co	ATPase_H+_	883	755	726	2026	1257	1428	25.33707	25.52994	27.45157	50.29191	40.52099	40.72242
protein_co	chromoson	0	2	0	0	1	0	0	0.040485	0	0	0.019298	0
protein_co	pleckstrin_	1	7	6	33	30	37	0.034178	0.281933	0.270226	0.975703	1.15189	1.256759
protein_co	phosphatid	305	222	152	278	169	174	11.37113	9.753575	7.467619	8.966265	7.078472	6.447074
protein_co	proteasom	1060	908	719	3191	2010	2475	43.87604	44.2909	39.21798	114.2645	93.4688	101.8137
protein_co	vesicle_tra	348	270	272	427	335	334	3.442995	3.147951	3.546181	3.654669	3.723497	3.284076
protein_co	translocase	226	209	138	467	234	359	8.955587	9.759757	7.206088	16.00905	10.41719	14.13806
protein_co	glutathione	237	247	148	456	337	416	2.342609	2.877104	1.927738	3.899235	3.74223	4.086528
protein_co	KIAA0586	260	194	248	530	427	320	2.578134	2.266945	3.24055	4.546436	4.756737	3.153492
protein_co	transmemb	385	323	440	429	495	376	2.618484	2.588802	3.943454	2.524117	3.782192	2.54148
protein_co	sterile_alph	51	48	48	71	54	58	1.053038	1.167945	1.306021	1.268222	1.252613	1.190177
protein_co	AHA1_activ	1762	1572	1347	3667	2925	3805	66.53497	69.95258	67.02649	119.7893	124.0849	142.7935
protein_co	dishevelled	96	113	121	484	464	460	0.875359	1.214229	1.453902	3.81789	4.753156	4.168526
protein_co	isthmin_2_	6	12	4	54	41	38	0.10442	0.246105	0.091733	0.812998	0.801615	0.657243
protein_co	serine_paln	841	727	869	1015	813	805	5.449618	5.551515	7.420354	5.689827	5.918473	5.184126
protein_co	Ras_and_Ra	485	399	324	917	640	680	6.294774	6.102649	5.541384	10.29605	9.331843	8.771158
protein_co	legumain	1496	1186	1129	1927	1199	1464	37.44668	34.98432	37.24007	41.72789	33.71708	36.41937
protein_co	alkB_alkyla	138	127	130	361	271	265	2.816445	3.054449	3.496232	6.37371	6.21356	5.37499
protein_co	SNW_dom	776	670	516	1241	891	1026	18.99316	19.32491	16.64256	26.27667	24.49979	24.95701
protein_co	chromogra	3	0	0	27	7	13	0.076986	0	0	0.599404	0.201809	0.331548
protein_co	inositol-tet	596	409	391	873	609	753	5.201588	4.206492	4.496776	6.591237	5.971123	6.53122
protein_co	dehydroger	1073	928	761	908	609	822	24.46412	24.9336	22.86385	17.9093	15.59898	18.62565

protein_co	protein_ph	477	415	510	619	559	499	3.085637	3.163601	4.347419	3.464018	4.062444	3.208017
protein_co	SIX_homeo	481	443	445	359	312	327	4.05165	4.397417	4.939485	2.616039	2.952504	2.737437
protein_co	UDP-N-acet	22	11	16	15	12	16	0.209932	0.123696	0.201192	0.123825	0.128643	0.151735
protein_co	ankyrin_rep	0	0	0	6	1	0	0	0	0	0.09669	0.020927	0
protein_co	centrosoma	96	96	71	302	263	294	1.090162	1.284689	1.062461	2.96681	3.355248	3.318003
protein_co	enhancer_c	1282	1246	1032	3495	2542	3593	60.81573	69.65512	64.51228	143.4294	135.4729	169.3927
protein_co	hypoxia_in	8313	7475	7779	4958	3773	3735	112.2128	118.9057	138.3704	57.89673	57.21638	50.10543
protein_co	KIAA0247	707	595	509	339	352	263	6.946786	6.889514	6.590481	2.881557	3.885583	2.568206
protein_co	serine/argi	2380	2409	1926	4210	3376	3875	41.39276	49.37321	44.14063	63.34211	65.96278	66.97748
protein_co	solute_carr	0	5	8	2	9	3	0	0.152239	0.27238	0.044704	0.261241	0.077034
protein_co	eukaryotic_	2492	2281	2102	6196	5029	5310	22.19158	23.93716	24.66651	47.73255	50.31192	46.99421
protein_co	serpin_pep	0	1	0	0	0	0	0	0.031008	0	0	0	0
protein_co	solute_carr	1	0	0	10	15	10	0.01005	0	0	0.086938	0.169351	0.099875
protein_co	dicer_1_rib	585	478	583	2049	2054	1838	2.99782	2.886587	3.936888	9.083531	11.82495	9.360626
protein_co	zinc_finger_	510	463	363	1505	1153	1436	6.063307	6.486755	5.686969	15.47886	15.3999	16.96694
protein_co	methylenet	907	733	786	2919	2202	2317	13.92618	13.26282	15.90311	38.77233	37.98317	35.35579
protein_co	T-cell_leuke	0	0	0	1	0	0	0	0	0	0.032831	0	0
protein_co	zinc_finger_	647	492	572	1211	895	936	8.167101	7.318732	9.514687	13.22424	12.69217	11.74219
protein_co	TEL2_telom	729	707	514	1997	1634	2050	11.64574	13.30963	10.82026	27.59819	29.32518	32.54641
protein_co	pecanex_ho	837	707	966	746	652	710	3.429957	3.414206	5.216451	2.644631	3.001649	2.891553
protein_co	bradykinin_	14	13	7	0	0	0	0.439344	0.480759	0.289474	0	0	0
protein_co	GSK3B_inte	185	197	179	597	444	588	2.554534	3.205629	3.257076	7.131441	6.887665	8.069134
protein_co	vaccinia_re	141	106	99	1395	887	993	4.277754	3.789742	3.957917	36.61288	30.23217	29.94026
protein_co	proteasom	1594	1515	1159	3823	2673	3283	37.57255	42.08255	35.99984	77.95602	70.78323	76.90647
protein_co	papilin_pro	926	854	654	18	22	30	8.292179	9.01203	7.717386	0.139442	0.221324	0.266986
protein_co	ribosomal_	1	1	9	24	28	36	0.012599	0.014847	0.149422	0.261583	0.396317	0.450763
protein_co	SMEK_hom	1113	951	1025	2103	1894	1849	14.34356	14.44273	17.40686	23.44574	27.42147	23.68145
protein_co	chromoson	143	110	97	106	68	81	3.206507	2.906671	2.866175	2.056198	1.712987	1.805056
protein_co	proteasom	3915	3364	2797	4889	4025	5280	160.1731	162.1888	150.7944	173.0377	185.0004	214.6848
protein_co	YY1_transc	1641	1495	1382	2621	2232	2155	12.9724	13.92708	14.39642	17.92428	19.82235	16.93046
protein_co	apoptotic_	6716	5698	5206	5347	6046	6734	72.04695	72.03349	73.59425	49.62244	72.86553	71.79392
protein_co	cyclin_B1_i	1067	961	726	2579	1517	1750	34.63399	36.75942	31.05343	72.41899	55.3188	56.45284
protein_co	thyroid_ho	729	568	741	686	655	620	3.860943	3.545041	5.171528	3.143062	3.897231	3.263376
protein_co	APEX_nucle	6109	4949	4021	6318	4804	5884	179.3769	171.2462	155.5841	160.4867	158.4705	171.7033
protein_co	poly(A)_bin	1132	1041	910	1718	1555	2895	21.65072	23.46302	22.93518	28.42577	33.41223	55.02806
protein_co	embryonal_	767	610	485	551	648	709	13.02301	12.20542	10.85157	8.093392	12.36061	11.96387
protein_co	Rho_GTPas	635	526	676	1686	1660	1291	3.500368	3.416904	4.910452	8.040083	10.28009	7.072547
protein_co	cyclin-depe	800	683	511	896	722	719	18.05319	18.16318	15.19567	17.49182	18.30418	16.12511
protein_co	dehydroger	38	42	17	38	23	23	0.378292	0.49272	0.223012	0.327258	0.257229	0.227552
protein_co	signal_reco	1025	946	843	1802	1246	1439	23.31952	25.36261	25.27308	35.46611	31.84658	32.53615
protein_co	copine_VI_	0	0	5	0	0	0	0	0	0.076832	0	0	0
protein_co	chromodor	1476	1209	1254	2256	2119	2024	9.495796	9.16597	10.63108	12.55588	15.31528	12.94092
protein_co	phosphoen	202	218	156	819	435	579	4.269094	5.429351	4.34454	14.97377	10.32815	12.16109
protein_co	KIAA0391	1	6	5	1	0	1	0.020245	0.143146	0.133391	0.017514	0	0.02012

protein_co	DDB1_and_	561	462	416	574	482	499	6.90856	6.704613	6.750762	6.115043	6.668386	6.107097
protein_co	proteasom	44	42	28	50	28	65	0.492474	0.553971	0.412975	0.484132	0.352077	0.723026
protein_co	nuclear_fac	1110	837	738	940	675	620	37.71791	33.51639	33.04577	27.6322	25.76781	20.93756
protein_co	ER_membr	119	105	63	175	210	283	6.61068	6.873779	4.611843	8.410082	13.10592	15.62411
protein_co	proteasom	1218	851	785	924	620	956	23.41399	19.27813	19.88532	15.36608	13.38964	18.26399
protein_co	breast_can	272	195	186	463	293	320	5.419628	4.578701	4.883692	7.980765	6.558692	6.336656
protein_co	REC8_hom	70	81	32	107	101	119	1.363956	1.859921	0.821651	1.803637	2.210919	2.304406
protein_co	transmemb	76	64	69	78	69	107	1.468436	1.457232	1.756813	1.303764	1.497751	2.054636
protein_co	Sec23_hom	2494	2178	2475	2579	2158	2097	31.32499	32.23736	40.9642	28.02263	30.45054	26.17596
protein_co	guanosine_	699	673	571	1262	1084	1193	17.13229	19.4384	18.44205	26.75843	29.8481	29.05952
protein_co	pinin_desm	1277	1168	978	3028	2363	2728	18.90538	20.3772	19.07956	38.7805	39.30134	40.13734
protein_co	Rab_geran	449	438	245	788	378	447	10.4947	12.06438	7.546139	15.93357	9.925782	10.38344
protein_co	nuclear_fac	2220	2116	1426	172	142	186	20.61912	23.16008	17.45306	1.382002	1.481681	1.71688
protein_co	phospholip	6927	5944	4603	2264	1700	1850	162.6263	164.4491	142.4037	45.98169	44.83772	43.16452
protein_co	PDX1_C-ter	516	440	372	706	449	563	9.944504	9.992938	9.447376	11.77067	9.7214	10.78329
protein_co	glutathione	1113	1058	844	1264	976	1186	30.70522	34.39615	30.68276	30.16666	30.24935	32.51707
protein_co	matrix_met	648	528	421	70	34	36	14.68569	14.10134	12.57292	1.372399	0.86566	0.810833
protein_co	transient_r	2086	1710	1573	2360	1610	1965	34.23277	33.06975	34.01663	33.50447	29.68265	32.04793
protein_co	phosphoryl	10482	8292	7146	4118	3456	4193	134.235	125.1377	120.5923	45.62165	49.72152	53.36495
protein_co	abhydrolas	1597	1196	1127	2158	1498	1827	39.93707	35.24597	37.13898	46.68589	42.08546	45.40665
protein_co	protein_C_	572	547	436	85	86	86	22.46458	25.31609	22.56438	2.887913	3.794458	3.356683
protein_co	GINS_comp	262	172	196	3202	2277	2779	4.269172	3.302767	4.208557	45.13638	41.68257	45.00291
protein_co	ninein-like	626	530	396	318	388	454	6.669564	6.654356	5.559722	2.930982	4.644125	4.80716
protein_co	CD40_mole	24	15	10	1	11	5	0.73317	0.539998	0.402558	0.026428	0.377516	0.1518
protein_co	ubiquinol-c	925	753	709	1022	780	888	13.46081	12.91313	13.59598	12.86599	12.75185	12.84257
protein_co	zinc_finger_	1249	910	952	1146	1118	1012	12.33184	10.588	12.38617	9.788427	12.40098	9.930142
protein_co	serum/gluc	7	6	2	8	0	8	0.154734	0.156295	0.058257	0.152982	0	0.175746
protein_co	intraflagell	605	530	467	853	545	660	18.22954	18.81929	18.54266	22.23476	18.44871	19.76396
protein_co	v-myb_mye	407	386	312	10072	7993	8875	8.164829	9.125299	8.247876	174.796	180.1406	176.9419
protein_co	hepatocyte	1	0	0	0	0	0	0.015851	0	0	0	0	0
protein_co	NDRG_fami	965	737	633	844	626	690	17.15516	15.43981	14.8288	12.97994	12.50233	12.19063
protein_co	Src-like-ada	3	0	2	2	0	5	0.057607	0	0.050608	0.033224	0	0.095419
protein_co	chromoson	170	106	141	250	314	313	7.692281	5.652222	8.40737	9.786091	15.96191	14.07538
protein_co	nuclear_fac	8	18	9	72	110	97	0.056283	0.149233	0.083438	0.438209	0.869415	0.678214
protein_co	regulating_	57	55	30	16	19	37	0.57998	0.65949	0.402248	0.140838	0.217191	0.374153
protein_co	poly(A)_bin	341	311	214	867	633	789	8.120953	8.728108	6.715854	17.86219	16.93579	18.67408
protein_co	serine/thre	859	706	682	1944	1366	1380	7.170658	6.945086	7.502138	14.03864	12.81049	11.44866
protein_co	sal-like_4_(	7	1	1	632	611	529	0.105973	0.01784	0.019949	8.277068	10.3917	7.95906
protein_co	activity-dep	1624	1410	1421	2237	2017	1945	13.79149	14.1108	15.90209	16.43442	19.24333	16.41552
protein_co	prefoldin_s	316	291	192	1198	727	967	11.44279	12.4178	9.161799	37.52879	29.57523	34.80013
protein_co	docking_pr	132	108	110	134	123	110	3.559965	3.432437	3.909303	3.126364	3.726713	2.948317
protein_co	cleavage_st	344	367	314	843	597	689	7.642342	9.608182	9.192476	16.20163	14.90018	15.21237
protein_co	bone_morp	2	1	4	2250	1961	2169	0.026385	0.015546	0.069537	25.67843	29.06361	28.43755
protein_co	RAE1_RNA_	612	468	443	1391	953	1090	9.96613	8.98107	9.506347	19.5959	17.4348	17.64052

protein_co	tumor_pro	2441	2192	1860	3741	2291	2984	54.71167	57.8975	54.93637	72.53755	57.68811	66.46923
protein_co	DnaJ_(Hsp4	1870	1580	1593	2284	2081	2521	18.72511	18.64434	21.02003	19.78527	23.41014	25.08796
protein_co	negative_el	968	751	697	2112	1272	1682	14.31077	13.08383	13.57861	27.01125	21.12632	24.71288
protein_co	cathepsin_	221	148	125	1021	761	1145	7.82606	6.176177	5.83305	31.27805	30.27503	40.29638
protein_co	PRP6_pre-r	1581	1394	1105	2413	1801	2080	27.49662	28.57046	25.32471	36.30511	35.18927	35.95178
protein_co	tubulin_be	3	8	0	12	10	12	0.04543	0.142764	0	0.157204	0.170126	0.180597
protein_co	slowmo_hc	594	555	528	1572	1131	1222	11.97523	13.18553	14.02704	27.41656	25.61587	24.48377
protein_co	histamine_	0	0	0	0	4	1	0	0	0	0	0.089471	0.019787
protein_co	GTP_bindir	432	436	362	868	593	783	7.8083	9.286804	8.62216	13.57236	12.04139	14.06514
protein_co	proteasom	2770	2150	2000	6813	4405	5989	143.3495	131.1179	136.3896	305.0127	256.1011	308.0211
protein_co	solute_carr	9	11	4	34	24	34	0.154097	0.221949	0.09025	0.50361	0.46165	0.57855
protein_co	neurotensi	21	7	12	0	0	0	0.269061	0.105691	0.202604	0	0	0
protein_co	MRG/MORF	453	371	303	580	550	601	14.65909	14.14783	12.92071	16.23678	19.99496	19.32827
protein_co	transcriptic	201	200	130	166	148	164	4.332712	5.080434	3.692682	3.095529	3.584054	3.513316
protein_co	death_indu	1605	1192	1276	1462	1855	1721	9.945025	8.703906	10.41877	7.836845	12.9129	10.59794
protein_co	GID_compl	595	518	461	1175	973	1006	20.11487	20.63655	20.53696	34.3638	36.95407	33.79932
protein_co	solute_carr	1	3	0	1	1	2	0.013262	0.046885	0	0.011473	0.014899	0.02636
protein_co	baculoviral	0	0	0	0	0	1	0	0	0	0	0	0.038461
protein_co	Na+/K+_tra	12	7	8	86	37	56	0.44426	0.305394	0.390284	2.75434	1.538887	2.06041
protein_co	ADP-ribosy	3281	2892	2084	1865	1862	2645	50.10078	52.04076	41.93443	24.63656	31.94236	40.13965
protein_co	arginine_va	0	0	0	1	0	0	0	0	0	0.073989	0	0
protein_co	collagen_ty	0	0	0	0	0	1	0	0	0	0	0	0.006498
protein_co	eukaryotic_	28	32	24	152	92	116	0.804312	1.083238	0.908475	3.777229	2.968955	3.311573
protein_co	protein_tyr	28	17	16	21	20	42	0.594127	0.425087	0.44738	0.385482	0.476761	0.885687
protein_co	glucocortic	559	443	355	716	648	771	6.491339	6.062243	5.432324	7.192809	8.453695	8.89788
protein_co	chromoson	2053	1505	1262	1971	1099	1440	57.62877	49.78448	46.68148	47.86301	34.65749	40.17192
protein_co	sperm_flag	6	8	6	10	4	5	0.165011	0.259274	0.217444	0.237916	0.123586	0.13666
protein_co	cell_divisio	8061	6508	5345	1236	960	984	118.7416	112.9714	103.752	15.75054	15.88672	14.40518
protein_co	isthmin_1_	79	89	52	125	108	104	1.613557	2.142171	1.399572	2.208666	2.478163	2.111058
protein_co	ring_finger_	460	394	459	218	179	175	7.289092	7.357308	9.58436	2.988375	3.186528	2.755899
protein_co	ADP-ribosy	668	557	435	746	607	781	11.92735	11.72006	10.23509	11.5231	12.17601	13.85888
protein_co	NADH_dehy	198	148	138	305	176	255	4.351315	3.83287	3.996402	5.798533	4.345272	5.569358
protein_co	sel-1_suppr	0	0	4	0	0	0	0	0	0.118847	0	0	0
protein_co	tribbles_hc	266	225	184	968	474	616	5.635176	5.617143	5.136632	17.74043	11.28115	12.96929
protein_co	Ras_associa	45	37	28	757	684	734	0.43898	0.425345	0.359936	6.388386	7.496136	7.116033
protein_co	casein_kina	2272	1945	1913	4051	3339	3363	27.23776	27.47829	30.22128	42.01344	44.97058	40.06817
protein_co	solute_carr	0	0	0	7	1	0	0	0	0	0.104769	0.019437	0
pseudogen	-	0	1	3	0	2	1	0	0.117491	0.394143	0	0.224015	0.099085
protein_co	angiopoieti	1	0	1	0	0	0	0.027545	0	0.036297	0	0	0
protein_co	R-spondin_	0	2	0	8	2	1	0	0.046094	0	0.13535	0.043942	0.019436
protein_co	CDP-diacyl	806	777	803	1645	1326	1233	4.589206	5.213515	6.024943	8.102732	8.481939	6.977105
protein_co	histocompa	5051	4396	3684	5609	3130	4091	134.2394	137.6789	129.02	128.9589	93.45362	108.0543
protein_co	syntaphilin	145	121	117	69	34	60	1.387393	1.364344	1.475204	0.571141	0.365476	0.570548
protein_co	myosin_ligl	7	5	6	27	22	20	0.125368	0.105527	0.141603	0.418326	0.442649	0.355981

protein_co	signal-regul	0	0	0	1	0	2	0	0	0	0.014131	0	0.032468
protein_co	Sec23_hom	732	611	613	2096	1438	1288	11.36113	11.17529	12.53735	28.14263	25.07369	19.86716
protein_co	fermitin_fa	34	30	8	757	575	645	0.349446	0.363353	0.108349	6.730688	6.639226	6.588247
protein_co	XK_Kell_blc	0	0	0	1	5	2	0	0	0	0.015738	0.102192	0.036161
protein_co	hydroxyaci	0	0	0	0	1	0	0	0	0	0	0.03347	0
protein_co	cerebral_ca	0	0	0	2	7	0	0	0	0	0.035284	0.160374	0
protein_co	phospholip	34	35	37	253	232	187	0.308588	0.374348	0.442524	1.986477	2.365577	1.686753
protein_co	myosin_ligl	1381	953	933	4438	4095	5410	60.97707	49.58758	54.28619	169.5209	203.1308	237.3995
protein_co	hemopoiet	1	0	0	0	0	0	0.02388	0	0	0	0	0
protein_co	transmemb	2396	2051	1934	2045	1620	1583	31.45998	31.73542	33.46284	23.22886	23.89657	20.65676
protein_co	TBC/LysM-a	2	8	2	0	1	1	0.050831	0.239607	0.066983	0	0.028553	0.025259
protein_co	crooked_ne	393	373	346	754	688	612	4.722154	5.281576	5.47846	7.837579	9.287206	7.30817
protein_co	protein_O-f	1935	1527	1498	1900	1498	1746	19.56845	18.19791	19.96283	16.62233	17.01909	17.54807
protein_co	SAM_doma	330	280	265	157	127	136	3.651866	3.651456	3.864396	1.503016	1.578897	1.495717
protein_co	p21_protei	0	0	0	2	3	4	0	0	0	0.019163	0.037328	0.044028
protein_co	kinesin_fam	1776	1510	1435	1117	1004	976	15.40606	15.43593	16.40346	8.382333	9.784339	8.41411
protein_co	maestro_he	21	18	19	56	32	39	0.324602	0.327877	0.387008	0.748829	0.555687	0.599109
protein_co	NOP56_rib	2332	1947	1554	8023	5039	6381	51.441	50.61205	45.17173	153.1019	124.8746	139.8876
protein_co	mannosida	695	636	500	1206	865	1184	19.21357	20.71989	18.21496	28.84255	26.8651	32.53004
protein_co	isocitrate_(	1209	939	809	1793	1381	1822	39.50967	36.16178	34.83858	50.68978	50.70138	59.17457
protein_co	microtubul	2032	1648	1690	6661	4909	5287	41.01262	39.19748	44.94851	116.3044	111.3104	106.0505
protein_co	jagged_1	618	488	498	1735	1936	1444	5.464763	5.08522	5.802925	13.27227	19.23257	12.68994
protein_co	CDK5_regu	305	276	197	845	620	793	6.093209	6.497741	5.186176	14.6038	13.91512	15.74451
protein_co	syntrophin	537	466	365	147	117	127	12.1389	12.41361	10.87259	2.874654	2.971256	2.85311
protein_co	TELO2_inte	276	225	235	1020	747	718	3.691691	3.546549	4.142085	11.80265	11.22499	9.544439
protein_co	E2F_transcr	150	81	78	987	708	910	3.172652	2.01894	2.174006	18.05974	16.82339	19.12856
protein_co	regulation_	337	313	322	880	617	729	4.605347	5.040619	5.7986	10.40347	9.472545	9.900785
protein_co	peroxisoma	14	15	5	11	23	20	0.42793	0.540309	0.201395	0.290871	0.789807	0.607553
protein_co	charged_m	2056	1703	1323	2601	2020	2527	66.128	64.54818	56.0734	72.37117	72.98989	80.77503
protein_co	bactericida	0	3	1	0	0	0	0	0.06551	0.024418	0	0	0
protein_co	cystatin_C	11465	9472	6268	4492	2599	2973	289.7224	282.07	208.7237	98.19985	73.7842	74.66423
protein_co	agouti_sign	1	5	6	6	4	9	0.086789	0.511375	0.686196	0.450481	0.390006	0.776273
protein_co	ARP5_actin	115	88	90	277	174	228	2.722815	2.455331	2.808003	5.673657	4.628269	5.364939
protein_co	WAP_four-d	0	0	0	487	363	475	0	0	0	27.26659	26.39335	30.55217
protein_co	adenosylhc	3580	2912	2589	6862	4790	5490	80.10514	76.7849	76.3386	132.8284	120.4098	122.0842
protein_co	protein_ph	0	2	0	2	1	1	0	0.019961	0	0.014653	0.009515	0.008417
protein_co	family_with	246	183	186	1831	1059	1237	5.361665	4.700269	5.342104	34.52359	25.93042	26.79439
protein_co	DEAH_(Asp-	178	174	179	289	208	246	2.834134	3.264801	3.755677	3.980717	3.720599	3.892649
protein_co	deoxynucle	404	291	270	791	617	731	16.57997	14.07351	14.60162	28.08289	28.44701	29.81463
protein_co	microtubul	671	513	396	162	145	176	22.56887	20.33348	17.55163	4.713737	5.479039	5.883147
protein_co	synapse_dif	37	40	28	173	124	147	0.776692	0.989496	0.774533	3.141638	2.924272	3.066719
protein_co	phosphatid	545	504	364	871	469	536	17.67944	19.2668	15.55995	24.44292	17.09204	17.2801
protein_co	troponin_C	0	5	1	0	5	0	0	0.399921	0.08944	0	0.381256	0
protein_co	acyl-CoA_th	263	215	157	310	226	270	4.551645	4.384885	3.580528	4.641275	4.394102	4.643934

protein_co	adipocyte_	2579	2176	1944	3231	2489	2848	56.18717	55.86654	55.81063	60.89558	60.91998	61.66453
protein_co	CUGBP_Ela	5	5	2	6	8	2	0.065327	0.076984	0.034434	0.067817	0.117425	0.025969
protein_co	zinc_finger_	1093	973	1108	540	633	537	6.713599	7.042959	8.968293	2.869406	4.368054	3.278077
protein_co	cadherin_2	0	10	2	7	4	3	0	0.16071	0.035942	0.082584	0.061284	0.04066
protein_co	ADNP_hom	408	368	421	1126	1012	987	4.005178	4.257127	5.446012	9.562315	11.1607	9.629161
protein_co	ribosome_l	187	159	123	182	143	181	6.238164	6.250566	5.406984	5.2523	5.359204	6.00072
protein_co	ubiquitin_s	1251	983	1024	3302	2219	2452	13.47765	12.48009	14.53757	30.77493	26.85736	26.25349
protein_co	VAMP_(vesi	2314	1809	1753	3983	2687	3002	17.97586	16.56044	17.94498	26.76699	23.45001	23.17643
protein_co	methyltran	157	114	129	271	199	234	1.601491	1.370366	1.734001	2.391426	2.280483	2.372194
protein_co	lipin_2	750	691	734	504	489	479	6.374337	6.920841	8.220621	3.705675	4.669084	4.045935
protein_co	structural_	874	639	954	1182	1167	994	5.245486	4.519415	7.544969	6.136981	7.86854	5.928848
protein_co	myomesin_	30	19	32	20	8	35	0.271632	0.202731	0.381807	0.156658	0.081376	0.314946
protein_co	myosin_ligl	1992	1689	1568	4740	3387	4511	85.80835	85.73871	89.00637	176.6369	163.9096	193.118
protein_co	centrosom	37	37	32	241	149	163	0.591966	0.697596	0.674652	3.335611	2.678124	2.591747
protein_co	ST8_alpha-l	16	9	15	62	20	36	0.311876	0.206734	0.385291	1.045483	0.437967	0.697388
protein_co	centrosom	362	315	340	624	715	514	2.219414	2.27587	2.746904	3.309614	4.924757	3.131861
protein_co	RNA_(guani	657	536	610	742	605	570	5.565157	5.350372	6.808896	5.437246	5.757269	4.798401
protein_co	SMAD_fami	153	105	150	492	480	494	2.623898	2.122032	3.389858	7.29934	9.247956	8.419612
protein_co	lipase_endo	123	115	127	334	396	399	1.564946	1.724246	2.129281	3.67624	5.660289	5.045183
protein_co	laminin_alp	252	264	309	1410	1488	1328	1.286016	1.587658	2.077969	6.224837	8.530959	6.735248
protein_co	ring_finger_	54	59	49	107	50	66	0.474886	0.611441	0.567841	0.814034	0.493986	0.576832
protein_co	ankyrin_rep	511	512	523	391	288	350	2.586562	3.05407	3.488498	1.71215	1.637734	1.760677
protein_co	nucleolar_p	0	0	1	1	16	8	0	0	0.01763	0.011574	0.240489	0.106372
protein_co	polymerase	549	461	478	506	405	417	4.740598	4.691036	5.439055	3.779848	3.928845	3.578545
protein_co	mindbomb	1225	1081	1464	1317	1321	1032	6.772422	7.042725	10.66556	6.298784	8.204646	5.670186
protein_co	retinoblast	177	133	149	1184	793	819	2.845599	2.519759	3.156614	16.46702	14.32262	13.08561
protein_co	RIO_kinase_	832	866	670	1018	726	721	10.9081	13.37983	11.57538	11.54613	10.69329	9.394435
protein_co	cleavage_st	241	195	200	849	651	799	5.535262	5.277921	6.053213	16.8691	16.79775	18.23802
protein_co	matrix-rem	9315	7960	9328	979	1209	899	50.35692	50.71034	66.45072	4.578488	7.342631	4.829984
protein_co	V-set_and_i	2	0	0	0	0	3	0.03272	0	0	0	0	0.048777
protein_co	proteasom	635	531	519	859	557	715	21.74485	21.42813	23.41989	25.44713	21.42826	24.33315
protein_co	autophagy_	121	97	84	247	166	196	2.56132	2.419676	2.343109	4.523123	3.947622	4.123292
protein_co	steroid_sul	198	179	179	395	330	307	1.607471	1.712529	1.914987	2.774201	3.009823	2.476999
protein_co	transducin_	1101	902	974	1327	1150	1001	9.93659	9.593204	11.58361	10.36058	11.65996	8.978293
protein_co	G_protein-r	5	3	4	275	155	205	0.15023	0.106222	0.158373	7.147956	5.23199	6.121385
protein_co	progesteron	4142	3478	3187	3671	2548	3007	114.747	113.545	116.3451	87.97895	79.30122	82.78935
protein_co	polymerase	168	115	129	649	537	516	1.621234	1.3078	1.640442	5.418062	5.821831	4.948751
protein_co	midline_1_	604	480	540	3622	3212	3049	4.947603	4.633469	5.828899	25.66666	29.55851	24.82133
protein_co	NFKB_activ	322	301	243	478	367	369	7.26951	8.007977	7.229202	9.335555	9.308171	8.279141
protein_co	Rhox_hom	0	0	0	1	7	0	0	0	0	0.059556	0.541393	0
protein_co	nuclear_tra	116	119	114	152	120	115	2.281261	2.757853	2.954314	2.585971	2.65123	2.247628
protein_co	guanylate_	0	3	1	0	0	0	0	0.050394	0.018784	0	0	0
protein_co	ATPase_Na-	0	0	0	0	0	2	0	0	0	0	0	0.027205
pseudogen	-	20	15	8	24	23	25	1.939231	1.713949	1.022173	2.013139	2.505396	2.409068

protein_co	ALG13_UDI	538	402	434	585	410	490	6.996378	6.160616	7.437304	6.581272	5.98996	6.332814
protein_co	phosphorib	322	264	218	777	540	516	6.788929	6.559283	6.056709	14.17194	12.79052	10.81197
protein_co	motile_spe	231	186	175	347	281	231	5.173168	4.908679	5.164372	6.722597	7.069684	5.141221
protein_co	Alport_syn	174	141	212	493	393	348	1.673643	1.598232	2.687103	4.102264	4.246736	3.326615
protein_co	chordin-lik	106	67	75	55	39	47	1.426111	1.062256	1.329669	0.640137	0.589469	0.628427
protein_co	WD_repeat	986	853	662	1206	646	924	19.98462	20.37394	17.6812	21.14605	14.70959	18.61232
protein_co	suppressor_	144	81	77	514	284	460	2.655348	1.760155	1.871046	8.199456	5.883372	8.429977
protein_co	P_antigen_	0	0	0	23	27	10	0	0	0	0.70507	1.074866	0.352169
protein_co	sushi-repea	2913	2462	2035	1317	918	951	82.29302	81.96296	75.75682	32.18632	29.13495	26.70009
protein_co	glycine_rec	1	0	2	20	14	11	0.016462	0	0.043385	0.284819	0.258913	0.179961
protein_co	X-linked_in	1027	946	978	1110	905	979	6.328763	6.86984	7.941857	5.917447	6.26536	5.995711
protein_co	stromal_an	868	860	902	1364	1355	1123	7.601784	8.875674	10.40967	10.33411	13.33166	9.774289
protein_co	ATPase_cla	659	517	699	452	415	400	5.038723	4.658356	7.042827	2.989761	3.564776	3.039518
protein_co	MCF.2_cell	0	0	0	0	2	4	0	0	0	0	0.030153	0.053348
protein_co	ATP-bindin	168	113	107	94	120	101	2.427425	1.924076	2.037301	1.174972	1.947901	1.450333
protein_co	coiled-coil_	218	193	137	403	253	348	4.976773	5.192252	4.121419	7.959016	6.488748	7.895511
protein_co	calcium_ch	0	0	0	0	3	1	0	0	0	0	0.029395	0.008668
protein_co	synaptophy	25	28	12	14	27	33	0.532391	0.702678	0.33675	0.257918	0.645957	0.698417
protein_co	proteolipid	1591	1316	970	582	297	405	78.06221	76.09106	62.71583	24.70339	16.37104	19.74855
protein_co	plastin_3	3493	3029	3240	7480	6130	6129	55.58247	56.79965	67.93899	102.9684	109.5844	96.92561
protein_co	N(alpha)-ac	278	256	158	449	236	408	8.305641	9.013126	6.220428	11.6048	7.921172	12.1143
protein_co	renin_bind	4	4	0	9	4	10	0.152568	0.179792	0	0.296967	0.1714	0.379064
protein_co	E74-like_fa	714	515	524	603	435	456	9.075599	7.714209	8.776941	6.63067	6.21177	5.760386
protein_co	SWI/SNF_re	2586	2035	2148	2224	1948	1840	33.39971	30.97317	36.55807	24.84917	28.26521	23.61792
protein_co	myotubula	2	0	7	13	14	6	0.040122	0	0.185048	0.22561	0.315522	0.119623
protein_co	ankyrin_rep	30	29	30	35	38	31	0.815732	0.929247	1.074935	0.823298	1.160804	0.837717
protein_co	zinc_finger_	8	9	3	48	64	67	0.058369	0.077383	0.028844	0.30297	0.524595	0.485824
protein_co	retinoblast	1421	1188	1081	3556	2312	2914	18.66265	18.38666	18.70854	40.40211	34.11271	38.03457
protein_co	potassium_	194	91	88	95	86	110	2.314752	1.279532	1.383631	0.980594	1.15279	1.304383
protein_co	ubiquitin-c	0	0	0	1	0	0	0	0	0	0.038714	0	0
protein_co	solute_carr	310	289	217	278	198	237	10.12443	11.1228	9.33907	7.85447	7.264794	7.692492
protein_co	fragile_X_m	542	431	431	3296	3552	3306	6.622206	6.205657	6.939297	34.83803	48.7557	40.14356
protein_co	pim-2_onc	101	89	68	246	141	226	2.576887	2.675907	2.286218	5.429653	4.041496	5.730494
protein_co	sex_comb_	39	39	49	129	114	98	0.491595	0.579315	0.813905	1.406681	1.614346	1.227661
protein_co	solute_carr	993	803	755	1020	856	1032	20.0727	19.12843	20.11122	17.83692	19.43925	20.73223
protein_co	polyglutam	747	642	534	951	674	1061	27.69392	28.04826	26.08795	30.50053	28.07197	39.09209
protein_co	retinoschis	0	0	0	0	0	4	0	0	0	0	0	0.074895
protein_co	proprotein	782	570	422	278	174	223	39.42844	33.86762	28.0382	12.12581	9.856009	11.17422
protein_co	emerin	1572	1278	1020	1818	1557	1868	60.35043	57.81836	51.60156	60.37883	67.15301	71.27124
protein_co	tafazzin	179	125	101	338	225	301	4.145423	3.411403	3.08228	6.771667	5.853929	6.927747
protein_co	RAB40A_m	1	0	1	0	1	0	0.051449	0	0.067797	0	0.0578	0
protein_co	phosphogly	13559	12212	9699	9963	6889	8371	146.885	155.8991	138.4559	93.36904	83.84072	90.12323
protein_co	GATA_bind	0	0	0	0	5	0	0	0	0	0	0.19865	0
protein_co	magnesium	1860	1598	1553	1922	1648	1529	24.33167	24.63444	26.77103	21.7508	24.2195	19.87815

protein_co spermine_s	1647	1442	1248	10740	7304	8404	47.46533	48.97284	47.39498	267.7628	236.4791	240.7014
protein_co phosphate_	49	38	29	6	12	2	0.420303	0.384111	0.327792	0.044523	0.115637	0.017049
protein_co ubiquitin-li	319	308	274	1001	743	858	7.089915	8.066927	8.024828	19.24631	18.55189	18.95166
protein_co CD99_mole	2351	1851	1698	425	440	382	25.22072	23.40014	24.00366	3.944181	5.302817	4.072658
protein_co early_endo	456	402	522	572	527	472	2.444668	2.539733	3.68774	2.652858	3.174057	2.514818
protein_co G_protein-r	0	0	0	10	5	6	0	0	0	0.234746	0.152424	0.161806
protein_co retinitis_pi	417	326	294	562	513	472	5.804995	5.347988	5.393217	6.768074	8.022915	6.530064
protein_co PHD_finger	124	94	110	513	416	375	1.331309	1.189302	1.556269	4.764721	5.01764	4.001271
protein_co cyclin-depe	2866	2281	1829	4479	3472	3824	48.04588	45.06219	40.40438	64.95671	65.38961	63.70998
protein_co ubiquitin_s	1485	1137	1016	1476	1061	1115	22.36625	20.18061	20.16486	19.23163	17.95276	16.68981
protein_co phosphate_	113	88	107	190	172	176	1.127253	1.034505	1.406571	1.639682	1.927616	1.744879
protein_co HIV-1_Tat_s	1014	799	778	1559	1282	1311	17.78144	16.51136	17.97808	23.65038	25.25609	22.84764
protein_co vestigial_lik	0	0	0	653	466	511	0	0	0	24.61456	22.81134	22.12821
protein_co TIMP_meta	8097	6876	4946	2141	1181	1693	302.9422	303.1647	243.851	69.29714	49.64032	62.95094
protein_co kelch-like_f	1022	951	1036	329	267	206	9.299707	10.19779	12.42261	2.589866	2.729472	1.862924
protein_co gamma-am	99	105	51	32	37	16	0.848633	1.060672	0.576089	0.2373	0.356316	0.136306
protein_co protocadhe	0	0	1	61	104	61	0	0	0.007603	0.304461	0.674095	0.349766
protein_co FYVE_RhoG	1084	969	805	816	785	826	13.4241	14.14122	13.13671	8.741966	10.92131	10.1659
protein_co protein_(pe	453	399	312	369	443	729	13.47319	13.98467	12.22817	9.494267	14.80215	21.54811
protein_co porcupine_	234	169	160	66	32	47	5.865621	4.9922	5.285097	1.431216	0.90115	1.170862
protein_co inter-alpha	0	0	0	0	1	0	0	0	0	0	0.011972	0
protein_co melanoma_	6889	5922	4973	5122	3669	3853	166.6106	168.7803	158.4892	107.164	99.68805	92.60938
protein_co RNA_bindir	4615	4375	3275	5845	4097	5366	113.0077	126.2471	105.6775	123.818	112.7071	130.586
protein_co Kruppel-lik	0	0	0	342	310	325	0	0	0	1.747348	2.056842	1.907582
protein_co sushi-repea	1650	1426	1414	107	45	60	40.85717	41.61127	46.13905	2.292087	1.251832	1.47654
protein_co synaptotag	362	323	270	60	66	67	3.953918	4.157466	3.886133	0.566935	0.809864	0.727283
protein_co zinc_finger_	0	10	1	55	27	29	0	0.103772	0.011604	0.418985	0.267107	0.253794
protein_co centromere	128	104	131	613	554	590	2.07739	1.989063	2.801652	8.6066	10.10106	9.516336
protein_co dystrophin	39	18	43	16	22	20	0.283729	0.154319	0.412233	0.100698	0.179809	0.144604
protein_co TAF7-like_R	0	6	0	9	7	11	0	0.1599	0	0.176074	0.177843	0.247225
protein_co polysaccha	404	274	247	724	544	579	17.80863	14.23334	14.34765	27.609	26.93997	25.36514
protein_co galactosida	661	520	435	1255	1086	1207	26.55083	24.61428	23.02506	43.60973	49.00671	48.18297
protein_co armadillo_r	1761	1645	1639	1025	1027	1213	24.99439	27.51416	30.6547	12.58549	16.37581	17.11015
protein_co brain_expr	271	276	217	642	555	694	10.80347	12.96612	11.39957	22.14074	24.85628	27.4956
protein_co KIAA0226-l	6	1	3	23	35	20	0.079911	0.015695	0.052652	0.265	0.523687	0.264725
protein_co sodium_lea	25	20	27	22	15	17	0.194179	0.183063	0.276351	0.147825	0.130889	0.131226
protein_co fibroblast_g	44	30	25	0	0	0	0.596977	0.47966	0.446971	0	0	0
protein_co 5-hydroxyt	85	78	107	0	0	0	1.262622	1.365388	2.094464	0	0	0
protein_co Nedd4_fam	579	466	515	1152	1044	963	6.62764	6.285985	7.768236	11.40764	13.42548	10.9551
protein_co tumor_nec	3	4	4	1	5	5	0.061512	0.09665	0.108076	0.017738	0.115174	0.101886
protein_co fibronectin	1341	1213	1395	1883	1775	1696	11.29397	12.03887	15.48199	13.71927	16.79442	14.19558
protein_co motilin_rec	0	1	0	0	0	0	0	0.044883	0	0	0	0
protein_co cytidine_ar	141	135	94	94	60	97	2.206527	2.489608	1.938442	1.272568	1.054849	1.508591
protein_co calcium_bi	210	100	139	425	308	309	3.024377	1.697163	2.637948	5.295031	4.983292	4.422672

protein_co	Kruppel-lik	129	119	84	795	522	547	1.91729	2.084262	1.645176	10.22182	8.71601	8.079698
protein_co	serine/thre	973	719	798	3963	2991	3081	11.85537	10.32377	12.81268	41.7724	40.94188	37.30814
protein_co	acid_phosp	5	0	7	10	14	10	0.1558	0	0.28743	0.269564	0.49009	0.309677
protein_co	DnaJ_(Hsp4	986	899	732	1078	991	905	9.336401	10.03158	9.133737	8.830481	10.54206	8.516494
protein_co	UDP-glucos	677	638	741	712	512	480	7.417436	8.237453	10.69838	6.748514	6.302084	5.226561
protein_co	Rho_guanir	1724	1457	1506	1701	1487	1437	16.51951	16.45229	19.01602	14.10026	16.00736	13.68441
protein_co	fibroblast_	5	2	5	27	25	41	0.062726	0.029568	0.082658	0.293026	0.352345	0.511179
protein_co	sarcoglycar	2	14	10	28	27	25	0.065198	0.537825	0.429577	0.789636	0.988824	0.809945
protein_co	poly_(ADP-	913	735	857	1545	1183	1061	8.829947	8.376869	10.92202	12.92644	12.85349	10.19794
protein_co	suppressor_	630	501	578	1508	1016	1110	8.751726	8.201588	10.58073	18.12247	15.85608	15.32448
protein_co	mitochond	248	178	142	604	323	464	10.15419	8.588566	7.661551	21.39407	14.85748	18.88083
protein_co	solute_carr	166	138	134	382	406	400	5.541113	5.428441	5.89425	11.03101	15.22523	13.26962
protein_co	karyopheri	685	650	701	1755	1258	1312	8.112882	9.072041	10.94051	17.98145	16.73841	15.44287
protein_co	fms-related	275	186	230	504	453	360	2.055163	1.638074	2.265042	3.25842	3.803302	2.67378
protein_co	regulator_c	952	866	623	364	221	278	52.49982	56.27893	45.27346	17.36542	13.69185	15.23615
protein_co	von_Willeb	270	212	253	426	405	340	2.00001	1.850594	2.469583	2.729863	3.37033	2.502977
protein_co	diacylglyce	118	80	123	66	88	71	1.412718	1.128679	1.940498	0.683566	1.1836	0.844776
protein_co	katanin_p6	431	303	371	648	493	440	3.021794	2.503441	3.427649	3.930299	3.883145	3.065843
protein_co	integrator_	432	345	384	546	428	405	6.071279	5.713769	7.111521	6.638227	6.75755	5.656674
protein_co	immunores	0	0	0	0	1	0	0	0	0	0	0.027472	0
protein_co	dehydroger	70	73	59	129	72	111	1.881152	2.31183	2.089357	2.999015	2.173739	2.964548
protein_co	mesenteric	0	0	0	8	0	1	0	0	0	0.154335	0	0.022163
protein_co	TSC22_don	4034	3354	3337	901	821	770	44.30788	43.41254	48.29877	8.561165	10.13065	8.405149
protein_co	ceroid-lipo	542	521	503	438	397	361	7.060536	7.998033	8.634579	4.936004	5.810024	4.67364
protein_co	olfactomed	0	0	0	0	1	0	0	0	0	0	0.02053	0
protein_co	mesothelin	3	11	3	2	5	4	0.065684	0.283815	0.086555	0.037882	0.122986	0.087037
protein_co	mahogunin	1954	1699	1443	2386	1940	2533	16.10065	16.49755	15.66824	17.00797	17.95849	20.74263
protein_co	zinc_finger_	577	486	502	341	647	464	5.024996	4.987734	5.761008	2.569078	6.33014	4.015943
protein_co	TNFRSF1A-a	295	280	195	143	143	171	8.320508	9.306641	7.247651	3.489208	4.531197	4.793289
protein_co	heat_shock	24	40	18	2	4	9	0.487935	0.958337	0.482235	0.035176	0.091361	0.181846
protein_co	coronin_ac	177	140	102	62	36	82	3.241285	3.021198	2.461382	0.982197	0.74062	1.492339
protein_co	mitogen-ac	1795	1573	1152	997	765	861	37.01951	38.2298	31.30787	17.78789	17.72461	17.64733
protein_co	glycerophо	41	58	32	38	21	31	1.553744	2.590185	1.598014	1.245783	0.894055	1.167527
protein_co	engulfment	40	56	29	114	72	115	0.836681	1.380369	0.799342	2.062851	1.691927	2.390603
protein_co	phosphoryl	479	367	373	1551	1001	1074	4.525921	4.086435	4.644245	12.67787	10.62563	10.08522
protein_co	LYR_motif_	420	344	289	583	435	486	13.11812	12.66158	11.89474	15.75266	15.26373	15.0858
protein_co	nuclear_tra	666	529	450	890	1087	1097	15.19117	14.21935	13.52584	17.56184	27.85451	24.86756
protein_co	nucleopori	658	523	537	2827	1837	2093	12.11658	11.34914	13.03057	45.03426	38.00253	38.30303
protein_co	centromere	707	657	427	1419	925	1193	12.65786	13.8616	10.07403	21.9779	18.60508	21.22711
protein_co	translin-ass	44	33	44	33	24	39	0.925468	0.817956	1.219541	0.600462	0.567112	0.815236
protein_co	nuclear_fac	1319	1422	1430	770	1871	1457	4.910976	6.239212	7.01607	2.480143	7.826109	5.391284
protein_co	lon_peptid	1097	987	919	1610	1091	1095	7.083336	7.510268	7.819546	8.993321	7.914163	7.026758
protein_co	NEDD4_bin	634	651	563	982	770	822	4.723415	5.71551	5.527263	6.329092	6.444759	6.08623
protein_co	cerebellin_	57	55	62	98	115	164	1.239276	1.409168	1.776314	1.843241	2.808924	3.543616

protein_co	ADP-ribosy	265	268	282	544	308	377	6.683832	7.965656	9.372675	11.86975	8.72729	9.449975
protein_co	plasmolipir	0	0	0	0	1	6	0	0	0	0	0.039206	0.208098
protein_co	zinc_finger_	828	584	641	548	563	477	5.722604	4.756454	5.837893	3.276475	4.371402	3.276358
protein_co	dihydroorc	228	200	144	416	276	435	5.464258	5.648504	4.54772	8.624873	7.431124	10.36085
protein_co	chemokine_	0	0	0	0	0	1	0	0	0	0	0	0.085551
protein_co	CCCTC-binc	649	463	473	1389	1145	1195	8.722697	7.333211	8.377261	16.14996	17.28863	15.96187
protein_co	adrenocort	295	256	169	721	447	572	6.182737	6.322747	4.667456	13.07245	10.52484	11.91419
protein_co	polymerase	757	658	565	2312	1450	2009	19.4829	19.95679	19.16201	51.47646	41.92517	51.3863
protein_co	par-6_parti	7	7	5	72	42	58	0.289295	0.340917	0.2723	2.574177	1.95003	2.382213
protein_co	zinc_finger_	155	131	80	157	142	150	4.199516	4.182596	2.856224	3.679851	4.322201	4.03895
protein_co	matrix_met	297	253	214	2106	1849	2053	3.699641	3.713905	3.512786	22.6947	25.87552	25.41568
protein_co	U6_snRNA_	594	478	409	2144	1612	1752	8.088207	7.670096	7.338781	25.25536	24.65925	23.7088
protein_co	cytochrom	1634	1503	1267	4351	3090	3448	19.84984	21.51647	20.28226	45.72534	42.17085	41.62764
protein_co	coiled-coil_	15	10	12	63	31	60	0.150629	0.118338	0.158794	0.547293	0.349726	0.598794
protein_co	protease_se	0	0	0	0	0	1	0	0	0	0	0	0.029069
protein_co	NME/NM23	480	357	250	328	176	243	23.77145	20.83482	16.31508	14.05242	9.792106	11.95998
protein_co	NDRG_fami	397	361	333	206	207	263	4.108205	4.402262	4.540886	1.844131	2.406473	2.704749
protein_co	proteasom	656	518	551	1736	1252	1436	20.79598	19.3514	23.01771	47.60892	44.58913	45.24178
protein_co	SET_domair	89	57	78	223	217	258	1.701607	1.284254	1.965163	3.688391	4.660987	4.902284
protein_co	solute_carr	697	661	550	952	805	840	8.111645	9.065353	8.434778	9.584647	10.52498	9.715498
protein_co	Vac14_hon	747	615	532	1493	1109	1402	10.95786	10.63133	10.28375	18.94646	18.2762	20.43915
protein_co	hyaluronan	31	21	16	101	125	128	0.388903	0.31046	0.264505	1.096135	1.761727	1.595876
protein_co	transport_a	241	136	184	252	204	217	2.649248	1.76178	2.665375	2.396454	2.519329	2.370691
protein_co	componen	1113	1044	841	1690	1044	1123	16.89316	18.67339	16.82079	22.19041	17.80185	16.93967
protein_co	sphingomy	22	18	17	26	17	55	0.213707	0.206051	0.21761	0.21849	0.185521	0.530967
protein_co	solute_carr	95	86	82	171	132	132	1.203204	1.283575	1.368562	1.873592	1.878187	1.661496
protein_co	solute_carr	273	210	257	370	401	319	2.2912	2.076954	2.84229	2.686366	3.780888	2.66073
protein_co	phospholip	447	320	300	293	209	258	7.582385	6.396691	6.705859	4.299609	3.982847	4.349383
protein_co	epithelial_s	7	1	7	1049	939	1249	0.097703	0.016448	0.128748	12.66624	14.72394	17.32532
protein_co	fatty_acid_	0	0	0	5	4	2	0	0	0	0.09447	0.098145	0.043411
protein_co	WD_repeat	671	639	496	818	608	666	9.613913	10.78911	9.364706	10.13897	9.786565	9.483344
protein_co	MON1_hon	604	475	467	969	893	840	5.249772	4.865239	5.348786	7.286019	8.719749	7.255919
protein_co	COX_assem	135	97	78	531	272	403	3.424549	2.899669	2.607348	11.65272	7.751533	10.15978
protein_co	axin_1	727	599	477	1166	953	1019	6.070679	5.894361	5.248752	8.422953	8.94015	8.456422
protein_co	host_cell_f	1636	1347	1006	639	434	653	63.45162	61.56503	51.41528	21.43993	18.91029	25.16994
protein_co	nitrogen_p	1380	1213	903	1325	851	1009	24.28809	25.15835	20.9429	20.17405	16.82646	17.6488
protein_co	malonyl-Co	78	75	54	161	151	182	0.919893	1.042343	0.839211	1.642598	2.000638	2.13316
protein_co	N-methylpu	826	673	543	558	484	497	36.28984	34.84394	31.4369	21.20812	23.88908	21.70057
protein_co	N-terminal_	16	13	4	18	2	16	0.410395	0.392946	0.1352	0.399409	0.057632	0.407861
protein_co	hydroxyste	481	359	353	523	469	500	7.236322	6.364648	6.998135	6.806714	7.926742	7.47571
protein_co	TATA_box_l	669	553	432	784	602	779	7.638026	7.440245	6.499404	7.743442	7.72148	8.838979
protein_co	N-acetylglu	253	257	207	230	175	251	4.076102	4.879381	4.394705	3.205645	3.167464	4.018906
protein_co	WAP_four-d	7	0	3	4	0	2	0.088721	0	0.050105	0.043858	0	0.025192
protein_co	SEC14-like_	4	0	0	3	0	1	0.032786	0	0	0.021272	0	0.008146

protein_co	coactosin-l	9534	7460	6463	22965	15408	17589	94.69783	87.31941	84.59289	197.3306	171.9334	173.6264
protein_co	ubiquitin_s	878	746	613	2453	1879	1728	15.14078	15.16002	13.92993	36.59437	36.40236	29.61468
protein_co	cysteine-ric	611	493	458	96	73	67	7.056489	6.709675	6.970241	0.959139	0.947151	0.76901
protein_co	tuberous_s	2264	1835	1533	1855	1571	1747	19.47018	18.59673	17.37283	13.80068	15.17815	14.93125
protein_co	zinc_finger_	325	289	221	505	304	420	2.92616	3.066336	2.622055	3.933409	3.074945	3.758146
protein_co	NME/NM23	4314	3644	2656	2695	1880	2326	122.723	122.1606	99.56544	66.32351	60.08314	65.76049
protein_co	ATP-bindin	1027	898	859	922	811	736	8.245435	8.496236	9.088059	6.40379	7.314979	5.872603
protein_co	NODAL_mo	108	95	149	112	144	133	1.313491	1.361552	2.387946	1.178378	1.967501	1.607551
protein_co	lipase_mat	707	551	467	375	321	399	11.1463	10.23694	9.702041	5.114529	5.685458	6.25164
protein_co	forkhead_b	24	29	35	12	10	6	0.494776	0.704534	0.950824	0.214014	0.231604	0.12293
protein_co	nuclear_pr	336	266	242	574	534	716	5.538037	5.166605	5.256138	8.184487	9.887964	11.72841
protein_co	methenylte	243	219	241	423	282	348	3.550831	3.77116	4.640616	5.347209	4.62937	5.053737
protein_co	chloride_ch	834	737	642	714	584	768	9.354404	9.741474	9.488989	6.928055	7.358885	8.56093
protein_co	hydroxyacy	231	205	172	169	85	125	5.561332	5.816046	5.456701	3.519789	2.298978	2.990794
protein_co	family_with	196	208	127	478	356	396	6.154469	7.696707	5.255004	12.98451	12.55838	12.35775
protein_co	solute_carr	2484	2055	1592	21398	15848	19536	28.98511	28.25805	24.47942	216.0029	207.7528	226.5524
protein_co	meteorin_g	1657	1205	865	979	734	949	26.38293	22.60969	18.14894	13.48485	13.12942	15.01676
protein_co	F-box_prot	609	468	446	502	373	385	5.433277	4.920367	5.243415	3.874461	3.738544	3.413618
protein_co	STIP1_hom	1327	935	724	1050	894	1323	37.91295	31.48005	27.25775	25.95189	28.6948	37.56524
protein_co	rhomboid_	42	68	22	46	20	74	1.419873	2.709046	0.980072	1.345306	0.75959	2.486232
protein_co	nucleotide_	111	111	93	139	146	185	4.785383	5.639282	5.283376	5.184078	7.071241	7.926384
protein_co	ubiquitin-c	2177	1796	1416	3215	2675	3366	35.42962	34.44462	30.36729	45.2639	48.90811	54.44171
protein_co	Mediterran	1	2	2	7	0	1	0.01427	0.033632	0.037608	0.086413	0	0.014182
protein_co	crystallin_r	2	4	0	10	4	16	0.07026	0.165595	0	0.303908	0.157866	0.55861
protein_co	eukaryotic_	1233	1035	887	770	622	773	12.34189	12.2086	11.69976	6.667642	6.994521	7.689669
protein_co	small_optic	1013	878	590	1854	1670	1942	11.30464	11.54646	8.676294	17.89864	20.93693	21.53804
protein_co	piezo-type_	1786	1394	1186	3389	3306	4043	11.71365	10.77409	10.25016	19.2285	24.35919	26.35265
protein_co	G1_to_S_ph	2514	2121	2191	6962	4831	4865	18.73239	18.62412	21.51321	44.87713	40.44028	36.02637
protein_co	zinc_finger_	116	102	101	206	145	167	2.717325	2.815729	3.11774	4.17459	3.815933	3.887852
protein_co	clusterin_a	243	227	180	266	203	193	2.509688	2.762781	2.449745	2.376611	2.355367	1.980982
protein_co	ubiquitin_f	2377	1707	1951	2573	2236	2375	24.62637	20.84068	26.63565	23.06078	26.02508	24.45369
protein_co	glutamyl-tR	564	473	377	940	877	787	7.538177	7.449986	6.639929	10.86871	13.16849	10.45374
protein_co	transcriptic	2713	2103	1535	2692	1598	2370	144.0611	131.5962	107.4089	123.6616	95.3285	125.0705
protein_co	golgi-associ	1202	1042	902	1716	1327	1464	10.65379	10.88365	10.53515	13.1577	13.21355	12.89586
protein_co	aquaporin_	0	2	1	0	0	4	0	0.091814	0.051334	0	0	0.154861
protein_co	calcineurin	277	240	243	758	395	428	4.871979	4.974437	5.632052	11.53341	7.804979	7.481333
protein_co	ubiquitin_s	163	125	183	398	398	321	0.80656	0.728897	1.193259	1.703707	2.212489	1.578569
protein_co	heme_oxyg	955	669	564	2231	1446	1802	23.54851	19.43987	18.32627	47.59076	40.05691	44.15953
protein_co	DnaJ_(Hsp4	1067	870	809	1829	1396	1841	16.85707	16.19735	16.84228	24.99737	24.7772	28.90554
protein_co	bifunctiona	1213	1083	1023	2085	1564	1627	21.1311	22.23294	23.48399	31.42176	30.60886	28.16817
protein_co	sal-like_1_(	665	505	476	751	755	730	6.70203	5.997678	6.321592	6.547683	8.548319	7.31168
protein_co	TOX_high_r	1	1	3	27	13	7	0.015507	0.018274	0.061303	0.362206	0.226475	0.107879
pseudogen	RNA_polym	0	2	0	4	0	1	0	0.058525	0	0.085927	0	0.024678
protein_co	retinoblast	550	431	495	520	493	429	5.935089	5.480862	7.038896	4.854348	5.976687	4.60078

protein_co	quinolinate	3129	2673	2368	2928	1867	2450	70.70097	71.17473	70.50766	57.23397	47.39289	55.01683
protein_co	xylosyltran	1279	928	1322	148	112	123	6.845772	5.853383	9.324341	0.685293	0.673471	0.654285
protein_co	PYD_and_C	14	24	14	28	18	43	0.651868	1.316891	0.859003	1.127853	0.941571	1.989801
protein_co	RPGRIP1-lil	437	371	369	304	325	313	2.823089	2.824387	3.141263	1.698947	2.358715	2.009542
protein_co	MYC-associ	466	383	246	1032	626	519	9.143997	8.856375	6.360922	17.51834	13.79982	10.12109
protein_co	syntaxin_4	799	655	429	537	375	633	26.63719	25.73297	18.84663	15.48741	14.04501	20.97273
protein_co	CDP-diacyl	1767	1401	1160	1540	1091	1336	39.75637	37.14629	34.39244	29.97463	27.57681	29.87351
protein_co	branched_c	1535	1261	881	1567	776	909	31.76874	30.75486	24.02715	28.05586	18.04273	18.69671
protein_co	K(lysine)_ac	411	363	296	963	660	765	8.703499	9.058698	8.259973	17.64174	15.70164	16.0999
protein_co	NODAL_mo	2636	2022	2126	2391	1773	1783	32.04419	28.96624	34.05666	25.1447	24.21373	21.54095
protein_co	interleukin	1	0	6	0	2	0	0.015733	0	0.124392	0	0.03535	0
protein_co	synaptotag	1	4	0	95	54	57	0.010397	0.049008	0	0.854457	0.630734	0.588963
protein_co	transmemb	12	2	4	136	85	100	0.129203	0.025376	0.056753	1.266758	1.028158	1.070044
protein_co	centriolar_	310	250	291	790	823	784	2.957597	2.810765	3.658518	6.520298	8.821171	7.433666
protein_co	chromosom	1081	813	788	1159	851	962	14.84545	13.15726	14.2603	13.76937	13.12944	13.12963
protein_co	solute_carr	0	0	0	26	17	23	0	0	0	0.335334	0.284734	0.340784
protein_co	ring_finger_	2590	2043	1759	2839	2598	3396	24.33745	22.62303	21.7809	23.07829	27.42606	31.71411
protein_co	lysine-rich_	203	127	136	646	562	668	2.245512	1.655504	1.982408	6.1818	6.984009	7.343541
protein_co	aquaporin_	0	4	0	0	0	0	0	0.082251	0	0	0	0
protein_co	alpha-_and	617	445	455	1378	1227	1423	11.49757	9.772101	11.17293	22.21432	25.68706	26.35332
protein_co	IQ_motif_c	16	12	15	26	14	13	0.201297	0.177912	0.248681	0.282978	0.197876	0.162543
protein_co	lactamase_	161	141	129	302	262	245	4.213297	4.348329	4.448573	6.837009	7.702763	6.371944
protein_co	coronin_ac	1003	798	876	272	146	136	14.70502	13.78715	16.92402	3.449821	2.404731	1.981587
protein_co	c-src_tyrosi	1293	1060	869	2925	2347	2499	24.73896	23.89989	21.90975	48.41409	50.44813	47.51807
protein_co	HECT_and_	716	560	691	786	900	701	2.504179	2.308062	3.184675	2.378142	3.536257	2.436576
protein_co	thyroid_ho	413	303	316	632	399	570	10.69175	9.243756	10.78005	14.15399	11.60435	14.66504
protein_co	mitochond	181	136	101	370	198	250	5.510247	4.879086	4.051806	9.744448	6.771841	7.563837
protein_co	RAS-like_fa	7	1	0	30	24	22	0.140587	0.023668	0	0.521232	0.541511	0.439116
protein_co	adaptor-rel	12	9	9	36	30	48	0.170046	0.150292	0.168059	0.441317	0.47759	0.675984
protein_co	acyl-CoA_sy	2	4	4	3	5	0	0.016656	0.039256	0.043897	0.021613	0.04678	0
protein_co	immunoglc	2094	1757	1714	123	127	102	17.03418	16.84315	18.37343	0.865591	1.160639	0.824621
protein_co	RAB11A_m	1834	1595	1790	4796	3411	3880	19.69448	20.18427	25.32987	44.55407	41.15058	41.40822
protein_co	cathepsin_l	62	65	47	83	66	98	1.498786	1.851691	1.497203	1.735758	1.792425	2.354419
pseudogen	golgin_A8_	0	3	3	0	0	1	0	0.106646	0.119253	0	0	0.02998
protein_co	tetratricop	387	344	284	314	246	267	5.322984	5.575832	5.147512	3.736258	3.801267	3.649767
protein_co	CD276_mo	4713	3683	3619	5570	4554	5424	71.92589	66.23638	72.77986	73.53701	78.07821	82.26538
protein_co	fumarylace	597	586	426	519	344	440	9.222578	10.66799	8.672062	6.935988	5.970153	6.755233
protein_co	KIAA1199	3043	2343	3806	14	35	31	21.89744	19.86876	36.09067	0.087153	0.282949	0.221698
protein_co	RNA_polym	609	531	458	1367	1173	1257	5.467367	5.617752	5.418278	10.61677	11.83063	11.21517
protein_co	homer_hor	69	59	45	104	74	93	0.589087	0.593594	0.506265	0.768116	0.709759	0.789083
protein_co	EH-domain	677	491	427	1689	1566	1739	9.947558	8.501908	8.267811	21.46943	25.85048	25.39435
protein_co	transmemb	435	401	381	558	420	370	7.407312	8.046793	8.549312	8.219939	8.034701	6.261563
protein_co	zinc_finger_	2935	2505	2880	1363	1403	1185	14.85486	14.94085	19.20825	5.967869	7.977506	5.960578
protein_co	centrosom	129	116	109	324	268	241	1.211959	1.28429	1.349458	2.633335	2.828668	2.250219

protein_co ATPase_clas	0	0	1	13	38	15	0	0	0.012064	0.102954	0.390815	0.136471
protein_co oculocutan	98	64	75	15	9	16	1.628442	1.253238	1.642262	0.215626	0.168011	0.264226
protein_co DTW_doma	227	233	205	486	297	328	4.484181	5.424008	5.33637	8.305324	6.591174	6.439332
protein_co transglutan	0	0	0	8	0	0	0	0	0	0.132415	0	0
protein_co family_with	116	116	117	230	147	180	1.30524	1.538146	1.734815	2.238841	1.858227	2.012865
protein_co GA_binding	391	295	329	940	674	738	6.863372	6.102248	7.610119	14.27419	13.29137	12.87439
protein_co tight_junct	1769	1496	1950	3125	2596	2419	11.7802	11.73988	17.11175	18.00271	19.42132	16.00923
protein_co Bcl2_modif	82	82	53	188	243	199	0.926213	1.091486	0.788874	1.837037	3.08356	2.23388
protein_co Dmx-like_2	253	245	306	198	234	200	1.255067	1.432252	2.000334	0.849717	1.304101	0.98602
protein_co secretogran	0	1	2	133	114	123	0	0.018848	0.042153	1.840258	2.048415	1.955144
protein_co DnaJ_(Hsp4	152	129	93	282	174	223	6.000769	6.001504	4.838169	9.63109	7.717233	8.749391
protein_co eukaryotic_	1164	1104	1000	3401	2289	2661	23.98728	26.81045	27.15581	60.6314	52.99353	54.49824
protein_co spastic_par	742	651	719	740	679	632	5.053025	5.224391	6.452251	4.359556	5.194771	4.277345
protein_co ras_homolo	6	14	8	71	69	91	0.186303	0.512275	0.327335	1.907168	2.406943	2.80814
protein_co vacuolar_p	777	515	575	1533	1297	1257	10.56101	8.248955	10.29882	18.0256	19.80495	16.97968
protein_co Opa_intera	40	19	28	341	192	274	1.713301	0.959035	1.580398	12.63546	9.238977	11.66363
protein_co solute_carr	141	99	111	81	62	72	1.04299	0.862985	1.081979	0.518333	0.515231	0.529302
protein_co biogenesis_	1039	924	872	1143	824	832	13.62539	14.27948	15.06901	12.96709	12.13975	10.84342
protein_co myelin_exp	33	24	40	834	845	725	0.314049	0.269154	0.501623	6.866131	9.034181	6.856945
protein_co serum/gluc	50	27	38	199	150	139	0.640157	0.407368	0.641114	2.204107	2.15753	1.768646
protein_co platelet-der	548	363	282	101	63	85	15.22922	11.88806	10.32716	2.428183	1.96692	2.347609
protein_co centrosom	256	249	192	295	284	252	3.103479	3.557258	3.06722	3.093812	3.867909	3.036121
protein_co zinc_finger_	131	143	141	775	543	626	1.087544	1.399003	1.542516	5.565964	5.06436	5.164873
protein_co BRF2_subu	111	113	105	129	131	150	2.257568	2.708342	2.814116	2.269711	2.993218	3.031928
protein_co tripartite_r	497	448	433	603	512	643	6.221725	6.609057	7.142942	6.530324	7.200679	7.999724
protein_co zinc_finger_	389	363	245	735	401	529	7.574125	8.329072	6.286136	12.38036	8.771549	10.23642
protein_co retinitis_pi	0	0	0	1	0	4	0	0	0	0.006451	0	0.029642
protein_co carbonic_a	17	6	15	135	93	129	0.524168	0.218012	0.609464	3.600962	3.221468	3.952948
protein_co frizzled_fam	69	71	72	651	623	512	0.266132	0.322711	0.365945	2.172161	2.699512	1.962582
protein_co integrator_	246	154	230	647	439	483	4.720364	3.482316	5.815714	10.74008	9.463548	9.210796
protein_co receptor-in	193	157	140	638	384	466	3.954184	3.790586	3.779744	11.30793	8.838526	9.488447
protein_co eyes_absen	36	41	49	359	329	292	0.440563	0.591285	0.790199	3.800695	4.523249	3.551388
protein_co nibrin	482	445	492	810	564	624	5.200236	5.657742	6.99481	7.560039	6.836034	6.69068
protein_co transient_r	1	3	1	10	0	3	0.010136	0.035834	0.013357	0.087687	0	0.030221
protein_co carboxypep	510	411	373	413	295	348	13.86744	13.16967	13.36503	9.714919	9.011503	9.404052
protein_co 24-dienoyl_	835	764	566	464	344	394	25.03156	26.98994	22.35901	12.03323	11.58534	11.73836
protein_co calbindin_2	6	6	1	6	1	6	0.058911	0.069423	0.012938	0.050963	0.01103	0.058547
protein_co inositol_m	1563	1435	1537	2066	1791	1691	11.4942	12.43595	14.89459	13.14357	14.79669	12.35871
protein_co secreted_fr	3914	3120	3792	9577	8487	7747	46.17002	43.37115	58.94438	97.73086	112.4715	90.8202
protein_co lysosomal_	4027	3434	2972	6168	3910	4519	67.18985	67.51953	65.34399	89.02857	73.29053	74.93315
protein_co ubiquitin-c	242	266	265	475	367	414	1.520499	1.969515	2.194074	2.581828	2.590513	2.585119
protein_co processing_	365	294	308	846	698	648	4.094822	3.886839	4.553314	8.210611	8.797243	7.224816
protein_co NIPA-like_d	252	276	246	155	95	84	2.912275	3.758789	3.746293	1.549625	1.233401	0.964763
protein_co inhibitor_c	747	562	581	583	400	576	7.906222	7.009577	8.103252	5.338017	4.756171	6.058715

protein_co plasminoge	3238	2473	2354	773	597	791	49.51558	44.56524	47.43581	10.22604	10.25625	12.02129
protein_co junctophili	17	23	11	293	263	199	0.205573	0.327756	0.175285	3.065116	3.572902	2.391548
protein_co dickkopf_h	0	0	0	1	1	0	0	0	0	0.051229	0.066528	0
protein_co serine/thre	242	228	222	703	524	460	2.402348	2.667242	2.904078	6.037246	5.843874	4.538245
protein_co ganglioside	98	80	86	369	321	324	1.415226	1.361434	1.636564	4.609873	5.207793	4.650014
protein_co RAB2A_mei	2340	1858	1917	2608	2041	2119	32.19385	30.1238	34.75473	31.04042	31.54635	28.97328
protein_co eukaryotic_	7609	7106	5621	8969	5231	6186	202.4261	222.7775	197.055	206.4173	156.341	163.553
protein_co ER_membr	345	333	315	681	497	596	6.680557	7.598798	8.037832	11.40785	10.81183	11.46963
protein_co epithelial_s	0	0	0	2001	1732	1621	0	0	0	24.30865	27.32421	22.62265
protein_co WNT1_indu	127	61	95	3	1	0	1.749091	0.990024	1.724119	0.035743	0.015472	0
protein_co N-myc_dov	4450	4108	3071	322	269	325	59.14824	64.34567	53.78936	3.702548	4.016827	4.293137
protein_co zinc_finger_	93	107	138	119	96	86	3.825573	5.186859	7.480445	4.234708	4.436432	3.51578
protein_co interleukin	53	54	69	140	52	72	1.351576	1.622802	2.318722	3.088558	1.489763	1.824765
protein_co stathmin-li	563	463	466	3235	1982	1963	13.40791	12.99394	14.62424	66.64843	53.02801	46.46036
protein_co armadillo_	488	462	376	1078	772	722	8.529285	9.515725	8.659952	16.29951	15.1586	12.54122
protein_co trichorhinc	1122	945	1187	384	464	389	5.945925	5.901542	8.289191	1.760438	2.762445	2.048735
protein_co sperm_assc	2	0	1	261	237	196	0.027488	0	0.018111	3.103197	3.659344	2.677143
protein_co chromatin_	389	371	303	1224	743	891	8.27735	9.302993	8.496091	22.53129	17.7615	18.84209
protein_co neurocalcin	90	45	45	79	86	65	1.251231	0.73725	0.824409	0.950135	1.343206	0.898086
protein_co sorting_nex	115	128	149	124	129	139	1.763677	2.313334	3.011219	1.645152	2.222594	2.118584
protein_co ubiquitin_p	1585	1512	1661	1475	1475	1148	8.149119	9.160945	11.25345	6.560492	8.519664	5.865876
protein_co gasdermin_	3	1	6	35	21	45	0.045876	0.018021	0.120907	0.463016	0.360772	0.683891
protein_co tissue_spec	1221	974	765	2186	1376	1880	29.11755	27.37191	24.04005	45.09748	36.86435	44.55604
protein_co pyrroline-5	287	199	202	361	278	392	5.673661	4.635981	5.262204	6.173788	6.174124	7.701534
protein_co eukaryotic_	4973	4259	3226	5202	4120	5634	70.81107	71.46566	60.53156	64.07905	65.90661	79.72769
protein_co squalene_e	2921	2468	2546	2303	1823	1748	52.22582	52.00031	59.98558	35.62137	36.61756	31.06024
protein_co SH2_domai	88	58	46	1731	1431	1491	1.389859	1.079501	0.957372	23.65093	25.39082	23.40321
protein_co integrator_	586	508	503	1114	746	863	11.06399	11.30277	12.5146	18.19543	15.82348	16.19327
protein_co exoribonuc	305	283	296	941	751	837	3.208226	3.507993	4.102907	8.562839	8.87471	8.749843
protein_co solute_carr	1067	817	1000	1894	1508	1627	12.17152	10.98271	15.03195	18.69061	19.32551	18.44496
protein_co myotubula	325	296	331	607	431	424	2.302707	2.471463	3.090424	3.720548	3.430691	2.985594
protein_co leptin_rece	375	389	318	940	703	785	6.256815	7.648543	6.991719	13.56791	13.1773	13.01671
protein_co dynactin_6	167	164	136	437	224	285	7.84485	9.078605	8.418639	17.75876	11.8213	13.30524
protein_co R3H_doma	453	386	282	690	563	620	13.52638	13.58244	11.09602	17.8236	18.88604	18.3986
protein_co glutathione	1371	1105	814	2283	1975	2194	23.30832	22.13823	18.23613	33.57704	37.72156	37.06976
protein_co tumor_nec	241	176	180	657	451	551	4.701098	4.045778	4.626894	11.08691	9.883434	10.68178
processed_ UBX_doma	244	240	170	402	210	306	7.95909	9.225542	7.307306	11.34391	7.69559	9.919839
protein_co protein_ph	1450	1330	1223	3387	2178	2579	38.26742	41.36375	42.53265	77.32846	64.57555	67.64289
protein_co glutamate-l	480	373	333	449	412	520	7.000462	6.41064	6.399772	5.664933	6.750435	7.536999
protein_co neurofilam	389	279	264	110	119	141	5.122897	4.329895	4.581469	1.253204	1.760606	1.845418
protein_co tumor_sup	2241	2045	1811	2349	1609	1990	32.21308	34.64103	34.30391	29.21033	25.98337	28.42844
processed_ neurofilam	706	617	564	1095	796	726	9.154137	9.427683	9.636662	12.28259	11.59511	9.355327
protein_co Rho_guanir	1144	974	942	1300	1141	1248	10.72318	10.75879	11.63545	10.54153	12.01523	11.62577
protein_co kelch_dom	281	252	219	560	603	778	3.25381	3.438694	3.34168	5.609665	7.844265	8.953135

protein_co minichrom	1480	1293	1315	10325	7239	7920	18.73121	19.28456	21.93132	113.0465	102.9276	99.61828
protein_co ADAM_met	0	0	0	0	2	1	0	0	0	0	0.044518	0.019691
protein_co potassium_	520	398	428	937	855	776	8.101624	7.307333	8.787135	12.62907	14.96525	12.01545
protein_co fibrinogen-	0	5	6	1	0	3	0	0.158586	0.212801	0.023284	0	0.080245
protein_co N-acylsphir	662	547	571	2210	1472	1685	13.43309	13.08014	15.26824	38.79478	33.55636	33.98033
protein_co BCL2/aden	1739	1572	1461	423	355	289	25.5026	27.16718	28.23384	5.366465	5.84874	4.212039
protein_co mannosida	1542	1329	1106	1330	938	971	22.15333	22.50022	20.93845	16.52986	15.13932	13.86384
protein_co potassium_	14	11	4	187	146	214	0.330881	0.306368	0.124577	3.823391	3.876555	5.026521
protein_co tubby_like_	0	0	0	4	3	1	0	0	0	0.104444	0.101726	0.029997
protein_co nucleobind	5951	5117	3816	2907	2439	3089	118.0854	119.6544	99.78137	49.90158	54.37098	60.91634
protein_co dihydrodio	0	0	1	0	1	1	0	0	0.064536	0	0.055019	0.048672
protein_co glycogen_s	2991	2711	1779	3322	2315	2536	44.30512	47.3232	34.72548	42.56966	38.52455	37.3333
protein_co mitogen-ac	0	0	4	15	4	1	0	0	0.103353	0.254438	0.088112	0.019487
protein_co enoyl_CoA_	561	545	345	777	409	462	21.04883	24.09732	17.05764	25.22023	17.24001	17.22728
protein_co heterogene	2732	2133	2240	4982	4849	5251	46.74686	43.01003	50.50735	73.74601	93.21226	89.29424
protein_co nuclear_fac	507	377	328	908	758	896	12.18388	10.67643	10.38691	18.87672	20.46425	21.39909
protein_co luteinizing_	1	2	3	2	7	11	0.102998	0.242754	0.407179	0.178206	0.809983	1.125982
protein_co tubulin_be	5	1	1	0	1	2	0.103725	0.024447	0.027337	0	0.023306	0.041234
protein_co seryl-tRNA_	19	11	15	12	12	34	0.489003	0.333624	0.508726	0.267179	0.346967	0.869654
protein_co potassium_	4	3	2	1	0	0	0.048436	0.04281	0.031914	0.010476	0	0
protein_co small_nucl	5863	5230	3777	6847	6225	8684	96.36543	101.3002	81.80562	97.35644	114.9449	141.8505
protein_co cleft_lip_ar	3686	2889	2588	4122	2799	3318	71.42771	65.97297	66.08615	69.10069	60.93451	63.89949
protein_co v-rel_reticu	463	367	292	208	170	151	10.68513	9.980949	8.880069	4.152647	4.407544	3.463261
protein_co CLK4-assoc	762	682	424	1224	825	1195	14.56881	15.36599	10.68242	20.2448	17.72034	22.70632
protein_co lin-7_homc	61	48	41	58	40	29	3.055251	2.833123	2.70605	2.51309	2.250744	1.443526
protein_co protein_ph	1106	950	773	1414	1090	1596	9.852388	9.972799	9.07404	10.89679	10.90842	14.12957
protein_co Fc_fragmen	991	959	657	270	145	220	19.56901	22.31624	17.09604	4.612348	3.216713	4.317453
protein_co PIH1_doma	701	528	422	1376	1048	1237	31.13392	27.63483	24.69807	52.86854	52.29091	54.60032
protein_co creatine_ki	0	8	3	0	0	0	0	0.301208	0.126306	0	0	0
protein_co Rho/Rac_gu	479	402	370	561	464	660	4.423293	4.37465	4.502427	4.48163	4.81368	6.057086
protein_co protein_ph	169	112	81	1195	857	1080	2.869477	2.240996	1.812324	17.55282	16.34729	18.22424
protein_co peroxisoma	29	18	9	33	23	39	1.141479	0.834929	0.466818	1.123691	1.01706	1.525612
protein_co excision_re	809	631	536	1355	996	1116	10.31285	9.479089	9.003881	14.94282	14.26391	14.13852
protein_co DOT1-like_l	1075	1033	762	1922	1916	2010	7.653519	8.666827	7.148954	11.83775	15.32489	14.22193
protein_co pleckstrin_	1338	989	865	3468	2321	3264	24.78483	21.58904	21.1145	55.57404	48.30077	60.08826
protein_co solute_carr	2	3	6	0	0	0	0.035615	0.062954	0.140794	0	0	0
protein_co ribonuclea	314	292	166	1570	1050	1166	11.1792	12.25099	7.787966	48.35527	41.99712	41.25621
protein_co kinesin_ligl	1	3	2	35	18	45	0.026391	0.093302	0.069555	0.799084	0.533682	1.180275
protein_co CD37_mole	401	373	325	44	85	78	6.69273	7.336262	7.147877	0.635294	1.593775	1.293788
protein_co splicing_fac	1921	1510	1090	2596	2284	2730	51.33753	47.5545	38.38565	60.01714	68.57294	72.50699
protein_co anti-Muller	138	127	72	375	244	317	2.963837	3.214297	2.03771	6.967379	5.887271	6.766188
protein_co dickkopf-lik	29	18	8	4	13	7	1.256374	0.918968	0.456715	0.149915	0.632723	0.30139
protein_co lymphobla	7	9	5	2	1	0	0.239552	0.362954	0.225479	0.05921	0.038446	0
protein_co ornithine_c	5514	4578	3493	8891	4783	6745	103.2237	100.994	86.16801	143.988	100.5917	125.4886

protein_co tRNA_meth	1269	1064	834	1737	1186	1816	26.04968	25.73887	22.56013	30.84634	27.35108	37.04813
protein_co syntaxin_1(	862	662	513	664	446	722	36.77287	33.28016	28.83849	24.50481	21.37491	30.61027
protein_co dystrophia_	675	652	400	848	730	852	10.64497	12.11701	8.312575	11.5691	12.9334	13.35334
protein_co radial_spok	0	4	0	0	0	0	0	0.101609	0	0	0	0
protein_co TBC1_dom	751	579	502	672	474	566	14.04404	12.75962	12.3706	10.87138	9.958172	10.51909
protein_co interleukin_	9	8	9	6	2	11	0.197951	0.207354	0.260851	0.114164	0.049419	0.240446
protein_co transducin-	2	0	0	0	5	0	0.05054	0	0	0	0.141947	0
protein_co coiled-coil_	474	475	292	591	374	509	13.05621	15.4184	10.59879	14.08281	11.57336	13.93369
protein_co prostate_tu	1181	1011	731	675	661	953	33.25708	33.55	27.12604	16.44376	20.91148	26.67085
protein_co amino-term	1482	1259	1020	1606	1164	1675	23.96413	23.99088	21.73444	22.4658	21.14538	26.9177
protein_co neuro-oncc	2	3	5	0	1	0	0.013569	0.023986	0.044703	0	0.007622	0
protein_co small_gluta	1854	1578	1295	4825	2909	3283	42.12558	42.25229	38.77401	94.84108	74.25556	74.13387
protein_co mediator_c	804	736	521	1275	925	1066	12.7477	13.75183	10.8855	17.48835	16.47656	16.79742
protein_co small_nucl	781	531	460	579	416	439	26.81382	21.48371	20.81136	17.19687	16.04538	14.97897
protein_co chromoson	1763	1407	966	2274	1521	2285	106.9129	100.5493	77.19511	119.2975	103.623	137.7126
protein_co translocase	996	834	610	1992	1405	1917	23.67725	23.36388	19.10894	40.96606	37.52297	45.29014
protein_co coiled-coil_	142	149	72	203	124	215	4.119244	5.093574	2.752305	5.094344	4.041103	6.198368
protein_co interleukin_	19	14	12	88	57	50	0.375749	0.326271	0.312723	1.50553	1.26639	0.982705
protein_co ASF1_anti-s	162	106	125	1328	891	972	4.165343	3.211802	4.235265	29.53907	25.73727	24.83772
protein_co troponin_T	26	21	21	3	8	4	1.183548	1.12652	1.259698	0.11814	0.409121	0.18096
protein_co vaccinia_re	487	400	346	801	529	635	11.73521	11.35871	10.98684	16.69773	14.32078	15.20707
protein_co family_with	1235	1049	783	2373	1641	1797	44.93617	44.97919	37.54271	74.69471	67.07902	64.98106
protein_co protein_ph	2151	1698	1563	2913	2507	2947	28.74933	26.74435	27.5284	33.68145	37.64356	39.14507
protein_co chromoson	125	141	96	180	101	133	1.931025	2.566872	1.954268	2.405545	1.752865	2.041923
protein_co mediator_c	152	123	123	199	153	178	2.078799	1.982354	2.21671	2.354426	2.350766	2.419349
protein_co olfactomed	1789	1662	1108	60	39	63	46.91007	51.35632	38.28515	1.361037	1.148866	1.641746
protein_co RAS_protei	0	1	2	0	0	0	0	0.014611	0.032676	0	0	0
protein_co A_kinase_(P	657	526	453	1236	941	1032	9.400604	8.869175	8.541288	15.29931	15.12617	14.67505
protein_co epoxide_hy	1	9	1	14	14	9	0.029057	0.308172	0.038289	0.351913	0.457005	0.259894
protein_co ilvB_(bacte	1469	1287	988	1417	1226	1697	18.30751	18.90137	16.22555	15.27708	17.16513	21.01837
protein_co zinc_finger_	163	125	110	127	76	84	1.557088	1.407157	1.384692	1.049524	0.815621	0.79747
protein_co synapse_de	1282	984	841	1116	769	843	17.71147	16.02023	15.31078	13.33809	11.93554	11.57454
protein_co solute_carr	0	0	0	217	182	185	0	0	0	3.044841	3.316365	2.982108
protein_co aurora_kina	8	8	9	12	5	4	0.263061	0.310001	0.389981	0.341358	0.184708	0.130718
protein_co processing_	514	431	358	969	630	752	8.038898	7.943607	7.378214	13.11053	11.06937	11.68856
protein_co cyclin_E1	45	24	50	331	241	322	1.166101	0.732895	1.707374	7.420185	7.016004	8.292572
protein_co URI1_prefo	989	745	804	1657	1033	1203	20.61364	18.29876	22.08255	29.87747	24.18843	24.91917
protein_co programme	1031	905	669	1656	1205	1810	15.76153	16.30404	13.47723	21.90095	20.69549	27.49969
protein_co ankyrin_rep	383	342	329	621	525	515	4.556495	4.794742	5.15778	6.391263	7.016822	6.089042
protein_co ribosomal_	23632	19253	13129	22618	16485	21611	523.6926	502.784	383.3914	433.6039	410.4062	475.949
protein_co translocase	1256	989	795	3248	1926	2867	25.81284	23.95243	21.53021	57.74645	44.46841	58.55764
protein_co fibrillarin	3932	3291	2385	7075	4717	6652	148.6886	146.6557	118.8467	231.448	200.3914	249.9919
protein_co dual-specifi	819	664	505	435	355	408	15.91728	15.20758	12.93335	7.313702	7.751083	7.880519
protein_co cyclin_N-te	13	6	5	2	3	4	0.378774	0.206013	0.191974	0.050412	0.098199	0.115826

protein_co	glucose-6-p	5015	4085	3321	3942	2746	3243	66.37477	63.71347	57.92096	45.13482	40.83022	42.65684
protein_co	v-akt_muri	3212	2845	2237	3498	3393	4499	32.08424	33.48926	29.44537	30.22728	38.07581	44.66238
protein_co	phospholip	15204	12913	9765	14296	9271	10610	369.227	369.5471	312.4947	300.34	252.9363	256.0711
protein_co	periaxin	214	168	160	96	131	122	2.059137	1.904969	2.02874	0.799108	1.416093	1.166651
protein_co	protein_inh	653	533	467	1314	1125	1550	10.94348	10.52632	10.31322	19.05026	21.18088	25.81569
protein_co	numb_hom	1242	994	782	490	418	529	23.69467	22.34717	19.65942	8.087014	8.958895	10.02985
protein_co	Epstein-Bar	22	19	17	81	38	50	0.982042	0.999466	0.99998	3.127918	1.905636	2.21813
protein_co	coiled-coil_	287	212	182	652	408	608	10.59558	9.223291	8.854196	20.82349	16.92202	22.30777
protein_co	Src_homol	0	0	0	13	10	12	0	0	0	0.231038	0.230795	0.245001
protein_co	tubulin_fol	2216	1833	1446	2670	1722	2324	79.64511	77.63524	68.48453	83.01635	69.52989	83.0109
protein_co	fibronectin	296	236	157	227	165	173	8.558457	8.041237	5.981887	5.677964	5.359654	4.97118
protein_co	polymerase	59	26	28	93	32	68	3.145537	1.633516	1.967142	4.289323	1.916646	3.602976
protein_co	ovo-like_3_	0	3	1	9	5	5	0	0.232212	0.086555	0.511402	0.368957	0.32639
protein_co	CAP-GLY_d	1559	1271	1116	121	110	110	24.4911	23.52962	23.10262	1.644412	1.94135	1.717373
protein_co	zinc_finger_	4	0	4	13	13	12	0.044526	0	0.058674	0.125186	0.162571	0.132752
protein_co	solute_carr	5057	4353	3463	7778	5215	6689	92.89473	94.23102	83.82729	123.603	107.6221	122.115
protein_co	protein_kir	625	533	442	1067	880	964	9.963301	10.01285	9.284966	14.71467	15.75995	15.27249
protein_co	tight_junct	22	2	1	271	215	260	0.347672	0.037246	0.020825	3.704926	3.817111	4.083479
protein_co	amyloid_be	852	711	663	114	111	107	18.07845	17.77863	18.5383	2.092615	2.646023	2.256394
protein_co	cactin_spli	374	370	315	640	590	866	5.481709	6.39077	6.084007	8.114978	9.715058	12.61455
protein_co	coiled-coil_	750	718	478	546	629	969	18.97073	21.402	15.93256	11.94754	17.87403	24.35882
protein_co	heterogene	4921	4255	3580	7712	7920	10123	73.28344	74.67223	70.25388	99.35335	132.5033	149.8205
protein_co	fizzy/cell_d	1264	1157	810	1854	1692	2227	12.83911	13.84931	10.84195	16.29148	19.30799	22.4811
protein_co	BCL2_bindi	448	377	264	561	506	709	12.90401	12.79661	10.02041	13.97888	16.37367	20.29563
protein_co	transformir	1207	818	710	1412	834	1074	23.07684	18.43018	17.88802	23.3543	17.91366	20.40718
protein_co	DENN/MAD	270	226	198	334	254	330	2.607455	2.571986	2.519725	2.790375	2.755725	3.167208
protein_co	ATP5S-like	1060	841	718	2184	1388	1683	24.21988	22.64483	21.61849	43.16997	35.62908	38.21728
protein_co	perilipin_3	2998	2630	2191	1875	1548	1460	68.03133	70.32993	65.51708	36.80795	39.46366	32.92607
protein_co	myosin_he	0	0	2	4	9	15	0	0	0.020192	0.026512	0.077465	0.114213
protein_co	mitochond	369	385	268	1038	697	801	12.05878	14.82671	11.54109	29.34522	25.58933	26.01472
protein_co	CD79a_mo	13	6	6	11	0	12	0.547085	0.297557	0.332734	0.400467	0	0.501883
protein_co	ribosomal_	36184	29595	17154	40240	26897	32793	812.0462	782.6896	507.2994	781.2412	678.1364	731.4
protein_co	glioma_tun	8526	7328	5121	5569	4444	5748	107.8554	109.2419	85.36625	60.94483	63.15674	72.26417
protein_co	natural_kill	0	1	0	0	3	0	0	0.074007	0	0	0.211658	0
protein_co	intercellula	133	152	133	3	1	6	2.347051	3.160978	3.092839	0.045799	0.019825	0.105228
protein_co	electron-tra	96	62	56	93	102	104	1.431241	1.089282	1.100181	1.199464	1.708404	1.540935
protein_co	CD33_mole	0	0	0	0	0	3	0	0	0	0	0	0.033385
protein_co	BRISC_and_	195	140	151	389	256	367	7.013243	5.933616	7.156424	12.10311	10.34364	13.11777
protein_co	tyrosine_ki	1590	1311	1107	1504	1229	1773	19.3642	18.81535	17.7658	15.84577	16.81525	21.45956
protein_co	sulfotransfe	3	0	0	0	1	0	0.079931	0	0	0	0.029933	0
protein_co	cell_divisio	8151	6364	4696	9190	6284	8787	268.3595	246.9126	203.7365	261.7487	232.4295	287.5122
protein_co	N-ethylmal	1411	1105	1022	1955	1280	1567	19.16361	17.68559	18.29094	22.96995	19.53032	21.1509
protein_co	Rab_accept	4295	3418	2511	1798	1054	1495	276.9568	259.7336	213.3686	100.3002	76.3552	95.80756
protein_co	ATPase_Na-	10	5	10	3	8	11	0.138662	0.081702	0.182722	0.035987	0.124622	0.151586

protein_co	Meis_home	1503	1285	931	104	74	104	36.25071	36.52311	29.5898	2.169971	2.005111	2.492875
protein_co	protein_tyr	5314	4261	4057	1077	1145	1144	38.27598	36.16791	38.50743	6.710942	9.265296	8.18918
protein_co	cornifelin	7	11	2	51	58	24	0.708579	1.31217	0.266781	4.46605	6.5958	2.414411
protein_co	multiple_E	3636	3096	2879	1912	2857	3296	17.55366	17.61375	18.31557	7.985364	15.49541	15.81396
protein_co	KDEL_(Lys-A	8494	7341	5611	6908	5242	6346	282.1084	287.3202	245.572	198.4811	195.5914	209.466
protein_co	cytohesin_1	759	713	549	830	744	1007	8.637621	9.562006	8.233027	8.171344	9.512056	11.38915
protein_co	glutamate-r	1076	783	729	3211	2123	2480	10.22519	8.76855	9.128959	26.39747	22.66512	23.4218
protein_co	glutamate_	74	55	46	69	68	82	0.769219	0.673734	0.630102	0.620484	0.794102	0.847114
protein_co	synaptogyr	0	0	0	3	0	0	0	0	0	0.137397	0	0
protein_co	C-type_lect	7	7	10	39	17	26	0.261161	0.307762	0.491637	1.258744	0.712537	0.964035
protein_co	coiled-coil_	1	5	4	11	0	12	0.016467	0.097026	0.086797	0.156699	0	0.196382
protein_co	caspase_rec	395	355	320	457	311	352	3.973341	4.208179	4.241735	3.976838	3.514537	3.518933
protein_co	ligase_I_DN	443	376	257	1670	1435	1679	5.717421	5.718622	4.370835	18.64558	20.80642	21.53559
protein_co	sialic_acid_	0	0	0	6	7	12	0	0	0	0.141646	0.214604	0.325448
protein_co	zinc_finger_	157	136	136	108	92	107	2.221202	2.267432	2.535491	1.321828	1.462262	1.504464
protein_co	phospholip	5	14	1	22	2	6	0.106052	0.349931	0.02795	0.403676	0.047657	0.126476
protein_co	sialic_acid_	0	0	0	0	0	2	0	0	0	0	0	0.042125
protein_co	hyaluronan	1	0	5	9	1	3	0.025091	0	0.165316	0.195351	0.028188	0.074807
protein_co	RAB3D_me	41	19	13	172	247	226	0.507976	0.277409	0.212245	1.843532	3.437995	2.78277
protein_co	D_site_of_a	35	22	25	17	7	20	0.321914	0.238452	0.303002	0.135264	0.07233	0.182815
protein_co	transmemb	16	24	16	64	33	44	0.646608	1.142981	0.852071	2.237504	1.498248	1.767189
protein_co	calcyphosin	106	114	77	87	80	103	1.596514	2.023386	1.528243	1.133572	1.353648	1.541749
protein_co	Lipid_phos	1844	1395	1094	69	42	42	35.79875	31.91452	27.98718	1.158828	0.916021	0.810337
protein_co	family_with	4	11	4	18	27	28	0.10995	0.356316	0.144887	0.428027	0.833775	0.764898
protein_co	Ras_interac	12	19	14	37	15	25	0.192047	0.358333	0.29525	0.512261	0.269691	0.397627
protein_co	fibroblast_g	0	0	2	0	1	2	0	0	0.106346	0	0.045332	0.080204
protein_co	branched_c	595	458	361	583	361	409	13.97511	12.67683	11.17327	11.84595	9.525646	9.547093
protein_co	mesoderm_	406	330	292	580	377	396	7.776427	7.448607	7.370072	9.610479	8.112309	7.538048
protein_co	pleckstrin_	1716	1401	1034	70	64	85	29.41928	28.3048	23.35986	1.038188	1.232661	1.448249
protein_co	protein_ph	7269	5994	5269	8357	5852	6141	117.2899	113.975	112.0337	116.6539	106.0814	98.47695
protein_co	transportin	2439	2281	1995	3233	3126	3653	25.2095	27.78337	27.17254	28.90821	36.29866	37.52423
protein_co	WD_repeat	123	115	109	181	96	189	2.541664	2.800386	2.968071	3.235598	2.228606	3.881364
protein_co	calcium_ch	2	1	0	0	0	0	0.039391	0.02321	0	0	0	0
protein_co	glutaryl-Co	296	247	205	550	462	568	8.011521	7.878205	7.311591	12.87802	14.04799	15.27852
protein_co	leukocyte_i	0	0	0	1	0	0	0	0	0	0.008259	0	0
protein_co	deoxyribon	198	163	107	319	206	268	5.361799	5.201637	3.818246	7.473069	6.267028	7.212565
protein_co	microtubul	25	16	13	20	16	23	0.273852	0.206539	0.187652	0.189526	0.196899	0.250388
protein_co	leukocyte_l	220	193	119	134	137	250	7.55319	7.808581	5.383807	3.979931	5.284177	8.530164
protein_co	PRP31_pre	690	567	415	1399	926	1158	17.18217	16.63868	13.61795	30.13766	25.90531	28.65808
protein_co	TCF3_(E2A)	285	246	190	353	348	484	12.52131	12.73642	11.00002	13.41661	17.17645	21.13295
protein_co	Janus_kinas	60	47	45	27	21	20	0.584768	0.539805	0.577936	0.227646	0.229933	0.193719
protein_co	ribosomal_	28031	23895	13895	30127	18311	21371	1066.85	1071.714	696.8805	991.9365	782.9357	808.35
pseudogen	-	4	0	0	1	0	0	0.0797	0	0	0.017237	0	0
protein_co	arrestin_do	219	162	103	22	6	20	3.093404	2.696588	1.917187	0.26883	0.095212	0.280758

protein_co	phosphoin	4	3	0	0	1	0	0.04885	0.043175	0	0	0.01372	0
protein_co	RAB3A_mei	109	105	53	51	27	24	3.77655	4.287115	2.4198	1.528628	1.050949	0.826399
protein_co	phosphodi	12	9	7	4	8	6	0.106254	0.09391	0.081676	0.03064	0.07958	0.052799
protein_co	inositol-3-p	398	303	245	3622	2178	2554	10.33375	9.270957	8.382542	81.35539	63.53043	65.90303
protein_co	elongation_	196	209	118	252	215	355	2.576716	3.237903	2.044218	2.865986	3.175397	4.638189
protein_co	CREB_regul	503	405	320	460	364	419	3.921844	3.721212	3.287813	3.102724	3.1884	3.246729
protein_co	Histone-lys	1595	1247	1211	1746	1667	2144	9.970585	9.186149	9.975597	9.44207	11.70697	13.3197
protein_co	cartilage_o	8	7	5	0	1	1	0.156457	0.161328	0.128857	0	0.021971	0.019436
protein_co	uroplakin_	4	4	0	10	5	0	0.173151	0.204048	0	0.37448	0.243156	0
protein_co	coatomer_	1573	1386	985	2164	1100	1599	47.04869	48.85276	38.82307	55.99369	36.96243	47.531
protein_co	DEAD_(Asp	1391	1106	852	2048	1352	1584	39.12908	36.66356	31.58253	49.83855	42.72659	44.28303
protein_co	ets_variant	70	38	43	7	27	8	2.358924	1.50906	1.909498	0.204069	1.022183	0.267926
protein_co	ATPase_H+/	2	0	3	1	5	6	0.028547	0	0.056428	0.012348	0.080178	0.085113
protein_co	armadillo_	800	651	507	2072	1140	1480	17.02283	16.32412	14.21623	38.14121	27.25183	31.29775
protein_co	transmemb	745	685	545	1368	671	1029	22.12061	23.96836	21.32417	35.13904	22.38269	30.36447
protein_co	glyceraldeh	3	1	2	3	1	1	0.106664	0.041899	0.093705	0.092274	0.039944	0.035335
pseudogen	-	0	2	0	0	0	2	0	0.343734	0	0	0	0.289885
protein_co	transmemb	75	40	52	31	23	13	2.312507	1.453412	2.112808	0.826888	0.796707	0.398359
protein_co	hepcidin_a	0	0	0	0	1	0	0	0	0	0	0.022666	0
protein_co	upstream_t	1088	978	694	1758	1115	1586	21.00649	22.25208	17.65708	29.36341	24.18514	30.43249
protein_co	lipolysis_st	28	26	17	3495	2527	3154	0.597721	0.654065	0.478216	64.54322	60.60308	66.91319
protein_co	KxDL_moti	568	595	405	1132	725	870	10.98265	13.5576	10.31926	18.93512	15.74874	16.71812
protein_co	FK506_bin	8848	7563	5201	8121	5730	7749	264.0484	265.9743	204.5315	209.6578	192.1065	229.8232
protein_co	SURP_and_	579	550	436	1070	827	953	12.64034	14.14979	12.54301	20.20818	20.28313	20.67678
protein_co	hepsin	0	1	1	51	49	47	0	0.026402	0.029523	0.988466	1.233314	1.046492
protein_co	zinc_finger_	81	52	71	128	71	103	1.454127	1.100089	1.679618	1.987881	1.43194	1.837656
protein_co	sodium_ch	193	159	104	36	21	43	2.953067	2.866951	2.096931	0.47652	0.360981	0.653874
protein_co	pre-B-cell_l	5	3	3	26	7	11	0.153009	0.108187	0.120977	0.688307	0.240654	0.33454
protein_co	Ets2_repres	1446	1172	1073	2024	1871	2914	28.37386	27.10097	27.745	34.35767	41.24516	56.82629
protein_co	glycogen_s	1021	894	660	2147	1523	1862	15.33847	15.82708	13.06577	27.90302	25.70426	27.80005
protein_co	ATPase_typ	2588	2122	1716	2169	1509	1587	28.97257	27.99466	25.31482	21.0061	18.97846	17.65669
protein_co	zinc_finger_	254	259	209	775	437	399	3.737358	4.490946	4.052397	9.864967	7.223729	5.834632
protein_co	glutamate_	3	1	7	7	5	9	0.045469	0.017861	0.139806	0.091781	0.085136	0.135564
protein_co	signal-indu	684	568	504	620	1000	894	4.533822	4.436738	4.40224	3.555192	7.44659	5.88919
protein_co	zinc_finger_	50	38	34	248	210	249	0.998133	0.893942	0.894401	4.282854	4.709631	4.940007
protein_co	ethylmalon	114	73	61	982	428	696	5.736952	4.329187	4.045209	42.75145	24.19743	34.8093
protein_co	cell_adhesi	117	97	81	1164	956	1400	2.843938	2.778517	2.594502	24.47655	26.10605	33.81987
protein_co	smg-9_hom	561	469	417	1168	794	1030	12.44235	12.258	12.18739	22.41019	19.78378	22.70317
protein_co	AVL9_hom	894	654	717	638	620	510	5.963116	5.14068	6.302164	3.681454	4.645971	3.380769
protein_co	RUN_doma	2	1	10	9	8	6	0.025831	0.01522	0.170196	0.100559	0.116079	0.077015
protein_co	chromoson	14	32	21	21	19	17	0.106399	0.286593	0.210311	0.138067	0.162223	0.128401
protein_co	GTP-bindin	223	226	195	535	402	454	1.567633	1.872212	1.806379	3.253541	3.174787	3.171794
protein_co	RAS_p21_p	37	29	28	5	8	14	0.349477	0.322791	0.348505	0.040855	0.08489	0.131418
protein_co	cyclin-depe	1346	1145	1521	3275	3146	2696	6.136633	6.151735	9.137957	12.91693	16.11361	12.21559

protein_co	peptidase_(	832	812	662	1510	981	1243	17.81833	20.49306	18.68256	27.97587	23.6027	26.45601
protein_co	DnaJ_(Hsp4	422	371	265	821	538	577	7.366007	7.631338	6.095374	12.39726	10.54996	10.00933
protein_co	tissue_factc	233	138	126	322	179	254	5.047157	3.522711	3.596634	6.034062	4.356051	5.468072
protein_co	Bet1_golgi_	305	225	241	382	236	289	4.50279	3.914456	4.688497	4.878746	3.914199	4.240229
protein_co	nicotinami	1576	1356	1330	1761	1315	1342	18.2093	18.46306	20.24993	17.60189	17.06915	15.40988
protein_co	TWIST_neig	316	237	255	845	517	566	4.243875	3.75086	4.512845	9.817371	7.800368	7.554427
protein_co	paraoxonas	0	0	0	0	0	1	0	0	0	0	0	0.021625
protein_co	paraoxonas	1201	1047	1054	2132	1404	1715	35.74038	36.71723	41.33249	54.8866	46.93884	50.72125
protein_co	integrin_be	18	32	34	16	32	17	0.170992	0.358228	0.425615	0.131488	0.341509	0.160495
protein_co	HMG-box_t	323	276	279	256	183	152	6.044518	6.086608	6.880154	4.144404	3.847329	2.826913
protein_co	dihydrouri(	72	65	44	224	148	138	1.671821	1.778598	1.346309	4.499542	3.860717	3.184535
protein_co	Sp4_transc	101	69	74	85	128	83	0.872844	0.702702	0.842717	0.635473	1.242722	0.712858
protein_co	WD_repeat	355	259	295	179	210	269	4.09635	3.521888	4.485651	1.786836	2.722307	3.084826
protein_co	dynein_axc	74	55	51	30	21	9	0.276123	0.241847	0.25077	0.09684	0.088032	0.033375
protein_co	Cbl_proto-(	185	162	203	342	358	279	4.16947	4.302602	6.028926	6.66804	9.064444	6.249178
protein_co	distal-less_I	2	0	2	3157	2510	2600	0.062726	0	0.082658	85.65589	88.43872	81.0406
protein_co	myotrophi	1744	1400	1852	1304	1895	1365	24.70013	23.36619	34.56437	15.97693	30.15165	19.213
protein_co	STEAP_fami	133	119	97	42	23	22	4.647625	4.900422	4.466692	1.269673	0.902935	0.764032
protein_co	pleiotrophi	1855	1640	1204	4119	3004	3867	60.84606	63.39274	52.04151	116.8808	110.6974	126.0586
protein_co	membrane_	148	144	169	413	392	353	2.036192	2.334676	3.063928	4.915527	6.058877	4.826601
protein_co	deafness_au	404	298	342	597	494	527	5.114338	4.445611	5.705175	6.538007	7.025611	6.630226
protein_co	ATPase_H+_	0	0	0	0	3	4	0	0	0	0	0.056915	0.067131
protein_co	zinc_finger_	292	220	200	1511	1419	1313	2.177292	1.933141	1.965163	9.746781	11.88681	9.729894
protein_co	tetratricop	185	168	139	323	203	192	2.278224	2.438041	2.255663	3.441044	2.80847	2.349825
protein_co	oxoglutarat	1607	1331	1226	3363	2500	2849	20.34828	19.86082	20.45678	36.83849	35.56321	35.85205
protein_co	ArfGAP_wit	10	1	0	16	11	23	0.224041	0.026402	0	0.310107	0.276866	0.512113
protein_co	transcriptic	3	4	0	27	13	8	0.023962	0.037651	0	0.186568	0.116655	0.063505
protein_co	H2A_histor	1109	841	848	3005	2358	2805	15.43416	13.79287	15.55186	36.17921	36.86756	38.79664
protein_co	caveolin_2	287	325	325	1467	784	911	4.602867	6.142385	6.868545	20.35353	14.12576	14.52027
protein_co	caveolin_1_	5674	4622	4621	6542	3908	4202	111.0899	106.6406	119.2219	110.8049	85.95854	81.76192
protein_co	met_proto-	313	242	312	1735	1532	1245	2.497443	2.275483	3.280504	11.97605	13.7328	9.872569
protein_co	ring_finger_	39	21	16	30	22	32	0.913584	0.579709	0.493899	0.60795	0.578969	0.744978
protein_co	limb_regio	522	476	536	1144	1000	892	5.627204	6.046948	7.614156	10.66869	12.11075	9.556451
pseudogen	NHP2_ribo	0	1	1	0	2	3	0	0.135038	0.151003	0	0.257472	0.34165
protein_co	wingless-ty	0	0	0	33	21	30	0	0	0	0.519905	0.429651	0.542973
protein_co	homeobox_	17	21	14	64	46	41	0.357567	0.520517	0.388036	1.164533	1.086966	0.857043
protein_co	DnaJ_(Hsp4	1911	1533	1642	3729	3057	3314	12.65894	11.96702	14.33325	21.36938	22.74998	21.81719
protein_co	homeobox_	9	9	10	18	19	16	0.230624	0.271776	0.337673	0.399022	0.546971	0.407466
protein_co	homeobox_	110	76	73	104	86	95	1.78471	1.453101	1.560748	1.459726	1.567554	1.531822
protein_co	LFNG_O-fuc	15	22	28	102	85	62	0.334083	0.577421	0.82178	1.965287	2.126821	1.372348
protein_co	homeobox_	108	102	68	9	9	10	3.45059	3.840403	2.862947	0.248757	0.323044	0.317526
protein_co	homeobox_	23	26	39	0	0	4	1.231186	1.640122	2.751029	0	0	0.212797
protein_co	BRCA1-assc	797	571	464	1471	1001	1186	7.87201	6.646155	6.039209	12.56907	11.10735	11.64184
protein_co	IQ_motif_c	679	673	599	532	636	620	5.252328	6.134854	6.105816	3.560055	5.526985	4.766322

protein_co	vasoactive_	0	0	0	3	10	7	0	0	0	0.034837	0.150801	0.093382
protein_co	tetraspanin	17	19	24	562	464	466	0.321887	0.423951	0.598826	9.205645	9.870109	8.769008
protein_co	single-stran	944	881	716	2797	1729	2353	19.07492	20.97847	19.06508	48.89295	39.24957	47.25224
protein_co	homeobox_	406	382	376	0	0	3	4.911802	5.446095	5.994286	0	0	0.03607
protein_co	cadherin-lil	154	130	143	34	52	38	1.526763	1.518802	1.868193	0.291604	0.579166	0.374407
protein_co	even-skippe	1	0	0	0	0	3	0.019521	0	0	0	0	0.058201
protein_co	3-hydroxyis	563	406	388	477	306	356	14.97778	12.72835	13.60209	10.97793	9.145543	9.412363
protein_co	Tax1_(hum	1038	864	869	1370	856	891	19.01479	18.65156	20.97726	21.7109	17.6164	16.22115
protein_co	carboxypep	71	47	50	1236	756	805	1.698514	1.324999	1.576215	25.57951	20.31803	19.13887
protein_co	chimerin_2	18	12	21	218	222	200	0.269954	0.212083	0.415022	2.828374	3.740412	2.980966
protein_co	growth_fac	1521	1340	1233	1214	1070	1075	14.82387	15.3902	15.83544	10.23562	11.71562	10.41239
protein_co	abhydrolas	140	119	87	752	523	722	4.745031	4.75297	3.885663	22.04915	19.91415	24.31968
protein_co	cordon-ble	2	0	0	386	379	380	0.013756	0	0	2.296788	2.928592	2.59755
protein_co	FK506_bin	1477	1443	1479	745	616	590	15.76489	18.1503	20.8024	6.879069	7.386525	6.258526
protein_co	pleckstrin_	100	73	119	192	293	206	1.73577	1.493215	2.721912	2.883079	5.713588	3.553605
protein_co	syntaxin_1/	164	158	95	144	91	130	4.144307	4.705137	3.16349	3.147992	2.583441	3.264834
protein_co	nucleotide-	256	271	196	278	289	268	2.93989	3.667478	2.966074	2.761843	3.728534	3.058691
protein_co	glycyl-tRNA	4379	3834	3439	5993	3738	4221	88.0139	90.81039	91.08425	104.2038	84.40432	84.31432
protein_co	corticotrop	0	0	3	0	2	0	0	0	0.082723	0	0.047017	0
protein_co	EPH_recept	26	24	22	169	189	304	0.312407	0.339833	0.348341	1.756699	2.551282	3.630202
protein_co	family_with	7	4	0	0	2	2	0.103719	0.069844	0	0	0.033292	0.029451
protein_co	growth_ho	0	2	1	1	1	0	0	0.077356	0.043251	0.028394	0.036873	0
pseudogen	NOP2/Sun_	4	9	12	13	28	41	0.11837	0.313857	0.467948	0.332804	0.93087	1.2058
protein_co	caspase_2_	524	421	393	1644	1287	1179	4.808646	4.552823	4.752465	13.05138	13.26842	10.75264
protein_co	coiled-coil-	2289	1953	1296	3130	2179	2751	134.4972	135.2311	100.3476	159.1016	143.838	160.6451
protein_co	heat_shock	7542	5830	3886	1991	1310	1582	274.4199	249.9797	186.3231	62.67053	53.54876	57.20648
protein_co	neuronal_p	398	360	322	175	145	133	7.803895	8.318364	8.319917	2.968448	3.194077	2.591729
protein_co	PDGFA_ass	3195	2624	2378	4087	3898	5816	66.43616	64.29906	65.15989	73.5193	91.05936	120.1898
protein_co	BUD31_hor	629	623	456	790	837	851	29.23607	34.12428	27.92981	31.7657	43.70618	39.31041
protein_co	pentatricop	8	20	14	56	43	60	0.075874	0.223532	0.174971	0.459466	0.458163	0.56554
protein_co	cytochrom	30	19	16	26	32	16	0.478382	0.357038	0.336209	0.358666	0.573262	0.253562
protein_co	zinc_finger_	2175	1911	2106	1080	1315	1216	12.22623	12.65905	15.60007	5.251945	8.304399	6.793235
protein_co	eukaryotic_	4904	4256	3452	9113	6909	7902	69.32514	70.90045	64.30517	111.446	109.7247	111.0163
protein_co	sorting_nex	797	703	618	1071	966	1471	8.926163	9.278311	9.120734	10.37669	12.15438	16.37302
protein_co	nudix_(nuc	197	222	173	375	353	597	11.96029	15.88311	13.84065	19.69563	24.07683	36.02132
protein_co	protein_tyr	3	1	0	39	29	17	0.019428	0.007632	0	0.21849	0.210985	0.109411
protein_co	TAF6_RNA_	642	445	427	832	763	912	12.46356	10.18062	10.9237	13.97312	16.64104	17.5959
protein_co	Wiskott-Ald	896	737	834	899	1086	887	10.69563	10.36748	13.11896	9.283701	14.56389	10.52281
protein_co	hyaluronog	0	0	0	3	1	0	0	0	0	0.057082	0.02471	0
protein_co	sperm_adh	0	0	0	20	14	9	0	0	0	0.389944	0.354475	0.201586
protein_co	aminoacyl_	281	241	204	1032	645	720	12.14402	12.27383	11.61772	38.58324	31.31589	30.92418
protein_co	transferrin_	18	45	14	22	11	8	0.304356	0.896662	0.311941	0.321806	0.208954	0.134434
protein_co	fascin_hom	3	1	3	5	6	3	0.070966	0.027877	0.093516	0.102321	0.159453	0.070528
protein_co	motile_spe	484	388	284	366	258	230	21.51422	20.32447	16.63541	14.07422	12.88395	10.16056

protein_co	procollager	9863	9335	6046	1183	647	710	306.7903	342.1795	247.8195	31.8332	22.60924	21.94828
protein_co	F-box_prot	13	11	7	2	9	7	0.302387	0.301522	0.214562	0.040245	0.235186	0.161818
protein_co	RNA_bindi	446	323	324	1019	832	951	8.408719	7.176366	8.049609	16.62004	17.62249	17.81907
protein_co	ubiquitin_s	358	245	308	463	479	412	3.676601	2.965081	4.168204	4.113461	5.526472	4.205041
protein_co	IMP_(inosi	1889	1356	1158	2443	1584	2006	34.71209	29.36403	28.04092	38.83607	32.7004	36.63443
protein_co	ArfGAP_wit	448	307	265	308	273	282	4.945281	3.993543	3.854727	2.941214	3.385514	3.093653
protein_co	LSM5_hom	401	411	289	1725	1165	1490	9.43107	11.3911	8.956725	35.0969	30.78163	34.82671
protein_co	serpin_pep	8265	6831	6147	761	350	467	137.1653	133.5958	134.431	10.92569	6.525571	7.702433
protein_co	adaptor-rel	2918	2641	2034	4099	3574	5257	118.2862	126.1608	108.6512	143.744	162.7618	211.7857
protein_co	monoacylg	0	0	0	0	1	0	0	0	0	0	0.027897	0
protein_co	core_1_syn	493	514	541	1311	1045	1023	4.204238	5.165479	6.079564	9.671773	10.01165	8.670131
protein_co	procollager	5159	4165	3317	4226	2747	3394	93.53513	88.98798	79.24822	66.28294	55.95217	61.15482
protein_co	replication	146	120	100	485	322	503	3.826428	3.706202	3.453628	10.99627	9.480815	13.10142
protein_co	zinc_finger_	2807	2230	1548	2474	1558	2085	37.54557	35.15024	27.28488	28.62721	23.41169	27.71609
protein_co	claudin_15	168	127	114	191	148	245	4.173668	3.718086	3.732057	4.104923	4.13066	6.049011
protein_co	glucocortic	136	160	146	120	91	93	1.518021	2.104583	2.147468	1.158733	1.141115	1.031648
protein_co	PHD_finger	568	578	483	1239	926	943	7.032386	8.43314	7.880184	13.27054	12.87996	11.60315
protein_co	nuclear_res	183	150	163	432	406	450	2.746089	2.65254	3.22319	5.608029	6.844451	6.710976
protein_co	transmemb	489	367	448	1040	831	829	4.024898	3.559748	4.859134	7.405296	7.684155	6.781257
protein_co	enhancer_c	241	162	195	1465	1008	1170	3.504197	2.775834	3.736292	18.42774	16.46573	16.90701
protein_co	centrosoma	211	199	222	445	285	329	2.978813	3.310709	4.129986	5.434803	4.52017	4.616006
protein_co	zinc_finger_	386	368	300	168	178	183	2.94032	3.303408	3.011365	1.107081	1.523268	1.385377
protein_co	secreted_fr	1783	1550	1334	1040	732	707	31.92215	32.70239	31.47251	16.10783	14.72316	12.57969
protein_co	mesoderm_	3476	3266	2907	7905	5148	6159	74.65432	82.66058	82.27256	146.8724	124.2118	131.4604
protein_co	mesenchym	734	609	551	0	0	1	15.54348	15.19765	15.37583	0	0	0.021046
protein_co	ankyrin_rep	341	306	293	676	508	478	6.946087	7.345381	7.86481	11.9123	11.62515	9.676613
protein_co	ARP3_actin	0	0	0	3	1	3	0	0	0	0.024117	0.01044	0.027706
protein_co	POU_class_	3	0	0	12	12	10	0.026806	0	0	0.092757	0.120458	0.0888
protein_co	tetraspanin	105	90	89	913	553	673	2.655903	2.682702	2.966523	19.97821	15.71437	16.91794
protein_co	retinoic_ac	0	1	0	6105	4620	7014	0	0.032749	0	146.7729	144.2408	193.7191
protein_co	anterior_gr	2	0	0	0	2	1	0.059551	0	0	0	0.066902	0.029592
protein_co	aryl_hydro	2165	1727	1921	1114	888	878	18.26279	17.16756	21.35361	8.129379	8.415331	7.360602
protein_co	coiled-coil-	914	914	730	2338	1835	2302	30.28039	35.68359	31.86933	67.00741	68.29681	75.79321
protein_co	transmemb	0	0	0	1	2	0	0	0	0	0.032027	0.083183	0
protein_co	GLI_family_	1748	1468	1662	1670	1952	1618	11.27447	11.15804	14.12604	9.318247	14.14437	10.37153
protein_co	proteasom	38	39	25	125	70	74	0.473243	0.572364	0.410276	1.34671	0.979373	0.915888
protein_co	mitochond	665	595	436	1049	710	903	12.87702	13.57743	11.12538	17.57244	15.44546	17.37765
protein_co	cytochrom	727	672	584	1032	811	954	11.9417	13.00793	12.64094	14.66474	14.96586	15.57363
protein_co	biliverdin_	599	484	403	231	163	224	27.36122	26.0532	24.25764	9.128168	8.364603	10.16872
protein_co	upregulato	480	388	299	583	345	536	4.491283	4.278268	3.686678	4.719117	3.62658	4.984293
protein_co	transmemb	1764	1528	1457	2381	1742	1837	22.08274	22.54161	24.03526	25.78557	24.49918	22.85458
pseudogen	stromal_an	64	70	76	239	153	199	1.581066	2.037863	2.474106	5.107764	4.246297	4.885766
protein_co	Ras_homol	609	533	414	3296	2227	2721	15.53786	16.02538	13.91904	72.74853	63.83271	68.99414
protein_co	protein_kir	117	113	124	1425	928	1039	1.874159	2.133075	2.617442	19.74688	16.70005	16.54039

protein_co	AE_binding	11104	9171	7280	891	860	836	144.0472	140.2004	124.4491	9.999222	12.53352	10.77808
protein_co	polymerase	3188	2698	2010	4609	2823	3540	78.2094	77.99912	64.97878	97.81611	77.80376	86.3085
protein_co	myosin_ligl	2	0	0	116	80	146	0.133858	0	0	6.716401	6.015263	9.711316
protein_co	glucokinase	64	68	52	0	1	1	1.241562	1.55455	1.329311	0	0.021794	0.01928
protein_co	B-cell_CLL/	537	459	356	1247	830	946	14.39459	14.49922	12.57505	28.91708	24.99494	25.20146
protein_co	YKT6_v-SNA	4134	3124	3299	4504	3712	4492	81.17881	72.29201	85.36686	76.51271	81.88969	87.66406
protein_co	transducin_	1272	1017	845	1057	756	875	27.71232	26.11042	24.25925	19.92158	18.50362	18.94539
protein_co	CAP-GLY_d	3028	2446	2235	258	270	294	28.81635	27.43131	28.02821	2.124055	2.886661	2.78061
protein_co	eukaryotic_	9942	8039	7534	10646	9835	12103	196.4686	187.2098	196.1913	181.9989	218.3448	237.6961
protein_co	LIM_domai	575	439	383	883	658	974	9.02225	8.117431	7.919187	11.9859	11.59904	15.18853
protein_co	spermatoge	1	3	8	23	23	17	0.012998	0.045952	0.137026	0.258624	0.335857	0.219602
protein_co	solute_carr	147	123	156	20	20	25	2.090899	2.061712	2.923985	0.246098	0.319591	0.353399
protein_co	LIM_homec	3	5	3	4	5	1	0.062186	0.122137	0.081946	0.071729	0.116437	0.020601
protein_co	fukutin	442	393	497	487	317	373	3.17761	3.329492	4.708358	3.028798	2.560275	2.664997
protein_co	fibronectin	87	94	126	158	85	102	0.604207	0.76931	1.153112	0.949262	0.663184	0.704005
protein_co	contactin_a	128	110	145	82	57	72	1.338161	1.355184	1.997566	0.741609	0.669456	0.748067
protein_co	spindlin_1	1266	1195	1265	2013	1762	1648	14.94721	16.62652	19.68121	20.56048	23.37122	19.33719
protein_co	nicotinami	347	278	237	511	335	435	8.961232	8.460385	8.065316	11.41621	9.719235	11.16444
protein_co	transmemb	856	759	876	1618	1477	1376	5.678884	5.933871	7.658225	9.286044	11.00826	9.072297
protein_co	prune_hom	2079	1863	2154	75	100	90	8.744286	9.233999	11.93852	0.272894	0.472519	0.376203
protein_co	multiple_E	307	206	258	238	279	185	2.580642	2.040628	2.85788	1.73073	2.63477	1.545506
protein_co	tripartite_r	32	31	38	80	81	94	0.380357	0.434221	0.595196	0.822612	1.081623	1.1104
protein_co	coronin_ac	14	10	11	728	648	593	0.13153	0.110715	0.136184	5.916877	6.839467	5.536847
protein_co	transformir	593	466	618	1799	1921	1679	4.817988	4.461738	6.616591	12.6446	17.53426	13.55724
protein_co	Sec61_beta	2356	2043	1494	1947	1543	2617	181.556	185.5286	151.7123	129.7969	133.5827	200.4235
protein_co	complemer	23	36	39	212	164	154	0.22293	0.411197	0.498127	1.777621	1.785802	1.483443
protein_co	osteoglycin	133	181	99	2	8	1	2.36996	3.800801	2.32466	0.030831	0.160151	0.017709
protein_co	asporin	63	69	55	7	4	5	1.350317	1.742815	1.553433	0.129794	0.096317	0.106506
protein_co	extracellula	33	32	50	8	13	6	0.537059	0.613713	1.072291	0.112632	0.237684	0.097044
protein_co	transducin-	1662	1313	1454	1496	1347	1051	18.16056	16.90714	20.93618	14.14142	16.53541	11.41329
protein_co	LIM_homec	0	0	0	1	0	2	0	0	0	0.012768	0	0.029336
protein_co	prostaglanc	680	560	475	1457	1159	1266	15.66574	15.20328	14.42017	29.03786	29.99677	28.98581
protein_co	sushi_doma	146	118	106	440	439	369	2.474195	2.356515	2.367128	6.45055	8.357851	6.214656
protein_co	alpha-1-mi	15	5	0	0	3	10	0.553776	0.21753	0	0	0.124427	0.366904
protein_co	AT-hook_tr	286	330	200	810	797	817	2.051643	2.789695	1.890604	5.026709	6.423077	5.824618
protein_co	tumor_nec	0	0	0	10	0	3	0	0	0	0.240288	0	0.082813
protein_co	dynamin_1	2932	2352	1793	295	225	252	47.23767	44.65488	38.06621	4.111588	4.072453	4.034918
protein_co	endoglin	4804	3755	3506	168	113	151	83.14107	76.58252	79.95752	2.515272	2.197051	2.597163
protein_co	adenylate_k	185	141	97	29	38	37	4.322191	3.882026	2.986336	0.586129	0.99739	0.8591
protein_co	cell_divisio	206	232	187	305	206	203	3.114176	4.133053	3.725224	3.988768	3.498583	3.049872
protein_co	relaxin_2	1	0	0	42	37	41	0.04498	0	0	1.634285	1.869676	1.832775
protein_co	relaxin_1	0	0	0	3	8	8	0	0	0	0.128649	0.445512	0.394113
protein_co	plasminoge	113	89	80	513	381	441	6.418812	5.957627	5.988265	25.20905	24.31365	24.8957
protein_co	TBC1_doma	771	598	599	834	727	830	10.44995	9.551424	10.69847	9.778875	11.06989	11.18015

protein_co	KIAA1432	571	568	791	979	915	672	4.462549	5.231212	8.146259	6.619003	8.033727	5.219463
protein_co	lysine_(K)-s	386	292	341	217	203	156	4.389951	3.913473	5.110479	2.134987	2.593687	1.763221
protein_co	dedicator_(	0	1	1	353	477	376	0	0.006725	0.00752	1.742698	3.058102	2.132466
protein_co	KN_motif_a	370	343	397	993	847	871	2.723226	2.974974	3.850413	6.322579	7.00349	6.371033
protein_co	ELAV_(emb	188	137	214	2730	2661	2127	2.615744	2.246286	3.923612	32.85966	41.59406	29.41132
protein_co	neuronal_c	4706	3744	3286	2442	2132	2332	49.91792	46.80017	45.9311	22.40852	25.40626	24.58344
protein_co	testis-speci	377	337	252	352	238	271	8.244013	8.684289	7.261606	6.658907	5.846868	5.88947
protein_co	potassium_	0	4	0	5	5	5	0	0.051667	0	0.047411	0.061569	0.054466
protein_co	carbonic_a	216	206	107	0	11	4	7.067525	7.943061	4.613517	0	0.404348	0.130072
protein_co	far_upstrea	1598	1366	1485	1734	1946	2221	27.08057	27.27965	33.16212	25.42103	37.0487	37.40583
protein_co	tyrosinase-r	2	4	3	5	2	0	0.037139	0.087531	0.073409	0.080321	0.041723	0
protein_co	cAMP_resp	1035	853	846	1538	964	1304	29.90935	29.04844	32.21601	38.44908	31.29628	37.45018
protein_co	RGP1_retrc	731	620	590	444	692	685	5.514373	5.511598	5.864967	2.897508	5.864539	5.135455
protein_co	multiple_P	583	541	623	981	1088	926	3.99697	4.370857	5.628403	5.818276	8.379927	6.309325
protein_co	LIM_homec	0	0	0	1	0	0	0	0	0	0.019059	0	0
protein_co	DEAD_(Asp-	145	95	131	399	362	255	1.661208	1.282587	1.977708	3.954504	4.659226	2.903394
protein_co	endothelial	4127	3406	2638	2674	2775	4678	270.0711	262.6608	227.4852	151.3798	204.012	304.238
protein_co	phosphatid	0	0	2	35	25	15	0	0	0.041837	0.480648	0.445846	0.236645
protein_co	GLIS_family	3635	3157	3530	89	77	53	28.86463	29.54223	36.93781	0.611385	0.686912	0.418261
protein_co	BCL2-assoc	715	587	495	1464	1090	1237	9.793741	9.475187	8.934754	17.34789	16.77329	16.83922
protein_co	Rap_guanir	1281	1014	1026	1826	2152	2054	10.84038	10.11208	11.44136	13.36778	20.45911	17.2745
protein_co	neural_pro	746	516	371	1061	617	826	18.05852	14.71974	11.83456	22.21886	16.77944	19.87161
protein_co	amyloid_be	646	559	617	114	137	115	5.234142	5.337426	6.587687	0.799063	1.247046	0.92602
protein_co	senataxin	1001	927	1050	1108	997	836	4.772938	5.208811	6.597446	4.570403	5.340673	3.961573
protein_co	SH3-domai	2	8	1	440	401	318	0.04128	0.194582	0.027198	7.856342	9.298184	6.522911
protein_co	prostaglanc	229	202	144	0	1	0	12.25833	12.74249	10.15765	0	0.060137	0
protein_co	ATP-bindin	1045	856	650	93	72	66	6.78481	6.549411	5.561213	0.522357	0.525174	0.425868
protein_co	Src_homol	236	192	153	413	326	412	4.489427	4.304148	3.835351	6.796604	6.966996	7.789072
protein_co	ubiquitin-c	2028	1753	1566	2915	2141	2328	26.34708	26.83821	26.80964	32.76167	31.24857	30.05779
protein_co	abhydrolas	264	261	247	612	536	479	5.346757	6.229226	6.592016	10.72262	12.19552	9.641213
protein_co	exosome_c	183	163	128	535	399	536	5.96197	6.257969	5.4952	15.07841	14.60363	17.35454
protein_co	zinc_finger_	3619	3031	2999	4339	3290	3099	33.44858	33.01278	36.52585	34.69299	34.16127	28.4656
protein_co	dishevelled	1575	1260	976	1866	1527	2099	25.74315	24.26939	21.0216	26.38492	28.03943	34.09598
protein_co	PDZ_and_L	826	733	552	8957	5301	6339	30.11657	31.49463	26.52158	282.5212	217.1363	229.6973
protein_co	cyclin_J	217	181	208	925	930	840	2.791785	2.74415	3.526309	10.29502	13.4417	10.74017
protein_co	GATA_bind	2	6	3	1787	1299	1354	0.0344	0.121614	0.067995	26.58955	25.10046	23.14471
protein_co	attractin-li	180	211	171	67	76	68	1.12388	1.552519	1.406949	0.361897	0.533102	0.421955
protein_co	Hermansky	1370	1032	902	1489	1013	1235	19.5866	17.38702	16.99338	18.41603	16.27035	17.54749
protein_co	phytanoyl-(	202	190	165	217	135	149	5.846955	6.480956	6.293571	5.433768	4.389967	4.286218
protein_co	Ras_associa	38	25	20	1001	719	796	0.462473	0.35855	0.320751	10.53901	9.830617	9.627766
protein_co	dynamin_b	1098	823	939	1057	839	796	8.981646	7.933421	10.12171	7.479827	7.710181	6.471073
protein_co	RAB11_fam	172	176	193	344	284	245	1.502368	1.811622	2.221467	2.599377	2.78686	2.126785
protein_co	chemokine	146	154	99	2657	2274	2313	2.188388	2.72019	1.955426	34.45291	38.29225	34.45535
protein_co	ER_lipid_ra	781	747	711	1733	1379	1307	7.138625	8.046208	8.563828	13.7033	14.16044	11.87268

protein_co eukaryotic_	8079	6349	6631	5308	6627	5767	78.16343	72.38664	84.53953	44.42628	72.02977	55.45052
protein_co cubilin_(int	43	53	57	17	10	7	0.190515	0.276722	0.33279	0.065159	0.049775	0.030823
protein_co tRNA_aspar	77	75	82	199	136	147	0.495317	0.568539	0.69509	1.10741	0.982834	0.939765
protein_co retinol_bin	0	0	0	6	2	3	0	0	0	0.064264	0.027818	0.036914
protein_co growth_dif	8	0	0	3	5	8	0.172306	0	0	0.055898	0.120984	0.171242
protein_co DEAD_(Asp	941	733	664	1096	748	894	19.62863	18.01821	18.2517	19.77762	17.52876	18.53308
protein_co mitogen-ac	431	353	374	713	518	525	3.936779	3.799667	4.501633	5.633992	5.315481	4.765765
protein_co SEC23_inte	838	721	841	1451	1027	1101	9.528469	9.660986	12.60114	14.27281	13.11894	12.4416
protein_co arginyltran	154	141	197	394	305	274	1.66386	1.795239	2.804769	3.682606	3.702072	2.942092
protein_co non-SMC_e	152	170	147	978	649	679	3.354327	4.420973	4.274782	18.67083	16.08998	14.8916
protein_co pleckstrin_	441	449	432	614	473	509	2.70878	3.25004	3.496663	3.262621	3.263964	3.107153
protein_co phosphatas	124	108	124	83	67	59	1.441204	1.479226	1.899154	0.834535	0.874838	0.681499
protein_co unc-5_hom	3121	2642	2457	1242	1367	1386	24.15273	24.09419	25.05604	8.314901	11.88475	10.65971
protein_co cadherin-re	2836	2471	2120	11	6	30	14.88752	15.28608	14.66516	0.049954	0.035385	0.156512
protein_co chromoson	64	78	77	306	224	209	0.72259	1.0378	1.145612	2.988796	2.841247	2.345135
protein_co sparc/ostec	35	37	54	42	25	31	0.3403	0.423939	0.691867	0.35327	0.273076	0.299547
protein_co mitochond	720	581	579	708	511	563	15.71856	14.94733	16.65688	13.37139	12.53286	12.21514
protein_co protein_ph	1158	1140	1045	1006	748	757	17.5109	20.31477	20.82337	13.16015	12.70722	11.37642
protein_co coiled-coil_	626	598	648	1219	1084	902	4.324251	4.867936	5.898566	7.28456	8.412304	6.192311
protein_co bone_morp	552	493	556	1219	958	952	8.10636	8.531803	10.75961	15.48651	15.80525	13.8942
protein_co multiple_ir	382	328	308	577	378	395	8.374103	8.473364	8.897346	10.94243	9.309274	8.605611
protein_co actin_alpha	1018	887	797	4406	3721	3907	30.69131	31.51362	31.66363	114.9146	126.0307	117.0633
protein_co lipase_A_ly	6107	5452	5576	870	641	581	116.2152	122.2638	139.8275	14.32245	13.70383	10.98805
protein_co T-cell_leuke	0	0	0	53	26	33	0	0	0	0.620804	0.395492	0.444057
protein_co chromoson	252	189	174	635	586	643	4.201931	3.713789	3.823248	9.159781	10.97729	10.65538
protein_co leucine_zip	3048	2429	1917	2826	2193	2683	28.10732	26.39606	23.29493	22.54445	22.71916	24.58866
protein_co sideroflexir	1986	1747	1415	708	502	530	33.97118	35.2153	31.89501	10.47678	9.646821	9.009837
protein_co Kazal-type_	122	142	132	38	32	44	3.376268	4.630976	4.813776	0.909753	0.994892	1.210151
protein_co F-box_and_	251	260	207	445	364	565	4.174738	5.096076	4.536915	6.402926	6.801519	9.339283
protein_co fibroblast_	3	0	1	0	0	0	0.132684	0	0.058282	0	0	0
protein_co nucleophos	976	819	663	1446	900	1473	58.91723	58.26174	52.74009	75.51336	61.03572	88.37001
protein_co tankyrase_1	1015	1047	1169	1203	1170	893	8.727482	10.60906	13.24562	8.948527	11.30207	7.631045
protein_co paired-like_	4	0	0	0	0	1	0.152239	0	0	0	0	0.037825
protein_co golgi_brefe	2411	1844	1703	2148	2281	2008	19.93452	17.96704	18.55488	15.36406	21.18766	16.49992
protein_co Rho_GTPas	2219	1779	2140	1926	1600	1588	16.39125	15.48595	20.83067	12.30762	13.27773	11.65775
protein_co cytoplasmi	13	15	13	24	10	14	0.089801	0.122105	0.118335	0.14342	0.077604	0.096111
protein_co F-box_and_	148	130	60	196	124	133	3.317217	3.433702	1.772141	3.800417	3.12236	2.962603
protein_co CUE_domai	1396	1164	900	1041	836	1027	62.05342	60.9734	52.71785	40.03078	41.748	45.36913
protein_co suppressor_	1195	1041	1020	905	857	894	12.65037	12.98653	14.22886	8.287944	10.19213	9.405511
protein_co ankyrin_rep	221	171	203	334	263	230	1.775142	1.618617	2.148679	2.320867	2.373261	1.836024
protein_co acyl-CoA_b	283	248	303	499	387	468	3.823967	3.948994	5.39517	5.83299	5.874727	6.28468
protein_co phospholys	168	111	92	134	106	120	5.483408	4.269444	3.95698	3.783633	3.886836	3.892531
protein_co La_ribonuc	1087	912	1024	2136	1876	1777	10.20334	10.08823	12.66624	17.34512	19.78312	16.57716
protein_co GTP_bindir	997	879	811	2702	2091	2318	11.23981	11.67777	12.04813	26.35193	26.48299	25.9709

protein_co chromoson	297	233	309	672	507	509	3.584106	3.313504	4.913803	7.015469	6.873556	6.104525
protein_co BRCA2_and	695	675	529	1979	1456	1664	15.73738	18.01186	15.78476	38.76648	37.03889	37.44644
protein_co mitochond	314	309	226	723	570	533	2.79527	3.241602	2.651169	5.567952	5.700567	4.715535
protein_co neuralized_	34	5	5	201	156	149	0.417245	0.072308	0.080857	2.133885	2.150729	1.817221
protein_co SH3_and_P	4784	4085	4269	247	349	348	22.08491	22.22304	25.96961	0.986426	1.810001	1.59659
protein_co pitrilysin_n	1453	1208	1280	1756	1264	1228	22.25145	21.80051	25.83078	23.26378	21.74647	18.68963
protein_co oligonuclec	343	260	253	273	186	256	12.81493	11.44729	12.45597	8.823642	7.807001	9.505432
protein_co mitogen-ac	97	73	85	242	208	245	1.658681	1.471029	1.915336	3.579889	3.995798	4.16358
protein_co dickkopf_1	165	134	149	498	351	507	4.880036	4.670366	5.807111	12.74182	11.6626	14.90242
protein_co early_B-cell	311	299	346	115	188	168	3.763348	4.263756	5.517279	1.203857	2.555765	2.02038
protein_co glutaredoxi	1302	1102	886	3538	2327	2850	35.88192	35.78932	32.17609	84.35009	72.04605	78.05833
protein_co sortilin-rela	5	2	3	184	172	133	0.036401	0.017158	0.02878	1.158828	1.406746	0.962276
protein_co family_with	774	707	858	1473	1405	1217	4.750328	5.113393	6.939125	7.82075	9.687418	7.423058
protein_co X-prolyl_an	1962	1696	1561	1634	992	1036	23.69303	24.1354	24.84044	17.07012	13.45805	12.43343
protein_co structural_	686	687	671	1572	1399	1429	8.827788	10.41817	11.3785	17.50021	20.22528	18.27552
protein_co soc-2_supp	633	520	644	676	567	493	8.499023	8.227649	11.39426	7.851905	8.552586	6.578424
protein_co transcriptic	506	376	407	1964	1615	1739	4.947939	4.332801	5.244488	16.61416	17.74171	16.89986
protein_co coiled-coil_	2089	1807	1968	2216	2294	1934	19.03179	19.40021	23.62659	17.46522	23.47922	17.51085
protein_co cullin_2	576	491	519	1358	873	949	6.868021	6.899184	8.154762	14.00786	11.69425	11.24566
protein_co cyclin_Y	1515	1184	1208	2352	1834	1963	20.25394	18.6533	21.28132	27.20177	27.54516	26.08116
protein_co ubiquitin-c	1545	1150	978	8363	5391	7289	81.06426	71.10594	67.61991	379.5998	317.7747	380.0831
protein_co ribosomal_	19928	16589	10572	18268	10921	13086	187.7239	184.1548	131.2344	148.8709	115.5759	122.5102
protein_co zinc_finger_	1935	1657	1615	2121	2734	2568	13.57551	13.69951	14.93078	12.87298	21.54879	17.90523
protein_co DnaJ_(Hsp4	133	131	80	4	1	3	5.882333	6.82773	4.662542	0.153046	0.049687	0.131865
protein_co peptidylpro	1076	925	729	2313	1621	1861	26.01119	26.35098	23.22257	48.37117	44.02304	44.70993
protein_co phenazine_	137	147	126	94	110	104	2.803601	3.545031	3.397825	1.664127	2.528933	2.115138
protein_co tetraspanin	2461	1957	1935	3902	3237	3358	22.89365	21.45366	23.72025	31.40174	33.82948	31.04516
protein_co leucine-rich	0	1	0	5	2	2	0	0.027244	0	0.099998	0.051944	0.045951
protein_co TBC1_doma	242	204	188	176	134	128	2.430144	2.414093	2.487765	1.528947	1.511717	1.277428
protein_co cytochrom	0	0	0	0	2	3	0	0	0	0	0.049194	0.065278
protein_co keratin_23_	0	0	2	40	20	34	0	0	0.07022	0.921971	0.59865	0.900291
protein_co crystallin_b	1	5	2	0	1	0	0.067613	0.398389	0.178195	0	0.075959	0
protein_co nuclear_fra	1605	1510	1848	2274	2887	2275	7.831364	8.682532	11.88226	9.598775	15.82553	11.03198
protein_co G_protein-r	1302	1142	965	2267	1689	2110	18.29331	18.90838	17.86666	27.5547	26.65999	29.46275
protein_co transcriptic	252	205	187	495	376	473	3.136875	3.007168	3.067419	5.330463	5.258158	5.851504
protein_co apoptosis_a	983	785	714	1543	1104	1386	24.30686	22.87453	23.26529	33.00687	30.66857	34.06029
protein_co dehydrogen	58	60	49	212	181	212	0.681593	0.830913	0.758802	2.155243	2.389598	2.475955
protein_co zinc_finger_	416	290	296	647	464	536	4.981555	4.092387	4.670873	6.702531	6.242213	6.378903
protein_co myeloid/ly	1088	903	788	502	640	738	7.600924	7.434167	7.25435	3.033921	5.023039	5.123934
protein_co proteasom	1270	1125	826	3821	2211	2905	86.97938	90.79715	74.54653	226.3876	170.1181	197.7281
protein_co CWC25_spl	321	278	226	436	321	430	6.584293	6.719794	6.108679	7.736661	7.397044	8.765611
protein_co ribosomal_	27387	23502	16037	23600	16151	20533	1112.736	1125.277	858.6291	829.512	737.2184	829.1054
protein_co F-box_and_	87	47	93	55	69	41	1.88379	1.199273	2.653573	1.030241	1.678461	0.882281
protein_co RUN_doma	4	6	1	9	9	6	0.057451	0.101554	0.018927	0.111826	0.145221	0.085644

protein_co	upstream_b	2244	1821	1719	2985	2958	3306	23.77418	22.73525	23.99902	27.35836	35.20708	34.8093
protein_co	proteasom	2661	2381	2026	5503	4313	5331	48.77977	51.43531	48.94058	87.26848	88.82259	97.12102
protein_co	cancer_sus	1346	1211	1105	2067	1615	1845	17.31258	18.35557	18.72897	22.9996	23.33664	23.58429
protein_co	Rap_guanir	187	153	120	123	74	121	2.656283	2.561128	2.246202	1.511474	1.180901	1.708157
protein_co	regulator_c	2	9	4	10	24	13	0.044358	0.235228	0.116905	0.191868	0.597998	0.286545
protein_co	ring_finger_	3	1	0	819	897	864	0.028488	0.011191	0	6.728126	9.569488	8.153998
protein_co	wingless-ty	23	19	17	145	96	88	0.362934	0.353314	0.353495	1.979386	1.701844	1.380041
protein_co	aspartoacyl	0	5	0	0	0	0	0	0.057437	0	0	0	0
protein_co	RAD51_hor	140	131	111	861	592	699	3.568483	3.934903	3.728322	18.98549	16.95221	17.7069
protein_co	septin_4	23	29	31	2	7	4	0.343579	0.510509	0.610232	0.025846	0.117475	0.059384
protein_co	myotubula	1153	784	992	904	1018	935	10.45401	8.376773	11.85223	7.090634	10.36932	8.425096
protein_co	tripartite_r	382	327	375	850	749	666	4.605662	4.646046	5.957921	8.86565	10.14517	7.980177
protein_co	DEAH_(Asp	536	524	467	872	643	599	7.619864	8.77851	8.74851	10.72413	10.26934	8.462894
protein_co	tubulin_de	61	53	45	341	226	256	1.306392	1.337601	1.269963	6.317729	5.437523	5.448704
protein_co	karyopheri	6349	5179	5154	9022	9221	9207	54.75197	52.63171	58.56979	67.30701	89.33498	78.90822
protein_co	golgi_SNAP	271	224	226	299	258	280	6.515445	6.346436	7.160083	6.218834	6.968568	6.690252
protein_co	pyridoxami	11	28	20	26	38	40	0.24295	0.728768	0.582088	0.496776	0.942881	0.877998
protein_co	ribosomal_	519	481	489	742	659	629	5.111884	5.582976	6.346836	6.322379	7.292024	6.157067
protein_co	tripartite_r	322	294	213	261	181	234	5.345563	5.751644	4.659636	3.748358	3.375711	3.860673
pseudogen	zinc_finger_	2	2	3	18	6	4	0.63025	0.742711	1.245773	4.907026	2.12414	1.252715
protein_co	CDK5_regu	647	554	443	646	505	691	12.41494	12.52729	11.20157	10.72348	10.88631	13.17735
protein_co	chromobox	2605	2472	2117	3870	3684	4249	56.94108	63.67567	60.97806	73.17992	90.46626	92.30268
protein_co	RecQ_prote	482	434	319	597	504	524	6.878048	7.298187	5.998514	7.369797	8.079747	7.431203
protein_co	phosphatid	143	125	107	262	142	317	5.628671	5.798116	5.549941	8.921422	6.279242	12.40049
protein_co	galactokina	422	316	249	241	174	179	11.97272	10.56512	9.309248	5.915078	5.545986	5.047114
protein_co	integrator_	237	229	276	428	389	290	2.134572	2.430553	3.275717	3.334796	3.936055	2.595794
protein_co	calmodulin	470	459	344	424	349	470	5.208764	5.994551	5.023774	4.065048	4.345216	5.176597
protein_co	mediator_c	760	633	845	928	931	717	3.844735	3.773668	5.63306	4.061289	5.291169	3.604804
protein_co	homeobox_	17	3	14	185	161	176	0.262084	0.054503	0.284416	2.467326	2.788475	2.696585
protein_co	enolase_3_	28	41	20	64	48	97	0.974588	1.681721	0.917334	1.927107	1.876952	3.3554
protein_co	profilin_1	7472	6466	4799	26561	14535	19108	306.4098	312.4702	259.3292	942.2655	669.6224	778.7368
protein_co	ring_finger_	1601	1448	1053	2981	2582	3550	44.26033	47.17359	38.3607	71.29323	80.19155	97.53518
protein_co	solute_carr	948	695	627	1632	1005	1430	23.06437	19.92623	20.10183	34.34918	27.46935	34.57633
protein_co	RAS_dexam	40	23	23	22	9	18	1.212852	0.821831	0.918989	0.577077	0.306577	0.542413
protein_co	cholinergic	1	4	2	2	1	1	0.021565	0.10165	0.056834	0.037311	0.024226	0.021431
protein_co	retinoic_ac	963	746	663	1172	1722	1935	6.653899	6.074295	6.036682	7.005523	13.36694	13.28742
protein_co	nucleopori	438	332	342	1650	1039	1070	7.952042	7.10313	8.182113	25.91502	21.19186	19.30625
protein_co	complemer	2362	1948	1611	7127	4821	5482	106.9689	103.9618	96.14084	279.2205	245.2809	246.7324
protein_co	solute_carr	1	0	8	62	29	47	0.008091	0	0.085298	0.43398	0.26361	0.37794
protein_co	bleomycin_	866	722	623	1904	1417	1651	19.42665	19.08642	18.41632	36.94963	35.71075	36.80754
protein_co	carboxypep	1925	1500	1993	1373	1398	1229	10.84856	9.961847	14.80075	6.693836	8.851111	6.883401
protein_co	golgi_SNAP	1018	853	723	1842	1189	1301	8.924314	8.812176	8.352186	13.96946	11.71003	11.3348
protein_co	coiled-coil_	1431	1299	1303	2071	1725	1888	21.85763	23.3819	26.22665	27.3657	29.60068	28.65993
protein_co	mediator_c	41	44	52	92	65	88	1.312322	1.659649	2.193283	2.54746	2.337324	2.799297

protein_co	developme	759	732	464	1104	776	997	7.521942	8.548824	6.059559	9.464993	8.639706	9.819582
protein_co	FtsJ_homol	1442	1202	1032	2119	2136	2260	21.4501	21.07054	20.2292	27.2683	35.69558	33.41044
protein_co	A_kinase_(F	391	294	346	581	486	435	5.08348	4.504419	5.927823	6.534667	7.09855	5.620607
protein_co	aldehyde_d	2	0	0	1	0	2	0.049385	0	0	0.021361	0	0.04908
protein_co	SWI/SNF_re	1265	1079	958	1983	1662	1922	24.65772	24.78511	24.60723	33.4386	36.39506	37.23277
protein_co	synaptogyr	59	37	63	1963	1158	1320	1.028827	0.760325	1.447657	29.6124	22.68548	22.87567
protein_co	B9_protein	193	204	134	160	127	128	7.55182	9.406576	6.909298	5.415983	5.582736	4.97753
protein_co	UTP6_smal	963	805	685	1993	1206	1570	11.62119	11.44794	10.89306	20.8063	16.35012	18.82928
protein_co	DEAD_(Asp	6292	5005	5909	10188	8333	9318	93.62134	87.76014	115.8604	131.1409	139.2953	137.7903
protein_co	chromoson	120	109	83	281	254	270	3.869013	4.141451	3.526402	7.837693	9.200294	8.651519
protein_co	cytohesin_	635	566	540	436	400	514	7.600617	7.983598	8.517335	4.514656	5.378785	6.114316
protein_co	proteasom	1151	858	917	5505	3805	4625	14.86947	13.06215	15.61077	61.52342	55.22349	59.38018
protein_co	lectin_gala	289	313	232	111	89	82	6.361724	8.119484	6.729764	2.113796	2.20098	1.793909
protein_co	acid-sensin	0	0	1	2	28	10	0	0	0.020262	0.026604	0.483684	0.152815
protein_co	chemokine_	9	5	1	0	0	0	0.588233	0.385109	0.086128	0	0	0
protein_co	chemokine_	181	137	125	248	160	172	9.620803	8.581445	8.755432	11.40374	9.554364	9.08596
protein_co	chemokine_	0	5	0	0	0	1	0	0.247374	0	0	0	0.041724
protein_co	peroxisoma	106	75	87	101	79	84	2.097849	1.749189	2.268937	1.72923	1.756485	1.65218
protein_co	HNF1_hom	1	1	0	1	0	1	0.015209	0.017922	0	0.013157	0	0.015115
protein_co	keratin_32	0	5	0	0	0	0	0	0.178251	0	0	0	0
protein_co	DEXH_(Asp	3	9	6	2	0	0	0.060689	0.214555	0.159946	0.035001	0	0
protein_co	K(lysine)_ac	651	548	447	1113	689	885	11.08543	10.99661	10.03029	16.39568	13.18074	14.97698
protein_co	RAB5C_mer	1152	949	753	1728	1329	2167	34.43706	33.4308	29.6622	44.6869	44.63213	64.37868
protein_co	N-acetylglu	625	539	457	366	235	312	13.00634	13.21815	12.53216	6.588993	5.494041	6.452667
pseudogen	hydroxyste	50	42	19	21	12	18	2.77178	2.743754	1.387961	1.007096	0.747341	0.991678
protein_co	hydroxyste	94	70	57	92	78	103	0.998887	0.876584	0.798175	0.845745	0.931177	1.087765
protein_co	MLX_MAX_	760	552	507	809	591	724	15.55884	13.3171	13.67749	14.32765	13.59252	14.73031
protein_co	contactin_	1572	1284	1077	312	216	265	15.77393	15.18306	14.24091	2.708351	2.43495	2.642669
protein_co	ABI_family_	1	0	0	13	6	18	0.025102	0	0	0.282307	0.169206	0.449053
protein_co	enhancer_c	371	330	225	185	195	267	4.248563	4.453375	3.395358	1.832749	2.508718	3.038709
protein_co	distal-less_l	4	0	0	8	2	13	0.104215	0	0	0.180311	0.058539	0.336606
processed_	protein_ph	3413	2858	2407	1578	1680	2100	43.45541	42.88219	40.38485	17.38111	24.03067	26.57275
protein_co	collagen_ty	397729	331378	284593	1653	1613	1706	3130.098	3073.275	2951.411	11.25399	14.26113	13.34318
protein_co	sarcoglycar	10	4	4	0	0	0	0.3697	0.174267	0.19487	0	0	0
protein_co	mitochond	923	758	506	1311	1024	1362	20.01825	19.37317	14.46138	24.59745	24.95016	29.35696
protein_co	vesicle_ami	10686	8901	7622	8884	7279	8751	206.923	203.1138	194.49	148.8213	158.3486	168.4073
protein_co	leucine_ric	3508	2851	2785	4523	3588	3753	63.82028	61.12282	66.76658	71.18503	73.33319	67.85585
protein_co	Rho_family	31	32	18	188	145	254	0.395082	0.480599	0.302296	2.072748	2.076073	3.217133
protein_co	arachidona	68	64	39	38	40	27	1.526712	1.693306	1.153846	0.738065	1.008921	0.602451
protein_co	histone_de	808	685	529	566	453	524	8.031604	8.023957	6.929173	4.867101	5.058691	5.176448
protein_co	ATP-bindin	31	13	32	8	6	7	0.287119	0.14189	0.390557	0.064099	0.062431	0.064433
protein_co	LUC7-like_3	2175	1991	1670	3677	2076	2755	16.35606	17.64403	16.54896	23.92082	17.53864	20.58973
protein_co	pancreatic_	3	0	0	0	0	0	0.282101	0	0	0	0	0
protein_co	membrane_	126	86	82	44	46	52	1.511229	1.215529	1.29601	0.456536	0.619822	0.61983

protein_co	SMAD_spec	464	387	482	1718	1177	1190	4.169148	4.097768	5.707044	13.35413	11.88105	10.6264
protein_co	dual_specif	973	907	924	1585	1349	1390	12.53323	13.7678	15.68401	17.66211	19.52141	17.79405
protein_co	calcium_ch	0	0	0	1	2	0	0	0	0	0.036291	0.094257	0
protein_co	elongation_	2044	1613	1448	4625	2956	3263	23.79318	22.12652	22.21135	46.5743	38.65673	37.74838
protein_co	hepatic_leu	7	8	7	1	8	1	0.066809	0.089977	0.088037	0.008257	0.085777	0.009485
protein_co	solute_carr	12	16	20	80	70	99	0.166875	0.262202	0.3665	0.962415	1.093594	1.368214
protein_co	protein_kir	7473	6162	6658	4532	4677	4269	92.95772	90.32735	109.1363	48.76895	65.35923	52.77476
protein_co	ephrin-B3	383	339	256	380	294	356	6.29311	6.564072	5.542955	5.401485	5.427039	5.813346
protein_co	family_with	2491	2103	1744	283	221	299	35.95311	35.76919	33.16989	3.533558	3.583473	4.288877
protein_co	tyrosine_3-	10115	8554	7660	18812	14479	15469	242.1973	241.368	241.6946	389.6739	389.4852	368.108
pseudogen	-	7	6	1	12	5	8	0.908301	0.917467	0.170988	1.347027	0.728872	1.031648
protein_co	monocyte_	993	822	963	1013	779	845	19.22136	18.75054	24.56382	16.96318	16.94031	16.25553
protein_co	RAN_guanii	1	0	2	3	2	8	0.046439	0	0.122392	0.120523	0.104344	0.369221
protein_co	DPH1_hom	300	221	162	303	204	267	6.092174	5.288718	4.335118	5.323003	4.654042	5.388551
protein_co	mitogen-ac	46	41	21	136	115	113	0.791705	0.831566	0.476277	2.024919	2.223579	1.932831
protein_co	dehydroger	110	102	97	443	316	355	2.677476	2.925769	3.111282	9.328237	8.641099	8.587581
protein_co	WD_repeat	3010	2884	2276	2149	2003	1962	38.05885	42.97258	37.92243	23.50653	28.45242	24.65459
protein_co	recoverin	1	2	0	6	0	0	0.01878	0.044262	0	0.097479	0	0
protein_co	myosin_hea	0	0	2	0	0	0	0	0	0.023162	0	0	0
protein_co	solute_carr	147	158	125	2756	1634	1920	3.952426	5.006227	4.428852	64.10451	49.35686	51.30471
protein_co	myosin_hea	23	15	27	38	61	43	0.201697	0.155013	0.312011	0.288282	0.600966	0.374756
protein_co	N-acetyltra	923	891	689	695	525	674	24.51808	27.89135	24.11786	15.97102	15.66726	17.79321
protein_co	transmemb	876	626	682	771	676	809	9.773722	8.23071	10.02709	7.441719	8.473281	8.970446
protein_co	SEBOX_hon	12	15	12	20	27	37	0.295622	0.435466	0.389558	0.426235	0.747254	0.905872
protein_co	tumor_nec	869	672	567	1591	1177	1251	12.68424	11.55902	10.90592	20.0899	19.30057	18.14728
protein_co	intraflagell	286	221	221	256	225	300	10.19604	9.284639	10.38228	7.8953	9.011503	10.6291
protein_co	transmemb	1618	1388	1221	3582	2375	2652	33.40816	33.77308	33.22191	63.98271	55.09177	54.41984
protein_co	cerebellar_	959	766	619	645	530	600	14.35815	13.51499	12.21252	8.354156	8.91466	8.927723
protein_co	peripheral_	2912	2600	2202	3260	1865	2435	84.84545	89.27248	84.54527	82.17085	61.0471	70.5092
protein_co	unc-119_h	534	479	357	622	406	480	6.748745	7.133856	5.94545	6.80041	5.764436	6.028824
protein_co	aldolase_C_	605	609	402	64	42	45	16.16009	19.16959	14.14977	1.478875	1.260337	1.194567
protein_co	suppressor_	3572	2934	2921	3199	2932	3181	29.01277	28.08309	31.26397	22.47786	26.75413	25.6774
protein_co	RAB34_mer	2991	2239	1972	5255	3612	4254	91.21343	80.46436	79.24723	138.6367	123.7483	128.9287
protein_co	PHD_finger	716	536	612	1036	936	944	4.936287	4.354711	5.559985	6.178886	7.249571	6.467986
protein_co	transmemb	810	703	705	2166	1637	1722	5.731383	5.861878	6.573525	13.25854	13.01284	12.10925
protein_co	gamma-am	0	0	0	0	2	0	0	0	0	0	0.009935	0
protein_co	gonadotrop	0	0	5	7	11	5	0	0	0.161191	0.148148	0.302327	0.121567
protein_co	SLAIN_mot	713	598	679	963	666	701	5.992527	5.922823	7.520125	7.001801	6.288452	5.855286
protein_co	OCIA_doma	1697	1541	1320	2431	1457	1773	46.88981	50.17719	48.06239	58.10915	45.22777	48.68722
protein_co	UDP_glucu	0	0	0	0	1	1	0	0	0	0	0.030801	0.027247
protein_co	cell_wall_b	0	0	0	1	2	2	0	0	0	0.018527	0.04812	0.042568
protein_co	DCN1_defe	761	794	804	1007	964	752	8.323987	10.23468	11.58878	9.528822	11.84603	8.174745
protein_co	ubiquitin_s	451	354	472	942	849	748	5.024492	4.647571	6.92935	9.078823	10.62606	8.281841
protein_co	sulfotransfe	57	70	32	0	0	0	1.695301	2.45345	1.254171	0	0	0

protein_co odontogen	1	0	0	0	0	1	0.040137	0	0	0	0	0.039889
protein_co cysteine-ric	198	185	128	117	95	109	8.77916	9.66644	7.478811	4.487832	4.732171	4.803125
protein_co neuromedi	1	0	0	17	12	9	0.064879	0	0	0.954144	0.874646	0.580302
protein_co KIAA1211	578	402	543	228	454	337	6.611905	5.419159	8.185277	2.256299	5.8345	3.831231
protein_co late_endos	519	521	423	1239	723	947	6.501745	7.691436	6.982931	13.42755	10.17536	11.79023
protein_co nuclear_fac	363	320	339	889	728	737	4.704426	4.887166	5.789413	9.967008	10.59938	9.492425
protein_co amphiregul	0	0	0	42	45	43	0	0	0	1.551253	2.1584	1.824519
protein_co mannosida	603	539	502	2464	2005	2030	4.297135	4.526449	4.714116	15.19027	16.05185	14.37697
protein_co ubiquitin-c	4025	3677	3323	8806	6382	7050	44.2182	47.60317	48.10612	83.69063	78.7664	76.9722
protein_co mitogen-ac	34	17	20	52	40	26	0.438275	0.25824	0.339729	0.579874	0.579264	0.333081
protein_co E74-like_fa	339	326	355	510	491	403	4.473329	5.069392	6.172972	5.821895	7.278832	5.285011
protein_co NADH_dehy	538	533	382	619	530	630	22.65891	26.45399	21.20093	22.55332	25.07736	26.36981
protein_co uncoupling	0	0	0	15	10	14	0	0	0	0.469893	0.406812	0.503828
protein_co TBC1_dom	762	621	640	1219	1326	1126	7.602909	7.301692	8.414719	10.52184	14.86337	11.16536
protein_co zinc_finger_	470	377	351	758	541	693	13.10283	12.38556	12.89464	18.28097	16.9439	19.20039
protein_co inositol_pc	634	441	678	344	336	319	3.800769	3.115501	5.356076	1.784036	2.262927	1.900564
protein_co GRB2-assoc	331	359	372	575	400	397	2.195648	2.806314	3.251715	3.299633	2.980875	2.617188
protein_co kelch-like_f	164	156	121	400	384	457	2.770365	3.105452	2.693477	5.845425	7.287413	7.672183
protein_co carboxypep	4729	4187	3524	1628	1230	1172	103.411	107.8965	101.5472	30.79745	30.21701	25.47033
protein_co ribosomal_	14589	12816	8183	9683	7650	10987	294.0069	304.3628	217.3098	168.8126	173.1979	220.0497
protein_co Wolfram_sy	578	540	433	777	621	642	8.372064	9.217339	8.264706	9.736183	10.10521	9.241647
protein_co annexin_A1	8	5	4	3	0	0	0.298891	0.22014	0.196932	0.096963	0	0
protein_co GrpE-like_1	733	707	582	1321	1009	1341	13.98405	15.89482	14.63143	21.80193	21.62566	25.42538
protein_co GAR1_ribo	652	624	581	1020	899	1259	28.20059	31.80551	33.11476	38.16575	43.6837	54.11854
protein_co FSHD_regio	384	324	238	702	437	585	18.92862	18.82088	15.45965	29.9356	24.20016	28.65849
protein_co chloride_ch	1427	1106	1320	1381	1238	1162	11.28912	10.31094	13.76084	9.451328	11.00287	9.135912
protein_co aminoadipa	280	327	247	557	461	449	6.55616	9.022905	7.621199	11.28261	12.12667	10.44835
protein_co UDP-N-acet	319	238	307	731	652	580	3.9211	3.447476	4.972679	7.77316	9.003552	7.085245
protein_co DEAH_(Asp-	2354	1877	2099	4424	3542	3683	41.1569	38.67297	48.35969	66.91359	69.5719	63.99523
protein_co superoxide_	216	146	122	16	22	7	7.493614	5.968944	5.577405	0.480198	0.857451	0.241349
protein_co Sep_(O-pho	102	67	80	132	120	133	0.982529	0.760549	1.015477	1.099974	1.298601	1.273229
protein_co carboxypep	48	50	31	2	7	4	0.683477	0.838996	0.581673	0.024636	0.111977	0.056605
protein_co tripartite_r	507	482	558	347	403	333	3.985313	4.464868	5.779942	2.359647	3.558841	2.601407
protein_co solute_carr	5	5	5	5	12	4	0.121703	0.14342	0.160375	0.105285	0.328143	0.096761
protein_co F-box_and_	634	512	578	557	488	520	6.74394	6.418026	8.101904	5.125576	5.831675	5.497148
protein_co nei_endonu	50	50	55	353	224	307	1.099273	1.295426	1.59343	6.713876	5.532643	6.707854
protein_co TBC1_dom	363	364	350	124	111	132	8.492082	10.03497	10.78973	2.509529	2.91729	3.068959
protein_co Wolf-Hirsch	690	691	664	4069	4054	3986	4.263455	5.031503	5.406492	21.7502	28.14138	24.47708
protein_co SH3_domai	1440	1178	1278	947	818	781	14.42752	13.90854	16.8731	8.208093	9.207286	7.776604
protein_co stromal_int	379	267	336	583	558	520	3.874978	3.21698	4.526934	5.156578	6.40934	5.283759
protein_co NK3_home	19	8	12	0	1	15	0.359114	0.178187	0.298879	0	0.021234	0.28176
protein_co major_facil	1983	1565	1263	2713	1429	1941	48.31201	44.9318	40.5481	57.18013	39.11233	46.99672
protein_co glycine_rec	26	27	18	41	20	16	0.440328	0.538858	0.401708	0.600689	0.380524	0.269298
protein_co bone_marr	47	42	35	199	125	163	1.248483	1.314744	1.225145	4.572997	3.730301	4.303106

protein_co	Rap_guanir	288	212	285	328	317	276	2.19413	1.903324	2.861208	2.161756	2.713177	2.089722
protein_co	HGF_activa	14	17	2	20	24	39	0.345053	0.493758	0.064957	0.426433	0.664535	0.955283
protein_co	sorting_nex	256	199	177	328	219	201	4.078512	3.736129	3.71595	4.520626	3.919719	3.182493
protein_co	LRP2_bindi	35	69	35	50	20	57	0.358818	0.833608	0.472834	0.443444	0.230348	0.580752
protein_co	UFM1-spec	461	356	329	372	274	267	10.39429	9.459128	9.775179	7.256045	6.940546	5.982944
protein_co	Kruppel-lik	1186	1037	1098	893	799	665	12.2585	12.63102	14.95511	7.984854	9.277872	6.830992
protein_co	kelch-like_f	373	383	345	535	441	425	5.765545	6.976496	7.02725	7.15399	7.658067	6.528751
protein_co	family_witl	32	34	40	138	116	115	0.565269	0.707769	0.931108	2.108859	2.302038	2.018891
protein_co	non-SMC_c	330	222	288	2242	1928	1593	3.748236	2.971482	4.310625	22.02985	24.60192	17.98202
protein_co	UDP-glucos	1502	1303	1075	1765	1309	1370	24.72555	25.27712	23.31951	25.13528	24.20833	22.41332
protein_co	peroxisome	21	24	15	34	49	21	0.175967	0.23699	0.16563	0.246465	0.461273	0.174881
protein_co	DEAD_(Asp-	0	1	3	18	6	2	0	0.027411	0.091955	0.362206	0.156791	0.046234
protein_co	crystallin_a	6	9	10	14	8	4	0.283866	0.501778	0.623443	0.572998	0.425208	0.188075
protein_co	developing	0	0	1	1	1	1	0	0	0.050553	0.033188	0.043098	0.038126
protein_co	HIV-1_Tat_i	56	44	58	706	610	593	1.69605	1.570401	2.3148	18.49773	20.75533	17.84905
protein_co	cathepsin_(	3712	3540	2980	2682	1728	2003	32.0844	36.05756	33.94197	20.05431	16.77949	17.20587
protein_co	coiled-coil_	365	335	272	918	587	764	9.162382	9.909857	8.997446	19.93523	16.55399	19.05981
protein_co	zinc_finger_	325	349	269	0	11	5	3.886565	4.918301	4.239061	0	0.147783	0.059424
protein_co	elongator_a	126	99	98	347	165	187	3.401614	3.14961	3.486385	8.104141	5.004348	5.01725
protein_co	zinc_finger_	896	723	603	1377	909	1197	17.93389	17.05343	15.90445	23.84314	20.43993	23.81059
protein_co	mitochond	1728	1377	1346	3083	1976	2493	35.36221	33.20754	36.2974	54.57983	45.42884	50.70229
protein_co	formin_bin	968	862	858	1367	1089	1255	12.91179	13.54956	15.0811	15.77402	16.31879	16.63659
protein_co	tectorin_al	6	4	10	18	15	9	0.042775	0.033605	0.093945	0.111013	0.120137	0.063766
protein_co	sterol-C5-d	834	665	850	2702	2135	2129	17.97752	16.89244	24.14446	50.38625	51.7024	45.60884
protein_co	cytotoxic_a	29	34	27	8	1	0	0.621826	0.859126	0.762903	0.148397	0.024089	0
protein_co	chromoson	86	100	93	60	55	53	1.564579	2.143908	2.229548	0.944307	1.124115	0.958263
protein_co	beta-13-glu	0	0	0	42	43	37	0	0	0	0.312265	0.415173	0.316026
protein_co	heat_shock	21367	17231	16682	56067	35774	40311	459.2733	436.4608	472.5096	1042.553	863.8617	861.1145
protein_co	purinergic_	0	0	0	0	2	0	0	0	0	0	0.064966	0
protein_co	von_Willeb	62	91	59	661	474	594	0.748027	1.29382	0.93802	6.89906	6.4247	7.122321
protein_co	DnaJ_(Hsp4	507	451	304	372	220	251	20.03066	20.99766	15.82689	12.71432	9.764703	9.855318
protein_co	sialic_acid_	381	332	307	187	193	192	3.612846	3.709963	3.836168	1.534013	2.056037	1.809403
protein_co	sorting_nex	412	306	255	462	323	421	4.627984	4.050636	3.774589	4.489517	4.076113	4.699876
protein_co	leupaxin	86	95	72	87	52	58	2.169093	2.823647	2.393023	1.898287	1.473439	1.453842
protein_co	deltex_hon	107	93	90	536	534	513	1.004021	1.028369	1.112849	4.350977	5.629234	4.783943
protein_co	autophagy_	546	482	398	551	610	602	4.533529	4.716262	4.354734	3.957841	5.690136	4.967638
protein_co	EH-domain_	3369	2762	2366	4139	3428	4042	39.19099	37.86309	36.26894	41.65275	44.7997	46.72951
protein_co	oxysterol_b	1436	1168	1230	1140	1129	955	14.95638	14.3358	16.88153	10.27164	13.21037	9.885189
protein_co	unc-93_hor	329	232	197	241	171	242	7.523796	6.252248	5.936659	4.767834	4.393253	5.500043
protein_co	pseudourid	223	184	175	251	240	202	6.405774	6.228618	6.624294	6.237398	7.7451	5.766705
protein_co	decapping_	200	138	78	521	280	431	4.291933	3.489869	2.20573	9.672164	6.750408	9.191997
protein_co	suppressor_	564	504	632	732	523	569	5.115422	5.386914	7.553605	5.743498	5.329091	5.128901
protein_co	FAD-depen	307	270	194	921	699	914	5.337565	5.531917	4.444689	13.85248	13.65309	15.79285
protein_co	protein_ph	1021	832	998	2203	1705	1713	10.55924	10.13999	13.60105	19.7099	19.80981	17.60654

protein_co	neurexin_2	4	1	2	15	13	11	0.031984	0.009423	0.021073	0.103758	0.116778	0.087412
protein_co	membrane-	0	0	0	33	17	21	0	0	0	0.625565	0.418498	0.457324
protein_co	membrane-	0	0	0	37	24	17	0	0	0	1.011074	0.851684	0.533675
protein_co	ST3_beta-g	556	470	361	578	418	440	14.96451	14.90708	12.80353	13.45794	12.63901	11.76928
protein_co	carnitine_p	2809	2219	2274	213	214	208	28.4234	26.45993	30.32143	1.86452	2.432692	2.09169
protein_co	cyclin_D1	3945	3053	3131	14485	14586	15690	48.49134	44.2233	50.71484	154.0277	201.42	191.6681
protein_co	coiled-coil_	889	678	576	1470	985	1310	24.86241	22.34489	21.2275	35.56492	30.94759	36.41015
protein_co	PRP19/PSC	1978	1644	1378	5627	3887	4855	48.54765	47.55004	44.56829	119.4763	107.178	118.4243
protein_co	transmemb	1513	1352	1311	3170	2169	2490	33.19508	34.95574	37.90289	60.16682	53.46178	54.29299
protein_co	cholecystol	0	0	0	29	23	29	0	0	0	0.62122	0.639825	0.713661
protein_co	hemopexin	23	27	29	11	11	26	0.737072	1.019654	1.224658	0.304956	0.396026	0.828066
protein_co	tripartite_r	466	303	360	330	236	300	5.582825	4.277774	5.683363	3.420149	3.176356	3.571897
protein_co	cysteine_ar	587	534	491	1830	1446	1431	5.796748	6.214335	6.389437	15.63365	16.04219	14.04415
protein_co	folate_rece	0	0	0	26	13	21	0	0	0	0.894644	0.580907	0.830124
protein_co	anaphase_p	42	72	43	100	106	86	1.501365	3.033029	2.025538	3.092431	4.256885	3.055239
protein_co	folate_rece	3	0	1	0	0	0	0.160427	0	0.070468	0	0	0
protein_co	pannexin_1	378	305	392	433	460	303	7.227048	6.871888	9.876203	7.161765	9.880434	5.757334
protein_co	Rho_guanir	1212	1079	945	1275	1255	1331	8.170697	8.572057	8.395047	7.435834	9.504938	8.917522
protein_co	apolipopro	1	1	0	0	0	0	0.087651	0.103291	0	0	0	0
protein_co	centrosom	1642	1414	1161	799	920	1063	15.27752	15.50373	14.23465	6.431164	9.616493	9.829303
protein_co	ring_finger_	626	524	559	1100	856	968	5.696298	5.61897	6.702935	8.659126	8.750668	8.753936
protein_co	KIAA1377	112	93	96	44	12	37	0.842363	0.824273	0.951453	0.286284	0.101394	0.276562
protein_co	eukaryotic_	14071	11680	13003	26603	22516	20580	110.0506	107.6509	134.0127	179.9953	197.8372	159.9641
protein_co	interleukin	0	1	1	0	0	0	0	0.012102	0.013533	0	0	0
protein_co	UDP-N-acet	20	18	14	171	89	124	0.422851	0.448474	0.39005	3.127641	2.11396	2.605488
protein_co	baculoviral	970	927	823	2686	2133	2069	12.60809	14.19922	14.09653	30.20276	31.1471	26.72685
protein_co	ubiquitinat	492	363	565	251	375	264	4.267896	3.710756	6.458505	1.883586	3.654509	2.275948
processed_	matrix_met	0	0	0	0	1	0	0	0	0	0	0.031754	0
protein_co	DEAD_(Asp-	1520	1253	1728	1124	1867	1417	17.73255	17.22605	26.56478	11.34376	24.46927	16.42885
protein_co	uroplakin_3	3	6	6	60	44	50	0.165786	0.390737	0.436931	2.868407	2.731671	2.746036
protein_co	Cbl_proto-(	606	543	589	1242	1403	1155	2.798277	2.954779	3.584001	4.961382	7.278213	5.300412
protein_co	poliovirus_	375	271	311	5042	6032	7173	3.399465	2.895047	3.715134	39.54077	61.43129	64.62339
protein_co	homeodom	906	801	1049	967	889	783	6.474695	6.745757	9.878737	5.97834	7.137431	5.561123
protein_co	KIAA1549-l	446	353	481	261	232	214	2.021894	1.885842	2.873449	1.023593	1.181573	0.964155
protein_co	F-box_prot	405	365	374	496	390	389	2.893536	3.07308	3.521116	3.065622	3.130311	2.76206
protein_co	pyruvate_d	378	341	296	651	512	540	7.995084	8.499487	8.250073	11.91174	12.16607	11.35101
protein_co	solute_carr	14	12	23	13	16	18	0.06337	0.064009	0.137188	0.050905	0.081362	0.080972
protein_co	COMM_dor	822	662	582	1078	710	847	24.93839	23.66801	23.26775	28.29296	24.19937	25.53817
protein_co	solute_carr	0	0	4	2	4	5	0	0	0.060942	0.020004	0.051955	0.057451
protein_co	CD5_molec	3	2	2	0	7	7	0.049309	0.038738	0.043318	0	0.129255	0.114343
protein_co	1-aminocyc	99	62	67	47	68	74	1.553857	1.146765	1.385752	0.63817	1.19904	1.154296
protein_co	midkine_(n	4513	3805	2655	18132	12612	18783	178.4337	177.2855	138.3282	620.1835	560.2018	738.0506
protein_co	autophagy/	715	619	535	759	707	747	7.073969	7.21697	6.975024	6.496238	7.858246	7.344925
protein_co	MAP-kinase	787	720	565	935	983	999	6.938312	7.480294	6.563906	7.131054	9.736024	8.752945

protein_co	protein_tyr	3	8	3	33	12	29	0.069904	0.219675	0.092117	0.665213	0.314133	0.67157
protein_co	N(alpha)-ac	466	428	297	1082	798	1019	5.241237	5.672817	4.40189	10.52781	10.08323	11.39021
protein_co	cysteinyl-tF	1333	1078	903	1452	961	1108	12.31164	11.73307	10.99027	11.60154	9.971451	10.17034
protein_co	solute_carr	170	182	123	117	73	92	3.415548	4.309133	3.256502	2.033576	1.64772	1.836999
protein_co	CD81_mole	12075	10870	8025	9806	5823	7562	122.1132	129.5424	106.9437	85.78874	66.15631	76.00142
protein_co	solute_carr	90	72	79	1785	1393	1490	1.430408	1.348519	1.654548	24.54249	24.8724	23.53495
protein_co	chromoson	2	1	1	0	0	0	0.035819	0.021105	0.023601	0	0	0
protein_co	ELMO/CED-	0	0	0	97	79	93	0	0	0	1.557677	1.647475	1.715676
protein_co	calcitonin-r	0	0	0	20	7	5	0	0	0	0.498627	0.226637	0.143206
protein_co	SRY_(sex_d	53	51	53	53	40	53	0.314383	0.356501	0.414281	0.271971	0.266559	0.312442
protein_co	chromoson	2234	1936	1850	4166	3009	3634	27.77599	28.36605	30.31049	44.80936	42.02983	44.90358
protein_co	phosphatid	1917	1489	1265	1357	1150	1449	24.0208	21.98706	20.8877	14.70985	16.18871	18.04444
protein_co	ribosomal_	13743	13218	8164	12815	10460	14569	936.3811	1061.314	733.0083	755.3578	800.6668	986.5304
protein_co	aryl_hydro	1121	927	710	778	485	613	48.60512	47.36562	40.56669	29.18227	23.62475	26.41475
protein_co	nucleopori	1513	1072	1206	3207	2577	2493	11.48713	9.59123	12.06576	21.06369	21.98042	18.81067
protein_co	NADH_dehy	1024	925	731	2126	1213	1664	17.647	18.78537	16.60057	31.69547	23.48447	28.49928
protein_co	T-cell_imm	1039	847	646	832	488	728	20.54751	19.73941	16.83492	14.2341	10.84208	14.30819
protein_co	choline_kir	213	199	185	776	659	608	4.457088	4.907177	5.101268	14.04741	15.49195	12.64401
protein_co	exophilin_5	2	12	3	422	310	302	0.010394	0.073491	0.020545	1.897236	1.809908	1.559776
protein_co	Hermansky	338	325	302	519	441	429	3.793525	4.298497	4.466507	5.039142	5.5605	4.785123
protein_co	general_tra	858	783	717	1235	845	874	15.23252	16.38149	16.77407	18.96769	16.8535	15.42075
protein_co	protein_tyr	4	1	1	4	2	3	0.054705	0.016117	0.018022	0.047325	0.030729	0.040776
protein_co	von_Willeb	4	1	0	35	70	57	0.023961	0.007059	0	0.181372	0.47107	0.33933
protein_co	proteasom	84	59	56	94	54	54	1.457569	1.206449	1.28048	1.411045	1.052671	0.931222
protein_co	leprecan-lik	3294	2725	2171	519	380	432	54.05692	52.69887	46.94857	7.368144	7.005843	7.045651
protein_co	PTPRF_inte	5465	4488	4730	4181	3422	3268	48.21239	46.65825	54.98756	31.90889	33.91545	28.65234
protein_co	PRP40_pre	140	134	150	103	110	169	2.057673	2.320921	2.905189	1.30963	1.816311	2.468566
protein_co	PR_domain	897	692	717	980	802	788	11.27983	10.25471	11.8813	10.66103	11.33009	9.84795
protein_co	C-type_lect	19	29	10	0	4	0	0.591693	1.064261	0.410372	0	0.139943	0
protein_co	coenzyme_	353	276	260	553	392	542	12.1747	11.2176	11.81658	16.49954	15.18864	18.57773
protein_co	selectin_P_	253	217	194	104	53	50	5.298288	5.355276	5.35367	1.884132	1.246924	1.040626
protein_co	coronin_ac	5311	4318	4433	6290	4827	4939	72.24296	69.2164	79.46059	74.01724	73.7642	66.76793
protein_co	acid-sensin	395	265	217	35	20	40	5.135484	4.060105	3.717739	0.393655	0.292121	0.516837
protein_co	D-amino-ac	0	0	0	1	1	1	0	0	0	0.019203	0.024937	0.02206
protein_co	caprin_fam	965	813	910	1314	1048	1216	7.808048	7.751983	9.702673	9.197579	9.526328	9.778188
protein_co	tetraspanin	1482	1302	1094	583	522	579	14.25223	14.75546	13.86395	4.850275	5.639678	5.533794
protein_co	potassium_	5694	4669	4586	2892	2341	2546	56.29244	54.39558	59.74499	24.73397	26.00058	25.01501
protein_co	solute_carr	410	385	353	689	585	576	5.222764	5.779422	5.925515	7.592744	8.371851	7.292034
protein_co	malectin	4888	4235	4420	4284	4176	4408	39.05457	39.87504	46.53693	29.611	37.48437	35.00192
protein_co	mevalonate	761	643	573	997	637	818	9.804842	9.762791	9.728489	11.11256	9.220287	10.47415
protein_co	cysteine-se	785	713	707	1060	1004	1086	9.299324	9.953558	11.03662	10.86302	13.36179	12.7856
protein_co	calcium/ca	846	701	606	725	676	758	8.000729	7.812397	7.552081	5.931441	7.182158	7.124232
protein_co	bridging_in	0	0	0	0	0	1	0	0	0	0	0	0.018919
protein_co	interleukin	11	20	11	20	8	18	0.559415	1.198612	0.737172	0.879902	0.457068	0.909753

protein_co ATP_syntha	9731	8215	7248	18833	12217	14504	287.9647	286.4814	282.6407	482.1301	406.1583	426.5591
protein_co prostaglanc	2965	2530	2284	10791	7098	8398	53.60999	53.90743	54.41917	168.7896	144.1803	150.906
protein_co synaptotag	0	0	0	34	62	48	0	0	0	0.349061	0.82661	0.566123
protein_co B-cell_CLL/	117	89	114	485	425	419	0.991849	0.889113	1.273501	3.556841	4.0476	3.53007
protein_co arginine/se	1029	801	669	1589	1318	1487	17.26118	15.83415	14.78822	23.05908	24.83817	24.78995
protein_co cytochrom	13	21	17	34	33	23	0.270958	0.515804	0.46692	0.613056	0.772719	0.476426
protein_co myogenic_t	0	0	1	4	5	1	0	0	0.04762	0.125048	0.202989	0.035914
protein_co lin-7_homc	462	449	459	46	46	24	4.001757	4.58313	5.239095	0.344691	0.447626	0.2066
protein_co keratin_18	185	152	138	35629	21145	26474	4.690653	4.541635	4.610792	781.4987	602.3076	667.0998
protein_co acyl-CoA_sy	23	28	15	346	385	319	0.253517	0.363701	0.217874	3.299276	4.767485	3.494458
protein_co tensin_like_	791	692	532	93	111	170	8.358548	8.617227	7.407997	0.850159	1.31773	1.785307
protein_co GLI_family_	118	120	104	4	4	6	1.729044	2.072108	2.008132	0.050705	0.065847	0.087375
protein_co protein_ph	154	140	157	1082	1107	835	1.283317	1.374828	1.724041	7.80016	10.36358	6.915273
protein_co methionyl_	2513	2123	1814	3675	2236	2601	36.94549	36.78121	35.14318	46.74007	36.93089	38.00309
protein_co leukotriene	1272	1168	977	1628	1219	1451	11.02324	11.92812	11.1571	12.20504	11.86792	12.49681
protein_co ELK3_ETS-d	875	764	814	840	746	704	11.01626	11.33513	13.50471	9.14889	10.55149	8.808631
protein_co solute_carr	1	1	1	1	0	0	0.014825	0.017471	0.019536	0.012825	0	0
protein_co wingless-ty	574	486	446	3184	2533	3200	13.19502	13.16563	13.51039	63.31903	65.41576	73.1068
protein_co mago-nashi	224	239	173	443	402	457	4.439829	5.582429	4.51855	7.596	8.951448	9.002104
protein_co transient_r	46	34	53	47	49	49	0.750011	0.653275	1.138729	0.662935	0.897542	0.793991
protein_co integrin_al	281	242	232	393	296	349	6.300898	6.394676	6.855181	7.623452	7.456532	7.777342
protein_co forkhead_b	499	385	404	2260	2053	1833	7.602174	6.912022	8.110609	29.78576	35.13786	27.75297
protein_co proline_ric	73	39	48	87	71	75	2.485333	1.564708	2.153465	2.562382	2.715621	2.537655
protein_co protein_arg	2	5	1	2	1	0	0.017949	0.05288	0.011826	0.015528	0.010082	0
protein_co poly_(ADP-	229	195	190	156	158	128	2.740391	2.749911	2.996163	1.61497	2.12414	1.522287
protein_co actin_relat	1455	1361	1009	3737	1862	2399	70.15405	77.33124	64.10852	155.8748	100.8599	114.9555
protein_co GPN-loop_(	250	179	167	643	420	498	8.251402	6.962222	7.263384	18.35954	15.57349	16.33528
protein_co vacuolar_p	760	784	620	2056	1248	1778	26.41836	32.11555	28.40002	61.82702	48.73667	61.42336
protein_co RAD51_ass	74	62	82	638	442	524	1.752856	1.730666	2.559548	13.07369	11.76213	12.33546
protein_co cut-like_ho	2	2	1	12	1	15	0.015471	0.018231	0.010193	0.080302	0.00869	0.115314
protein_co SH2B_adap	837	659	772	406	291	307	8.196747	7.605163	9.962496	3.439577	3.201534	2.987886
protein_co A_kinase_(F	15	25	19	46	29	32	0.239335	0.47007	0.399488	0.634946	0.519832	0.507429
protein_co MANSC_do	29	25	9	373	220	241	0.585318	0.594622	0.239371	6.512768	4.988449	4.834154
protein_co potassium_	56	61	69	0	2	0	0.371702	0.477138	0.603519	0	0.014914	0
protein_co dual_specif	224	130	179	330	440	317	3.32365	2.273096	3.499896	4.235885	7.334474	4.674511
protein_co cAMP_resp	402	321	322	408	307	276	5.669227	5.334699	5.983958	4.977611	4.863907	3.868268
protein_co acyl-CoA_d	664	526	444	430	486	493	8.634935	8.060905	7.60867	4.837516	7.100294	6.371586
protein_co aldehyde_d	674	635	477	810	568	762	17.68198	19.63142	16.49013	18.38311	16.7405	19.86715
protein_co cyclin-depe	889	707	663	849	788	903	17.71341	16.60072	17.408	14.63428	17.63908	17.88125
protein_co G_protein-(	0	1	0	0	0	0	0	0.060104	0	0	0	0
protein_co N(alpha)-ac	494	479	459	994	859	747	4.35663	4.978131	5.334224	7.58356	8.510713	6.547176
protein_co germ_cell_(	16	13	8	3	1	3	0.354417	0.339347	0.233517	0.057488	0.024885	0.066043
protein_co sodium_ch	42	17	32	383	339	388	0.627228	0.29918	0.629739	4.94809	5.687542	5.758604
protein_co lymphotox	869	654	563	125	98	124	19.80444	17.56417	16.90776	2.464427	2.5091	2.808499

protein_co 2-oxoglutar	17	10	13	11	6	15	0.389947	0.270311	0.392947	0.218279	0.154617	0.341946
protein_co cyclin-depe	1362	1082	987	1697	1335	1158	39.7934	37.2536	38.0002	42.89224	43.81918	33.62421
protein_co 2'-5'-oligoa	3	2	8	17	14	9	0.023638	0.018571	0.083064	0.115878	0.123927	0.070476
protein_co 2'-5'-oligoa	1	0	2	0	2	0	0.011183	0	0.029473	0	0.025127	0
protein_co ADP-ribosy	2	0	0	6	2	7	0.020644	0	0	0.053576	0.023192	0.071807
protein_co matrix_Gla	234	237	157	1	0	3	8.817219	10.52377	7.795612	0.032597	0	0.112343
protein_co RAS_protei	0	0	0	6	15	15	0	0	0	0.071992	0.233728	0.206762
protein_co Rho_GDP_(	169	114	121	2912	1807	1962	7.12343	5.662581	6.720826	106.1834	85.56766	82.18851
protein_co general_tra	511	479	432	1227	932	1082	8.126419	8.976787	9.05309	16.88052	16.65111	17.10075
protein_co eukaryotic_	729	782	578	1875	1149	1455	15.58094	19.69609	16.27904	34.66813	27.58895	30.90571
protein_co DEAD_(Asp	426	344	241	912	660	744	8.150655	7.75619	6.076238	15.09527	14.18652	14.14704
protein_co solute_carr	1833	1478	1827	7166	7116	6556	12.03085	11.43182	15.80182	40.68869	52.47094	42.76441
protein_co RERG/RAS-l	0	0	0	1	0	2	0	0	0	0.039929	0	0.091742
protein_co endonuclea	0	1	3	17	4	8	0	0.025855	0.086734	0.322661	0.098592	0.174435
protein_co chromosom	333	306	357	1038	885	790	6.293949	6.815653	8.891643	16.97225	18.79193	14.83938
protein_co vitamin_D_	211	144	168	87	86	59	2.340362	1.882219	2.455527	0.834801	1.071638	0.650373
protein_co frizzled_fam	0	0	0	65	44	63	0	0	0	0.907047	0.797361	1.009959
protein_co replication_	251	250	181	1000	757	876	5.441519	6.38695	5.170825	18.75467	18.43705	18.87384
protein_co syntaxin_2	968	858	744	959	744	664	15.38483	16.06985	15.58207	13.18557	13.28432	10.48806
protein_co G_protein-(	0	0	0	6	1	2	0	0	0	0.038785	0.008395	0.014852
protein_co coatomer_[	3816	3178	2665	3953	2541	2860	106.496	104.5167	98.00693	95.43652	79.667	79.32324
protein_co TBC1_doma	39	40	24	82	43	73	0.277775	0.335734	0.225255	0.505248	0.344069	0.516726
protein_co cullin-assoc	1985	1778	1959	3208	2927	2680	9.340314	9.859158	12.14703	13.05865	15.47294	12.53272
protein_co RAB5B_mer	284	201	275	188	207	225	4.472113	3.729903	5.706396	2.561033	3.661962	3.521166
protein_co Mdm1_nuc	86	60	79	169	126	130	1.56029	1.282818	1.888725	2.652507	2.568186	2.344012
protein_co nucleopori	369	336	292	2245	1539	1520	5.347722	5.738373	5.576479	28.14633	25.05706	21.89251
protein_co CCR4-NOT_	845	665	609	1219	887	1007	9.41198	8.728769	8.938742	11.74603	11.09933	11.14714
protein_co timeless_ci	377	310	279	1581	1504	1565	4.560959	4.419606	4.447887	16.54663	20.44145	18.8165
protein_co cleavage_ar	1218	1031	1026	2819	2327	2219	9.746392	9.722151	10.81879	19.51438	20.91905	17.6467
protein_co KRR1_smal	724	593	710	751	610	522	9.405958	9.078754	12.15507	8.440485	8.903143	6.739763
protein_co mitochond	1623	1369	1153	1909	1824	3114	75.63665	75.1838	70.80727	76.96313	95.49654	144.2255
protein_co glyceraldeh	67682	57094	43873	62993	44931	49991	1911.015	1899.715	1632.386	1538.672	1425.233	1402.789
protein_co NOP2_nucl	766	593	571	2357	1670	2164	13.34852	12.17772	13.11219	35.53259	32.69413	37.47755
protein_co chromodor	4589	3897	3900	5924	6431	6214	36.92192	36.94909	41.34906	41.23294	58.12912	49.68749
protein_co acrosin_bir	6	7	0	1	0	2	0.164328	0.225926	0	0.023693	0	0.054438
protein_co UHRF1_bin	291	266	281	184	172	157	2.981004	3.211133	3.793243	1.630611	1.979462	1.598376
protein_co COP9_signa	1627	1338	1051	1432	927	1085	40.496	39.24531	34.47165	30.83405	25.9211	26.83885
protein_co inhibitor_c	427	318	211	329	207	331	13.2275	11.60872	8.613255	8.816758	7.203929	10.19032
protein_co guanine_nu	51	59	49	57	38	42	0.941091	1.282982	1.191496	0.909912	0.78776	0.77023
protein_co cell_divisio	258	210	163	1724	1082	1363	4.682474	4.491403	3.898325	27.06799	22.06134	24.58449
protein_co choline_ph	488	358	320	610	416	471	5.95007	5.143898	5.141467	6.434208	5.698291	5.707328
protein_co ubiquitin_s	2196	1952	1716	3502	2974	3861	36.54776	38.28383	37.63401	50.42055	55.60559	63.86132
protein_co triosephosp	20899	18593	13484	15238	10160	12673	627.5745	657.9552	533.5724	395.8501	342.754	378.2064
protein_co N-acetylglu	479	359	485	881	726	714	4.448121	3.928643	5.934957	7.077501	7.574025	6.589446

protein_co	splA/ryano	84	75	55	112	77	135	2.972623	3.127727	2.564827	3.428795	3.06126	4.747926
protein_co	enolase_2_	1147	1157	728	139	135	108	21.47977	25.53329	17.96522	2.251874	2.840201	2.010017
protein_co	atrophin_1	6028	5065	3945	5894	4330	4698	74.3369	73.60677	64.10812	62.87881	59.98852	57.57764
protein_co	chromoson	2198	1940	1104	1175	643	782	118.7391	123.5022	78.59047	54.91195	39.02348	41.98386
protein_co	protein_tyr	9	5	3	377	264	329	0.197541	0.129328	0.08677	7.158452	6.509802	7.176626
protein_co	lysophosph	572	488	392	670	528	694	10.43496	10.49111	9.423572	10.57383	10.82126	12.58241
protein_co	5'-nucleoti	628	506	488	766	709	718	4.613146	4.380212	4.723808	4.867762	5.851037	5.241694
protein_co	Nanog_hon	0	0	0	0	4	1	0	0	0	0	0.113234	0.025042
protein_co	suppressor_	889	756	806	1415	1363	1422	9.610893	9.631432	11.48238	13.2337	16.55415	15.27817
protein_co	golgi_trans	759	831	741	869	687	730	12.45188	16.06576	16.0194	12.3332	12.6619	11.90216
protein_co	glycogen_s	0	0	1	0	1	0	0	0	0.022274	0	0.01899	0
protein_co	lactate_deh	13892	11991	9827	21126	16571	18868	478.19	486.4052	445.7502	629.0947	640.8163	645.4629
protein_co	protein_kir	334	248	255	782	494	531	4.399675	3.849753	4.426384	8.911357	7.310551	6.951496
protein_co	cytidine_m	445	440	391	1371	1064	1259	13.1834	15.36128	15.26438	35.13727	35.41263	37.06832
protein_co	host_cell_f	209	196	246	96	74	73	2.717924	3.003683	4.215615	1.080004	1.081115	0.94346
protein_co	ST8_alpha-l	105	75	52	25	11	31	2.385753	2.008189	1.556949	0.491405	0.280788	0.700015
protein_co	C-type_lect	5	3	2	7	1	3	0.206639	0.146107	0.10892	0.250267	0.046429	0.123218
protein_co	C2_calcium	332	277	322	373	398	342	3.96222	3.895717	5.063971	3.85099	5.336207	4.056358
protein_co	activation-i	0	1	0	0	0	0	0	0.022131	0	0	0	0
protein_co	RAB35_mer	1545	1296	1150	2579	2007	2735	27.7738	27.45484	27.24203	40.10709	40.53248	48.86228
protein_co	polyhomec	356	301	313	387	437	418	3.642635	3.629437	4.220315	3.425624	5.023381	4.250613
protein_co	cytochrom	84	69	50	129	86	82	5.797971	5.612455	4.547802	7.702815	6.668747	5.62497
protein_co	regulatory_	0	0	1	0	2	0	0	0	0.017639	0	0.030076	0
protein_co	resistance_	234	252	215	282	268	230	2.414382	3.064063	2.923232	2.51711	3.106518	2.358455
protein_co	serine/argi	3225	2751	2289	5674	4287	6122	100.1964	100.721	93.7137	152.5018	149.6322	189.0277
pseudogen	-	144	101	83	405	288	452	1.945267	1.607849	1.477508	4.732982	4.370774	6.06827
protein_co	FGFR1_onc	453	440	394	701	611	599	8.143385	9.321087	9.333356	10.90154	12.33949	10.70147
protein_co	killer_cell_l	0	1	0	0	10	1	0	0.043085	0	0	0.410745	0.036336
protein_co	collagen_ty	17923	15974	19381	2445	2402	1930	80.94015	85.0108	115.3358	9.552019	12.1864	8.662042
protein_co	butyrophili	248	239	224	10	4	7	2.887479	3.279232	3.436766	0.100723	0.052321	0.080998
protein_co	tyrosyl-DN/	462	436	403	799	670	627	11.53714	12.83068	13.26161	17.261	18.79663	15.56085
protein_co	fyn-related_	4	6	6	0	5	14	0.074329	0.131389	0.146922	0	0.10438	0.258546
protein_co	dermatan_s	497	462	475	724	697	634	6.183707	6.773944	7.78791	7.79281	9.742589	7.839555
protein_co	RWD_dom	1023	781	755	1345	812	1043	9.807794	8.823763	9.538442	11.15529	8.745825	9.937786
protein_co	radial_spok	5	6	4	12	19	13	0.093701	0.132505	0.09878	0.194544	0.400015	0.242118
protein_co	male_germ	48	46	36	60	73	58	0.637843	0.72034	0.630391	0.689743	1.089795	0.765968
protein_co	transmemb	1832	1578	1225	2437	1616	2207	82.40263	83.64302	72.60834	94.82747	81.65937	98.65693
protein_co	PAK1_inter	346	294	241	1161	778	924	10.17644	10.19	9.340528	29.54029	25.70681	27.00855
protein_co	glucosamin	0	1	0	545	451	461	0	0.013787	0	5.516111	5.927876	5.360238
protein_co	small_integ	58	66	94	130	108	126	1.261536	1.691697	2.694227	2.446121	2.63903	2.723653
protein_co	neural_pre	312	218	279	802	709	614	3.347708	2.756491	3.944863	7.444411	8.546499	6.547431
protein_co	centrosom	216	172	196	210	228	195	1.490324	1.3985	1.782041	1.253456	1.767302	1.337122
protein_co	androgen-d	2	0	0	4	8	8	0.054947	0	0	0.095068	0.246916	0.218429
protein_co	ASF1_anti-s	241	165	199	699	387	530	5.401685	4.358161	5.877601	13.55353	9.744784	11.80586

protein_co minichrom	94	49	77	210	194	197	0.655486	0.402661	0.707557	1.26683	1.519801	1.365249
protein_co family_witl	0	5	1	49	24	17	0	0.075329	0.016847	0.541933	0.344705	0.215996
protein_co RNA_guany	326	271	325	567	501	482	3.892369	3.813052	5.113457	5.856558	6.720215	5.719434
protein_co mannosida	1822	1520	1934	1058	980	847	19.23783	18.91291	26.90909	9.663989	11.62473	8.887934
protein_co gamma-am	15	3	3	5	5	8	0.469613	0.110682	0.123767	0.13542	0.17586	0.248913
protein_co serine_incc	3071	2612	2553	2147	1487	1511	48.07268	48.18354	52.66282	29.07459	26.15041	23.50675
protein_co HD_domair	569	590	408	1627	1016	1400	18.65228	22.7918	17.62441	46.13921	37.41643	45.6097
protein_co tumor_pro	66	48	21	1800	1144	1354	1.403819	1.203138	0.588601	33.12094	27.33646	28.62171
protein_co histidine_t	197	159	149	541	538	655	3.149917	2.995968	3.139453	7.4833	9.664163	10.4084
protein_co nuclear_rec	132	144	169	1110	1070	1024	1.265751	1.627211	2.135482	9.207894	11.52676	9.75852
protein_co family_witl	314	289	329	145	137	129	3.038471	3.295568	4.195233	1.213826	1.489344	1.24058
protein_co SAM_and_S	894	780	874	751	727	626	6.137887	6.310781	7.907289	4.460508	5.607443	4.271352
protein_co uronyl-2-su	505	456	479	173	132	140	6.368557	6.776752	7.960127	1.887377	1.870134	1.754637
protein_co UL16_bind	78	64	64	40	25	26	1.315095	1.271597	1.421927	0.583426	0.473534	0.435658
protein_co F-box_prot	258	221	182	1160	857	864	5.253376	5.302957	4.88343	20.43336	19.60418	17.48405
protein_co mitochond	361	251	251	540	470	491	5.199048	4.25988	4.763489	6.727804	7.604375	7.027611
protein_co peroxisome	1106	964	818	756	634	740	15.51477	15.93582	15.12092	9.174344	9.99145	10.31648
protein_co Fanconi_an	187	152	121	444	290	332	3.876259	3.712974	3.305152	7.961908	6.753334	6.839415
protein_co tubby_like_	3	3	6	14	11	47	0.073461	0.086569	0.193608	0.29657	0.302606	1.143784
protein_co solute_carr	0	3	1	5	3	4	0	0.051235	0.019098	0.062687	0.048844	0.057612
protein_co mitogen-ac	1037	801	811	1282	1129	1175	12.71123	11.5704	13.0998	13.5944	15.54719	14.31385
protein_co potassium_	1215	1131	1085	2531	1960	2099	11.44747	12.55749	13.47093	20.62948	20.74618	19.65419
protein_co serine/thre	1209	1059	1031	1314	1021	1093	17.89867	18.47556	20.11352	16.82879	16.98124	16.08142
protein_co serine/argi	3178	2808	2589	9821	7329	8593	81.91163	85.28955	87.93434	218.983	212.2196	220.1132
protein_co superoxide_	2369	1919	1443	1666	1323	1473	29.15323	27.82939	23.40038	17.73616	18.29071	18.01499
protein_co mitochond	808	682	453	1493	1164	1487	39.79193	39.57994	29.39792	63.60722	64.39997	72.77869
protein_co interleukin_	0	0	1	0	2	0	0	0	0.075338	0	0.128458	0
protein_co minichrom	567	429	432	5570	4231	4594	9.472245	8.445672	9.510173	80.49855	79.40758	76.27294
protein_co ring_finger_	301	297	262	525	371	406	2.829913	3.290562	3.245956	4.27001	3.918587	3.793519
protein_co phosphatas	48	44	36	34	58	52	0.531181	0.5738	0.524975	0.325494	0.721071	0.571892
protein_co MAM_dom	589	548	480	71	64	76	2.904457	3.184471	3.119074	0.30288	0.354551	0.372454
protein_co intestinal_c	360	283	369	360	295	245	3.060664	2.83535	4.134037	2.647761	2.817632	2.070089
protein_co F-box_prot	650	562	596	1036	684	833	7.548069	7.690701	9.120183	10.40747	8.923344	9.613403
protein_co CD83_mole	139	136	69	74	42	34	2.978065	3.433724	1.948064	1.371558	1.010922	0.723949
protein_co MDN1_mid	930	700	916	1545	1802	1345	2.673933	2.371771	3.470546	3.8429	5.820649	3.843257
protein_co SAYSVFN_m	254	199	147	164	101	178	6.656937	6.146118	5.076833	3.718327	2.973796	4.636288
protein_co bone_morp	11	15	14	282	263	279	0.147356	0.236796	0.247137	3.268039	3.958038	3.714403
protein_co BTB_and_C	49	36	26	331	397	307	0.28466	0.246457	0.199039	1.663496	2.591017	1.772469
protein_co RNA_bindir	203	213	207	80	41	49	3.975961	4.916236	5.342582	1.355498	0.90215	0.953788
protein_co CAP_adeny	165	160	228	725	524	605	2.634277	3.010264	4.796752	10.01333	9.398486	9.599367
protein_co triggering_	0	0	0	0	2	2	0	0	0	0	0.036024	0.031868
protein_co zinc_finger_	598	493	550	904	627	630	3.340232	3.24511	4.048302	4.368243	3.934522	3.497241
protein_co BCL2-assoc	777	876	676	1534	996	1180	23.43883	31.14054	26.87178	40.03164	33.75385	35.37583
protein_co RAB23_mer	1430	1246	1298	652	512	464	25.35352	26.03319	30.32577	10.0003	10.19815	8.175793

protein_co translocatc	0	0	0	0	5	1	0	0	0	0	0.310417	0.054921
protein_co four_and_a	0	1	0	0	0	0	0	0.030718	0	0	0	0
protein_co G_protein-(	27	43	41	74	71	76	0.650322	1.220506	1.301317	1.54191	1.921197	1.81923
protein_co KH_domair	0	1	0	6	3	5	0	0.030315	0	0.133525	0.0867	0.127828
protein_co F-box_and_	233	213	179	204	210	128	3.959952	4.265999	4.008869	2.99935	4.009612	2.16199
protein_co cyclin_C	682	614	741	2126	1247	1676	14.59998	15.48972	20.9036	39.37261	29.99048	35.65756
protein_co PR_domair	0	0	0	2	0	1	0	0	0	0.028323	0	0.016269
protein_co E2F_transci	390	334	306	845	648	758	4.352232	4.392391	4.499908	8.157689	8.124029	8.406714
protein_co protein_tyr	2164	1908	1988	5063	4078	4269	22.51657	23.3954	27.25814	45.57387	47.66957	44.14493
protein_co activating_	1172	987	1306	2049	1573	1465	7.616848	7.559132	11.18473	11.52	11.48485	9.462262
protein_co blood_vess	157	133	156	348	254	264	1.493037	1.490492	1.954926	2.862946	2.713649	2.49508
protein_co collagen_ty	1	0	0	1	1	2	0.01112	0	0	0.00962	0.012492	0.022102
protein_co mediator_c	454	356	482	590	477	380	4.5825	4.234515	6.411039	5.151831	5.408963	3.811885
protein_co WAS_prote	544	408	409	752	555	578	8.944069	7.905029	8.861237	10.69589	10.25128	9.444385
protein_co glycosylphc	1	0	3	13	8	18	0.015174	0	0.059986	0.170647	0.136374	0.27144
protein_co aldehyde_d	15	10	13	81	64	53	0.151318	0.118879	0.172813	0.706881	0.725316	0.531354
protein_co absent_in_(	140	157	183	141	125	140	0.982468	1.298366	1.692296	0.855998	0.985484	0.976401
protein_co vanin_1	0	0	0	0	1	0	0	0	0	0	0.019149	0
protein_co vanin_2	0	0	0	2	0	0	0	0	0	0.043247	0	0
protein_co acyl-CoA_th	356	295	238	448	349	431	4.292187	4.191387	3.781294	4.672719	4.727191	5.164349
protein_co small_ArfGA	138	112	80	171	141	141	2.191976	2.096437	1.674486	2.349719	2.516083	2.225797
protein_co ribosomal_	15717	14000	8582	20285	14064	19055	1302.15	1366.867	936.946	1453.882	1309.029	1568.953
protein_co chromosor	3482	3033	2843	2788	2550	2531	44.59133	45.77213	47.97702	30.88712	36.68689	32.21242
protein_co beta-13-glu	32	16	31	2	2	12	0.258052	0.152049	0.329423	0.013952	0.018119	0.096172
protein_co geminin_DI	221	175	186	2073	1302	1589	9.270966	8.65123	10.28207	75.23069	61.36105	66.24701
protein_co eyes_absen	51	37	58	120	127	78	0.473766	0.405044	0.709997	0.964357	1.325398	0.720108
protein_co sine_oculis	854	608	644	64	106	132	8.643015	7.251336	8.588712	0.560338	1.205209	1.327672
protein_co nuclear_rec	0	0	0	3	3	1	0	0	0	0.042776	0.05555	0.01638
protein_co sorting_nex	3401	3157	2503	3222	2258	2563	102.5939	112.2268	99.49715	84.08209	76.52229	76.8375
protein_co HBS1-like_(	1063	803	854	1266	962	978	7.856523	6.993906	8.317443	8.094571	7.987691	7.183658
protein_co tripartite_r	489	352	359	241	241	199	7.953347	6.746691	7.694322	3.390948	4.403593	3.21665
protein_co peroxisoma	40	39	41	117	66	100	1.375984	1.580976	1.858541	3.481788	2.550624	3.418717
protein_co zinc_finger_	220	177	164	564	334	420	2.110349	2.000839	2.073053	4.680301	3.599376	4.003968
protein_co FIG4_homc	212	202	170	335	224	239	3.727496	4.185427	3.93881	5.095527	4.424645	4.176273
protein_co PERP_TP53	1652	1346	1372	9535	6721	7353	43.53336	41.79885	47.64322	217.3681	198.9734	192.569
protein_co KIAA1244	7	13	5	120	135	100	0.02491	0.054516	0.023447	0.36942	0.539709	0.35366
protein_co solute_carr	3	2	1	130	99	75	0.063327	0.049751	0.027816	2.373946	2.347734	1.573387
protein_co headcase_h	408	294	355	319	292	305	3.847511	3.267188	4.411465	2.602396	3.09351	2.858441
protein_co G_protein-(	2	9	3	2192	1997	1655	0.01507	0.079916	0.029788	14.28853	16.90484	12.39343
protein_co phosphatas	225	235	261	458	409	351	1.249787	1.538256	1.91042	2.200808	2.552266	1.937628
protein_co epilepsy_pr	51	30	50	87	84	106	0.743185	0.515175	0.960133	1.096753	1.375166	1.53512
protein_co solute_carr	5488	4839	4024	3061	2602	3636	120.6061	125.3193	116.5328	58.19446	64.2409	79.41249
protein_co chemokine	0	0	0	0	2	2	0	0	0	0	0.029605	0.026189
protein_co unc-93_hor	0	0	0	5	0	2	0	0	0	0.10822	0	0.04973

protein_co solute_carr	0	0	0	2	0	0	0	0	0	0.024511	0	0
protein_co PHD_finger	718	656	537	770	624	787	16.31401	17.56496	16.07849	15.13526	15.92831	17.77136
protein_co cutA_divale	3035	2471	2007	3883	2246	2853	116.6008	111.8723	101.6073	129.0545	96.9397	108.9317
protein_co PARK2_co-r	7	5	5	1	0	3	0.228899	0.192674	0.215452	0.028288	0	0.097494
protein_co QKI_KH_do	2706	2324	2580	3331	3068	2766	15.13879	15.32168	19.02032	16.12133	19.28269	15.37889
protein_co chromoson	2	3	3	15	14	6	0.057607	0.10183	0.113868	0.373767	0.453027	0.171754
protein_co phosphodi	134	113	153	326	347	301	0.861666	0.856287	1.296463	1.813488	2.506759	1.923579
protein_co MyoD_fami	1287	995	825	3729	2638	3674	41.82631	38.10669	35.33131	104.8399	96.31521	118.6642
protein_co transcriptic	58	67	52	44	47	62	1.183267	1.610781	1.397954	0.776552	1.077213	1.25706
protein_co SPARC_rela	2	0	1	101	74	83	0.033613	0	0.022147	1.468473	1.397212	1.386338
protein_co cyclin_D3	1717	1331	1235	1097	925	1051	37.96979	34.68591	35.98899	20.98638	22.98046	23.09832
protein_co bystin-like	535	413	385	1421	843	1197	13.95931	12.69893	13.23749	32.07503	24.71079	31.03944
protein_co family_with	601	591	628	612	558	499	6.17217	7.152502	8.498805	5.437232	6.437936	5.092999
protein_co TATA_box_l	259	193	172	646	385	548	7.205317	6.327289	6.305457	15.54708	12.0327	15.15108
protein_co guanylate_c	13	8	9	19	3	2	0.618358	0.448429	0.564124	0.781832	0.160312	0.094545
protein_co peripherin_	93	83	66	0	7	1	1.655519	1.74115	1.54821	0	0.13999	0.017691
protein_co GLTSCR1-lil	204	183	133	112	117	123	1.653899	1.748385	1.420906	0.785525	1.065648	0.991046
protein_co protein_ph	1495	1138	1064	1671	1325	1310	26.00092	23.32366	24.38506	25.14125	25.88883	22.64271
protein_co mitochond	383	383	266	659	544	767	12.76851	15.04691	11.68579	19.00597	20.37462	25.41245
protein_co protein_tyr	4468	3928	3164	4744	5492	5948	44.78235	46.39512	41.78929	41.13404	61.84054	59.24808
protein_co serum_resp	1402	1193	1149	2319	2295	2732	17.67221	17.72109	19.08524	25.28754	32.49934	34.22419
protein_co cullin_9	301	248	237	243	322	311	1.955244	1.898424	2.028699	1.365538	2.349846	2.007726
protein_co nudix_(nuc	186	125	186	200	212	251	7.219226	5.717351	9.513175	6.715382	9.244058	9.681911
protein_co 2'-deoxynu	485	483	331	197	241	397	30.78703	36.13102	27.68783	10.81821	17.18669	25.0453
protein_co dual_specif	209	157	159	555	376	436	2.89348	2.561421	2.900722	6.647069	5.84805	5.998882
protein_co exocyst_co	277	313	350	950	754	684	3.296169	4.389157	5.488233	9.779492	10.07976	8.089011
protein_co cytochrom	1863	1621	1206	2667	1969	2635	107.9093	110.6461	92.0509	133.6386	128.127	151.6827
protein_co transmemb	4003	3512	4141	5056	4977	5067	46.13034	47.69388	62.88414	50.40472	64.4344	58.03121
protein_co GDP-mann	445	409	287	416	215	366	13.44677	14.56426	11.42812	10.87463	7.2987	10.99129
protein_co SUMO1/ser	1186	1181	1081	1792	1338	1383	9.448912	11.08802	11.349	12.35089	11.97574	10.95037
protein_co interphoto	1	4	3	15	14	9	0.009136	0.043063	0.036116	0.118548	0.143686	0.081713
protein_co vascular_er	2397	2445	1713	539	465	455	10.42982	12.53703	9.822019	2.028899	2.273058	1.967567
protein_co PRP4_pre-r	983	856	902	1704	1511	1423	7.681328	7.882494	9.288041	11.51902	13.26467	11.05089
protein_co TTK_protei	162	144	126	1140	751	783	2.3024	2.411767	2.359778	14.01631	11.99098	11.05954
protein_co solute_carr	201	150	153	1252	738	949	4.282149	3.765859	4.295285	23.07454	17.66327	20.09285
protein_co WNT1_indu	6	0	2	4	5	5	0.126451	0	0.055544	0.072928	0.118384	0.104725
protein_co butyrophili	570	480	417	494	305	453	9.693661	9.619695	9.345098	7.267799	5.827226	7.656333
protein_co laminin_alp	4720	3846	4070	28	32	22	38.16733	36.64934	43.36896	0.195871	0.290703	0.1768
protein_co family_with	2188	2090	2069	485	447	396	20.45108	23.0209	25.4838	3.921693	4.693809	3.678525
protein_co chloride_in	0	0	2	25	28	34	0	0	0.051429	0.422032	0.613832	0.659373
protein_co fibrosin-like	1284	1003	796	2653	1887	2169	12.20838	11.23831	9.973343	21.82193	20.15644	20.49567
protein_co ectonucleo	0	0	0	27	19	26	0	0	0	0.322528	0.294742	0.356798
protein_co lymphocyte	0	0	0	1	2	0	0	0	0	0.038261	0.099375	0
protein_co protease_se	6	2	2	157	126	118	0.093124	0.03658	0.040905	2.108012	2.197	1.820128

protein_co	T-box_18	691	574	704	33	20	14	8.299053	8.123992	11.14187	0.342868	0.269854	0.167105
protein_co	erbb2_inte	880	781	850	1116	1221	1005	5.387773	5.634881	6.85773	5.910903	8.398299	6.115083
protein_co	protocadhe	1640	1341	1443	710	562	578	31.73364	30.5782	36.79401	11.88495	12.21691	11.1151
protein_co	histidyl-tRN	568	404	418	473	515	551	12.11055	10.15088	11.74428	8.724479	12.33592	11.67553
protein_co	nudix_(nuc	139	145	162	189	187	158	2.107331	2.590556	3.236441	2.478807	3.184993	2.38059
protein_co	centrosoma	96	72	77	241	286	272	2.088059	1.845487	2.206973	4.534731	6.988542	5.879631
protein_co	mannosida	1539	1427	1646	1844	1853	1541	14.55192	15.90057	20.50908	15.08362	19.68367	14.48085
protein_co	sema_doma	1438	1213	1418	638	569	509	6.472466	6.433967	8.410503	2.484246	2.877214	2.276871
protein_co	complemer	704	628	614	1	7	4	8.7551	9.203546	10.06217	0.010758	0.097799	0.049438
protein_co	PAP_associ	717	670	502	1065	770	839	9.831311	10.82615	9.070491	12.63295	11.86129	11.4331
protein_co	growth_ho	73	53	58	24	13	21	0.84752	0.725121	0.88734	0.241047	0.169559	0.242302
protein_co	3-hydroxy-	2885	2249	2987	1651	1853	1757	43.56382	40.01997	59.43609	21.56703	31.43436	26.36705
protein_co	death-assoc	4465	3657	3400	3413	2364	2562	101.0609	97.54251	101.4088	66.82842	60.11162	57.63027
protein_co	NME/NM23	8	4	4	39	21	37	0.355011	0.209179	0.233909	1.497198	1.046936	1.631785
protein_co	bromodom	881	694	704	1193	878	986	10.62922	9.867157	11.19265	12.45171	11.90061	11.82257
protein_co	kinesin_fam	669	593	607	3232	2589	2676	11.06452	11.55761	13.22909	46.24244	48.1047	43.98475
protein_co	nicotinami	812	808	819	821	705	688	6.630894	7.775611	8.813224	5.799923	6.467765	5.583598
protein_co	mitochond	600	571	514	1499	787	886	7.334241	8.225212	8.279457	15.85143	10.80756	10.76335
protein_co	heat_shock	3660	2943	2915	8875	6856	7404	58.34509	55.28669	61.23456	122.3924	122.7844	117.3003
protein_co	mitochond	1793	1426	1285	2736	2010	1900	21.4032	20.05973	20.21326	28.25385	26.95526	22.5404
protein_co	prefoldin_s	626	489	398	1762	1007	1209	24.51262	22.56479	20.53682	59.68763	44.299	47.0491
protein_co	heparin-bir	66	61	64	268	137	147	1.46442	1.594992	1.87127	5.144219	3.415004	3.241519
protein_co	solute_carr	0	2	6	0	0	0	0	0.037324	0.125211	0	0	0
protein_co	lysyl_oxida	5590	5105	4666	1702	1104	1177	58.00473	62.42441	63.80154	15.27827	12.86974	12.13774
protein_co	amyloid_be	238	287	177	177	129	156	4.498378	6.392459	4.408462	2.894111	2.739162	2.930308
protein_co	transmemb	92	107	60	223	165	213	2.493892	3.418068	2.143265	5.229471	5.024847	5.738245
protein_co	secreted_pr	127197	109164	90991	40628	28279	30546	1819.491	1840.177	1715.166	502.7609	454.45	434.2472
protein_co	IK_cytokine	1381	1214	1049	1772	1580	1728	37.22582	38.56349	37.26155	41.32162	47.84722	46.29179
protein_co	3-hydroxy-	2266	2034	2243	3267	2814	2768	26.16451	27.67648	34.12847	32.63359	36.50278	31.76351
protein_co	collagen_ty	529	467	515	796	865	689	4.955899	5.155737	6.357829	6.451235	9.103994	6.414985
protein_co	Fas_associa	1466	1115	1252	1761	1528	1470	17.1897	15.40694	19.34521	17.86309	20.12828	17.13016
protein_co	heart_and_	0	0	0	11901	9199	10131	0	0	0	313.6092	314.798	306.6933
protein_co	protocadhe	100	100	96	58	43	28	1.668484	1.966206	2.110708	0.837169	0.806008	0.46429
protein_co	protocadhe	132	121	135	621	406	477	2.406409	2.599489	3.243128	9.793774	8.315159	8.642184
protein_co	protocadhe	16	8	25	9	4	5	0.279556	0.16472	0.575605	0.136036	0.078516	0.086822
protein_co	protocadhe	24	16	26	10	2	3	0.342014	0.268695	0.488249	0.123281	0.032019	0.042488
protein_co	phosphodi	84	65	65	57	70	33	0.746649	0.68086	0.761352	0.438304	0.699012	0.291515
protein_co	CDC-like_ki	352	325	275	343	200	234	5.006779	5.447612	5.154461	4.220587	3.195912	3.307815
protein_co	protocadhe	340	217	299	142	108	112	6.784749	5.102954	7.862503	2.451355	2.421183	2.221174
protein_co	hepatitis_A	0	0	0	0	0	1	0	0	0	0	0	0.028517
protein_co	glutamate_	0	0	0	0	7	11	0	0	0	0	0.067773	0.094214
protein_co	ring_finger_	872	711	661	870	464	487	4.641986	4.460299	4.636856	4.006541	2.774945	2.576475
protein_co	tRNA-histid	466	413	315	409	304	352	7.940297	8.29293	7.072879	6.028887	5.819337	5.960781
protein_co	arylsulfatas	571	476	519	766	590	627	5.674734	5.574725	6.796911	6.585688	6.587346	6.192793

protein_co clathrin_in	1433	1299	1314	2334	1710	1794	19.02795	20.32648	22.99196	26.8108	25.50886	23.67434
protein_co thrombosp	19	30	16	19	11	27	0.312191	0.580891	0.346435	0.270074	0.203052	0.4409
protein_co CCR4-NOT_	881	792	899	1691	1704	1722	7.399812	7.839296	9.950371	12.28716	16.07916	14.37433
protein_co interleukin	0	1	0	5	0	3	0	0.022596	0	0.082939	0	0.057168
protein_co tetratricop	731	671	548	1569	1002	1164	26.38028	28.5359	26.06018	48.98329	40.62363	41.74694
protein_co mutS_hom	268	253	187	570	394	418	3.467299	3.857306	3.188107	6.379613	5.726665	5.374554
protein_co Ras_protei	25	15	19	1155	1010	1087	0.162058	0.114585	0.1623	6.477009	7.355293	7.002752
protein_co gamma-am	0	0	0	4	8	0	0	0	0	0.045167	0.11731	0
protein_co cyclin_G1	5630	5096	4940	5469	3506	3643	121.2603	129.3441	140.2077	101.9016	84.83424	77.97925
protein_co polymerase	112	125	98	325	198	289	1.80499	2.373962	2.081218	4.531094	3.58485	4.628755
protein_co drosha_rib	947	732	775	1676	1559	1478	9.450541	8.608448	10.19162	14.46917	17.47841	14.65854
protein_co cadherin_6	28	45	39	341	446	340	0.174888	0.331223	0.320997	1.842547	3.129573	2.110521
protein_co lamin_B1	788	597	606	5139	4336	4403	12.00504	10.71812	12.16591	67.72966	74.21225	66.66465
protein_co arrestin_do	1103	1000	1002	568	536	458	13.94315	14.89678	16.69122	6.211504	7.612009	5.753877
protein_co golgi_phos	1570	1244	1182	2365	1900	1952	30.54662	28.52273	30.30511	39.80684	41.53041	37.74444
protein_co SUB1_hom	2258	2004	1808	3645	2266	3036	27.97584	29.2593	29.51837	39.06787	31.54047	37.3827
protein_co natriuretic_	1667	1444	1808	155	269	222	12.02844	12.27857	17.19122	0.967539	2.180594	1.591975
protein_co family_witl	593	500	515	383	339	323	7.280614	7.234199	8.332117	4.067945	4.675866	3.941173
protein_co solute_carr	11	3	9	2823	2943	2813	0.180911	0.058143	0.195051	40.16474	54.3764	45.97804
protein_co threonyl-tR	3335	2759	2490	6369	4420	4676	40.9268	39.8998	40.26671	67.61549	60.93731	57.02904
protein_co iroquois_ho	0	0	0	59	48	66	0	0	0	1.064671	1.12484	1.368214
protein_co leucyl/cysti	359	321	419	271	484	224	1.490419	1.570456	2.292253	0.973299	2.257398	0.924212
protein_co phosphodi	538	486	479	845	801	646	3.459943	3.683241	4.059355	4.701175	5.787197	4.128848
protein_co RAD1_hom	287	232	211	914	555	626	2.633287	2.508484	2.551136	7.254801	5.72082	5.708214
protein_co BRX1_biog	205	195	158	1711	738	888	4.560044	5.1116	4.631344	32.92518	18.44253	19.63079
protein_co alanine--gly	1	3	0	0	0	0	0.022395	0.079172	0	0	0	0
protein_co prolactin_r	113	88	188	303	285	194	0.512186	0.470045	1.122902	1.188105	1.451253	0.873898
protein_co solute_carr	184	104	114	461	388	440	1.847713	1.230714	1.508538	4.004798	4.377211	4.391157
protein_co interleukin	0	0	1	0	2	0	0	0	0.113252	0	0.193104	0
protein_co RAD50_hor	531	447	521	842	793	696	4.261281	4.227272	5.509576	5.845487	7.149371	5.550914
protein_co interleukin	0	0	0	0	1	0	0	0	0	0	0.065719	0
protein_co ST8_alpha-l	13	20	22	111	56	80	0.191976	0.348049	0.428115	1.418041	0.929052	1.174093
protein_co glucosamin	693	654	668	1803	1433	1544	12.31145	13.6918	15.63821	27.70987	28.60033	27.26043
protein_co protocadhe	31	26	16	26	13	25	0.250102	0.247193	0.170102	0.181465	0.117828	0.20045
protein_co S-phase_kir	3769	3403	2671	5348	3230	4202	98.14786	104.4296	91.65653	120.4784	94.49445	108.7478
protein_co nucleopori	568	470	540	2762	2017	1979	3.692802	3.600913	4.626326	15.53439	14.73203	12.78684
protein_co protein_ph	1142	1004	962	4429	2267	2884	13.00465	13.47328	14.43585	43.63161	29.00235	32.63905
protein_co fibroblast_g	41	23	27	339	323	333	0.593055	0.392054	0.514647	4.24203	5.248831	4.787016
protein_co nuclear_rec	852	728	862	295	239	209	6.190739	6.233635	8.25363	1.854334	1.950967	1.509242
protein_co chromoson	1213	1074	1048	2253	1502	1688	27.32656	28.51252	31.11146	43.90848	38.01397	37.79256
protein_co peptidylpro	314	335	282	758	566	577	7.674733	9.649072	9.082754	16.0275	15.54172	14.01584
protein_co leukemia_in	2281	1751	2504	325	412	296	11.96931	10.82772	17.31463	1.475334	2.428792	1.543638
protein_co tripartite_r	243	173	212	167	178	162	3.073259	2.578375	3.533162	1.827142	2.529076	2.036186
protein_co trafficking_	193	190	171	299	246	263	1.70464	1.977589	1.990244	2.284597	2.440954	2.308558

protein_co complemer	3	2	4	0	1	0	0.058541	0.045992	0.102858	0	0.021923	0
protein_co SEC24_fam	648	530	742	720	657	589	5.446224	5.249325	8.217869	5.234992	6.203473	4.919777
protein_co thioredoxir	1056	831	820	705	595	662	15.75696	14.61223	16.12342	9.100403	9.974118	9.816939
protein_co tetratricop	118	60	129	130	117	100	2.391668	1.433103	3.44543	2.279425	2.66412	2.01432
protein_co arginyl-tRN	1874	1729	1488	3933	2746	2985	46.23086	50.26486	48.37268	83.9362	76.10479	73.18404
protein_co WW_and_C	69	58	45	1408	1240	1411	0.512332	0.507502	0.440301	9.04416	10.34364	10.41212
protein_co H2A_histor	1153	872	983	4135	3445	3583	5.558274	4.953752	6.244519	17.24444	18.65731	17.16592
protein_co transcriptic	1032	957	927	2112	1807	1767	11.73939	12.82876	13.89569	20.78369	23.0926	19.97616
protein_co dihydropyr	409	313	339	1515	1527	1289	3.954139	3.56599	4.318801	12.67081	16.58505	12.38486
protein_co SMAD_fami	1140	901	1112	1206	1190	1044	8.608292	8.017593	11.06501	7.878117	10.09504	7.834698
protein_co casein_kina	2250	1770	2112	2119	2513	1887	19.63363	18.20113	24.28549	15.99602	24.6354	16.36438
protein_co HMG_box_	1513	1263	1249	1502	1242	1376	15.18478	14.93757	16.51836	13.04075	14.00362	13.72454
protein_co endoplasm	7512	6438	4829	3044	2794	3248	69.93015	70.62638	59.23807	24.51413	29.22028	30.04931
protein_co platelet-de	2983	2548	2164	324	234	273	27.6234	27.80548	26.40681	2.595565	2.434382	2.512443
protein_co caudal_typ	2	0	0	0	4	6	0.060263	0	0	0	0.135403	0.179672
protein_co ATPase_H+_	2609	2335	1848	3044	1880	2329	96.38734	101.6576	89.96688	97.28672	78.02842	85.5116
protein_co BCL2/aden	97	135	82	283	163	166	3.835158	6.290025	4.272285	9.679679	7.24016	6.522728
protein_co stanniocalc	5754	5061	4654	2357	1963	2395	56.90687	58.98455	60.65352	20.16589	21.81043	23.54019
protein_co cytoplasmi	276	230	411	275	284	205	1.540832	1.513148	3.023591	1.328134	1.781204	1.137391
protein_co histamine_	26	31	23	2	1	16	0.444739	0.624885	0.518435	0.029595	0.019217	0.271995
protein_co drebrin_1	8981	7628	6376	10376	8763	10530	154.7731	154.9133	144.7951	154.6906	169.6574	180.347
protein_co zinc_finger_	340	280	203	448	356	374	6.488802	6.297247	5.105244	7.396507	7.632814	7.093603
protein_co unc-5_hom	45	33	28	1	0	3	0.624959	0.540083	0.512427	0.012014	0	0.041407
protein_co enoyl-CoA_	24	20	19	96	76	94	0.330022	0.324092	0.344286	1.141999	1.17407	1.284603
protein_co contactin_	19	36	23	33	31	38	0.20329	0.453912	0.324284	0.305449	0.372626	0.404069
protein_co structural_	645	513	770	1989	2099	1500	6.241444	5.849919	9.81863	16.65034	22.81849	14.42535
protein_co Selenoprot	441	365	303	923	599	975	14.29699	13.94459	12.94444	25.88634	21.81633	31.41378
protein_co ARP8_actin	467	395	425	519	491	423	6.812743	6.790618	8.170128	6.549912	8.047031	6.132748
protein_co TBCC_dom	169	155	144	328	203	216	2.925778	3.16223	3.285125	4.912374	3.948205	3.716362
protein_co translocase	943	799	618	1885	1269	1713	20.85353	20.82197	18.00907	36.06138	31.52671	37.6474
protein_co cereblon	211	177	184	405	294	285	1.984817	1.962087	2.280818	3.295763	3.106951	2.664358
protein_co kininogen_	0	0	0	0	2	0	0	0	0	0	0.034629	0
protein_co histidine-ri	0	0	0	3	0	0	0	0	0	0.032162	0	0
protein_co B-cell_CLL/	1451	1338	1205	315	225	260	18.38616	19.9796	20.12081	3.453005	3.202987	3.274211
protein_co homogenti	1	0	1	4	2	0	0.026404	0	0.034795	0.091369	0.059328	0
protein_co claudin_16	4	0	0	3	0	0	0.0647	0	0	0.041979	0	0
protein_co ADP-ribosy	79	39	73	102	55	56	2.452984	1.427051	2.986932	2.739876	1.918578	1.728086
protein_co nephronop	840	717	640	771	628	653	5.713057	5.74666	5.735933	4.536351	4.798417	4.413794
protein_co CD86_mole	0	0	0	0	0	1	0	0	0	0	0	0.019429
protein_co angiomotir	1294	1088	1212	3166	2879	2700	15.15276	15.0139	18.7023	32.0724	37.87462	31.4218
protein_co nitrilase_fa	326	238	202	719	425	765	10.42826	8.97177	8.514914	19.89693	15.27327	24.32009
protein_co family_witl	1299	1284	763	561	418	462	22.53288	26.247	17.44082	8.418475	8.145784	7.964512
protein_co 8-oxoguani	389	366	292	355	297	319	4.137843	4.587886	4.093003	3.266749	3.549196	3.372289
protein_co karyopheri	1038	838	1046	2431	1764	1747	8.045791	7.6546	10.6841	16.30119	15.36098	13.4578

protein_co propionyl_	304	267	230	821	664	733	2.642703	2.735226	2.634738	6.174204	6.484731	6.332693
protein_co ubiquitin_p	983	841	917	1468	1372	1065	10.04846	10.13093	12.35237	12.98181	15.75612	10.81946
protein_co armadillo_	518	489	471	765	505	493	5.725143	6.369019	6.859813	7.314439	6.270426	5.415183
protein_co centrosom	131	100	138	245	190	189	2.538532	2.283592	3.523914	4.107149	4.136319	3.639845
protein_co retinol_bin	1	3	2	0	8	9	0.076284	0.269688	0.201047	0	0.685601	0.682315
protein_co retinol_bin	5	3	6	186	141	143	0.136798	0.096725	0.21632	4.402375	4.333904	3.888273
protein_co solute_carr	970	824	1006	1105	975	821	11.07218	11.08398	15.13192	10.91155	12.50302	9.313526
protein_co G_protein-	0	1	1	1	1	3	0	0.019261	0.021539	0.01414	0.018362	0.048732
protein_co ring_finger_	1498	1185	966	1695	1251	1761	28.70272	26.75695	24.39064	28.09596	26.92884	33.5336
protein_co transcriptic	571	447	427	394	364	432	3.050076	2.813774	3.005642	1.820681	2.184364	2.293338
protein_co 5'-3'_exorib	563	531	634	255	317	234	2.938557	3.266083	4.360635	1.151407	1.858806	1.213811
protein_co K(lysine)_ac	254	200	304	146	117	85	2.782332	2.581739	4.388173	1.383538	1.439827	0.925345
protein_co butyrylcho	83	64	70	29	22	30	1.738861	1.580061	1.932501	0.525591	0.517796	0.624623
protein_co serpin_pep	0	0	0	0	0	1	0	0	0	0	0	0.028641
protein_co programme	405	283	300	1304	801	1036	10.37305	8.541716	10.12529	28.89297	23.048	26.37066
protein_co wingless-ty	4798	3771	4949	1211	1228	1020	42.04086	38.93812	57.14308	9.179489	12.08812	8.882213
protein_co 6-phosphot	865	692	574	231	214	259	12.77021	12.03913	11.16679	2.950236	3.549316	3.800067
protein_co collagen_ty	344	291	173	166	219	341	1.963314	1.957183	1.301105	0.819601	1.404186	1.934173
protein_co fibroblast_	169	152	187	61	48	47	2.925778	3.101025	4.2661	0.913582	0.933566	0.808653
protein_co protein_kir	1109	977	1046	1315	1069	1064	9.073028	9.419381	11.27683	9.306994	9.825337	8.651113
protein_co hairy_and_	47	38	16	886	604	659	1.576823	1.502366	0.707359	25.71472	22.76518	21.97253
protein_co ubiquitin_s	646	529	484	900	816	766	9.658255	9.320279	9.535563	11.6405	13.70583	11.38163
protein_co ArfGAP_wit	778	630	793	1045	862	827	5.752527	5.489423	7.726576	6.684337	7.160369	6.07707
protein_co epithelial_c	333	240	302	1552	1269	1240	4.040649	3.431826	4.828905	16.29152	17.29886	14.95334
protein_co guanine_nu	0	0	0	0	1	0	0	0	0	0	0.024607	0
protein_co guanine_nu	10480	8668	7049	6946	5020	6517	142.7745	139.1603	126.5469	81.86289	76.83199	88.23617
protein_co TRK-fused_p	3041	2710	2330	4010	2662	2891	49.21845	51.68779	49.69381	56.14601	48.4026	46.50175
protein_co ubiquitin_s	445	471	530	456	458	367	2.347424	2.927922	3.684191	2.080939	2.714226	1.924009
protein_co hyaluronog	31	19	19	17	15	17	0.652034	0.470944	0.52662	0.309329	0.354445	0.355359
protein_co tumor_sup	560	446	344	1513	1150	1373	17.5322	16.45472	14.19194	40.97797	40.44784	42.71975
protein_co nitrogen_p	242	218	153	254	163	204	4.115554	4.368945	3.428777	3.736885	3.114222	3.447885
protein_co ribosomal_	14874	13890	8515	13898	10329	14919	424.0411	466.6481	319.8893	342.7642	330.8168	422.6974
protein_co cytochrom	229	118	160	281	171	218	7.908342	4.802187	7.28123	8.394972	6.6343	7.481972
protein_co chromoson	123	134	82	332	217	257	1.847303	2.371619	1.622862	4.313542	3.661354	3.835975
protein_co fragile_X_m	3164	2637	2536	3155	2739	2702	51.11544	50.20337	53.98831	44.09385	49.71149	43.38211
protein_co Cbl_proto-	570	516	517	457	413	393	4.450792	4.748093	5.319707	3.087035	3.622943	3.049752
protein_co bobby_sox_	631	442	651	1294	1440	1233	3.740847	3.087948	5.085767	6.636482	9.590741	7.264628
protein_co intraflagell	951	794	820	644	450	500	15.71867	15.46546	17.8601	9.208397	8.355967	8.213245
protein_co guanine_nu	641	557	769	473	578	414	10.21836	10.46371	16.15416	6.523	10.35142	6.558933
protein_co HERV-H_LTI	1	1	4	0	0	0	0.019858	0.023401	0.104671	0	0	0
protein_co IQ_motif_c	143	123	99	92	108	96	2.329404	2.361136	2.125097	1.296461	1.97643	1.554138
protein_co glucan_(14	1263	1113	1074	948	850	847	19.31941	20.06286	21.64859	12.54474	14.60691	12.87608
protein_co uridine_mo	444	347	311	1416	1101	1328	8.843417	8.144673	8.162671	24.39851	24.63619	26.28723
protein_co nuclear_ca	1606	1362	1184	2432	1755	2335	20.43337	20.42107	19.85093	26.76831	25.08537	29.52507

protein_co sorting_nex	348	316	333	886	672	721	7.351742	7.866928	9.270221	16.19227	15.94885	15.13756
protein_co chromoson	74	79	57	439	367	366	1.052561	1.324189	1.068379	5.401859	5.864498	5.173762
protein_co FERM_dom	13	9	8	259	216	159	0.130818	0.106727	0.106084	2.254689	2.441893	1.590122
protein_co solute_carr	750	668	655	679	445	536	10.37245	10.88689	11.93703	8.123683	6.913998	7.367067
protein_co rhophilin_a	0	0	0	0	2	1	0	0	0	0	0.058025	0.025665
protein_co plexin_A1	3330	2615	2569	2291	2380	2365	19.44557	17.99514	19.76857	11.57349	15.61358	13.72515
protein_co ATPase_H+_	849	702	706	1476	1087	1125	9.790221	9.539574	10.72814	14.72428	14.08197	12.89279
protein_co ankyrin_rep	156	106	104	197	168	187	1.63185	1.306678	1.433587	1.782728	1.974304	1.944048
protein_co podocalyxi	605	507	444	461	307	423	14.65201	14.46962	14.16967	9.658415	8.352748	10.18104
protein_co uroplakin_	12	1	2	15	17	13	0.299949	0.029456	0.065877	0.324355	0.47738	0.322938
protein_co chondroitin	7	20	8	17	15	23	0.089062	0.299869	0.134128	0.187114	0.214405	0.290825
protein_co kelch-like_f	256	200	292	677	534	486	2.933527	2.700768	4.409281	6.711225	6.874489	5.534725
protein_co SREBF_chap	1291	1007	841	2360	1856	2291	15.55458	14.29778	13.35251	24.59841	25.12228	27.43259
protein_co EF-hand_an	0	0	1	0	0	0	0	0	0.025925	0	0	0
protein_co KIAA1257	1	0	1	3	8	17	0.008774	0	0.011562	0.02277	0.078854	0.148233
protein_co NIMA-relate	211	152	116	156	62	111	3.833408	3.254267	2.777124	2.451829	1.265445	2.004173
protein_co mitochond	1778	1604	1501	4079	2564	3129	55.17531	58.65763	61.38024	109.5039	89.38819	96.50021
protein_co phospholip	152	123	122	7	11	17	2.436279	2.323249	2.576785	0.097061	0.198073	0.270796
protein_co HemK_met	320	304	228	351	236	375	2.783164	3.115799	2.613115	2.640942	2.30595	3.241378
protein_co cytokine_in	87	85	65	37	42	45	0.9135	1.051757	0.899368	0.336089	0.495436	0.469582
protein_co mitogen-ac	616	495	427	1396	1101	1397	10.91421	10.33532	9.969519	21.39735	21.91532	24.59901
protein_co activin_A_r	43	13	14	61	77	71	0.423922	0.151032	0.181878	0.520248	0.85282	0.695642
protein_co WD_repeat	362	269	313	571	422	402	3.891297	3.407573	4.433687	5.309883	5.096211	4.294588
protein_co COMM_dor	412	288	348	1314	883	1051	5.885507	4.848264	6.550896	16.23847	14.17087	14.92104
protein_co golgi_reass	464	373	377	865	631	683	6.599844	6.252182	7.066297	10.64375	10.0831	9.654862
protein_co peroxisoma	54	49	42	15	18	14	0.314778	0.3366	0.322623	0.075642	0.117878	0.081105
protein_co ribosomal_	486	360	296	1441	882	1225	16.30502	14.23294	13.08614	41.8227	33.24319	40.84424
protein_co ATP-bindin	464	423	459	672	685	685	4.148728	4.457019	5.408098	5.197917	6.880764	6.086915
protein_co arylacetam	0	1	0	0	1	0	0	0.038088	0	0	0.03631	0
protein_co abhydrolas	426	362	241	165	77	110	10.08625	10.10034	7.519209	3.379615	2.048142	2.588348
protein_co eukaryotic_	647	516	438	957	696	800	33.91369	31.87334	30.25378	43.3956	40.98538	41.6745
protein_co Rho_guanin	67	76	47	167	148	161	0.675114	0.902449	0.624072	1.455732	1.675378	1.612269
protein_co kelch-like_f	131	131	162	23	33	55	1.802305	2.123907	2.93702	0.273746	0.510059	0.75202
protein_co phospholip	2	1	3	28	34	34	0.016511	0.009728	0.032635	0.199964	0.315325	0.278946
protein_co vasoactive_	1	1	1	134	65	102	0.014084	0.016597	0.018559	1.632629	1.028448	1.427676
protein_co dynein_axo	192	203	166	39	44	63	0.764261	0.952234	0.87073	0.134298	0.196762	0.249224
protein_co signal_sequ	9836	8286	7422	11338	6410	8185	140.1312	139.1132	139.3388	139.7384	102.5944	115.8897
protein_co zinc_finger_	670	619	415	126	97	158	6.440978	7.01253	5.257266	1.047878	1.047606	1.509537
protein_co troponin_C	5	12	2	46	25	50	0.364106	1.029784	0.191921	2.897867	2.045252	3.618573
protein_co natural_kill	1717	1424	1607	1437	1368	1371	11.41382	11.15521	14.07705	8.263816	10.21636	9.057492
protein_co chloride_ch	125	114	120	247	149	214	2.011436	2.161763	2.544557	3.438398	2.69359	3.422312
protein_co forkhead_b	1259	1075	1017	105	113	126	9.369231	9.42744	9.973188	0.675975	0.944726	0.931877
protein_co eukaryotic_	9420	7891	7448	18280	19921	24751	88.00144	86.87164	91.68818	147.7332	209.0735	229.7954
protein_co signal_pept	952	934	778	1463	1109	1467	39.5603	45.73794	42.60269	52.59325	51.77299	60.58462

protein_co	NIMA-relat	308	227	222	578	487	431	4.380931	3.804947	4.161056	7.112243	7.782045	6.0926
protein_co	solute_carr	594	506	402	512	432	576	7.060384	7.087605	6.296551	5.264715	5.768657	6.804152
protein_co	INO80_con	181	237	231	365	359	296	0.677866	1.045974	1.14002	1.182555	1.510459	1.101709
protein_co	eukaryotic_	8003	6888	4852	10875	6939	9024	385.8714	391.3722	308.28	453.6094	375.8683	432.4127
protein_co	ADAM_met	616	522	564	156	133	122	5.154363	5.14721	6.218823	1.129229	1.250245	1.014527
protein_co	deoxyguan	496	351	339	617	493	650	22.95344	19.14169	20.67286	24.70098	25.63079	29.89435
protein_co	MOB_kinas	671	603	656	1109	1095	932	14.95722	15.83992	19.26935	21.38568	27.42153	20.64686
protein_co	KAT8_regul	804	594	654	857	685	711	8.102905	7.054695	8.685549	7.471856	7.755759	7.121376
protein_co	lectin_man	464	349	383	880	545	804	10.19279	9.034572	11.08686	16.72325	13.44995	17.55257
protein_co	rhotekin	444	442	309	1567	1337	1659	8.883523	10.42153	8.146959	27.12278	30.05265	32.98817
protein_co	tubulin_tyr	908	717	839	1587	1220	1305	9.280004	8.635522	11.2995	14.03144	14.00784	13.25508
protein_co	interleukin	4	10	6	10	11	4	0.099701	0.293728	0.197071	0.215626	0.30802	0.099085
protein_co	chemokine	5	11	1	0	0	0	0.318538	0.82583	0.083951	0	0	0
protein_co	phosphoin	664	589	800	579	620	502	3.550431	3.71138	5.636868	2.678272	3.724378	2.667635
protein_co	Kv_channel	903	705	650	17	10	5	13.06881	12.02388	12.39643	0.212843	0.162591	0.071916
protein_co	fumarylace	1377	1151	952	481	397	435	15.32473	15.09529	13.96146	4.630917	4.96362	4.811249
protein_co	nucleolin	13704	11406	10256	26688	23258	26579	179.8471	176.3992	177.3654	302.9948	342.908	346.6606
protein_co	ARP1_actin	870	695	531	1304	952	1288	20.58028	19.37421	16.55241	26.68533	25.29985	30.28011
protein_co	solute_carr	998	855	874	1013	911	895	11.97532	12.0901	13.81983	10.51548	12.28073	10.67307
protein_co	zeta-chain_	1	0	0	27	33	38	0.016175	0	0	0.377809	0.599666	0.610857
protein_co	ARP3_actin	3834	3227	3435	9273	7421	7179	30.21372	29.96803	35.67087	63.21721	65.69973	56.22451
protein_co	STEAP_fami	1095	917	830	1048	925	998	13.53816	13.36047	13.52254	11.20907	12.84802	12.26269
protein_co	erythrocyte	183	226	208	604	562	582	1.461708	2.127282	2.189312	4.173588	5.04307	4.620003
protein_co	transcriptic	0	0	0	26	36	41	0	0	0	0.12815	0.230428	0.232154
protein_co	Pre-mRNA_	1227	1049	825	2148	1469	1787	84.36182	84.99315	74.74637	127.7611	113.4677	122.1056
protein_co	tumor_pro	835	635	553	926	819	1260	22.12499	19.82793	19.30886	21.22612	24.37977	33.18003
protein_co	DnaJ_(Hsp4	69	61	57	58	85	78	0.731757	0.76235	0.796576	0.532119	1.012711	0.822095
protein_co	proopiome	0	0	3	28	10	12	0	0	0.146767	0.899277	0.417082	0.442755
protein_co	signal_tran	490	447	476	402	297	372	4.55027	4.891653	5.824824	3.229461	3.098465	3.433157
protein_co	otoferlin	0	1	0	0	0	1	0	0.008718	0	0	0	0.007352
protein_co	glycerol-3-p	310	260	308	1034	976	877	2.71672	2.68512	3.556876	7.839111	9.609087	7.638226
protein_co	centromere	106	87	80	666	448	585	3.864838	3.738108	3.843707	21.00694	18.3507	21.19781
protein_co	cytohesin_	3	0	0	4	0	0	0.070276	0	0	0.08106	0	0
protein_co	activin_A_r	688	535	635	419	315	309	11.96171	10.96139	14.54834	6.30205	6.152681	5.33916
protein_co	tetratricop	945	655	774	1149	1520	1120	6.594943	5.38676	7.117952	6.93685	11.91714	7.767959
protein_co	solute_carr	12	5	2	2	0	0	0.184249	0.090469	0.040466	0.026565	0	0
protein_co	MpV17_mi	1001	900	725	1050	694	1095	26.35203	27.92091	25.15086	23.9129	20.52525	28.64863
protein_co	general_tra	795	643	512	1757	1422	1551	10.54311	10.04893	8.947595	20.15748	21.18606	20.44198
protein_co	eukaryotic_	501	364	384	1098	755	937	6.178299	5.289805	6.240182	11.71377	10.45989	11.48366
protein_co	nuclear_rec	2788	2281	2013	3629	2197	2456	51.12556	49.29214	48.6434	57.56987	45.26103	44.7593
protein_co	integrin_be	4	3	1	181	155	209	0.045297	0.040035	0.014923	1.773177	1.971929	2.352158
protein_co	fibronectin	525	465	345	44	28	29	16.7737	17.50772	14.52525	1.216145	1.005025	0.920825
protein_co	integrin_al	415	282	460	102	108	80	5.244811	4.19989	7.660804	1.11518	1.533397	1.004804
protein_co	proteasom	839	747	724	3069	2077	2322	9.083332	9.530395	10.32896	28.74373	25.26206	24.9836

protein_co sorting_ne	2383	2042	1818	2343	1679	2157	61.72133	62.32668	62.04973	52.49845	48.85522	55.52275
protein_co GPR75-ASB	10	2	7	15	10	25	0.199928	0.047121	0.18442	0.259435	0.224607	0.496734
protein_co protein_ph	2466	1901	1772	5459	4115	5049	34.79544	31.60956	32.9479	66.63545	65.23012	70.8018
protein_co phosphodi	5	4	3	52	17	18	0.054187	0.051085	0.042843	0.487522	0.206979	0.19387
protein_co receptor_a	165	172	107	99	74	80	6.352919	7.804138	5.428852	3.297521	3.200886	3.061181
protein_co proprotein	64	65	45	52	15	41	1.186768	1.420386	1.099596	0.834166	0.312483	0.755578
protein_co adenomatc	492	376	290	121	135	136	2.235791	2.013544	1.736597	0.47568	0.689206	0.614207
protein_co interferon_	3	0	5	202	120	165	0.044179	0	0.097028	2.573402	1.985288	2.414831
protein_co ribosomal_	21868	16614	10963	24064	15334	17545	719.0768	643.7949	475.0403	684.5372	566.4619	573.3624
protein_co grancalcin_	15	19	6	700	484	485	0.398652	0.595064	0.21013	16.09399	14.45098	12.81015
protein_co INO80_con	695	618	525	386	258	433	18.03627	18.89981	17.95379	8.665871	7.521954	11.16759
protein_co mannosyl-c	1273	1117	859	1776	1772	2228	23.27941	24.07153	20.70006	28.09632	36.4046	40.49192
protein_co tetratricop	362	297	273	438	363	441	4.761401	4.603517	4.73177	4.983831	5.363915	5.76467
protein_co NADH_deh	561	399	274	607	417	540	7.934784	6.650469	5.106903	7.42718	6.626091	7.590592
protein_co polycomb_	287	268	176	308	157	221	8.478831	9.330308	6.851751	7.871687	5.210781	6.488675
protein_co growth_fac	54	43	62	190	115	150	1.200174	1.126227	1.815837	3.653145	2.871423	3.313227
protein_co CAP-GLY_d	260	224	252	231	153	153	3.206303	3.255265	4.095119	2.464372	2.119687	1.875134
protein_co T-cell_leuke	2	1	3	3	0	2	0.04957	0.029208	0.097982	0.064324	0	0.049264
protein_co spectrin_be	6770	5307	6589	5168	6360	5634	39.49427	36.48393	50.65237	26.0814	41.6823	32.66419
protein_co ancient_ub	1822	1471	1078	2723	1479	1925	56.90766	54.14298	44.36862	73.57547	51.89669	59.75342
protein_co reticulon_4	7379	5941	5729	11024	7721	8133	81.55566	77.37902	83.43922	105.4044	95.86922	89.33404
protein_co HtrA_serine	276	217	187	390	316	458	6.173094	5.719534	5.511506	7.546081	7.940173	10.1805
protein_co lysyl_oxida	1033	869	794	92	73	114	15.61623	15.48114	15.81726	1.203169	1.239789	1.712736
protein_co docking_pr	482	299	317	88	89	100	9.987303	7.300952	8.655562	1.577418	2.071764	2.059258
protein_co UDP-N-acet	11	10	7	919	677	646	0.150556	0.161292	0.126252	10.88138	10.40982	8.787145
protein_co polymerase	315	245	200	457	346	446	13.36251	12.24759	11.18001	16.77091	16.48932	18.80278
protein_co tachykinin_	1	0	0	2	6	6	0.022839	0	0	0.039516	0.15395	0.136188
protein_co coiled-coil_	909	834	873	704	546	439	4.905042	5.30337	6.207659	3.286355	3.309943	2.354252
protein_co acyl-CoA_d	0	0	1	158	171	173	0	0	0.027433	2.845547	3.999364	3.579328
protein_co eva-1_hom	408	273	330	161	89	113	11.90079	9.383939	12.68423	4.062603	2.91645	3.275696
protein_co mitochond	343	361	281	987	735	821	5.219535	6.473691	5.634804	12.99325	12.56533	12.41625
protein_co LanC_lantil	670	556	665	1044	906	830	7.419047	7.255298	9.703531	10.00085	11.27069	9.134002
protein_co WD_repeat	736	704	637	2214	1324	1455	9.067855	10.22131	10.34192	23.59757	18.32584	17.81556
protein_co EGF_contai	255	244	191	454	300	382	4.46427	5.033931	4.406345	6.875894	5.900389	6.646352
protein_co regeneratin	0	0	0	8	7	22	0	0	0	0.40665	0.462077	1.284694
protein_co Fanconi_an	132	111	135	301	256	312	4.115554	4.07835	5.546551	8.118652	8.966923	9.667599
protein_co fibronectin	338402	276584	350128	25954	24936	20032	1953.477	1881.523	2663.404	129.6113	161.7153	114.9236
protein_co signal_tran	848	706	745	1089	1007	916	10.41623	10.21943	12.05885	11.57193	13.89611	11.18201
protein_co glutaminas	838	654	938	3547	3150	3012	9.177607	8.440541	13.53702	33.60544	38.75655	32.7831
protein_co poly(A)_pol	183	178	181	335	250	254	1.595028	1.828287	2.078886	2.525952	2.447972	2.200192
protein_co dynein_axo	0	0	2	6	1	0	0	0	0.010905	0.021477	0.004648	0
protein_co peroxisom	98	61	57	149	111	121	2.799901	2.053778	2.145983	3.682697	3.562778	3.435672
protein_co unc-50_ho	326	330	301	530	417	572	7.946024	9.478799	9.667932	11.17561	11.41872	13.856
protein_co insulin-like	48380	40228	30453	13911	9080	11926	580.264	568.5849	481.3097	144.3381	122.3474	142.1557

protein_co	ELMO/CED-	302	251	205	282	290	369	3.358156	3.289082	3.00388	2.712727	3.622772	4.077838
protein_co	insulin-like	14943	12948	11292	296	364	389	127.2884	129.9753	126.7525	2.181251	3.483384	3.29314
protein_co	ubiquitin_s	1833	1593	2061	1757	1765	1440	8.544584	8.750872	12.66022	7.085381	9.243197	6.671148
protein_co	EF-hand_dc	14	8	5	651	349	455	0.328098	0.220939	0.154412	13.19836	9.188621	10.59734
protein_co	potassium_	8	0	4	5	3	11	0.143569	0	0.094594	0.077625	0.060484	0.196188
protein_co	chaperonin	3051	2534	2212	6803	4675	5276	64.09642	62.73433	61.23666	123.6389	110.3373	110.1554
protein_co	gamma-glu	1531	1242	1267	1120	993	1129	25.15601	24.0489	27.4333	15.92017	18.3301	18.43615
protein_co	EH_domain	350	298	373	728	739	581	3.587483	3.599524	5.038084	6.455296	8.50972	5.918444
protein_co	orthodenti	0	0	3	50	64	53	0	0	0.073153	0.8004	1.330464	0.974675
protein_co	thioredoxir	311	289	270	877	563	732	10.05782	11.01408	11.50647	24.53613	20.45507	23.52687
protein_co	coenzyme_	335	287	276	554	374	389	7.921051	7.996998	8.599672	11.33211	9.934789	9.141074
protein_co	splicing_fac	4485	3976	4106	5584	4488	4069	54.76023	57.20794	66.06274	58.98088	61.56087	49.37421
protein_co	ST3_beta-g	93	59	79	156	97	102	1.411962	1.0556	1.580527	2.048933	1.654478	1.53904
protein_co	carbohydra	231	173	174	401	296	358	4.31067	3.804398	4.278749	6.473515	6.205453	6.639348
protein_co	phosducin-	231	250	167	638	444	535	9.146873	11.66562	8.713888	21.85468	19.75116	21.05349
protein_co	MOB_famil	193	183	193	654	445	566	2.563375	2.864264	3.377901	7.514421	6.639936	7.471037
protein_co	heat_shock	139	92	130	447	244	450	7.746103	6.041759	9.546554	21.54959	15.27592	24.92244
protein_co	lysine_(K)-s	960	810	882	605	493	433	5.814364	5.781268	7.039379	3.169928	3.354493	2.606325
protein_co	phospholip	187	172	158	255	152	175	2.275854	2.466825	2.533931	2.684763	2.078239	2.116657
protein_co	charged_m	1085	942	972	1272	857	1019	18.11447	18.53335	21.38439	18.37156	16.07407	16.90751
protein_co	zinc_finger_	270	293	261	741	604	587	2.368921	3.029434	3.017603	5.624294	5.953506	5.118404
protein_co	interleukin	26	16	12	0	0	5	0.872285	0.632575	0.530519	0	0	0.166711
protein_co	protein_kir	0	0	0	0	1	0	0	0	0	0	0.02557	0
protein_co	SET_and_M	0	0	0	9	8	18	0	0	0	0.092982	0.107333	0.213637
protein_co	interleukin	4453	3859	3988	71	76	59	45.83827	46.81203	54.09605	0.632262	0.878897	0.603583
protein_co	wingless-ty	0	0	0	725	553	570	0	0	0	19.49748	19.31308	17.6101
protein_co	interleukin	13	9	7	0	2	1	0.263187	0.214719	0.186747	0	0.045488	0.02012
protein_co	interleukin	0	0	1	0	0	0	0	0	0.017467	0	0	0
protein_co	interleukin	25	42	21	11	8	9	0.343416	0.679887	0.380132	0.130718	0.123458	0.122866
protein_co	interleukin	4	0	6	4	4	0	0.076366	0	0.150948	0.066064	0.085793	0
protein_co	solute_carr	2	0	5	29	12	14	0.019572	0	0.064476	0.245502	0.131924	0.136155
protein_co	four_and_a	1157	1011	821	1605	1034	1273	12.54922	12.92235	11.73441	15.05987	12.59949	13.72212
protein_co	melanophil	447	377	391	239	153	215	6.190067	6.152282	7.135088	2.86318	2.380281	2.958938
protein_co	cyclin_Pas1	449	363	338	544	326	472	11.46672	10.92462	11.37481	12.01862	9.353183	11.97966
protein_co	UDP-glucur	777	636	562	1541	1043	1174	14.15038	13.64933	13.48709	24.27799	21.33931	21.24833
protein_co	ATP-bindin	41	20	12	16	11	10	0.719689	0.413712	0.277573	0.242965	0.216921	0.17445
protein_co	serine/thre	514	432	328	524	296	561	9.48803	9.397315	7.978506	8.367722	6.138379	10.29166
protein_co	solute_carr	0	0	0	18	6	2	0	0	0	0.160012	0.069265	0.020425
protein_co	high_densit	24039	19502	17970	12587	11461	11075	199.7251	190.9425	196.743	90.46937	106.9764	91.44705
protein_co	protein_ph	957	737	611	1369	902	1168	21.23409	19.27064	17.86478	26.27775	22.48419	25.75575
protein_co	PAS_domai	104	104	127	510	514	529	1.064141	1.254025	1.712396	4.514388	5.908508	5.379365
protein_co	serine/thre	3094	2398	2087	5914	3900	4712	35.4621	32.38921	31.5211	58.63926	50.21781	53.67339
protein_co	thyroid_pe	0	0	0	8	16	15	0	0	0	0.067964	0.176519	0.146394
protein_co	protein_C_	2	0	1	0	0	3	0.057141	0	0.037649	0	0	0.085182

protein_co inhibitor_c	654	606	499	2599	1705	2040	16.96394	18.52375	17.05629	58.32012	49.68468	52.58827
protein_co TATA_box_l	190	168	162	442	314	372	4.213988	4.390925	4.734668	8.480568	7.823811	8.199592
protein_co hippocalcir	171	143	133	3073	1782	2166	1.893518	1.866021	1.940706	29.43736	22.16818	23.83644
protein_co ornithine_(	810	634	629	6529	4154	4875	16.16367	14.90909	16.54018	112.7105	93.12588	96.68055
protein_co baculoviral	997	734	1063	1482	1250	1064	3.361279	2.916168	4.722561	4.322357	4.734439	3.56501
protein_co nucleolar_p	391	341	309	791	627	558	6.2106	6.382903	6.467703	10.86917	11.18854	8.808473
protein_co pleckstrin_	1437	1208	1267	2993	2570	2557	17.66339	17.49811	20.52242	31.82636	35.48946	31.23616
protein_co golgi_reass(	1975	1668	1532	2753	2160	2425	32.95256	32.79632	33.68337	39.73665	40.48786	40.21086
protein_co striatin_cal	417	275	487	662	612	540	2.702791	2.100468	4.15949	3.711909	4.456325	3.478402
protein_co CCAAT/enh	402	406	423	1016	752	702	6.145619	7.314299	8.521475	13.43681	12.91536	10.66563
protein_co protein_kir	1375	1117	1422	859	802	730	11.91194	11.40355	16.23358	6.437778	7.805545	6.285102
protein_co DDB1_and_	314	262	308	574	389	390	2.852346	2.804665	3.686872	4.510736	3.969824	3.520844
protein_co glutaminyl-	82	74	59	24	14	37	2.496355	2.654797	2.366897	0.632072	0.478817	1.119448
protein_co RAB3_GTPa	1080	891	936	1108	941	927	11.63538	11.31206	13.28824	10.32666	11.38926	9.925361
protein_co solute_carr	394	345	316	338	218	233	7.001931	7.225165	7.4002	5.196385	4.352383	4.115164
protein_co regulator_c	67	78	62	80	36	47	1.555722	2.134317	1.897072	1.606979	0.939093	1.084588
protein_co distal-less_l	29	19	26	2064	1531	1519	0.625882	0.483231	0.73944	38.53605	37.12093	32.58082
protein_co lactase	0	0	0	8	3	11	0	0	0	0.058352	0.028417	0.092173
protein_co aspartyl-tRI	873	722	709	2008	1374	1346	19.57539	19.07833	20.94967	38.95138	34.61241	29.99513
protein_co serine/argir	1143	1020	812	4103	2955	3471	21.1801	22.27353	19.82772	65.77281	61.51604	63.92137
protein_co syndecan_1	1400	1075	1077	4343	3551	4819	22.52124	20.37885	22.83046	60.43897	64.17471	77.04257
protein_co phospholip	35	32	28	0	3	8	0.27801	0.299536	0.293079	0	0.026771	0.063153
protein_co solute_carr	313	259	200	531	449	464	2.862417	2.791229	2.410201	4.200936	4.613005	4.217122
protein_co son_of_sev(	612	534	667	742	571	562	3.804143	3.911594	5.463439	3.989995	3.987407	3.471774
protein_co kynurenina	7	2	1	37	19	23	0.205311	0.069128	0.03865	0.938814	0.626062	0.670428
protein_co WAS/WASL	2903	2527	2554	247	229	182	33.50506	34.3697	38.84356	2.466172	2.969258	2.087586
protein_co origin_recc	348	259	252	966	776	912	4.272603	3.747315	4.077075	10.26014	10.70346	11.12802
protein_co cytochrom	2174	1862	1534	2040	1443	1760	37.66156	38.01242	35.01861	30.57257	28.08369	30.30129
protein_co partner_of_	272	247	202	1492	909	1114	6.299191	6.740931	6.164559	29.8915	23.64987	25.63957
protein_co origin_recc	204	231	188	1000	574	638	3.494003	4.662428	4.243124	14.81686	11.0447	10.85984
protein_co pleckstrin	1	0	0	9	22	23	0.018453	0	0	0.14367	0.456072	0.421793
protein_co Rho_family	1567	1219	1454	2616	1739	1751	29.87344	27.3859	36.52712	43.14366	37.24473	33.17508
protein_co activating_	659	523	690	736	598	638	8.354434	7.813406	11.52698	8.071838	8.516906	8.038258
protein_co thyroid_ad	385	352	397	663	574	535	2.937352	3.16479	3.991357	4.375944	4.919899	4.056567
protein_co AP2_associ	316	220	276	117	262	226	3.718461	3.050745	4.279766	1.191036	3.46359	2.642982
protein_co trafficking_	1169	975	1301	864	765	674	9.506609	9.343784	13.94194	6.07838	6.989105	5.447292
protein_co chromosor	140	114	110	152	96	102	2.871654	2.755599	2.973251	2.697185	2.2122	2.079284
protein_co TIA1_cytot(	1572	1344	1373	1635	1322	1412	17.90903	18.04371	20.61222	16.11388	16.91998	15.98688
protein_co prenylcyste	2404	2207	2481	2446	2126	2065	23.81107	25.76047	32.38217	20.95868	23.65684	20.32704
protein_co KISS1_recep	0	1	2	12	5	6	0	0.037136	0.083052	0.327135	0.177012	0.187907
protein_co endothelial	911	631	842	12479	15159	14235	9.346753	7.629197	11.38385	110.7606	174.7278	145.1475
protein_co AT_rich_int	1031	836	607	7149	6937	9637	9.122876	8.71739	7.077772	54.72445	68.95946	84.74705
protein_co SMT3_supp	1273	1176	1098	3236	2257	2919	43.87623	47.76561	49.86985	96.4878	87.39397	99.98725
protein_co glutamate_	14	33	18	10	2	21	0.225899	0.62749	0.382731	0.139588	0.036255	0.336756

protein_co	ventral_ant	3	7	0	2	1	0	0.138468	0.380745	0	0.079859	0.051853	0
protein_co	ATPase_H+_	6	1	0	0	0	0	0.166743	0.032749	0	0	0	0
protein_co	nuclear_fac	1233	1161	1072	2140	1232	1362	22.87986	25.38807	26.21319	34.35319	25.68326	25.11754
protein_co	mutS_hom	940	700	755	2501	2636	2265	11.49828	10.09044	12.16989	26.46559	36.22424	27.53485
protein_co	pleckstrin_	168	153	142	172	142	131	3.194715	3.428636	3.558328	2.82953	3.033614	2.475733
protein_co	sepiapterin	137	137	75	226	179	224	4.900619	5.77508	3.535301	6.993617	7.193371	7.963208
protein_co	EPH_recept	481	313	411	305	310	246	4.012704	3.077113	4.518233	2.201177	2.905379	2.039561
protein_co	par-3_parti	29	13	37	83	96	66	0.187826	0.099222	0.315787	0.465049	0.698518	0.424826
protein_co	phenylalan	986	819	804	2543	1754	1952	15.49416	15.16638	16.64876	34.57008	30.9649	30.4846
protein_co	Alstrom_sy	268	193	250	393	375	280	1.097987	0.931809	1.3497	1.392893	1.726008	1.140066
protein_co	B-cell_CLL/	1111	878	877	857	1105	938	9.368819	8.72514	9.745524	6.251937	10.46844	7.861099
protein_co	paired_rela	12605	11191	12264	1126	1227	943	155.7706	162.9741	199.7145	12.03771	17.03477	11.58148
protein_co	24-dehydrc	6234	4847	5647	10519	8855	8893	77.6551	71.15137	92.69488	113.355	123.9198	110.0934
protein_co	DnaJ_(Hsp4	457	446	354	701	593	530	3.840933	4.417356	3.920654	5.096846	5.599177	4.426964
protein_co	MAP/microc	47	32	26	257	213	267	0.47576	0.381722	0.346816	2.250539	2.422251	2.686033
protein_co	MORN_repe	44	79	47	82	97	73	1.221502	2.584494	1.719389	1.969329	3.025256	2.014067
protein_co	glutathione	302	269	227	220	127	171	13.01969	13.66637	12.89598	8.205016	6.151011	7.326549
protein_co	calcyclin_b	951	825	704	3964	2490	3086	17.76531	18.16157	17.33005	64.06029	52.25654	57.2925
protein_co	sterol_carri	1391	1197	1073	1044	802	1043	14.15083	14.35014	14.38432	9.187943	9.165966	10.54505
protein_co	pappalysin_	30	26	27	110	74	63	0.163989	0.167484	0.194487	0.520173	0.454437	0.342249
protein_co	Ral_GEF_wi	270	257	298	370	398	323	2.450132	2.748311	3.5635	2.904627	4.057493	2.912982
protein_co	angiopoieti	261	255	212	12	12	13	4.12712	4.751754	4.417508	0.164154	0.213175	0.204296
protein_co	centrosoma	515	435	404	879	698	695	4.24418	4.224574	4.387355	6.266693	6.462358	5.692211
protein_co	family_with	1035	1064	1059	1595	1297	1243	9.156739	11.09301	12.34614	12.20743	12.89109	10.92902
protein_co	transcriptic	108	98	95	260	158	221	1.395564	1.492311	1.61765	2.906447	2.293677	2.838102
protein_co	transmemb	1857	1770	1386	1089	806	1021	39.75391	44.65276	39.09903	20.16782	19.38439	21.72218
protein_co	leucine_ric	526	413	388	1661	1343	1533	13.67058	12.64906	13.28824	37.34511	39.21264	39.59614
protein_co	WD_repeat	278	217	167	845	545	624	2.417079	2.223376	1.913363	6.355736	5.323432	5.391882
protein_co	mitochond	1932	1609	1237	3610	2279	2737	64.6536	63.4525	54.54942	104.5095	85.67991	91.02696
protein_co	isoprenylcy	1465	1160	1323	5453	4968	5579	16.25625	15.16868	19.34538	52.34572	61.93175	61.52458
protein_co	ribosomal_	8709	8018	6448	7000	6051	8737	202.3094	219.4931	197.382	140.6724	157.9152	201.7064
protein_co	chromodor	11	15	5	3	13	17	0.060372	0.097016	0.036162	0.014244	0.080156	0.092726
protein_co	quiescin_Q	8495	6956	5965	2200	1582	1839	48.30134	46.60821	44.69316	10.82135	10.10535	10.39171
protein_co	syntaxin_bi	417	366	366	686	478	511	8.705203	9.003907	10.06836	12.38882	11.21037	10.60165
protein_co	PHD_finger	588	435	511	764	627	637	8.456752	7.372633	9.684607	9.505668	10.13078	9.104904
protein_co	ERBB_recep	1176	1036	945	4516	3987	3969	20.05754	20.82271	21.23914	66.63269	76.39513	67.27615
protein_co	parkinson_	3733	3233	2528	4533	3842	5236	181.6441	185.3856	162.097	190.8147	210.0243	253.2051
protein_co	KIAA1324	6	5	3	16	27	15	0.053243	0.052286	0.03508	0.122826	0.269167	0.132285
protein_co	opioid_rec	0	0	0	45	37	19	0	0	0	1.161754	1.240479	0.56351
protein_co	adenosine_	1663	1496	1190	588	526	678	22.58037	23.93743	21.2922	6.906837	8.023681	9.149096
protein_co	serine/argi	1332	1106	1010	3305	2553	2715	29.54227	28.90692	29.51861	63.41239	63.61207	59.8438
protein_co	mitochond	333	349	230	682	438	590	7.296917	9.012135	6.641372	12.92833	10.78247	12.84863
protein_co	potassium_	55	66	63	186	146	173	0.383277	0.542002	0.578529	1.121311	1.143015	1.198135
protein_co	ER_degrada	680	537	844	566	469	400	5.218886	4.856801	8.535838	3.757927	4.043811	3.050974

protein_co	WD_repeat	211	190	152	1342	762	866	4.336394	4.601579	4.116467	23.85952	17.59342	17.6878
protein_co	ATP_syntha	2988	2432	2072	5121	3355	4297	50.12284	48.07572	45.8015	74.31438	63.22614	71.6358
protein_co	RAP1A_me	825	713	642	1268	843	1073	8.693535	8.853991	8.914814	11.55912	9.979737	11.23704
protein_co	histone_de	1366	1245	1111	2205	1756	2012	30.01968	32.24272	32.17393	41.92054	43.35397	43.94332
protein_co	capping_pr	2946	2542	2458	5226	3861	4021	51.64376	52.51312	56.78084	79.25334	76.03858	70.05334
protein_co	S100P_bin	549	467	382	792	559	651	6.731034	6.747353	6.17174	8.400355	7.699638	7.932317
protein_co	ring_finger	153	160	160	879	672	716	3.117772	3.8422	4.29643	15.49547	15.38407	14.50025
protein_co	secretory_c	1618	1285	1094	1922	1115	1241	55.73099	52.1589	49.65584	57.27098	43.14616	42.48148
protein_co	tripartite_r	193	117	152	224	222	199	2.972829	2.12376	3.085254	2.984857	3.841622	3.046318
protein_co	ash1_(absen	892	764	1023	446	508	487	3.954393	3.99131	5.976205	1.71046	2.530042	2.145624
protein_co	discs_large_	1	3	2	8	10	15	0.01373	0.048538	0.036184	0.095018	0.154243	0.204671
protein_co	splicing_fac	4728	4044	4045	12781	10764	11183	66.80145	67.33279	75.31158	156.2199	170.8564	157.0277
protein_co	ras_homolo	133	138	97	816	860	817	1.610511	1.969238	1.547813	8.548012	11.69929	9.83204
protein_co	gon-4-like_	655	532	675	553	633	623	4.495832	4.30316	6.105305	3.28365	4.881143	4.24978
protein_co	Rho/Rac_gu	1899	1718	1266	1486	1518	1709	22.66853	24.16733	19.91439	15.34547	20.35726	20.2745
protein_co	late_endos	714	533	461	609	519	836	43.54824	38.30952	37.0517	32.1331	35.56221	50.67436
protein_co	myocyte_en	1065	1010	818	410	442	471	9.452164	10.56356	9.566868	3.147955	4.407101	4.154437
protein_co	dedicator_c	998	773	913	1385	1230	1031	7.431099	6.782801	8.958351	8.921446	10.28908	7.629407
protein_co	spermidine	3424	2799	2161	6447	3071	3611	143.1832	137.9331	119.0825	233.2271	144.2737	150.0706
protein_co	deleted_in_	1	5	4	0	5	1	0.075307	0.443725	0.396946	0	0.423015	0.074842
protein_co	F-box_prot	123	75	105	159	120	212	4.174194	2.99941	4.695606	4.667965	4.575071	7.150115
protein_co	F-box_prot	54	45	24	9	13	8	1.880798	1.847005	1.101526	0.271178	0.508676	0.276916
protein_co	chromosom	396	363	336	580	497	499	2.042341	2.20621	2.283533	2.587761	2.879643	2.557663
protein_co	SWT1_RNA	80	93	94	154	107	112	1.105817	1.514898	1.712206	1.841523	1.661599	1.538583
protein_co	MAD2_mit	625	441	452	704	439	599	17.78931	14.79193	16.95323	17.33464	14.0376	16.94399
protein_co	DnaJ_(Hsp4	19	11	23	350	294	310	0.175149	0.119496	0.279393	2.791157	3.044736	2.840041
protein_co	leptin_rece	261	239	289	160	104	126	1.679543	1.812406	2.450661	0.890704	0.751853	0.805807
protein_co	influenza_v	1004	984	1041	4274	3583	3934	12.65843	14.62003	17.29545	46.61694	50.75071	49.29356
protein_co	KIAA2013	1532	1205	1021	2968	1888	2204	28.81194	26.70594	25.30313	48.28815	39.89006	41.19409
protein_co	mitofusin_	1439	1122	1232	2754	2675	2864	16.78389	15.42169	18.93553	27.7881	35.05135	33.1982
protein_co	proteoglyca	17	21	25	44	15	31	0.178429	0.259743	0.345774	0.399515	0.176871	0.323362
protein_co	migration_	368	321	228	1334	732	1057	11.39982	11.71823	9.307214	35.74941	25.47476	32.54128
protein_co	smg-7_hom	1122	856	1008	3132	2862	2451	9.949714	8.945376	11.77913	24.02716	28.51258	21.60084
protein_co	neutrophil_	15	13	5	11	11	11	0.348908	0.356345	0.153259	0.221348	0.28745	0.254286
protein_co	phosducin	2	0	2	2	1	3	0.085251	0	0.11234	0.07375	0.047887	0.127087
protein_co	solute_carr	272	244	259	423	464	462	2.336896	2.4704	2.932277	3.143937	4.47855	3.944773
protein_co	phospholip	213	212	225	46	56	25	3.922237	4.600417	5.459735	0.732782	1.158487	0.457513
protein_co	growth_arr	1486	1275	1161	1985	1567	2116	52.58711	53.17136	54.14116	60.76927	62.29864	74.41934
protein_co	PRAME_fam	1	0	0	2	1	0	0.02451	0	0	0.042406	0.027535	0
protein_co	PRAME_fam	3	0	0	0	3	3	0.088927	0	0	0	0.099904	0.088377
protein_co	wntless_ho	5435	4454	4695	4524	4135	4381	104.7068	101.119	119.1916	75.3982	89.49524	83.87997
protein_co	PR_domain	1194	1070	1013	1011	1146	1065	7.944143	8.389452	8.881514	5.819114	8.565967	7.042097
protein_co	regulator_c	254	234	239	147	72	105	10.00522	10.86215	12.40582	5.009255	3.18621	4.110473
protein_co	retinal_pig	14	8	8	2	0	1	0.283975	0.191227	0.213834	0.035095	0	0.020159

protein_co	TROVE_dor	1025	1033	853	1385	1184	1076	6.914439	8.211841	7.582579	8.082503	8.972921	7.213649
protein_co	adenosine_	0	0	1	0	0	0	0	0	0.029165	0	0	0
protein_co	ubiquitin_(	316	298	237	1183	863	959	8.754241	9.728699	8.651961	28.3517	26.85909	26.40339
protein_co	breast_carc	313	305	234	1219	695	874	12.75637	14.64839	12.56706	42.97834	31.82122	35.40006
protein_co	serine/argir	2291	2030	2205	3142	2566	2674	30.26143	31.59858	38.38025	35.90323	38.07765	35.10229
protein_co	cystathiona	140	119	96	189	113	116	3.626095	3.632162	3.276553	4.23483	3.288052	2.985925
protein_co	agmatine_u	15	16	12	36	23	53	0.317646	0.399281	0.334864	0.659504	0.547178	1.115418
protein_co	olfactomed	4337	3900	3044	1600	1327	1454	111.2967	117.9409	102.9372	35.52024	38.25717	37.08232
protein_co	complemer	2	1	2	0	0	0	0.053884	0.031749	0.071006	0	0	0
protein_co	pleckstrin_	1782	1380	1316	1828	1540	1872	22.88715	20.88672	22.2728	20.31063	22.2205	23.89459
protein_co	crystallin_z	497	377	447	1106	753	840	9.076121	8.113202	10.75688	17.47278	15.44856	15.24519
protein_co	putative_h	381	323	390	454	419	464	4.675595	4.671126	6.306834	4.81982	5.776636	5.658998
protein_co	zinc_finger_	744	484	438	664	523	642	14.21953	10.90096	11.03116	10.97851	11.22957	12.1943
protein_co	CD58_mole	121	96	77	238	120	181	4.82369	4.509956	4.04501	8.207936	5.37433	7.171041
protein_co	transcriptic	14	19	5	22	22	29	0.33859	0.541511	0.15935	0.460291	0.597748	0.697034
protein_co	transcriptic	196	203	192	870	681	748	2.126754	2.595759	2.745347	8.166642	8.301517	8.066266
protein_co	nuclear_rec	0	0	0	6	2	8	0	0	0	0.054029	0.023388	0.082759
protein_co	kinesin_fan	110	93	95	104	140	112	0.588531	0.586363	0.669784	0.481363	0.841499	0.59553
protein_co	transmemb	1214	1058	807	1805	1191	1733	22.2235	22.82373	19.46714	28.58472	24.49371	31.52841
protein_co	ADP-ribosy	408	346	308	1070	701	1000	12.9496	12.94134	12.88195	29.37939	24.99557	31.5432
protein_co	MAP7_dom	4723	3641	2925	7944	5899	7161	72.34963	65.72735	59.04444	105.2739	101.5186	109.0189
protein_co	tryptophan	382	323	281	348	239	315	7.1944	7.168707	6.973846	5.669875	5.056828	5.895918
protein_co	hydroxyaci	0	1	0	0	0	0	0	0.037403	0	0	0	0
protein_co	-	164	190	70	131	63	85	4.723788	6.449221	2.656926	3.264231	2.03862	2.433185
protein_co	organic_sol	98	90	72	105	84	91	3.546287	3.837933	3.433326	3.287003	3.414885	3.272644
protein_co	mitochond	966	900	609	2272	1380	1989	24.04372	26.39819	19.97454	48.92107	38.58804	49.20044
protein_co	exocyst_co	372	312	344	383	412	338	3.861578	3.816661	4.705602	3.439408	4.804721	3.48697
protein_co	glyceronep	874	876	788	1054	751	777	17.50678	20.67789	20.79965	18.26411	16.89989	15.46769
protein_co	translin-ass	399	295	363	784	584	603	3.752613	3.269565	4.498858	6.378814	6.170534	5.636218
protein_co	chromoson	307	256	207	659	544	793	6.32408	6.214498	5.619066	11.74377	12.58945	16.23461
protein_co	Ras-related	653	607	606	769	602	705	12.65391	13.8614	15.47458	12.89142	13.1056	13.5772
protein_co	tubulin_fol	515	453	375	868	549	629	13.77001	14.27356	13.21274	20.0775	16.49105	16.71426
protein_co	nidogen_1	10761	9216	9723	4084	4006	3107	97.15178	98.05002	115.6733	31.89678	40.63106	27.87719
protein_co	lectin_gala	177	146	171	440	288	282	1.459588	1.418786	1.858181	3.138866	2.668079	2.311084
protein_co	hippocalcir	0	0	0	3	1	0	0	0	0	0.028294	0.012248	0
protein_co	5-methylte	1015	838	896	1142	1107	1009	5.103534	4.965421	5.936737	4.967457	6.25319	5.042034
protein_co	bone_morp	13	9	16	16	10	13	0.142728	0.116443	0.231483	0.151967	0.123343	0.141846
protein_co	v-myc_mye	7	3	4	29	19	24	0.113817	0.057483	0.085704	0.407914	0.347065	0.387819
protein_co	signal-indu	842	555	688	1219	1331	1175	6.663127	5.175664	7.17446	8.345122	11.83295	9.240883
protein_co	zona_pellu	0	0	0	0	0	1	0	0	0	0	0	0.029246
protein_co	rearranged_	547	480	450	591	451	408	4.636363	4.794446	5.026173	4.333518	4.294531	3.436845
protein_co	kynurenine	10	0	3	5	1	0	0.100629	0	0.039781	0.043527	0.011305	0
protein_co	zinc_finger_	31	47	25	43	47	48	0.782628	1.398294	0.831703	0.939129	1.333032	1.204327
protein_co	potassium_	7	1	0	14	7	11	0.090409	0.01522	0	0.156425	0.101569	0.141194

protein_co	regulating_	16	0	4	52	54	51	0.117078	0	0.03857	0.32917	0.443911	0.37088
protein_co	v-akt_muri	376	308	358	338	331	249	3.882546	3.747888	4.871319	3.019315	3.839775	2.555276
protein_co	ets_variant	512	491	505	801	948	902	5.159077	5.830296	6.705454	6.982285	10.73147	9.032713
protein_co	acyl-CoA_d	300	241	194	719	542	694	6.06426	5.74091	5.167651	12.57328	12.30849	13.94202
protein_co	ST6_(alpha-	48	36	45	32	24	20	0.677464	0.598763	0.836936	0.390713	0.380544	0.280533
protein_co	latrophilin_	840	663	843	2705	2118	2015	7.056559	6.563482	9.332029	19.65821	19.98889	16.8228
protein_co	peptidyl_ar	0	0	1	26	45	23	0	0	0.016056	0.274056	0.615976	0.278509
protein_co	succinate_d	651	620	463	1566	914	1073	29.89123	33.54761	28.01422	62.20389	47.14743	48.96347
protein_co	microfibrill	1267	992	737	2448	1559	2051	28.29027	26.10233	21.68517	47.28626	39.10711	45.51304
protein_co	ribosome_p	315	261	295	1044	560	818	12.04073	11.75682	14.85933	34.52278	24.04802	31.07458
protein_co	lysine_(K)-s	2385	2209	2112	2477	2185	1888	16.97557	18.52843	19.8091	15.25193	17.47175	13.35511
protein_co	UDP-N-acte	1291	1043	949	902	532	588	29.1582	27.76041	28.24461	17.62398	13.4988	13.19841
protein_co	actin-like_8	3	0	0	1	0	5	0.085343	0	0	0.02461	0	0.14136
protein_co	chitobiase_	286	300	254	130	81	89	4.912759	6.072784	5.749472	1.931816	1.563124	1.519354
protein_co	regulator_d	444	360	511	1617	1285	1544	6.228352	5.951135	9.445956	19.6229	20.25081	21.5252
protein_co	kelch-like_f	568	540	469	656	667	600	8.952213	10.02958	9.74069	8.944353	11.81019	9.398163
protein_co	synovial_sa	325	258	271	1190	1022	1104	2.94469	2.754755	3.235641	9.32752	10.40294	9.941111
protein_co	zinc_finger_	581	518	520	992	813	837	5.059	5.31527	5.966596	7.472453	7.952947	7.243086
protein_co	retinoblast	293	262	263	679	451	502	3.522187	3.711532	4.166154	7.061185	6.090744	5.997333
protein_co	guanylate_l	213	151	194	25	40	42	3.065914	2.561323	3.679738	0.311303	0.646829	0.600813
protein_co	guanylate_l	221	241	212	6	3	1	3.855011	4.954017	4.873086	0.090541	0.05879	0.017336
processed_	PINK1_anti	88	99	84	230	111	181	1.048572	1.390138	1.318955	2.370864	1.485894	2.143404
protein_co	kinesin_fan	35	37	27	45	22	54	0.466852	0.581594	0.47458	0.519262	0.329673	0.715837
protein_co	G_protein-r	159	140	115	184	105	160	3.118791	3.236118	2.9725	3.122267	2.313809	3.119025
protein_co	cyclin-depe	16	4	6	279	184	213	0.213579	0.062923	0.105542	3.221859	2.759347	2.825717
protein_co	RAB7_mem	277	221	198	149	100	99	4.481863	4.213841	4.221617	2.085586	1.817724	1.591929
protein_co	CD160_mo	36	45	25	13	20	13	0.562371	0.8284	0.51463	0.175682	0.350994	0.201824
protein_co	thioredoxir	1453	1266	1169	453	288	308	26.28058	26.98424	27.86241	7.088112	5.852089	5.536429
protein_co	endothelin_	1841	1637	1436	3162	3198	3342	19.11441	20.02917	19.647	28.40089	37.30221	34.48444
protein_co	3-hydroxyn	684	655	528	449	307	363	16.83479	18.99766	17.1246	9.560069	8.48866	8.87908
protein_co	UDP-galact	429	402	250	1457	986	1229	10.95595	12.09834	8.413324	32.18958	28.28908	31.1928
protein_co	inhibitor_d	4280	3304	3032	8754	5761	7608	181.1251	164.7714	169.0826	320.4825	273.8935	319.9742
protein_co	complemer	0	0	0	2	2	0	0	0	0	0.021603	0.028055	0
protein_co	CD46_mole	1524	1293	1370	2148	1893	1730	10.30949	10.30761	12.21259	12.57041	14.38639	11.63076
protein_co	PRP3_pre-r	620	623	527	1251	1008	984	12.64872	14.97786	14.16773	22.07878	23.10278	19.95076
protein_co	anterior_pl	2301	1905	1535	3359	2718	4110	51.77103	50.5094	45.51068	65.37974	68.70189	91.90129
protein_co	leucine_pro	6629	5170	4123	1962	1312	1484	116.943	107.479	95.84606	29.9425	26.00213	26.01774
protein_co	solute_carr	2127	1745	1318	11314	7662	8435	33.93776	32.81091	27.71188	156.169	137.3431	133.7551
protein_co	EBNA1_bin	860	648	529	4869	2757	3649	30.29225	26.8977	24.55408	148.3665	109.0985	127.737
protein_co	cell_divisio	535	422	373	7575	4488	5701	15.9389	14.81577	14.64362	195.2317	150.2127	168.7972
protein_co	myeloproli	0	0	1	2	4	5	0	0	0.035776	0.046973	0.122002	0.134908
protein_co	artemin	3	2	1	74	98	105	0.081741	0.064218	0.035905	1.744271	2.999815	2.843271
protein_co	importin_1	487	441	386	969	761	744	6.621023	7.065482	6.915415	11.3968	11.62331	10.05261
protein_co	ATPase_H+_	1167	1010	905	1881	1244	1858	25.40384	25.90938	25.96043	35.42259	30.42271	40.1961

protein_co	UDP-Gal:be	1884	1524	1166	2053	1483	1742	37.9387	36.16542	30.94104	35.76461	33.54994	34.86256
protein_co	ERI1_exoril	915	888	611	1777	986	1178	28.76545	32.89804	25.31197	48.32818	34.82379	36.80484
protein_co	patched_2	50	36	45	8	5	11	0.615879	0.522559	0.730421	0.085247	0.06919	0.134657
protein_co	aldo-keto_r	1462	1138	968	1542	1093	1326	42.57411	39.05239	37.14569	38.84594	35.75752	38.37526
protein_co	peroxiredo	5574	4875	3941	15266	10850	12910	239.3294	246.6668	222.9822	567.0447	523.3688	550.89
protein_co	phosphoin	1920	1533	1853	660	599	566	18.12207	17.05124	23.04713	5.389067	6.351591	5.309244
protein_co	tetraspanin	23	15	6	17	13	6	0.753958	0.579453	0.259182	0.482094	0.478754	0.19547
protein_co	basic_leuci	367	241	311	619	472	411	7.067786	5.469423	7.892463	10.31267	10.21194	7.866269
protein_co	coiled-coil_	16	1	5	50	17	21	0.416244	0.030657	0.171409	1.12528	0.49685	0.542946
protein_co	solute_carr	112	86	111	527	421	370	1.615198	1.461549	2.109432	6.574782	6.820856	5.302969
protein_co	fatty_acid_	19	21	8	60	36	38	0.480362	0.625665	0.266526	1.31229	1.022509	0.954792
protein_co	NOP2/Sun_	336	242	249	587	419	467	4.094884	3.47556	3.998862	6.188756	5.736742	5.656253
protein_co	transmemb	1086	1012	1058	1965	1371	1317	9.419056	10.34344	12.092	14.74359	13.3587	11.35202
protein_co	down-regul	904	784	826	1370	1067	1113	14.76208	15.08698	17.77436	19.35364	19.57458	18.06275
protein_co	calponin_3	3617	3005	2959	7931	5784	6632	88.44692	86.59359	95.34852	167.7742	158.8955	161.1715
protein_co	proline-rich	3287	2776	3352	5412	5728	4688	16.78729	16.70734	22.55899	23.91122	32.86495	23.79458
protein_co	coagulation	723	621	475	745	468	572	16.73648	16.94044	14.48953	14.91919	12.17085	13.15926
protein_co	ATP-bindin	526	423	457	1555	1365	1272	6.37668	6.043052	7.300623	16.30806	18.59048	15.32518
protein_co	vesicle-assc	265	268	263	143	130	140	2.719396	3.240921	3.556453	1.269479	1.498715	1.42779
protein_co	DPH5_hom	364	308	296	322	305	337	8.92567	8.900149	9.564582	6.830592	8.40211	8.212568
protein_co	Fas_ligand_	0	0	0	0	1	0	0	0	0	0	0.031502	0
protein_co	polypyrimi	403	402	383	485	395	418	6.951848	8.172	8.706203	7.23769	7.654932	7.166071
protein_co	tumor_nec	30	53	33	32	19	24	0.457703	0.952896	0.663455	0.422353	0.325661	0.363901
protein_co	peroxiredo	4432	4140	3280	12388	8101	10180	134.0003	147.5073	130.6816	324.0188	275.1653	305.8887
protein_co	aspartyl-tRI	341	345	256	1473	968	1023	5.149138	6.139123	5.093953	19.24181	16.42119	15.35202
protein_co	hydroxyste	8	10	8	4	2	0	0.286749	0.422395	0.377865	0.124032	0.080536	0
protein_co	interferon_	6	5	3	457	371	385	0.073768	0.072443	0.048604	4.860683	5.124377	4.704229
protein_co	digestive_o	291	250	294	618	359	403	1.824039	1.846665	2.428416	3.351139	2.528043	2.510474
protein_co	Lipid_phos	0	0	6	9	1	0	0	0	0.101253	0.099707	0.014387	0
protein_co	Lipid_phos	4	4	2	18	23	15	0.039442	0.04648	0.025987	0.153544	0.254786	0.146994
protein_co	serpin_pep	0	1	2	0	3	0	0	0.039139	0.087532	0	0.111937	0
protein_co	RCAN_fami	38	30	27	383	325	241	0.724175	0.673734	0.678045	6.314248	6.958126	4.56443
protein_co	SYF2_homc	563	542	463	682	556	671	15.19153	17.23453	16.463	15.9199	16.85454	17.9939
protein_co	chromoson	773	680	480	867	509	753	13.48826	13.98275	11.03704	13.08756	9.977997	13.05813
protein_co	solute_carr	270	247	303	476	479	509	2.583421	2.785066	3.8204	3.940047	5.148918	4.84015
protein_co	REST_corep	437	423	413	654	603	546	5.448708	6.215264	6.785736	7.054283	8.446533	6.765726
protein_co	stathmin_1	2633	2002	1771	11312	7655	8911	47.30018	42.38216	41.92425	175.7982	154.4921	159.0919
protein_co	mitochond	462	457	328	374	233	317	7.498081	8.740402	7.014824	5.251009	4.24828	5.113015
protein_co	mannosida	963	747	691	48	37	39	10.98517	10.04172	10.38708	0.47368	0.474167	0.442135
protein_co	NIMA-relat	86	91	109	755	545	580	2.136521	2.66414	3.568371	16.22627	15.21088	14.32011
protein_co	ribosomal_	80	86	58	1055	860	958	1.322698	1.675623	1.26367	15.0899	15.97417	15.74149
protein_co	dehydrodo	677	648	605	1063	777	974	10.73728	12.11122	12.64433	14.58485	13.84445	15.35233
protein_co	neudesin_n	842	780	510	750	602	752	47.32093	51.65863	37.76993	36.4641	38.00903	42.00187
protein_co	NSL1_MIND	246	230	170	764	564	585	5.620839	6.192999	5.118583	15.10158	14.47752	13.28408

protein_co	prospero_h	17	11	8	77	158	135	0.105907	0.080756	0.065675	0.414982	1.105813	0.835832
protein_co	AT_rich_int	1894	1582	1603	2858	3470	2649	11.6906	11.50722	13.03842	15.26096	24.06219	16.24981
protein_co	centromere	724	494	581	2948	2737	2437	3.718762	2.990156	3.932518	13.09937	15.79369	12.44013
protein_co	replication	318	303	220	1591	1065	1236	9.609153	10.78966	8.760229	41.59022	36.15403	37.11813
protein_co	protein_ph	769	692	629	1426	1045	980	15.35708	16.28529	16.55266	24.6357	23.44486	19.44993
protein_co	syntaxin_1	802	686	683	761	494	478	13.78976	13.89996	15.47526	11.31957	9.542417	8.168079
protein_co	mitochond	14	23	25	55	40	46	0.34846	0.67462	0.819973	1.184269	1.118494	1.137869
protein_co	solute_carr	11	6	10	4	6	5	0.154511	0.099317	0.185098	0.048606	0.094682	0.069798
protein_co	oxysterol_b	600	597	564	3474	2755	2716	7.027566	8.240149	8.704976	35.20031	36.25136	31.61499
protein_co	thioredoxir	864	737	582	2143	1111	1568	19.09058	19.19022	16.94584	40.96288	27.57836	34.4319
protein_co	extended_s	1984	1664	1600	3452	2828	2766	17.62331	17.41832	18.7284	26.52648	28.22112	24.41786
protein_co	CD3e_mole	68	75	50	463	241	303	1.095553	1.423944	1.061523	6.453102	4.36205	4.851509
protein_co	mesoderm_	1034	835	755	2040	1580	1971	12.85905	12.2372	12.37286	21.94733	22.07469	24.36042
protein_co	reticulocall	1232	1116	1059	3497	2305	2516	16.57096	17.6892	18.77015	40.69074	34.83028	33.63236
protein_co	cholinergic	0	0	0	1	0	0	0	0	0	0.017461	0	0
protein_co	mucin_5B_	17	10	14	0	10	18	0.050212	0.034807	0.05449	0	0.033182	0.052837
protein_co	cathepsin_l	2938	2282	1754	2116	1323	1757	73.26455	67.0602	57.63768	45.6479	37.06389	43.54352
protein_co	collectin_s	2	2	3	9	10	14	0.068004	0.080138	0.134419	0.264734	0.38199	0.473087
protein_co	stromal_an	562	401	595	386	472	377	4.915387	4.133071	6.857617	2.920598	4.637805	3.27697
protein_co	alpha-14-N	1	1	0	0	0	0	0.029893	0.035227	0	0	0	0
protein_co	serine/thre	1960	1724	1272	1971	1748	2231	29.20471	30.27201	24.97577	25.4066	29.26088	33.03742
protein_co	myeloid/ly	1007	797	1070	1290	1619	1282	3.212702	2.996446	4.498416	3.560358	5.802791	4.064795
protein_co	trehalase_(l	25	23	26	2	3	2	0.477807	0.518021	0.654818	0.033068	0.064414	0.037988
protein_co	intraflagell	499	431	325	516	327	384	14.52312	14.78236	12.46458	12.99188	10.69193	11.10709
protein_co	matrix_met	3	4	3	0	0	0	0.051971	0.081659	0.068485	0	0	0
protein_co	apolipopro	11	14	0	3	2	14	0.474614	0.71184	0	0.111978	0.096945	0.600323
protein_co	zinc_finger_	0	0	0	0	5	2	0	0	0	0	0.064201	0.022718
protein_co	solute_carr	9	12	5	0	1	0	0.091033	0.143036	0.066644	0	0.011363	0
protein_co	kaptin_(act	181	150	121	222	156	275	5.666659	5.534098	4.991932	6.01263	5.486838	8.556395
protein_co	ribosomal_	11194	10142	7646	8300	7195	10140	405.3499	432.7882	364.8496	260.0075	292.7012	364.9155
protein_co	kinesin_fan	128	121	117	574	637	551	0.931598	1.037794	1.12212	3.614046	5.208435	3.985475
protein_co	troponin_T	17	7	6	120	91	146	0.298605	0.144895	0.138878	1.823447	1.795723	2.548657
protein_co	DEAD_(Asp	184	156	164	463	296	339	3.359015	3.35603	3.945234	7.312032	6.070645	6.150401
protein_co	calmodulin	738	659	865	1003	1061	903	5.314262	5.592154	8.208003	6.248137	8.583236	6.462253
protein_co	activating_	543	411	495	1208	819	825	3.834973	3.420672	4.606834	7.380613	6.498236	5.790634
protein_co	crystallin_g	0	0	0	0	4	0	0	0	0	0	0.384335	0
protein_co	melanoregu	72	53	47	199	155	207	2.900876	2.5164	2.495338	6.936059	7.015805	8.288515
protein_co	FAST_kinas	355	320	324	1199	784	848	3.759562	3.993613	4.521565	10.98477	9.327689	8.925128
protein_co	neuropilin_	957	845	883	1734	2453	1966	7.605003	7.913184	9.246619	11.92064	21.89949	15.52675
protein_co	cAMP_resp	556	559	522	698	645	610	3.847738	4.55879	4.760318	4.178776	5.014636	4.195369
protein_co	Kruppel-lik	317	281	310	353	447	405	2.006971	2.096502	2.586297	1.933391	3.179351	2.548277
protein_co	transthyret	4	1	0	5	3	7	0.221279	0.065191	0	0.239284	0.186445	0.384847
protein_co	UDP-Gal:be	90	94	81	667	584	494	1.07628	1.3247	1.276446	6.900355	7.845931	5.871096
protein_co	chromoson	216	202	129	12	16	18	9.140891	10.0738	7.193816	0.439318	0.760683	0.757037

protein_co carbonic_a	31	24	31	65	54	42	0.917881	0.837419	1.209542	1.664949	1.796253	1.235901
protein_co cancer_sus	0	0	3	1	0	2	0	0	0.085599	0.018732	0	0.043038
protein_co lymphoid-r	9	6	3	0	0	5	0.175495	0.137873	0.077086	0	0	0.096895
protein_co ATPase_cla	0	0	0	0	3	0	0	0	0	0	0.023583	0
protein_co signal_pept	1561	1426	1250	1629	1404	1693	30.51732	32.85262	32.2024	27.55038	30.83611	32.8935
protein_co ubiquitin_s	349	330	284	341	292	374	4.382449	4.88329	4.699424	3.704323	4.1193	4.667375
protein_co ELOVL_fatt	225	177	183	525	454	595	3.915754	3.630055	4.196805	7.90415	8.876419	10.29105
protein_co filamin_A_i	6	4	0	30	23	17	0.069355	0.054487	0	0.299993	0.298678	0.195292
processed_ caspase_8_	147	134	175	293	335	269	1.059685	1.138338	1.662388	1.827217	2.713022	1.927176
protein_co high_mobil	341	322	244	2027	1256	1793	20.70284	23.03767	19.52092	106.4614	85.66715	108.1846
protein_co ubiquitin_p	83	78	80	201	104	158	1.349955	1.495005	1.714612	2.828135	1.900306	2.553923
protein_co cannabinoi	0	0	1	10	5	16	0	0	0.007774	0.051035	0.033138	0.093807
protein_co ankyrin_rep	1060	808	912	666	672	596	13.79146	12.38862	15.6363	7.496208	9.822516	7.706555
protein_co SH3-domai	122	84	92	31	51	31	0.888052	0.720551	0.882472	0.195211	0.417059	0.224259
protein_co PHD_finger	669	496	547	726	769	638	4.301898	3.758571	4.635068	4.038626	5.555324	4.077221
protein_co pleiomorph	1309	1178	1030	238	210	191	15.64329	16.58978	16.22036	2.460528	2.8194	2.268461
protein_co F-box_prot	332	279	408	645	612	530	4.016547	3.977645	6.504438	6.750524	8.31793	6.37236
protein_co tumor_nec	297	242	251	941	872	888	3.547716	3.40655	3.950944	9.724	11.70194	10.5418
protein_co A_kinase_(P	41	44	42	161	147	136	0.734794	0.929269	0.991895	2.496149	2.959702	2.422312
protein_co RAB32_mer	411	333	320	998	612	848	17.879	17.07076	18.34367	37.55736	29.90901	36.66123
protein_co v-myb_mye	11	1	5	19	12	12	0.158592	0.01699	0.094994	0.236977	0.194366	0.171941
protein_co aldehyde_d	20	18	10	2	0	10	0.413925	0.439007	0.272726	0.035808	0	0.205684
protein_co serum/gluc	1411	1173	1181	883	604	673	13.64628	13.3688	15.05123	7.38773	6.56256	6.468625
protein_co ring_finger_	687	659	565	692	555	562	15.35266	17.3548	16.63835	13.37815	13.93378	12.48168
protein_co arginase_liv	0	5	5	1	0	0	0	0.203615	0.227687	0.029895	0	0
protein_co connective_	536	451	496	2797	1368	1807	12.13184	12.02944	14.79375	54.7668	34.7854	40.64711
protein_co transcriptic	0	3	1	11	2	8	0	0.041126	0.015329	0.110698	0.026138	0.092488
protein_co polyamine_	10	4	10	16	29	7	0.134539	0.063418	0.177289	0.186222	0.438323	0.093596
protein_co F-box_and_	842	638	616	1472	1196	1207	13.16878	11.75875	12.69547	19.9161	21.01424	18.76076
protein_co mediator_c	935	761	769	1819	1312	1693	20.67662	19.83169	22.40934	34.79875	32.59499	37.20785
protein_co solute_carr	42	19	67	28	27	23	0.490194	0.261324	1.030454	0.282709	0.354023	0.266782
protein_co transmemb	241	194	212	490	349	350	2.815886	2.671203	3.264139	4.952872	4.581129	4.064206
protein_co zinc_finger_	124	138	125	320	228	255	1.673383	2.194623	2.222893	3.735827	3.456668	3.41998
protein_co vesicle-assc	7	6	8	789	663	994	0.460356	0.465002	0.6933	44.88862	48.98451	64.96691
protein_co DNA_cross-	152	129	139	453	396	419	2.042394	2.042644	2.461192	5.265712	5.977783	5.595251
protein_co myosin_ligh	2587	2237	1954	10035	5830	7606	109.6544	111.7385	109.1413	367.968	277.6178	320.4023
protein_co forkhead_b	1988	1619	1706	763	903	678	14.33683	13.75912	16.21253	4.760191	7.316	4.859328
protein_co armadillo_t	68	62	60	41	36	36	1.110764	1.193471	1.291514	0.579375	0.66064	0.58442
protein_co ribophorin_	6202	5380	4962	9002	4754	5456	130.7607	133.6702	137.8596	164.1903	112.6039	114.3219
protein_co TGFB-induc	406	379	287	780	643	636	5.949085	6.544409	5.541672	9.887392	10.58484	9.261704
protein_co calsequestr	0	0	0	25	19	25	0	0	0	0.428187	0.422604	0.491904
protein_co olfactomed	0	0	0	13	5	4	0	0	0	0.182914	0.091361	0.064656
protein_co polycystic_	889	760	850	1093	1058	997	9.308652	9.377902	11.7284	9.900752	12.44571	10.37504
protein_co ATP-bindin	26	23	39	2371	2094	1987	0.307315	0.320366	0.60745	24.24407	27.80589	23.34095

protein_co	secreted_pl	3	10	1	13548	7785	9862	0.095447	0.374926	0.041925	372.8868	278.2572	311.8268
protein_co	FAM47E-ST	14	22	12	28	15	32	0.216718	0.401325	0.244783	0.374962	0.260859	0.492295
protein_co	cyclin_I	6680	6082	4758	7279	4749	5237	127.5779	136.8839	119.7452	120.2634	101.8943	99.40108
protein_co	retinoic_ac	24	19	19	9	20	23	0.650914	0.607258	0.679048	0.211163	0.609384	0.61994
protein_co	major_facil	1992	1550	1735	681	504	494	43.52392	39.90961	49.95431	12.87208	12.37138	10.72693
protein_co	RAB3_GTPa	897	737	988	855	734	713	6.543761	6.335918	9.497881	5.395902	6.015616	5.169329
protein_co	family_witl	132	117	100	298	234	263	2.923938	3.054127	2.918966	5.710491	5.823165	5.789747
protein_co	periplakin	69	82	57	1532	1645	1680	0.585593	0.820102	0.637465	11.24782	15.68418	14.16986
protein_co	ubinuclein_	1353	1059	1004	1348	1721	1614	11.30511	10.42749	11.05466	9.743833	16.155	13.40263
pseudogen	basic_trans	0	1	0	0	0	0	0	0.130792	0	0	0	0
protein_co	Kruppel-lik	365	319	322	218	190	165	1.816627	1.870987	2.111853	0.938626	1.062369	0.816143
protein_co	ubiquitin_(	5	4	1	6	7	7	0.313631	0.295676	0.082658	0.325585	0.493284	0.436372
protein_co	protocadhe	77	27	64	95	124	71	0.541866	0.223909	0.593493	0.578346	0.980329	0.496557
protein_co	HCLS1_bin(	912	753	674	595	540	584	11.07898	10.77971	10.78946	6.252948	7.369664	7.050621
protein_co	chromoson	345	261	272	924	674	698	6.291644	5.609093	6.536553	14.5774	13.80874	12.65057
protein_co	WD_repeat	256	222	256	302	227	201	1.947255	1.989953	2.566006	1.987251	1.939804	1.519457
protein_co	cyclin_D2	2847	2478	1870	7923	6914	7411	23.25972	23.85753	20.13231	55.99764	63.45934	60.17326
protein_co	fibroblast_	0	0	0	0	1	0	0	0	0	0	0.019707	0
pseudogen	-	1	0	0	0	0	0	0.017261	0	0	0	0	0
protein_co	elongation_	602	518	573	661	430	531	5.271333	5.345161	6.611704	5.007125	4.230011	4.620916
protein_co	dynein_axo	24	17	25	13	7	4	0.102516	0.085573	0.14072	0.048038	0.033591	0.01698
protein_co	cytochrom	257	253	190	434	346	373	5.161546	5.987897	5.028461	7.540487	7.806778	7.445008
protein_co	NADH_deh	538	482	338	768	710	1091	37.72484	39.82899	31.23177	46.5875	55.931	76.02904
protein_co	general_tra	505	439	462	1247	817	939	6.243625	6.396126	7.527005	13.33751	11.34793	11.53774
protein_co	SATB_home	164	168	179	234	236	243	1.401731	1.692144	2.016085	1.730214	2.266115	2.064129
protein_co	ubiquitin-c	503	460	447	1183	758	1097	10.5882	11.41088	12.39928	21.54279	17.92554	22.94935
protein_co	transient_r	0	0	1	11	2	8	0	0	0.008269	0.059712	0.014099	0.049889
protein_co	guanine_de	7	9	1	89	71	69	0.069398	0.105148	0.013064	0.763315	0.790785	0.679844
protein_co	Kruppel-lik	524	481	510	16	25	17	5.350257	5.78756	6.861962	0.141327	0.286769	0.172505
protein_co	tight_junct	519	432	448	2301	2315	1926	5.958876	5.845044	6.778128	22.85476	29.8605	21.97672
protein_co	chromoson	0	0	0	1	0	1	0	0	0	0.05732	0	0.06585
protein_co	integrin_be	1392	1131	919	929	947	1190	15.16647	14.52161	13.19458	8.756366	11.59162	12.88552
protein_co	cleavage_ar	560	530	456	2007	1267	1281	9.390864	10.47371	10.07667	29.11574	23.86949	21.34894
protein_co	phosphatid	35	21	26	13	16	20	0.686018	0.485058	0.671546	0.220432	0.352319	0.389589
protein_co	SUMO1/ser	558	486	442	1167	759	817	4.683113	4.806664	4.888296	8.472943	7.156345	6.81447
protein_co	coiled-coil_	870	748	581	919	536	578	9.432452	9.556834	8.30073	8.619536	6.528587	6.227917
protein_co	chromoson	1915	1511	1509	2607	2177	2155	26.27838	24.43439	27.28688	30.94809	33.56119	29.38913
protein_co	tripartite_r	58	32	59	25	21	14	0.329461	0.214207	0.441635	0.122851	0.134012	0.079034
protein_co	HEAT_repea	670	674	788	1310	1330	996	4.199179	4.978019	6.508046	7.102707	9.364623	6.203811
protein_co	polypyrimi	641	566	655	2982	2915	2276	4.667195	4.856478	6.284548	18.78316	23.84435	16.46948
protein_co	RAD23_hor	3757	3124	3174	11365	11296	12807	48.28825	47.31713	53.75787	126.3667	163.1075	163.5902
protein_co	FK506_bin(	824	716	667	741	606	680	4.953262	5.072058	5.283537	3.853411	4.092473	4.0624
protein_co	catenin_(ca	682	626	565	2113	1210	1236	14.32768	15.4979	15.64137	38.40202	28.55788	25.80594
protein_co	family_witl	279	218	187	584	378	416	6.96395	6.412317	6.150747	12.61035	10.59967	10.3194

protein_co	WD_repeat	656	449	448	2912	1711	2327	19.78877	15.96131	17.80852	75.99226	57.98478	69.76233
protein_co	SET_nuclea	6321	5328	5199	17893	13547	16359	114.7993	114.0315	124.4251	281.1252	276.4049	295.2704
protein_co	protein_ph	4530	3469	3038	3602	3189	4624	84.92305	76.63705	75.04988	58.41631	67.16314	86.14992
protein_co	GLE1_RNA_	483	409	321	805	758	713	7.699639	7.683403	6.743154	11.10151	13.57505	11.29594
protein_co	RAB14_mer	1688	1448	1474	2540	1927	1980	21.55957	21.79431	24.80846	28.06495	27.6502	25.13289
protein_co	centriolin	173	151	129	226	253	192	1.195665	1.229836	1.174865	1.351247	1.964413	1.318786
protein_co	tripartite_r	528	469	461	514	457	440	7.52027	7.871898	8.652374	6.333236	7.312482	6.22819
protein_co	F-box_and_	571	541	528	765	800	826	14.03403	15.66934	17.10075	16.26563	22.08948	20.17605
protein_co	PHD_finger	612	445	391	1425	1171	1459	7.639681	6.546225	6.431842	15.38869	16.42214	18.10042
protein_co	NIMA-relat	1383	1103	1259	1429	958	1024	20.23139	19.01455	24.26968	18.08418	15.74411	14.8872
protein_co	B-box_and_	1	0	1	223	188	270	0.022634	0	0.029826	4.366463	4.78045	6.073447
protein_co	protein_ph	883	714	585	1880	1410	1462	10.74888	10.24255	9.384116	19.7981	19.28283	17.68722
protein_co	NADH_deh	753	524	464	1032	658	1041	39.86457	32.69117	32.37016	47.26447	39.13515	54.77123
protein_co	haloacid_d	111	124	54	389	236	392	3.204171	4.218145	2.054099	9.714163	7.65339	11.24575
protein_co	RNA_bindi	356	318	303	490	291	325	3.789102	3.9886	4.249754	4.511754	3.479592	3.43779
protein_co	solute_carr	1	3	0	3	1	0	0.021159	0.074805	0	0.054915	0.023771	0
protein_co	hydroxyste	724	630	570	1078	819	836	11.44158	11.73262	11.87017	14.73768	14.54053	13.12995
protein_co	mitogen-ac	1389	1045	1112	2898	1871	2156	21.65981	19.20329	22.8503	39.09432	32.77745	33.41263
protein_co	nuclear_rec	18	9	14	54	59	50	0.191276	0.112704	0.196043	0.496415	0.704351	0.528041
protein_co	inversin	227	204	192	222	226	221	3.24012	3.431409	3.611364	2.741266	3.624038	3.134997
protein_co	UDP-N-acet	13	15	7	34	29	24	0.251639	0.342163	0.178553	0.569347	0.63064	0.461696
protein_co	DENN/MAD	1045	810	629	597	437	550	11.04258	10.08664	8.758703	5.457474	5.18782	5.775994
protein_co	ALG2_alph	579	565	478	1001	656	680	10.33474	11.88438	11.24304	15.45674	13.15448	12.06256
protein_co	colony_stir	0	0	0	1	11	3	0	0	0	0.00754	0.107711	0.025987
protein_co	3-ketodihy	452	415	358	666	468	554	4.393121	4.753242	4.58514	5.599793	5.110103	5.351236
protein_co	vacuolar_p	802	724	673	1355	1168	1108	12.77337	13.58866	14.12476	18.66953	20.89888	17.53802
protein_co	one_cut_ho	5	5	3	12	10	12	0.016419	0.019349	0.012982	0.034089	0.036891	0.039162
protein_co	chromoson	727	562	387	1200	864	1207	14.89478	13.56885	10.44829	21.26884	19.88668	24.5763
protein_co	zinc_finger_	508	445	314	825	625	786	10.58403	10.92583	8.620886	14.86977	14.62906	16.27495
protein_co	YLP_motif-	1178	1079	1159	1035	1806	1306	8.887629	9.593325	11.52282	6.75529	15.30761	9.792497
protein_co	DDB1_and_	195	160	173	211	187	164	3.564742	3.446836	4.167489	3.336868	3.840468	2.979525
protein_co	prospero_h	47	35	31	32	14	22	0.778301	0.683006	0.676466	0.458419	0.260451	0.362061
protein_co	FCF1_small	1013	878	749	1724	1388	1926	22.23434	22.70996	21.66364	32.7352	34.22578	42.01271
protein_co	placental_g	138	56	106	92	90	71	2.058568	0.984422	2.08366	1.187236	1.508265	1.052578
protein_co	interferon_	174	167	159	59	53	97	9.820611	11.10741	11.82555	2.880741	3.36058	5.440899
protein_co	coiled-coil_	23	29	35	22	24	34	0.392029	0.5825	0.786128	0.324397	0.459569	0.575943
protein_co	NIMA-relat	1025	834	913	948	946	983	9.787972	9.385167	11.48879	7.831415	10.14867	9.328934
protein_co	acylphosph	87	73	45	134	118	202	5.8376	5.772249	3.978894	7.778268	8.895004	13.47026
protein_co	intraflagell	410	338	263	248	223	291	12.29791	11.94734	10.39532	6.4352	7.514521	8.674611
protein_co	Niemann-P	2148	2006	1585	5928	3434	4955	79.19029	87.15166	77.00195	189.064	142.2286	181.5478
protein_co	dynein_axo	126	111	159	83	129	110	2.885193	2.995259	4.797734	1.644165	3.318509	2.503264
protein_co	interferon_	3837	2875	2593	959	1024	1120	48.9835	43.25168	43.62098	10.59107	14.68612	14.20973
protein_co	acyl-CoA_th	476	356	285	209	234	210	14.20514	12.51975	11.20774	5.3957	7.845189	6.22827
protein_co	latent_tran	517	355	494	434	329	313	3.194875	2.585227	4.022769	2.32015	2.284064	1.922283

protein_co apoptosis_	669	482	641	1015	885	887	6.491482	5.511526	8.196163	8.520141	9.647395	8.55364
protein_co mutL_hom	260	212	236	258	216	210	1.743244	1.67505	2.085123	1.496469	1.627001	1.39931
protein_co tubulin_tyr	963	787	817	585	490	454	10.88665	10.48455	12.17096	5.721196	6.22319	5.100743
protein_co feline_leuk	439	390	302	114	66	73	6.40427	6.704661	5.805597	1.438709	1.081678	1.05837
protein_co ATP-bindin	559	485	371	719	524	793	9.838436	10.05919	8.604447	10.94728	10.36083	13.87066
protein_co dihydrolipo	1582	1375	1330	2404	1943	2273	29.51115	30.22661	32.69386	38.79513	40.71942	42.13944
protein_co protein_ph	0	0	0	0	0	1	0	0	0	0	0	0.013602
protein_co transformir	18990	16324	13291	163	244	221	371.2517	376.0773	342.4017	2.756729	5.358982	4.293835
protein_co zinc_finger_	1	2	7	27	18	20	0.022133	0.052164	0.204157	0.516961	0.447561	0.439917
protein_co SRA_stem-l	506	468	289	1239	1058	969	30.96895	33.75429	23.30819	65.60098	72.74627	58.9399
protein_co RNA_bindir	1467	1388	1277	2880	2420	2175	11.34119	12.64518	13.0093	19.26122	21.01807	16.7108
protein_co aldehyde_d	198	166	147	339	263	292	1.906222	1.883318	1.864921	2.823391	2.844547	2.793836
protein_co G_protein-r	18	11	14	19	22	14	0.333312	0.240037	0.341618	0.304365	0.457667	0.257641
protein_co estrogen-re	0	0	2	3	6	3	0	0	0.051429	0.050644	0.131535	0.05818
protein_co eukaryotic_	287	242	231	696	450	560	9.885534	9.822922	10.48492	20.73913	17.41325	19.16973
protein_co NRDE-2_ne	193	183	169	293	372	330	1.753194	1.958983	2.022992	2.302519	3.796335	2.979176
protein_co coenzyme_	48	36	28	54	21	42	0.814738	0.720089	0.626281	0.792928	0.400447	0.708493
protein_co zinc_finger_	30	20	22	17	16	16	0.610623	0.479721	0.590078	0.299339	0.365865	0.323654
protein_co ras_homolo	1239	1085	1164	822	579	666	22.04837	22.75317	27.29562	12.65435	11.57531	11.77847
protein_co G_protein-r	29	39	14	106	61	56	0.725905	1.150412	0.46179	2.295359	1.715381	1.393091
protein_co suppressor_	476	471	438	962	546	597	5.614954	6.547375	6.808449	9.816967	7.235707	6.998794
protein_co kelch-like_f	437	318	390	444	521	483	3.62337	3.107173	4.261187	3.184763	4.853086	3.980045
protein_co DNA_(cytos	777	617	619	750	729	752	9.188106	8.597996	9.645627	7.672365	9.684598	8.837562
protein_co transmemb	2210	1878	1635	2246	1578	1920	39.1303	39.18534	38.14815	34.40279	31.38896	33.78561
protein_co ATPase_fam	208	163	161	267	283	210	1.358969	1.254992	1.38614	1.509109	2.077216	1.363563
protein_co FK506_bin	17	13	19	34	23	27	0.562147	0.506584	0.827922	0.972619	0.854432	0.887308
protein_co atlastin_GT	373	310	364	1132	839	850	6.885283	6.743444	8.854196	18.07683	17.39899	15.59342
protein_co yippee-like_	1303	1183	1030	396	331	309	26.94614	28.82995	28.06882	7.084518	7.69005	6.35068
protein_co family_with	1413	1197	1355	1383	1127	1160	21.09578	21.05982	26.65799	17.86235	18.90281	17.21159
protein_co Yip1_doma	503	431	459	638	474	647	3.653858	3.689505	4.393708	4.009289	3.86822	4.670869
protein_co aftiphilin	224	191	169	239	253	284	2.537181	2.549434	2.522464	2.341878	3.219385	3.196917
protein_co lectin_gala	58	48	61	408	363	375	0.86764	0.846174	1.202475	5.280009	6.100525	5.575097
protein_co cannabinoi	370	278	276	322	185	191	10.02978	8.880588	9.85902	7.551074	5.633919	5.145563
protein_co B-cell_CLL/	173	106	79	22	17	15	1.541365	1.112942	0.927516	0.169568	0.17016	0.132819
protein_co cysteine-ric	127	162	125	281	160	283	3.442656	5.175019	4.465136	6.589602	4.872579	7.624053
protein_co epithelial_c	5	0	2	5841	4056	4777	0.153541	0	0.080932	155.169	139.9271	145.7873
protein_co solute_carr	1828	1596	1598	577	417	525	28.01046	28.81934	32.26678	7.648616	7.178425	7.994899
protein_co opioid_gro	607	430	532	794	513	541	18.78152	15.67897	21.69145	21.25326	17.83235	16.636
protein_co family_with	620	527	640	941	918	813	4.761157	4.769123	6.476429	6.251345	7.91977	6.204703
protein_co insulin-deg	258	191	252	985	713	731	2.324107	2.027575	2.991381	7.676012	7.215642	6.544303
protein_co tectorin_be	0	0	0	3	0	0	0	0	0	0.050644	0	0
protein_co ELOVL_fatty	0	1	1	1	2	0	0	0.045505	0.050885	0.033405	0.086763	0
protein_co interferon-i	94	50	75	21	34	15	1.993771	1.249754	2.096252	0.385327	0.810169	0.31619
protein_co NK2_home	0	0	1	0	0	0	0	0	0.033316	0	0	0

protein_co interferon-i	52	41	44	0	1	0	0.789032	0.733132	0.879789	0	0.017047	0
protein_co glycerol-3-p	237	180	145	315	290	228	1.970013	1.763195	1.588268	2.265137	2.70812	1.883499
protein_co cutC_copp	187	133	141	312	210	188	7.355101	6.164612	7.308041	10.61609	9.279304	7.348768
protein_co protein_ph	325	262	217	7	10	10	6.816887	6.476064	5.997873	0.127018	0.235642	0.208455
protein_co pyridine_n	88	96	68	37	56	90	1.626111	2.090479	1.655813	0.591469	1.162531	1.652797
protein_co cyclin_M1	3	0	1	22	13	22	0.026653	0	0.011707	0.169085	0.129751	0.194246
protein_co MAX_intera	405	355	307	270	221	223	6.178992	6.382606	6.172141	3.563604	3.787947	3.381249
protein_co survival_m	542	511	453	1219	826	1015	14.12802	15.69676	15.5602	27.48836	24.18863	26.29407
protein_co chromoson	164	141	161	254	174	227	2.902816	2.941046	3.755228	3.889309	3.459983	3.993109
protein_co helicase_ly	271	231	182	2140	1753	1993	2.876882	2.889827	2.546003	19.65303	20.90661	21.02663
protein_co tectonic_fa	1237	1074	1019	1877	1175	1186	23.90946	24.4631	25.95428	31.38538	25.5145	22.78213
protein_co family_with	368	245	318	692	569	565	7.533753	5.91067	8.578779	12.25555	13.08654	11.49534
protein_co arginine_va	135	116	67	89	83	74	4.905308	4.96704	3.208058	2.7976	3.388127	2.67223
protein_co WD_repeat	892	777	899	1079	884	870	9.532371	9.785076	12.65991	9.975175	10.61298	9.239851
protein_co chromoson	595	531	466	726	542	646	7.647461	8.042701	7.892617	8.072349	7.826159	8.251682
protein_co Kv_channel	59	33	36	16	18	22	1.193549	0.7867	0.959678	0.280009	0.409082	0.442304
protein_co coiled-coil_	19	15	21	13	9	3	0.303616	0.282468	0.442206	0.179712	0.161571	0.047643
protein_co glutamic-ox	420	367	308	1754	1051	1199	11.42025	11.75978	11.036	41.259	32.10539	32.40074
protein_co chromoson	0	0	1	0	0	0	0	0	0.04749	0	0	0
protein_co secreted_fr	1	4	4	0	0	0	0.028835	0.135921	0.15199	0	0	0
protein_co guanine_nu	702	548	697	1268	1160	1020	7.550707	6.946054	9.879116	11.79866	14.01708	10.90336
protein_co homeobox_	0	6	8	697	437	527	0	0.205335	0.306147	17.51061	14.25725	15.20988
protein_co KAT8_regul	676	588	577	810	917	733	3.934922	4.033423	4.425884	4.078847	5.996637	4.240363
protein_co homeobox_	25	5	12	118	86	111	0.648469	0.152836	0.410171	2.647854	2.50609	2.861421
protein_co corticotrop	0	0	0	0	0	3	0	0	0	0	0	0.062265
protein_co homeobox_	199	149	176	228	221	217	2.503626	2.209071	2.917856	2.4815	3.123616	2.713225
protein_co homeobox_	0	0	0	0	4	1	0	0	0	0	0.117774	0.026047
protein_co dual_specif	1555	1467	1202	384	257	192	40.77427	45.33076	41.53317	8.710639	7.570733	5.003416
protein_co pantothena	1269	1233	1380	2373	1978	1903	6.394643	7.321918	9.163652	10.34464	11.19773	9.530224
protein_co msh_home	151	138	97	7119	5306	5600	3.567198	3.841815	3.019651	145.4897	140.8207	131.4764
protein_co TEK_tyrosir	138	134	183	73	50	54	1.534844	1.756293	2.682076	0.702378	0.624747	0.596882
protein_co RNA_termi	115	109	87	347	254	238	2.852959	3.186627	2.844145	7.447151	7.079139	5.867921
protein_co caspase_act	122	163	136	566	392	352	2.314153	3.643569	3.399429	9.287775	8.353479	6.635667
protein_co equatorin_	3	0	0	8	3	0	0.154048	0	0	0.355375	0.173063	0
protein_co MOB_kinas	96	91	134	934	675	706	0.787471	0.879653	1.448447	6.627855	6.220366	5.755426
protein_co insulin-like	0	0	0	1	0	0	0	0	0	0.023463	0	0
protein_co melan-A	22	12	20	4	10	16	0.482278	0.310001	0.57775	0.075857	0.246277	0.348582
protein_co CD274_mo	8	11	14	66	19	37	0.116226	0.188327	0.268026	0.829508	0.31011	0.534226
protein_co interferon_	0	0	0	8	5	2	0	0	0	0.2373	0.192603	0.068153
protein_co interferon_	1	0	0	0	0	0	0.050954	0	0	0	0	0
protein_co glutamate_	92	88	125	0	0	0	0.866496	0.976716	1.551398	0	0	0
protein_co nucleopori	851	788	627	3189	2216	2499	11.62953	12.69012	11.29106	37.70075	34.02133	33.93973
protein_co methylenet	1389	1036	950	3700	2520	2895	20.40373	17.93388	18.38932	47.01885	41.58693	42.26351
protein_co low_densit	310	228	246	506	353	419	5.034266	4.363314	5.264346	7.108664	6.440184	6.762358

protein_co	coiled-coil_	14	19	16	2	0	5	0.139739	0.223485	0.210447	0.01727	0	0.049598
protein_co	protein-L-is	1126	938	913	2521	1925	2240	30.04615	29.49581	32.10377	58.19508	57.70723	59.40296
protein_co	pleckstrin_	175	188	183	340	316	258	1.280182	1.620684	1.764085	2.151669	2.596986	1.875698
protein_co	cysteine-ric	320	265	260	538	318	342	12.69949	12.39336	13.59704	18.47062	14.17792	13.48876
protein_co	WD_repeat	713	630	505	770	731	827	9.251698	9.633399	8.634916	8.643421	10.6561	10.66466
protein_co	ArfGAP_wit	157	124	105	620	576	490	1.583188	1.473539	1.395266	5.408633	6.525358	4.910645
protein_co	protocadhe	7	12	6	0	1	0	0.136698	0.276154	0.1544	0	0.021939	0
protein_co	protocadhe	180	174	166	26	53	44	2.910623	3.315658	3.537173	0.363705	0.962805	0.707092
protein_co	protocadhe	173	134	168	72	48	44	3.293345	3.006097	4.214395	1.185732	1.026553	0.832441
protein_co	protocadhe	25	20	26	6	4	3	0.388586	0.36634	0.532544	0.080679	0.069848	0.046342
protein_co	solute_carr	0	5	1	0	3	1	0	0.22014	0.049233	0	0.125919	0.037131
protein_co	tenascin_N	0	0	0	3	0	8	0	0	0	0.027435	0	0.084048
protein_co	mitochond	386	307	284	652	423	552	9.662044	9.055808	9.367741	14.11862	11.89518	13.73189
protein_co	centromere	177	185	161	387	307	319	3.789145	4.667097	4.541807	7.167075	7.383383	6.786851
protein_co	tumor_nec	3	2	1	1	3	1	0.079095	0.062139	0.034743	0.022808	0.088858	0.026202
protein_co	SEC16_hon	13	7	5	0	0	0	0.172706	0.109589	0.087532	0	0	0
protein_co	golgin_RAB	197	199	180	255	221	209	4.227554	5.032492	5.090146	4.733977	5.328001	4.457372
protein_co	acetyl-CoA_	879	749	652	1937	1291	1374	14.63369	14.69447	14.30367	27.89701	24.14573	22.73324
protein_co	t-complex_	3535	3110	2770	8782	6024	6768	74.88852	77.64139	77.32865	160.9468	143.3705	142.4938
protein_co	tubulin_tyr	0	0	0	0	1	5	0	0	0	0	0.022193	0.098161
protein_co	sorting_nex	862	663	857	1043	955	834	6.983188	6.329467	9.148758	7.309603	8.691584	6.714632
protein_co	potassium_	0	0	0	1	4	6	0	0	0	0.00771	0.040051	0.053146
protein_co	Myb/SANT-	276	255	170	471	333	375	4.734839	5.155175	3.843084	6.990047	6.417848	6.393477
protein_co	tumor_pro	4	0	1	10	21	12	0.073657	0	0.024265	0.159301	0.434433	0.219606
protein_co	arrestin_3_	27	11	9	16	14	13	1.101238	0.52871	0.483721	0.564547	0.641497	0.526951
protein_co	PDZ_domai	767	644	530	868	499	554	38.93168	38.52128	35.45018	38.11453	28.45492	27.94648
protein_co	solute_carr	93	92	81	105	72	75	1.313988	1.531804	1.508093	1.283396	1.142852	1.053124
protein_co	NudC_dom	224	230	196	1413	858	947	2.812137	3.402698	3.242495	15.34595	12.1011	11.81539
protein_co	enhancer_c	796	763	615	1664	1296	1673	14.20803	16.04917	14.46541	25.69433	25.98813	29.67745
protein_co	microtubul	145	156	174	1215	924	928	2.118809	2.686306	3.350486	15.359	15.16858	13.47663
protein_co	KIAA1217	1249	1027	999	1418	1604	1340	8.956156	8.678342	9.439729	8.796268	12.92149	9.549347
pseudogen	septin_7_p	0	1	0	1	1	1	0	0.083967	0	0.061641	0.080048	0.070813
protein_co	plexin_dom	121	80	98	167	164	174	2.157582	1.681044	2.302729	2.576092	3.285298	3.083478
protein_co	enhancer_c	327	328	280	427	333	345	2.343854	2.770536	2.644695	2.64773	2.681489	2.457602
protein_co	IQ_motif_a	0	1	0	0	1	0	0	0.008794	0	0	0.008384	0
protein_co	coiled-coil_	116	112	117	421	297	303	2.590112	2.947037	3.442558	8.132155	7.450168	6.723769
protein_co	TAF12_RNA	333	344	290	446	396	475	12.9723	15.79204	14.88694	15.0304	17.33073	18.38975
protein_co	ecto-NOX_c	408	279	279	286	221	180	7.243436	5.837081	6.527148	4.392517	4.40784	3.175898
protein_co	tumor_nec	6	13	9	0	1	0	0.144516	0.36899	0.285655	0	0.027059	0
protein_co	mitochond	174	179	106	275	210	232	4.215896	5.11094	3.384397	5.764164	5.716221	5.58648
protein_co	SPG20_opp	9	6	4	20	10	16	0.841818	0.661354	0.493027	1.618336	1.050811	1.487323
protein_co	spermatoge	5	3	0	8	8	6	0.120705	0.085346	0	0.167073	0.216966	0.143951
protein_co	DnaJ_(Hsp4	426	348	307	1922	1300	1576	8.886077	8.554346	8.438663	34.68302	30.46442	32.67129
protein_co	proline_an	441	336	380	1533	1290	1069	4.517604	4.056168	5.129653	13.58547	14.84596	10.88321

protein_co ubiquitin-f	1685	1612	1283	2464	1953	1856	35.20346	39.68785	35.32214	44.53374	45.83917	38.53657
protein_co WW_doma	295	270	228	651	476	544	5.965467	6.434181	6.075641	11.3885	10.8138	10.93279
protein_co E74-like_fa	662	548	688	951	861	788	9.828081	9.587346	13.45966	12.2139	14.36028	11.62644
protein_co SMAD_fami	115	139	136	153	116	139	1.088736	1.550768	1.696675	1.253082	1.233764	1.307824
protein_co heat_shock	1078	952	1113	4989	3611	3620	15.80022	16.44328	21.49683	63.25879	59.45945	52.73058
protein_co kelch_repe	75	74	85	190	180	178	0.838736	0.97522	1.252615	1.838148	2.261442	1.978306
protein_co ALG5_dolic	506	493	324	616	368	526	23.2133	26.65264	19.58692	24.44725	18.96632	23.98179
protein_co exosome_c	365	380	211	1831	1114	1375	7.975016	9.784291	6.075135	34.60908	27.34469	29.85733
protein_co eukaryotic_	1808	1572	1635	5075	3995	4054	24.70762	25.31583	29.4432	59.99728	61.33358	55.05869
protein_co transformir	10552	8810	8226	8623	6449	6930	119.8527	117.9223	123.1222	84.72945	82.29139	78.22685
protein_co family_witl	1013	952	1018	1189	1226	1244	12.25811	13.57557	16.23292	12.44683	16.66685	14.96043
protein_co SIL1_homo	729	631	530	404	287	316	20.06967	20.47148	19.22753	9.621819	8.876541	8.645887
protein_co poly(A)_bin	394	290	313	417	522	604	9.092743	7.886853	9.518704	8.325259	13.53375	13.85305
protein_co myotilin	0	0	0	4	1	2	0	0	0	0.078389	0.02545	0.045027
protein_co lysine_(K)-s	974	839	877	1591	1727	1458	7.56855	7.682857	8.980243	10.69515	15.07631	11.25955
protein_co early_grow	641	572	391	50	79	87	10.81427	11.37214	8.692621	0.729747	1.497322	1.458707
protein_co stress-assoc	3097	2795	2365	3876	3228	3606	41.67724	44.32478	41.93954	45.12368	48.8023	48.22732
protein_co plastin_1	5	8	10	441	332	335	0.070494	0.132917	0.185788	5.37878	5.25859	4.69393
protein_co ZFP30_zinc	158	169	139	406	253	280	1.37351	1.731285	1.592298	3.05326	2.470839	2.419037
protein_co nuclear_rec	266	223	234	575	399	439	5.635176	5.567212	6.532456	10.53796	9.496155	9.242724
protein_co UTP20_sma	445	435	467	2021	1340	1276	2.610387	3.007054	3.609912	10.25591	8.830773	7.43884
protein_co thymopoie	791	735	774	4258	3086	3272	9.871836	10.80976	12.72909	45.97165	43.26796	40.58302
protein_co ADP-ribosy	1203	1124	1130	1435	1077	1111	19.65073	21.63647	24.32351	20.27813	19.76414	18.03586
protein_co glycosyltra	1029	880	805	117	86	95	28.97675	29.20277	29.87204	2.850251	2.720707	2.658689
protein_co MTERF_dor	171	135	118	103	51	75	2.798427	2.603506	2.544688	1.458203	0.937642	1.2198
protein_co suppressor_	100	82	80	476	341	349	1.418189	1.370424	1.495061	5.839882	5.432973	4.918913
protein_co nuclear_tra	273	235	245	716	494	599	4.115288	4.174578	4.866744	9.337134	8.365918	8.973752
protein_co coiled-coil_	232	214	169	214	170	170	12.99715	14.12801	12.47618	10.37139	10.69937	9.464961
protein_co apoptotic_	968	739	799	1258	1055	1067	7.26391	6.535015	7.900902	8.166552	8.893989	7.957362
protein_co dual_specif	312	261	276	1115	792	763	2.98313	2.940798	3.477455	9.222644	8.507301	7.250229
protein_co clusterin	1668	1474	1129	1956	1118	1321	28.67064	29.85698	25.57232	29.08528	21.58899	22.56596
protein_co tumor_nec	4795	4152	3955	5296	4427	5009	61.22819	62.47802	66.54939	58.50241	63.50697	63.56579
protein_co sorbin_and	1361	1107	781	2910	2130	2761	20.8305	19.96624	15.7517	38.52987	36.62437	41.99693
protein_co protein_tyr	36	47	42	370	374	426	0.404215	0.621893	0.621433	3.593976	4.717708	4.753677
protein_co cholinergic	0	0	0	0	0	2	0	0	0	0	0	0.02588
protein_co protein_ph	188	150	146	332	193	233	4.546782	4.275084	4.65301	6.946202	5.243879	5.600308
protein_co PDZ_and_L	315	282	193	479	329	520	3.631623	3.831302	2.932124	4.777368	4.261232	5.958037
protein_co epoxide_hy	2	0	1	100	64	48	0.03372	0	0.022218	1.458564	1.212248	0.804291
protein_co ring_finger_	307	289	263	412	322	317	3.948709	4.38048	4.457664	4.584341	4.652878	4.052151
protein_co natriuretic_	0	0	0	1012	553	842	0	0	0	66.78457	47.39219	63.83434
protein_co UbiA_preny	221	164	207	656	490	525	3.208985	2.80625	3.960779	8.240286	7.993198	7.576077
protein_co TAR_DNA_b	2034	1744	1666	5305	4045	4329	39.18558	39.59396	42.29462	88.41455	87.54734	82.88436
protein_co tumor_nec	2	0	3	36	26	23	0.028725	0	0.05678	0.447303	0.419526	0.328303
protein_co zinc_finger_	670	530	444	2263	1454	1863	10.12863	9.441889	8.844916	29.59535	24.69388	27.98971

protein_co	lysophosph	632	537	597	2727	1933	2101	12.99872	13.01562	16.18053	48.52122	44.6647	42.94566
protein_co	cysteine-ric	139	137	152	1418	1324	1293	1.716538	1.99373	2.473529	15.14879	18.36858	15.8689
protein_co	COP9_signa	764	631	596	858	811	921	7.107173	6.917353	7.306083	6.904843	8.475658	8.514767
protein_co	retinol_deh	199	143	174	691	481	496	2.667829	2.259166	3.073895	8.013939	7.244344	6.608399
protein_co	eosinophil_	1	3	2	5	0	2	0.01955	0.069115	0.051524	0.084562	0	0.038858
protein_co	A_kinase_(A	275	207	205	844	679	749	3.560473	3.158293	3.497548	9.453235	9.87629	9.637546
protein_co	coilin	360	259	282	761	633	614	7.191984	6.097518	7.423866	13.15206	14.20689	12.19058
protein_co	tripartite_r	655	482	546	739	777	703	6.047498	5.244312	6.642963	5.90258	8.059433	6.450589
protein_co	serine_carb	655	596	544	199	234	218	17.856	19.1468	19.54234	4.693091	7.166511	5.906212
protein_co	speckle-typ	644	544	480	542	421	433	11.0408	10.99058	10.84403	8.038538	8.108601	7.377553
protein_co	T-box_2	4875	3823	3314	184	173	207	49.46097	45.70876	44.3073	1.614986	1.971892	2.087219
protein_co	solute_carr	753	577	496	1492	917	1087	16.02918	14.47435	13.91338	27.47566	21.9298	22.99617
protein_co	T-box_4	75	95	64	4	8	4	1.168503	1.744213	1.313964	0.053913	0.140026	0.061935
protein_co	dynein_ligh	1694	1417	1270	3538	4161	5565	35.87282	35.36137	35.43975	64.81461	98.99172	117.1189
protein_co	testis_expr	4	0	0	5	0	3	0.04298	0	0	0.046477	0	0.032036
protein_co	family_with	85	74	69	235	190	187	1.902742	1.95209	2.035377	4.550843	4.778192	4.160181
protein_co	non-SMC_c	216	189	178	1262	954	1096	3.873731	3.994336	4.206594	19.57934	19.22088	19.53421
protein_co	lecithin_re	0	0	0	143	126	127	0	0	0	1.309325	1.498194	1.335863
protein_co	KIAA0922	213	156	189	548	389	317	2.247644	1.939901	2.628116	5.002551	4.611547	3.324428
protein_co	meiotic_nu	35	39	25	330	193	225	1.914189	2.513555	1.801738	15.61326	11.85832	12.22951
protein_co	tripartite_r	18	14	10	920	543	658	0.280029	0.256664	0.205005	12.38172	9.49028	10.17339
protein_co	ATP-bindin	9	2	2	7	3	10	0.097999	0.025663	0.028697	0.065938	0.036698	0.108215
protein_co	PAP_associ	359	313	348	570	390	378	2.423593	2.490099	3.095846	3.328918	2.957869	2.536102
protein_co	adenylate_(	61	65	87	90	139	136	0.519781	0.652696	0.976888	0.663432	1.330622	1.1517
protein_co	centrosom	714	600	500	1202	837	931	13.02097	12.89447	12.01572	18.96324	17.14824	16.87347
protein_co	teashirt_zir	494	396	423	34	48	46	5.052715	4.773095	5.701288	0.300843	0.551554	0.46759
protein_co	enoyl_CoA_	15	15	11	663	505	717	0.136516	0.160876	0.131923	5.219989	5.163373	6.485177
protein_co	taste_recep	0	0	2	0	0	0	0	0	0.11225	0	0	0
protein_co	phospholip	13	5	6	90	62	46	0.28369	0.128581	0.172539	1.699053	1.519995	0.997628
protein_co	taste_recep	3	1	4	1	0	3	0.152421	0.059873	0.267805	0.043953	0	0.15148
protein_co	proline-rich	4	0	0	0	0	0	0.148398	0	0	0	0	0
protein_co	pyridine_nu	94	85	74	121	125	123	1.367533	1.457257	1.418654	1.522855	2.043003	1.778381
protein_co	potassium_	4	1	2	595	474	582	0.088641	0.026115	0.058404	11.40659	11.80058	12.81765
protein_co	taste_recep	2	0	0	0	0	0	0.096608	0	0	0	0	0
protein_co	BCL2-like_1	4	0	1	4	0	14	0.103857	0	0.034214	0.089846	0	0.361254
protein_co	paraspeckle	568	481	477	1277	1116	1219	12.49293	12.46718	13.82513	24.29797	27.57587	26.64584
protein_co	zinc_finger_	165	129	85	217	192	162	1.586787	1.461947	1.077181	1.805334	2.074364	1.548315
protein_co	alpha-1-B_g	34	23	26	1	0	1	0.782266	0.623606	0.788286	0.019904	0	0.022866
protein_co	zinc_finger_	102	67	90	127	142	152	0.94257	0.729617	1.09595	1.015266	1.474181	1.395939
protein_co	zinc_finger_	168	126	134	179	153	148	3.223663	2.849168	3.388286	2.971368	3.29823	2.822356
protein_co	PDZ_domai	5065	4042	3969	228	249	203	63.12291	59.36234	65.18137	2.458133	3.48623	2.514278
protein_co	regulator_c	0	1	0	0	0	0	0	0.010999	0	0	0	0
protein_co	LIM_homeo	57	47	51	62	83	80	0.426039	0.41398	0.502319	0.400894	0.696951	0.594257
protein_co	ring_finger_	321	266	302	845	596	606	4.712717	4.60209	5.842627	10.73213	9.830185	8.841962

protein_co	tRNA_meth	303	309	349	600	477	428	3.588618	4.312709	5.446842	6.147504	6.346759	5.037766
protein_co	SEC22_vesi	118	193	133	167	129	137	1.47754	2.847879	2.19454	1.808992	1.814663	1.704855
protein_co	cystatin_A_	7	3	0	12	10	10	0.451385	0.22797	0	0.669412	0.724433	0.640853
protein_co	developme	1	0	1	1957	1313	1453	0.017398	0	0.022926	29.45398	25.66279	25.12265
protein_co	popeye_do	23	14	20	80	47	52	0.621881	0.446082	0.712597	1.871253	1.427665	1.397309
protein_co	UDP-Gal:be	223	176	147	567	363	429	2.037598	1.895105	1.769969	4.481874	3.726227	3.895655
protein_co	N(alpha)-ac	1708	1487	1650	3493	3072	3277	25.11059	25.76244	31.96596	44.42532	50.73869	47.8801
protein_co	CD80_mole	1	0	0	0	0	2	0.019428	0	0	0	0	0.038616
protein_co	kinesin_fam	147	88	149	639	441	452	2.181145	1.538711	2.913321	8.202214	7.351143	6.665233
protein_co	desumoylat	1005	765	931	1927	1537	1492	12.64394	11.34188	15.43479	20.97303	21.72397	18.65498
protein_co	mitogen-ac	816	614	534	568	396	414	13.58486	12.04593	11.71497	8.180433	7.406435	6.849754
protein_co	cryptochro	473	380	357	629	510	470	5.957909	5.640575	5.925646	6.854036	7.216921	5.88356
protein_co	peroxisoma	487	386	283	480	333	475	15.73048	14.6929	12.04576	13.41274	12.08388	15.24812
protein_co	DEP_domai	34	32	39	134	66	116	0.894629	0.99225	1.35227	3.050225	1.950999	3.033414
protein_co	catalase	727	596	609	225	192	231	16.71942	16.15251	18.45606	4.476435	4.960633	5.27969
protein_co	paired_imn	431	363	252	698	665	1067	5.251454	5.212139	4.04611	7.357339	9.102758	12.92041
protein_co	zinc_finger_	803	804	806	1060	1016	979	4.168214	4.918103	5.513208	4.759961	5.924849	5.050412
protein_co	gap_junctic	0	0	0	8	1	1	0	0	0	0.171934	0.02791	0.02469
protein_co	gap_junctic	28	32	22	10	25	30	0.284465	0.383114	0.294529	0.087889	0.285338	0.302902
protein_co	TBC1_doma	282	273	220	440	338	351	2.580702	2.94414	2.653055	3.483409	3.474997	3.192313
protein_co	brain-speci	623	525	464	244	213	196	6.104431	6.062106	5.991146	2.068283	2.344692	1.908635
protein_co	hypocretin	3	0	3	4	5	5	0.079372	0	0.104593	0.091552	0.148615	0.131469
protein_co	zinc_finger_	368	305	229	1032	658	844	11.26144	10.99899	9.234562	27.3205	22.62148	25.66836
protein_co	fatty_acid_	837	698	710	153	141	276	61.11946	60.06432	68.3199	9.665148	11.56704	20.02962
protein_co	KH_domain	4052	3512	3181	6387	5609	5681	77.80809	79.47251	80.4922	106.1	121.0012	108.4151
protein_co	transmemb	421	335	287	714	400	442	10.67952	10.01432	9.593705	15.66862	11.39931	11.14299
protein_co	chemokine	0	0	0	8	0	0	0	0	0	0.204004	0	0
protein_co	chemokine	0	0	0	0	0	2	0	0	0	0	0	0.039397
protein_co	ring_finger_	788	640	560	759	594	593	11.7184	11.21577	10.974	9.76443	9.923791	8.764082
protein_co	polymerase	473	379	305	148	112	146	15.62139	14.75044	13.27374	4.22847	4.155523	4.792047
protein_co	growth_ho	1	0	0	0	0	0	0.045171	0	0	0	0	0
protein_co	tumor_nec	1	0	0	2	0	0	0.027108	0	0	0.046901	0	0
protein_co	zinc_finger_	331	329	308	542	395	407	5.810169	6.805558	7.124367	8.23044	7.789452	7.100106
protein_co	SLIT_and_N	3	2	3	0	0	4	0.034868	0.027393	0.045947	0	0	0.046203
protein_co	phosphatid	496	435	525	298	303	238	2.887796	2.984566	4.027903	1.500943	1.981876	1.377119
protein_co	PDS5_regul	1295	1081	1360	2382	1832	1672	9.553872	9.398152	13.22158	15.20248	15.18393	12.25902
protein_co	transmemb	0	0	0	1	6	0	0	0	0	0.023669	0.184421	0
protein_co	lipoic_acid	227	252	198	444	291	419	6.770482	8.8573	7.782045	11.45618	9.7507	12.41988
protein_co	carboxypep	0	0	0	322	289	294	0	0	0	4.149479	4.836393	4.352428
protein_co	transmemb	78	59	47	917	355	568	4.133531	3.684561	3.282156	42.03964	21.13509	29.9147
protein_co	zinc_finger_	112	103	109	86	104	136	1.373816	1.488864	1.761862	0.912582	1.433155	1.657903
protein_co	CUB_and_S	61	56	56	20	23	20	0.235998	0.255314	0.285497	0.066938	0.099967	0.076899
protein_co	hippocalcin	2	1	3	8	6	11	0.072127	0.042498	0.142568	0.249585	0.24309	0.394247
protein_co	ligand_dep	262	255	247	545	349	374	3.991522	4.578092	4.958714	7.18285	5.973265	5.662634

protein_co	chloride_ch	777	623	573	917	765	711	8.52542	8.055452	8.284842	8.704165	9.42986	7.753076
protein_co	G-protein_s	245	216	200	349	301	285	3.918593	4.071223	4.215304	4.828948	5.408535	4.530213
protein_co	glycosyltra	318	241	216	255	193	200	5.699132	5.089859	5.101174	3.953528	3.885867	3.562224
protein_co	chemokine_	7	5	1	78	40	49	0.19556	0.164611	0.036814	1.885126	1.255428	1.360469
protein_co	zinc_finger_	130	125	125	242	231	200	1.009139	1.14347	1.278653	1.625122	2.014507	1.542934
protein_co	activin_A_r	208	168	124	203	181	162	1.922438	1.829808	1.510239	1.623111	1.879389	1.488037
protein_co	polymerase	265	237	239	192	182	176	2.373433	2.50142	2.820745	1.487632	1.831267	1.566583
protein_co	synaptic_ve	0	0	0	17	46	27	0	0	0	0.108771	0.382215	0.19846
protein_co	ribosomal_	12335	11125	6709	17770	10115	12998	801.2603	851.6116	574.2845	998.5847	738.1582	839.1134
protein_co	mitochond	341	368	218	395	312	286	16.35225	20.79591	13.77572	16.38638	16.80841	13.63009
protein_co	general_tra	1268	990	808	1776	1105	1401	34.98133	32.18544	29.37401	42.38606	34.24747	38.41182
protein_co	RAS-like_fa	328	207	184	133	99	160	11.25382	8.369579	8.319147	3.94767	3.816018	5.455767
protein_co	ubiquitin-li	962	873	887	2477	2115	1979	11.61707	12.42347	14.11497	25.8768	28.69333	23.75073
protein_co	forty-two-t	1085	976	965	1136	979	860	15.72003	16.66405	18.42407	14.23852	15.93512	12.38316
protein_co	MTERF_dor	436	414	323	495	379	421	5.09655	5.702919	4.97539	5.005621	4.977119	4.890818
protein_co	X-prolyl_an	7	12	3	0	0	1	0.113329	0.228946	0.064003	0	0	0.01609
protein_co	SAM_and_S	1	0	0	0	0	2	0.02016	0	0	0	0	0.040072
protein_co	oculocereb	793	679	676	1131	1161	1194	8.132935	8.206367	9.13599	10.03459	13.3769	12.16993
protein_co	progestage	0	0	0	24	10	23	0	0	0	1.110276	0.600767	1.222347
protein_co	odorant_bi	0	0	0	0	0	1	0	0	0	0	0	0.057565
protein_co	mitochond	516	431	343	1103	630	850	16.65704	16.3958	14.59074	30.80256	22.84746	27.26948
protein_co	T-box_22	0	0	0	2	1	0	0	0	0	0.038961	0.025298	0
protein_co	fibromodul	1796	1515	1369	11	3	4	28.72569	28.55511	28.85376	0.152202	0.053906	0.063582
protein_co	lymphocyt	0	0	1	0	0	0	0	0	0.023077	0	0	0
protein_co	plasminoge	0	4	0	0	1	4	0	0.091044	0	0	0.021699	0.076781
protein_co	KIAA1191	1872	1597	1494	2157	1605	1783	33.13458	33.311	34.84665	33.0285	31.91536	31.36438
protein_co	coatomer_	7210	6184	5765	4752	3949	3547	79.70444	80.56081	83.98107	45.44506	49.04372	38.96889
protein_co	heparan_su	0	1	0	6	9	3	0	0.026961	0	0.118753	0.231324	0.068212
protein_co	retinoblast	913	753	793	1423	1299	1217	7.456823	7.247448	8.534755	10.05428	11.91904	9.878324
protein_co	zinc_finger_	980	954	867	1324	1218	1127	13.49341	15.4793	15.73076	15.77055	18.84049	15.4216
protein_co	serine_activ	114	68	98	726	431	504	1.503931	1.057156	1.703664	8.285573	6.38777	6.607895
protein_co	annexin_A1	4378	3607	2972	5237	4044	4743	33.2772	32.30905	29.76834	34.43631	34.53275	35.82892
protein_co	LIM_domai	7	7	3	15	11	18	0.068173	0.080337	0.038501	0.126377	0.120352	0.174219
protein_co	family_with	342	322	262	694	477	474	5.016852	5.56632	5.064555	8.806994	7.860907	6.910241
protein_co	family_with	1012	942	803	1646	1357	1736	26.03318	28.55648	27.22056	36.63022	39.21711	44.38192
protein_co	zinc_finger_	319	288	186	566	448	579	8.190193	8.713708	6.292905	12.57138	12.92202	14.77378
protein_co	N(alpha)-ac	151	173	96	321	184	227	2.922885	3.946281	2.448729	5.375301	4.001305	4.36687
protein_co	ribosomal_	23026	20653	14559	26514	16199	19953	1007.454	1064.871	839.408	1003.564	796.24	867.61
protein_co	outer_dens	715	651	617	959	689	811	6.614155	7.0967	7.521221	7.674498	7.160389	7.455879
protein_co	prostaglan	205	214	169	16	18	2	2.438855	3.000219	2.649437	0.16467	0.240577	0.023647
pseudogen	spermatog	49	32	18	5	13	6	1.309495	1.007778	0.633892	0.115595	0.390301	0.159356
protein_co	tRNA_meth	148	140	138	276	199	213	2.50408	2.791397	3.076808	4.039788	3.782585	3.581589
protein_co	leucine_ric	29	9	13	18	18	17	1.047264	0.383008	0.618638	0.562333	0.730264	0.610122
protein_co	RWD_dom	54	43	58	58	43	54	1.858787	1.74426	2.630865	1.727137	1.662851	1.847307

protein_co zinc_finger_	451	426	458	808	767	715	4.19031	4.664298	5.607508	6.494474	8.005972	6.602149
protein_co coiled-coil_	91	94	95	271	280	290	0.989856	1.204941	1.361724	2.550134	3.421668	3.135006
protein_co RNA_polym	194	177	175	357	264	297	3.302429	3.550684	3.925587	5.257302	5.04876	5.024557
protein_co PQ_loop_re	1075	893	716	876	703	797	19.71305	19.29762	17.30187	13.89672	14.48271	14.5249
protein_co neuroblast	584	435	556	327	259	241	8.381009	7.356645	10.51461	4.059702	4.175729	3.437242
protein_co Bardet-Biec	279	259	262	650	478	449	3.667876	4.012521	4.538858	7.392423	7.059719	5.866329
protein_co PMS2_post	341	259	274	402	361	464	6.32325	5.659692	6.69532	6.448743	7.520422	8.550935
protein_co zinc_finger_	1348	1145	831	1875	1592	1937	13.88144	13.89495	11.27666	16.70355	18.41775	19.82366
protein_co septin_7	2480	2332	2259	4469	3599	3635	18.82077	20.85553	22.59106	29.33992	30.68432	27.41572
protein_co endonuclea	195	174	114	101	124	122	2.166525	2.278167	1.669048	0.970764	1.547747	1.347096
protein_co KIAA0087	0	0	0	1	0	0	0	0	0	0.010693	0	0
protein_co kelch-like_f	577	467	466	640	483	480	9.245446	8.81812	9.839494	8.871459	8.694573	7.643688
protein_co HERPUD_fa	344	342	316	746	636	599	5.957377	6.979589	7.211383	11.17631	12.37379	10.30939
protein_co chromobox	2409	2186	2042	5750	3790	5115	59.93179	64.08815	66.9439	123.7517	105.9275	126.4666
protein_co heterogene	11058	9499	8695	21984	21723	28012	93.16065	94.30634	96.52956	160.2233	205.6008	234.5361
protein_co WAS/WASL	0	3	5	48	34	50	0	0.046767	0.087161	0.549312	0.505293	0.657347
protein_co neurexophi	0	0	0	0	0	2	0	0	0	0	0	0.036025
protein_co neuropepti	3	0	0	980	786	975	0.225281	0	0	63.66373	66.30932	72.76411
protein_co family_witl	789	670	877	878	843	650	6.591517	6.596146	9.654789	6.345501	7.911977	5.396739
protein_co homeobox_	27	25	20	6	3	11	0.707627	0.772125	0.690726	0.136036	0.088331	0.286512
protein_co inhibin_be	1113	944	1174	479	418	408	9.716907	9.712074	13.50628	3.617691	4.099758	3.539995
protein_co FK506_bin	4975	4178	3351	2148	2075	2045	76.07783	75.29056	67.5265	28.41596	35.64776	31.07907
protein_co 5'-nucleoti	279	247	240	666	459	555	8.260927	8.618439	9.364199	17.05932	15.26815	16.33154
protein_co ADP-ribosy	540	465	401	458	350	467	9.041156	9.174666	8.847273	6.633744	6.583356	7.770639
protein_co CCZ1_vacu	235	185	153	511	228	292	4.339426	4.025717	3.722979	8.162972	4.72986	5.358669
protein_co polymerase	475	438	320	289	233	278	7.814472	8.491555	6.937306	4.113078	4.306367	4.545278
protein_co receptor_(C	0	0	0	3	0	0	0	0	0	0.103852	0	0
protein_co FtsJ_RNA_n	470	308	287	1295	983	1232	9.909306	7.652497	7.97374	23.61991	23.28348	25.81462
protein_co twist_basic	5342	4286	3635	3586	4069	4097	169.7544	160.5005	152.2146	98.58036	145.2626	129.3876
protein_co smu-1_sup	1313	1144	1133	2478	2010	2138	9.760113	10.02128	11.09826	15.93509	16.78554	15.79456
protein_co GLI_pathog	774	678	579	238	177	206	15.16518	15.65466	14.94927	4.0341	3.896091	4.011286
protein_co solute_carr	292	187	218	310	240	306	8.275573	6.245453	8.141539	7.600461	7.641445	8.61879
protein_co clathrin_lig	4794	4004	3370	6810	4326	5401	134.2853	132.1696	124.3927	165.0215	136.1338	150.3537
protein_co reversion-in	547	543	557	172	160	125	5.924452	6.930552	7.949703	1.611582	1.946839	1.34549
protein_co aconitase_1	1437	1192	1244	718	540	546	21.12641	20.65153	24.1004	9.131801	8.91891	7.977582
protein_co KIAA1045	2	0	0	0	0	4	0.018517	0	0	0	0	0.036806
protein_co dynein_axo	9	7	0	1	7	6	0.190664	0.174756	0	0.018327	0.166599	0.126324
protein_co DDB1_and_	491	451	443	515	406	414	3.332141	3.606828	3.961689	3.023514	3.095401	2.792234
protein_co ciliary_neu	0	0	0	7	6	22	0	0	0	0.156234	0.173906	0.564088
protein_co KIAA1549	345	286	338	525	471	400	1.475454	1.441384	1.904838	1.942356	2.262958	1.700107
protein_co tripartite_r	325	301	356	1319	1031	974	2.045877	2.232902	2.953119	7.182967	7.291281	6.09347
protein_co chromoson	256	216	250	803	614	681	5.261217	5.231269	6.770505	14.2766	14.17632	13.90923
protein_co caldesmon_	12284	10559	12161	13196	11465	10610	143.1178	144.9718	186.7058	133.0023	150.0641	122.851
protein_co aldo-keto_r	0	1	0	8	1	1	0	0.026582	0	0.15611	0.025341	0.022418

protein_co	nudix_(nuc	24	21	13	253	218	240	0.634974	0.654744	0.453235	5.790666	6.479635	6.310531
protein_co	surfactant_	2	0	0	3	0	0	0.047867	0	0	0.062114	0	0
protein_co	neurogenin	0	0	0	0	1	0	0	0	0	0	0.043224	0
protein_co	plasminoge	151	133	112	913	590	687	3.007558	3.121734	2.939612	15.73153	13.20195	13.59889
protein_co	serglycin	115	131	106	0	0	0	5.039913	6.765557	6.121612	0	0	0
protein_co	carbohydra	726	542	658	1480	1702	1412	5.51437	4.851384	6.585974	9.724875	14.52339	10.65869
protein_co	bicaudal_C	612	578	507	161	144	122	5.91995	6.588728	6.462632	1.347273	1.56487	1.172833
protein_co	CDGSH_iro	361	263	211	1032	674	718	7.709439	6.618787	5.937899	19.06594	16.17054	15.23876
protein_co	early_grow	19	16	9	0	3	0	0.338908	0.336322	0.211546	0	0.060117	0
protein_co	ecdysonele	636	483	442	1428	942	902	10.97115	9.818597	10.04737	21.31015	18.25556	15.46363
protein_co	prolyl_4-hy	5640	5489	4696	1282	1090	1104	101.664	116.5973	111.5452	19.99121	22.07312	19.77729
protein_co	solute_carr	252	236	192	269	212	194	7.554434	8.337205	7.584683	6.976164	7.139804	5.779799
protein_co	ZW10_inte	351	285	266	2463	2161	2671	9.475925	9.067059	9.463046	57.52305	65.54179	71.6635
protein_co	vacuolar_p	894	826	834	1902	1691	1898	14.65756	15.9592	18.01876	26.97724	31.14704	30.92644
protein_co	RNA_bindi	731	562	509	1406	1162	1315	8.751666	7.92897	8.030192	14.56202	15.6289	15.6462
protein_co	citron_(rhc	501	362	441	940	925	807	3.04587	2.593518	3.533028	4.943841	6.317779	4.875923
protein_co	intraflagell	445	316	352	486	393	402	7.580033	6.343154	7.901118	7.161605	7.520603	6.805292
protein_co	acyl-CoA_d	97	95	84	101	91	107	2.633475	3.039402	3.005188	2.372148	2.775543	2.887027
protein_co	hydrogen_	28	15	19	25	15	17	0.67718	0.427508	0.605529	0.523057	0.407555	0.408606
pseudogen	NME/NM23	0	0	0	2	1	4	0	0	0	0.132176	0.085824	0.303689
protein_co	DEAD_(Asp	1737	1408	1131	2063	2043	2688	20.99509	20.05523	18.01422	21.57149	27.74185	32.28917
protein_co	mediator_c	1161	986	1306	973	1299	936	6.44958	6.454806	9.560425	4.676006	8.106948	5.16755
protein_co	cyclin-depe	204	142	149	41	32	31	3.718995	3.05064	3.579452	0.64661	0.655382	0.561651
protein_co	ring_finger_	1502	1233	1322	1351	1022	1022	25.78384	24.94295	29.90501	20.06301	19.70959	17.43565
protein_co	Ras_associa	1497	1393	1616	755	618	588	14.38342	15.77243	20.46052	6.275531	6.670802	5.614712
protein_co	basic_helix	547	459	420	24	25	10	7.547231	7.463114	7.636325	0.286467	0.387516	0.137123
protein_co	sarcospan	85	75	75	5	1	10	1.614055	1.678293	1.876702	0.082136	0.021333	0.188716
protein_co	inositol_14	948	649	1027	476	677	446	4.774813	3.85212	6.816372	2.074044	3.830767	2.232506
protein_co	coiled-coil_	123	130	85	382	246	269	2.378284	2.962164	2.16577	6.389767	5.343709	5.169167
protein_co	N-terminal_	141	146	121	86	69	98	1.411359	1.72218	1.596021	0.744698	0.77592	0.974887
protein_co	WW_doma	399	384	452	775	665	536	4.50778	5.112439	6.729194	7.57451	8.440351	6.018167
protein_co	acyl-CoA_th	722	629	562	1300	907	1117	12.26288	12.58963	12.57843	19.10124	17.3066	18.85463
protein_co	peroxiredo	3789	3543	2545	3367	1877	2592	199.5954	219.94	176.6642	153.4377	111.0809	135.6971
protein_co	DEAD_(Asp	965	789	591	3576	2130	2975	26.84606	25.86648	21.66584	86.06247	66.57052	82.25265
protein_co	protein_kir	1455	1069	830	1725	1294	1640	21.89572	18.9575	16.45922	22.45683	21.87659	24.5273
protein_co	chromoson	4226	3622	2846	5030	3817	5275	226.446	228.7129	200.9578	233.1665	229.7769	280.91
protein_co	CD97_mole	92	90	63	456	426	488	1.527783	1.76126	1.378634	6.55091	7.947535	8.053845
protein_co	WD_repeat	67	80	43	93	49	114	2.396653	3.37231	2.026906	2.877904	1.969135	4.052704
protein_co	GIPC_PDZ_	2315	1766	1539	4321	3280	4280	59.17837	53.19977	51.84244	95.55629	94.19653	108.734
protein_co	SPRY_doma	211	211	188	585	441	515	3.61975	4.265655	4.249999	8.681905	8.499313	8.780375
protein_co	emopamil_	1098	925	750	943	642	891	56.65615	56.24625	50.99655	42.09393	37.21592	45.69115
protein_co	ATPase_Cu-	210	197	184	129	163	132	1.674843	1.851519	1.933782	0.890036	1.460466	1.046257
protein_co	zinc_finger_	977	723	756	1506	1484	1302	6.450904	5.625633	6.57783	8.602289	11.00801	8.543713
pseudogen	guanylate_	0	0	0	0	0	2	0	0	0	0	0	0.036652

protein_co	neurolysin_	892	701	719	1921	1498	1422	5.452415	5.049509	5.791456	10.15815	10.28691	8.6384
protein_co	centromere	93	73	93	959	615	694	2.839396	2.626473	3.741629	25.32938	21.0944	21.05776
protein_co	optineurin	1270	1100	942	1198	825	910	19.09545	19.49063	18.6643	15.58281	13.93571	13.59806
protein_co	inter-alpha	57	41	58	1626	1453	1726	0.434505	0.368308	0.582616	10.72268	12.44327	13.07586
protein_co	activating_	301	204	199	432	338	306	7.306391	5.835441	6.36538	9.071585	9.217267	7.381889
protein_co	Ts_translati	178	164	149	530	287	382	4.299041	4.667695	4.742121	11.07364	7.787221	9.169054
protein_co	Rho_GTPas	2	0	5	2	11	3	0.036361	0	0.119786	0.031455	0.224669	0.054204
protein_co	NCK-associ	0	0	1	1	1	3	0	0	0.01478	0.009703	0.012601	0.033441
protein_co	matrix_met	199	220	132	102	59	61	2.743557	3.574297	2.398113	1.216533	0.913823	0.835796
protein_co	prefoldin_s	3661	3277	2209	3148	2140	2857	97.88736	103.2548	77.83186	72.81563	64.28205	75.91835
protein_co	spermatoge	1066	953	902	807	520	581	17.00877	17.91908	18.96518	11.13916	9.32112	9.213009
protein_co	ORM1-like_	87	88	74	195	158	252	2.151269	2.564278	2.411248	4.171316	4.389162	6.192779
protein_co	nuclear_rec	94	96	50	100	78	111	1.028831	1.23821	0.721142	0.946845	0.959091	1.207393
protein_co	phosphodi	0	0	0	2	0	0	0	0	0	0.019349	0	0
protein_co	homeobox_	2	0	4	8	2	3	0.043448	0	0.114507	0.150345	0.048811	0.064769
protein_co	cyclin-depe	296	305	251	1456	997	1301	6.031768	7.324195	6.740025	25.66713	22.82428	26.34753
protein_co	low_densit	32313	27891	27469	3546	4456	3853	114.834	116.8058	128.6385	10.90172	17.79047	13.60824
protein_co	homeobox_	50	71	35	0	0	0	0.811729	1.358334	0.748763	0	0	0
protein_co	chromoson	445	292	284	346	361	532	16.37161	12.65964	13.76843	11.01211	14.92064	19.45148
protein_co	nuclear_fac	4	0	0	61	46	65	0.115529	0	0	1.524132	1.492576	1.865746
protein_co	IKAROS_fan	193	145	161	145	177	136	1.954028	1.73001	2.147999	1.270002	2.013241	1.368428
protein_co	single-stran	313	306	193	472	355	451	6.356168	7.322841	5.164677	8.291938	8.098945	9.102009
protein_co	tubulin_alp	1580	1170	1093	4167	2984	3326	26.15596	22.82478	23.84342	59.67606	55.49598	54.71993
protein_co	methyltran	240	208	171	92	63	103	4.600231	4.698279	4.31916	1.525525	1.356619	1.962074
protein_co	kelch_repea	50	69	54	63	54	45	0.859711	1.398101	1.22352	0.9371	1.043098	0.768961
protein_co	sarcosine_d	2	2	7	4	2	1	0.031663	0.037313	0.146036	0.054783	0.035572	0.015734
protein_co	dopamine_	2	0	0	0	0	0	0.038321	0	0	0	0	0
protein_co	ATP_syntha	375	302	257	1149	716	844	4.774621	4.531288	4.311968	12.65583	10.24164	10.67972
protein_co	SCL/TAL1_i	130	90	86	981	710	692	1.317192	1.074621	1.148257	8.598799	8.081895	6.968215
protein_co	Holliday_ju	268	225	173	1747	1177	1147	4.651864	4.602373	3.957065	26.23301	22.95185	19.78633
protein_co	interleukin	16	7	17	0	0	0	0.565458	0.291531	0.791706	0	0	0
protein_co	collagen_ty	1	9	11	0	5	4	0.015135	0.160517	0.219381	0	0.085014	0.060165
protein_co	adenosylm	1691	1355	1491	3579	2695	2665	26.03933	24.58853	30.25511	47.67722	46.62234	40.78431
protein_co	NADH_dehy	188	157	113	968	464	697	4.148773	4.082899	3.286057	18.47993	11.50347	15.28637
protein_co	ubiquitin_s	197	148	211	368	244	217	1.667366	1.476161	2.353326	2.694484	2.320084	1.8253
protein_co	proteolipid	124	92	124	207	237	281	2.095335	1.832005	2.761139	3.025973	4.499136	4.718975
protein_co	serpin_pep	0	1	0	0	2	1	0	0.03322	0	0	0.06334	0.028016
protein_co	mortality_f	7489	6647	6070	7459	5585	6255	144.2252	150.8517	154.0426	124.2685	120.8341	119.7166
protein_co	RAB9B_mer	34	38	35	35	25	12	0.480254	0.632533	0.651471	0.427685	0.396718	0.168455
protein_co	Nik_related	69	46	94	1010	920	708	0.452992	0.355882	0.813213	5.736222	6.785447	4.619388
protein_co	family_with	404	387	521	970	893	707	2.868199	3.23777	4.874168	5.957481	7.122435	4.988351
protein_co	ESX_homec	0	2	0	16	11	2	0	0.083462	0	0.490156	0.437615	0.070387
protein_co	RAB9A_mer	370	331	275	726	458	542	9.606752	10.12768	9.408976	16.30702	13.35948	13.98569
protein_co	methyltran	317	264	265	396	356	353	7.472082	7.333197	8.231198	8.074963	9.427171	8.269261

protein_co	tetratricop	205	226	228	281	229	251	1.979734	2.571986	2.901501	2.347591	2.484492	2.408998
protein_co	N-myc_(anc	182	139	165	181	127	145	4.601366	4.141306	5.497107	3.95874	3.607183	3.643284
protein_co	tumor_nec	83	75	47	1	0	0	3.090086	3.290492	2.305819	0.032207	0	0
protein_co	activin_A_r	5	3	1	1	0	0	0.078199	0.055292	0.02061	0.01353	0	0
protein_co	bromodom	241	167	294	311	346	259	1.539242	1.256937	2.474412	1.718357	2.482648	1.643991
protein_co	solute_carr	465	354	417	436	386	348	4.258357	3.820318	5.032224	3.45413	3.971234	3.167218
protein_co	lysophosph	507	493	563	840	919	820	3.449124	3.952345	5.047125	4.943598	7.023692	5.544015
protein_co	basic_leuci	7	10	6	26	17	18	0.157228	0.264691	0.17759	0.505206	0.428974	0.401804
protein_co	G0/G1swit	95	52	59	180	130	144	5.807615	3.746145	4.752926	9.519403	8.928255	8.748757
protein_co	potassium_	22	31	34	173	167	136	0.216006	0.358683	0.439902	1.469438	1.842077	1.327061
protein_co	RAP2C_mer	455	339	403	890	682	705	6.182791	5.428501	7.216274	10.46228	10.41134	9.520766
protein_co	exosome_c	240	181	188	1237	728	811	3.273014	2.908856	3.378541	14.59383	11.15365	10.99176
protein_co	phospholip	520	399	382	705	470	556	5.267761	4.763242	5.099421	6.178383	5.348963	5.597668
protein_co	B9_protein	82	61	70	154	101	118	4.227032	3.7056	4.755044	6.867606	5.849141	6.045237
protein_co	aarF_doma	629	514	378	726	576	803	13.63073	13.12619	10.79432	13.61032	14.02298	17.29393
protein_co	6-phospho	94	99	92	139	172	141	0.701502	0.870649	0.904739	0.897385	1.442044	1.045754
protein_co	complemer	0	0	1	0	0	0	0	0	0.031103	0	0	0
protein_co	complemer	0	1	0	9	9	6	0	0.031319	0	0.206923	0.268716	0.158476
pseudogen	zinc_finger_	44	34	33	51	62	66	1.213231	1.104783	1.199056	1.216533	1.920576	1.808608
protein_co	RAB38_mer	26	17	24	213	149	158	0.939567	0.723953	1.14288	6.658817	6.049086	5.674416
protein_co	G_protein-r	0	0	0	9	2	12	0	0	0	0.096261	0.02778	0.147447
protein_co	argonaute_	219	173	190	251	418	307	3.245822	3.021578	3.710813	3.218232	6.959948	4.52198
protein_co	MAX_dimer	4852	4021	3300	1160	986	1131	60.75442	59.33327	54.451	12.56545	13.87021	14.07438
pseudogen	postmeioti	44	36	33	48	58	45	1.909347	1.840949	1.88704	1.801924	2.827544	1.940682
protein_co	CDC28_prc	440	312	321	1833	1164	1719	38.00006	31.75362	36.53183	136.9484	112.9363	147.5425
protein_co	dynein_ass	5	3	1	19	11	17	0.106908	0.075591	0.028176	0.351446	0.264231	0.361243
protein_co	acyl-CoA_sy	1237	1009	1215	2332	1857	1875	11.53161	11.08456	14.92558	18.80666	19.44828	17.37125
protein_co	chondroiti	12187	9715	7910	8608	5507	6322	214.136	201.1606	183.1489	130.8453	108.7069	110.397
protein_co	aspartyl_an	719	732	532	737	467	600	15.69673	18.83209	15.30477	13.91909	11.45371	13.01791
protein_co	inhibin_alp	8	6	9	94	65	98	0.288507	0.254991	0.427704	2.932627	2.63347	3.512382
protein_co	monoacylg	1	1	0	0	0	0	0.050516	0.05953	0	0	0	0
protein_co	obscurin-lil	1849	1599	1220	6576	5716	7387	16.75876	17.07892	14.57134	51.56199	58.20311	66.53997
protein_co	family_with	0	0	0	0	0	3	0	0	0	0	0	0.060849
protein_co	solute_carr	1793	1498	1295	1603	1307	1585	20.32617	20.01217	19.34549	15.72069	16.64562	17.85723
protein_co	enkurin_do	158	113	78	194	156	226	5.297452	4.464733	3.446191	5.626971	5.876025	7.530573
protein_co	glucosamin	17	17	9	7	16	4	0.436045	0.513852	0.3042	0.155326	0.461054	0.101965
protein_co	family_with	1478	1180	1149	1301	1082	1051	25.68837	24.16859	26.31583	19.56152	21.12703	18.15409
protein_co	family_with	0	1	0	0	0	2	0	0.068483	0	0	0	0.115508
protein_co	sorting_nex	519	418	276	162	182	191	8.846225	8.396031	6.199184	2.388739	3.485067	3.235442
protein_co	secretory_l	2	0	0	1	0	0	0.177654	0	0	0.076844	0	0
protein_co	WAP_four-r	4	11	1	1	4	6	0.211764	0.686265	0.069763	0.045799	0.237904	0.315684
protein_co	tocopherol	747	609	558	630	534	609	6.343748	6.094663	6.244452	4.628378	5.094665	5.139871
protein_co	phosphatid	916	808	835	385	423	403	7.198152	7.482453	8.646629	2.617275	3.73435	3.147315
protein_co	potassium_	12	11	5	100	103	86	0.139994	0.151226	0.076866	1.009231	1.349938	0.997093

protein_co solute_carr	1	8	6	5	7	3	0.008764	0.082619	0.06929	0.037907	0.068918	0.026128
protein_co Rho_GTPas	0	3	4	68	76	74	0	0.065879	0.098224	1.096208	1.591049	1.370447
protein_co syndecan_4	710	533	499	2699	2784	3344	14.38504	12.72586	13.32257	47.30626	63.36814	67.3331
protein_co nuclear_rec	563	475	622	639	699	458	3.754349	3.732734	5.465772	3.686296	5.236638	3.035299
protein_co phosphatid	2221	1877	1587	1963	1003	1137	52.60937	52.39453	49.53661	40.22517	26.69098	26.76607
protein_co matrilin_4	6	2	3	6	2	5	0.139196	0.054678	0.091713	0.120418	0.052126	0.115281
protein_co nuclear_rec	871	650	674	1585	1302	1385	14.32037	12.5938	14.60262	22.54387	24.04896	22.63058
protein_co VAMP_(vesi	953	818	749	2277	1828	2084	6.357456	6.43059	6.584261	13.14064	13.69985	13.81649
protein_co par-6_parti	3	4	0	282	215	255	0.034415	0.054074	0	2.798546	2.770817	2.907169
protein_co ATP_syntha	1929	1674	1284	1973	1466	2230	27.86444	28.49579	24.44094	24.65518	23.79037	32.01346
protein_co chromodor	648	535	657	423	457	358	3.171174	3.085361	4.236872	1.790806	2.512525	1.741156
protein_co phospholip	2167	1991	1799	2042	2159	2217	20.88533	22.61314	22.84801	17.02555	23.37675	21.23527
protein_co TOX_high_r	6	9	5	68	52	52	0.121937	0.215543	0.133903	1.195518	1.187235	1.050261
protein_co serine/argir	3293	2903	2778	5080	3630	3916	47.33497	49.17501	52.6208	63.1709	58.62003	55.94261
protein_co ganglioside	1	4	2	9	6	7	0.023374	0.110177	0.061601	0.181982	0.157552	0.162604
protein_co ADP-ribosy	595	510	684	599	716	547	3.558506	3.594413	5.390656	3.099135	4.81075	3.25123
protein_co zinc_finger_	634	601	580	715	533	414	4.553601	5.08683	5.489446	4.442575	4.300728	2.955124
protein_co endothelin_	0	2	2	0	0	1	0	0.046996	0.052552	0	0	0.019817
protein_co CSE1_chror	1384	1323	1194	8413	5392	5651	20.6221	23.23078	23.44423	108.4453	90.2601	83.68196
protein_co RAB22A_m	934	642	731	863	614	616	5.703217	4.619714	5.882002	4.558761	4.21202	3.738207
protein_co prostaglanc	1451	1215	870	17	9	9	13.76902	13.58686	10.87902	0.139556	0.095946	0.084877
protein_co staufen_RN	1927	1625	1471	3665	2856	2917	28.86737	28.68706	29.03842	47.4966	48.06543	43.42818
protein_co cadherin_2	9	8	12	3	6	15	0.149739	0.156852	0.263092	0.043179	0.112148	0.248023
protein_co snail_homc	611	484	380	325	287	354	19.18562	17.90964	15.72363	8.828377	10.12431	11.04708
protein_co molybdenu	249	158	177	421	312	340	5.363022	4.010277	5.023637	7.84432	7.549425	7.277777
protein_co syntaxin_1(	1082	842	813	1154	793	1006	11.60262	10.64016	11.48826	10.70527	9.553251	10.72103
protein_co protein_ph	81	49	89	62	53	77	1.193493	0.850821	1.728063	0.790296	0.877324	1.127549
protein_co prostate_tr	737	600	539	23	9	17	8.05315	7.726035	7.761075	0.217415	0.110482	0.184611
protein_co ring_finger_	1290	995	927	1805	1359	1755	27.9893	25.4409	26.50433	33.87993	33.12614	37.8433
protein_co DEAD_(Asp-	707	646	564	1423	1051	1140	7.593687	8.176602	7.982652	13.22212	12.68192	12.1688
protein_co recombinat	0	1	0	0	0	2	0	0.034092	0	0	0	0.057502
protein_co breast_carc	52	43	52	159	115	177	1.837738	1.790836	2.421689	4.861166	4.565908	6.216747
protein_co potassium_	0	4	0	0	0	0	0	0.189054	0	0	0	0
protein_co TP53_targe	19	18	16	5	9	21	0.957068	1.068486	1.062048	0.217883	0.509309	1.05128
protein_co phosphoen	1	0	0	0	1	1	0.010434	0	0	0	0.011722	0.010369
protein_co neuralized_	39	38	40	32	22	23	1.61557	1.855034	2.183514	1.146764	1.023842	0.946888
protein_co 5-methylte	288	195	244	601	419	433	4.656996	3.715824	5.199218	8.407191	7.611609	6.958425
protein_co FAST_kinas(	83	64	67	173	116	153	1.829352	1.662288	1.945937	3.298589	2.872276	3.351353
protein_co peptidase_I	1299	999	808	896	589	701	36.17588	32.78556	29.65215	21.58644	18.42784	19.4016
protein_co carbohydra	1	7	3	36	18	15	0.021364	0.176237	0.084459	0.665359	0.432028	0.318487
protein_co IQ_motif_a	204	178	166	23	48	23	1.7967	1.847449	1.926585	0.175241	0.474937	0.201318
protein_co vesicle-assc	540	529	548	826	559	603	10.80428	12.47283	14.44833	14.29701	12.56502	11.99028
protein_co interleukin_	0	0	0	0	2	1	0	0	0	0	0.052218	0.023097
protein_co Xg_blood_g	23	35	16	1	12	4	0.421768	0.756346	0.386634	0.015864	0.247215	0.072898

protein_co	STAM_bind	624	522	528	1054	780	845	4.937256	4.867194	5.505158	7.214474	6.933375	6.644578
protein_co	N-acetylglu	1742	1629	1195	1081	912	1233	21.01714	23.1608	18.99889	11.28273	12.36145	14.78421
protein_co	methylmal	167	125	91	91	74	109	10.57553	9.328309	7.59385	4.985288	5.264615	6.859966
protein_co	poly(A)_bin	7	0	1	33	37	32	0.05902	0	0.011111	0.240701	0.350471	0.26814
protein_co	small_nucl	343	309	268	545	349	428	10.077	10.69801	10.37545	13.8515	11.51892	12.49657
protein_co	M-phase_pl	613	598	456	1010	691	907	13.06475	15.01927	12.80679	18.62194	16.54503	19.21133
protein_co	interleukin	2	1	2	0	3	0	0.10142	0.059758	0.133646	0	0.170908	0
protein_co	ATPase_am	84	97	102	71	68	62	0.537732	0.731755	0.860442	0.393195	0.48904	0.394446
protein_co	ubiquitin_s	3947	3202	2962	4138	4242	4277	40.06099	38.2986	39.61634	36.33356	48.36979	43.14231
protein_co	premature_	3	0	0	151	180	131	0.0403	0	0	1.754792	2.716484	1.748907
protein_co	hypoxia_in	685	690	413	19	9	16	6.138216	7.286312	4.876817	0.147288	0.090603	0.142489
protein_co	zinc_finger_	129	141	85	212	186	173	2.661492	3.428164	2.310943	3.783853	4.311193	3.547245
protein_co	zinc_finger_	282	235	223	251	241	224	3.830005	3.761189	3.991075	2.949083	3.677192	3.023486
protein_co	LY6/PLAUR	2	1	6	68	62	50	0.062504	0.036829	0.247095	1.838445	2.176805	1.552953
protein_co	pregnancy_	0	0	0	0	3	1	0	0	0	0	0.072005	0.021232
protein_co	carcinoemb	0	0	0	2	4	4	0	0	0	0.039739	0.103212	0.091304
protein_co	Norrie_dise	0	10	0	0	1	0	0	0.340359	0	0	0.032447	0
protein_co	ubiquitin_s	1204	886	1267	1652	1417	1300	6.224095	5.397474	8.631001	7.38793	8.229409	6.678866
protein_co	coagulation	0	0	0	0	2	1	0	0	0	0	0.029745	0.013157
protein_co	glutamate_	28	35	33	22	10	18	0.382147	0.562921	0.5935	0.259751	0.153328	0.244149
protein_co	transcriptic	443	378	356	342	377	329	3.067337	3.084301	3.248199	2.048552	2.932569	2.263932
protein_co	protein_kir	1	0	3	24	21	17	0.012395	0	0.049003	0.257357	0.292436	0.209421
protein_co	butyrophili	398	387	296	138	128	173	5.869224	6.725362	5.75207	1.760515	2.12059	2.53544
protein_co	sirtuin_5	118	77	77	243	166	178	2.670815	2.053807	2.296611	4.758074	4.221036	4.003976
protein_co	histone_clu	2	2	1	4	4	3	0.296588	0.349511	0.195415	0.513153	0.666397	0.442135
protein_co	MRS2_mag	193	159	172	2358	1920	1842	3.084097	2.994159	3.621879	32.59699	34.46839	29.25297
protein_co	Werner_he	756	672	538	1239	1088	1128	12.35671	12.94367	11.58773	17.51925	19.97833	18.32314
protein_co	ribosomal_	899	717	663	2290	1494	1850	41.06467	38.59534	39.90773	90.49137	76.66697	83.98274
pseudogen	butyrophili	126	123	129	25	38	25	2.606708	2.998707	3.516789	0.44743	0.883191	0.51401
protein_co	butyrophili	2	2	0	0	0	0	0.036574	0.0431	0	0	0	0
protein_co	small_nucl	1411	1192	772	3526	2144	2696	70.87262	70.55614	51.09796	153.2134	120.9833	134.5802
protein_co	serpin_pep	1269	1088	805	562	417	487	20.57645	20.78954	17.20044	7.883303	7.596158	7.847792
protein_co	exportin_5	853	738	704	2789	2056	2059	8.425125	8.589952	9.162939	23.83081	22.8139	20.21126
protein_co	ATP-bindin	784	626	648	752	693	892	8.157575	7.675849	8.884946	6.769021	8.100788	9.224004
protein_co	histone_clu	4	1	3	1	8	9	0.272541	0.080293	0.269356	0.058943	0.612365	0.609429
protein_co	histone_clu	0	0	0	2	0	0	0	0	0	0.244914	0	0
protein_co	peroxisoma	709	713	445	547	547	689	10.79217	12.78966	8.926009	7.202991	9.354033	10.42297
protein_co	NAD(P)H_d	319	216	179	189	147	168	11.14731	8.894884	8.242658	5.713527	5.770931	5.834429
protein_co	prickle_hor	147	130	91	108	90	75	1.971707	2.054828	1.608426	1.253175	1.356177	0.99976
protein_co	O-acyl-ADP	197	202	193	519	474	574	3.131945	3.784481	4.043337	7.138028	8.465941	9.069209
protein_co	unc-5_hom	2	4	1	28	23	31	0.035459	0.083574	0.023363	0.429461	0.45812	0.546228
protein_co	alanyl-tRNA	680	589	451	832	759	912	9.340912	9.534606	8.163788	9.88705	11.71308	12.45044
protein_co	zinc_finger_	57	63	48	86	78	72	0.739798	0.963576	0.820946	0.965606	1.137318	0.928711
protein_co	ribosomal_	30	21	34	104	46	72	2.033585	1.677519	3.03707	6.098702	3.503063	4.850463

protein_co	molybdenu	187	131	117	233	251	210	2.32612	1.920299	1.917835	2.507318	3.507626	2.596088
protein_co	histone_clu	81	56	60	132	101	119	5.972452	4.865895	5.829801	8.419854	8.366389	8.720156
protein_co	mediator_c	254	274	251	659	460	574	5.167953	6.569653	6.729663	11.59934	10.51457	11.60664
protein_co	olfactory_r	3	2	3	25	8	20	0.168602	0.132458	0.222176	1.21547	0.505103	1.117071
protein_co	tubulin_fol	311	340	244	574	367	517	7.704562	9.925984	7.965485	12.30162	10.21416	12.72881
protein_co	SAM_point	4	0	4	1	4	5	0.111749	0	0.147258	0.024168	0.125543	0.138823
protein_co	t-complex_	1	2	0	1	1	2	0.024442	0.057606	0	0.021144	0.027459	0.048582
protein_co	MAD2L1_b	269	280	186	670	402	533	9.387691	11.5152	8.553705	20.2276	15.76092	18.48602
protein_co	histone_clu	12	6	5	6	26	20	1.345957	0.793064	0.739018	0.582189	3.276216	2.229409
protein_co	apolipopro	0	3	3	1	3	3	0	0.162609	0.181833	0.039791	0.15502	0.137135
protein_co	kelch_dom	1691	1471	1135	2855	2303	3282	46.89535	48.07352	41.47791	68.49443	71.7512	90.45538
protein_co	glycine_N-r	5	9	6	0	8	11	0.246926	0.523778	0.390466	0	0.44385	0.539883
protein_co	dynein_axo	0	0	0	2	2	3	0	0	0	0.006444	0.008368	0.011104
protein_co	triggering_	0	0	0	2	0	0	0	0	0	0.044725	0	0
protein_co	male-enhar	726	570	526	824	914	1383	35.294	32.65473	33.6965	34.65408	49.91826	66.81839
protein_co	kelch-like_f	9	1	13	13	7	2	0.082965	0.010863	0.157918	0.103672	0.072494	0.018323
protein_co	collagen_ty	601	577	530	149	86	135	7.332919	8.296317	8.521443	1.572721	1.178827	1.636989
protein_co	cyclin-depe	19188	15537	14048	9530	7332	8226	449.2843	428.7121	433.4518	193.0401	192.8693	191.4211
protein_co	SRY_(sex_d	4345	3603	3495	981	1271	1295	47.17568	46.09987	50.00465	9.214259	15.50326	13.97358
protein_co	glyoxalase_	2615	2273	2186	5120	3422	3620	68.8075	70.48077	75.79649	116.5459	101.1564	94.66345
protein_co	copine_V	1	1	0	3	0	0	0.013585	0.016009	0	0.035257	0	0
protein_co	ras_respons	829	716	667	1222	1368	1159	4.84042	4.926615	5.132029	6.172523	8.973536	6.725453
protein_co	signal_sequ	3945	3519	3455	3457	2466	2696	21.60019	22.7058	24.92834	16.37468	15.16885	14.67034
protein_co	RIO_kinase_	394	251	296	1082	666	735	7.423043	5.572712	7.34873	17.63502	14.09643	13.76204
protein_co	neuritin_1	566	416	379	10	13	15	18.45111	15.98109	16.28096	0.282013	0.4761	0.485967
protein_co	solute_carr	448	351	399	537	413	488	11.09853	10.24712	13.02553	11.50866	11.49441	12.01481
protein_co	ribonuclea	158	126	100	225	143	154	5.640376	5.300643	4.7042	6.948586	5.735035	5.46363
protein_co	ataxin_1	957	815	819	566	732	594	4.778771	4.795888	5.389184	2.445027	4.10643	2.947816
protein_co	nucleopori	867	783	777	2199	2193	1950	8.365198	8.902787	9.878999	18.35462	23.77086	18.69827
protein_co	DEK_oncog	1070	756	993	4858	3791	3899	16.52958	13.7628	20.21446	64.92299	65.79317	59.86057
protein_co	eukaryotic_	52	51	44	221	101	212	2.556111	2.954294	2.850125	9.397918	5.577593	10.35671
protein_co	runt-relate	899	831	709	272	254	226	8.352747	9.098667	8.680619	2.186259	2.651261	2.086833
protein_co	opsin_5	0	4	0	4	2	0	0	0.0713	0	0.052342	0.033986	0
protein_co	glial_cells_	0	0	0	1	0	1	0	0	0	0.018762	0	0.021554
protein_co	leucine_ric	1122	951	870	1839	1562	1621	13.59263	13.57683	13.8888	19.27327	21.2589	19.51656
antisense	-	0	0	2	0	3	0	0	0	0.06254	0	0.079977	0
protein_co	RAB17_mer	4	1	0	20	11	18	0.06595	0.019429	0	0.285263	0.203748	0.29494
protein_co	chemokine_	98	96	75	11	7	11	3.019917	3.486159	3.045545	0.293241	0.242335	0.336877
protein_co	epiregulin	35	12	22	136	129	106	0.401155	0.162081	0.332278	1.348485	1.661051	1.207424
protein_co	tripartite_r	0	0	0	6	0	1	0	0	0	0.168688	0	0.032298
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.024118	0
protein_co	myelin_reg	86	87	75	50	49	47	0.768167	0.915764	0.882782	0.386358	0.491702	0.41722
protein_co	AHNAK_nuc	21726	18047	22815	25620	32769	31710	61.22298	59.93034	84.72078	62.45638	103.7402	88.80564
protein_co	ER_membra	1109	896	805	1272	820	856	21.14208	20.12942	20.22306	20.97811	17.56221	16.21809

protein_co ssu-2_hom	1	0	0	3	4	7	0.016446	0	0	0.042683	0.073906	0.114414
protein_co SH3_domai	9	9	6	28	32	40	0.081741	0.096327	0.07181	0.219998	0.32651	0.36105
protein_co CCR4-NOT_	2244	1872	2224	4220	3561	2742	14.02427	13.78702	18.31585	22.81565	25.00221	17.03078
protein_co leucine_ric	20	35	18	12	5	11	0.545783	1.125552	0.647288	0.283292	0.153288	0.298327
protein_co Bardet-Biec	551	445	460	417	430	400	4.803308	4.57147	5.284227	3.144763	4.211204	3.46544
protein_co metallothic	3	4	1	66	42	65	0.252903	0.397374	0.111088	4.813261	3.977689	5.445722
protein_co metallothic	3191	2128	1928	1337	1087	1357	187.0816	147.0222	148.9519	67.81078	71.59504	79.06674
protein_co chromoson	316	231	266	467	407	408	5.839216	5.030215	6.477149	7.465301	8.449109	7.492681
protein_co glutamic-o:	930	790	685	4586	2673	3003	19.99802	20.01881	19.41017	85.31023	64.57316	64.17546
protein_co docking_pr	461	433	358	6172	5514	7039	8.648405	9.572603	8.850197	100.1668	116.212	131.2368
protein_co G_protein-r	5	5	3	3	0	10	0.155892	0.183709	0.123257	0.080917	0	0.309859
protein_co citrate_lyas	23	19	27	26	29	22	0.214866	0.20917	0.332382	0.210124	0.304359	0.204254
protein_co transmemb	206	185	181	797	554	523	3.027719	3.204256	3.505595	10.13374	9.147601	7.639408
protein_co RAP2A_mer	1635	1467	1562	916	825	722	15.7752	16.67993	19.85971	7.645671	8.942524	6.923154
protein_co ATP-bindin	651	555	632	343	261	197	5.904504	5.932018	7.553605	2.691284	2.659451	1.775735
protein_co ephrin-B2	1600	1321	1491	3040	3087	2882	18.98803	18.47438	23.31698	31.21019	41.15717	33.99096
protein_co SRY_(sex_d	0	1	0	2	1	9	0	0.024915	0	0.036581	0.023752	0.189108
protein_co transmemb	3000	2613	2710	3597	2813	2881	46.30408	47.52745	55.11909	48.02876	48.77719	44.19273
protein_co chromoson	53	54	49	405	277	330	1.029678	1.236307	1.254459	6.80681	6.045809	6.37161
protein_co kinesin_fam	0	0	1	0	0	1	0	0	0.043251	0	0	0.032619
protein_co interferon_	226	210	195	140	120	101	2.321883	2.542485	2.639984	1.244294	1.38504	1.031248
protein_co UPF3_regul	339	271	267	654	483	499	7.547097	7.109787	7.832967	12.59566	12.08026	11.04054
protein_co ring_finger_	173	157	116	229	110	172	7.072426	7.563609	6.249066	8.098803	5.052008	6.988121
protein_co septin_6	513	395	411	398	331	331	5.785839	5.249926	6.108374	3.883248	4.193977	3.710109
protein_co transmemb	2	0	2	228	143	171	0.030914	0	0.040738	3.048803	2.483228	2.626862
protein_co NADH_dehy	738	625	527	527	519	1048	51.00581	50.90383	47.99641	31.50917	40.29765	71.98371
protein_co amelogenir	2738	2533	1689	0	0	1	173.5957	189.2552	141.114	0	0	0.063011
protein_co ATP_synthas	116	84	99	213	126	203	3.058344	2.609845	3.439524	4.858151	3.732055	5.31905
protein_co bone_morp	1597	1391	1195	2440	1717	2054	44.10369	45.26934	43.48833	58.29386	53.27081	56.37416
protein_co prostaglanc	437	444	352	0	0	0	9.708441	11.62407	10.30494	0	0	0
protein_co family_with	957	686	615	921	814	768	10.45492	8.83161	8.853574	8.704249	9.990383	8.338339
protein_co G_protein-r	176	176	169	118	92	97	4.231433	4.986485	5.354221	2.454256	2.484916	2.317694
protein_co SRY_(sex_d	270	225	234	2715	2617	2457	3.632546	3.567278	4.148566	31.5995	39.55489	32.85203
protein_co tektin_3	10	8	5	4	0	5	0.290885	0.274232	0.191657	0.100657	0	0.144544
protein_co myosin_hea	2	3	0	6	2	3	0.016703	0.029526	0	0.04335	0.018765	0.0249
protein_co heparan_su	1387	1245	1079	136	164	144	13.6816	14.47228	14.02545	1.160546	1.817412	1.411668
protein_co solute_carr	5	1	17	19	26	22	0.095047	0.022401	0.425844	0.312452	0.555251	0.415623
protein_co mitochond	601	501	376	1841	1234	1515	18.53089	18.20399	15.27722	49.10646	42.74507	46.42416
protein_co golgi-associ	602	572	494	1011	764	813	6.19807	6.940059	6.702268	9.004802	8.836951	8.318791
protein_co armadillo_r	171	91	96	426	342	330	4.258189	2.670406	3.150176	9.177015	9.567622	8.166809
protein_co nucleoporin	570	514	347	1846	1148	1350	13.51382	14.36063	10.84096	37.86152	30.57696	31.80876
protein_co solute_carr	28	29	24	178	151	130	0.635928	0.776167	0.718283	3.4973	3.852794	2.934289
protein_co MIF4G_dor	29	36	12	134	114	132	1.002801	1.466988	0.546806	4.008526	4.428644	4.536286
protein_co 5'_3'-nucle	554	507	305	767	632	818	22.30366	24.05367	16.18084	26.71313	28.58462	32.72874

protein_co	misato_hor	277	247	222	494	349	412	5.88942	6.188662	6.219859	9.086209	8.336183	8.705618
protein_co	chromoson	0	0	0	0	0	1	0	0	0	0	0	0.019508
protein_co	transcriptic	268	199	193	499	379	422	4.648816	4.067876	4.411636	7.488091	7.385771	7.274944
protein_co	general_tra	899	758	837	1353	1316	1295	5.263071	5.229448	6.457134	6.852363	8.655347	7.534579
protein_co	DEAD_(Asp-	319	287	245	681	443	490	3.689792	3.912012	3.734325	6.814301	5.756572	5.632704
protein_co	BarH-like_h	4	2	4	0	2	0	0.090459	0.0533	0.119203	0	0.050812	0
protein_co	protein_ph	2803	2209	1480	1554	1261	1709	35.83521	33.28049	24.93351	17.18703	18.11136	21.71394
protein_co	membrane_	4336	3704	2732	5935	4610	5435	75.53542	76.03954	62.71579	89.44275	90.22178	94.09587
protein_co	src-related_	6	2	1	0	7	5	0.209529	0.082306	0.046018	0	0.274625	0.173529
protein_co	opiate_rece	40	30	30	20	13	6	0.628566	0.555545	0.621222	0.271884	0.2295	0.093703
protein_co	SLC2A4_reg	1501	1173	978	1794	1266	1647	45.90666	42.27661	39.41565	47.46576	43.49885	50.06086
protein_co	chromoson	4	6	7	0	3	3	0.186248	0.329223	0.429501	0	0.156929	0.138823
protein_co	pancreatic_	3297	2737	1779	3508	2528	2931	201.0904	196.7226	142.9826	185.0951	173.2202	177.6633
protein_co	interleukin	11	4	1	2	2	5	0.357051	0.153005	0.042773	0.056161	0.072932	0.161294
protein_co	plasminoge	5	3	6	10	4	0	0.127446	0.090112	0.201531	0.220505	0.114542	0
protein_co	interleukin	0	0	0	0	4	0	0	0	0	0	0.308165	0
protein_co	coiled-coil-	181	144	134	368	271	322	2.928582	2.74567	2.857054	5.150977	4.926031	5.177789
protein_co	paired_box	412	344	334	34	64	54	5.340766	5.25499	5.70542	0.381284	0.932042	0.69568
protein_co	insulin_ind	431	408	282	234	213	208	7.164072	7.991898	6.176843	3.364818	3.97751	3.43602
protein_co	polymerase	243	223	299	830	582	583	2.822436	3.052318	4.576398	8.339862	7.594336	6.729704
pseudogen	5-hydroxyt	6	0	0	0	3	0	0.266258	0	0	0	0.149562	0
protein_co	coiled-coil_	470	375	481	663	625	572	3.606648	3.391129	4.863913	4.401315	5.388092	4.362261
protein_co	pleckstrin_	301	199	224	208	185	188	2.845578	2.216993	2.790531	1.701102	1.964829	1.766329
protein_co	solute_carr	1600	1273	1025	1378	1009	1168	24.73156	23.1882	20.87806	18.42654	17.52152	17.94254
protein_co	persephin	153	154	87	253	183	192	2.071074	2.456587	1.551881	2.962701	2.782944	2.582945
protein_co	general_tra	4501	3855	2415	3587	2981	4289	87.25281	88.0647	61.69108	60.15404	64.92044	82.62968
protein_co	alkB_alkyla	662	519	401	697	474	719	31.57382	29.17048	25.20277	28.75841	25.39782	34.08063
protein_co	ClpP_caseir	1121	1041	654	2404	1353	1579	44.09127	48.25084	33.89687	81.79834	59.78523	61.72183
protein_co	tumor_nec	368	298	277	59	28	23	11.75757	11.22	11.6623	1.63074	1.005025	0.73031
protein_co	glutamate_	23	23	22	5	3	7	0.23543	0.27744	0.29675	0.044276	0.034499	0.07121
protein_co	THO_comp	1054	945	1016	1286	1010	936	9.948263	10.51104	12.63674	10.50052	10.70969	8.779952
protein_co	mediator_c	988	783	974	805	1306	1146	8.950325	8.358931	11.62721	6.308713	13.2915	10.31754
protein_co	ribosomal_	22342	19964	12778	21577	14841	18459	383.9038	404.2547	289.3331	320.741	286.4921	315.2232
protein_co	autophagy_	120	126	120	265	199	212	2.162328	2.67558	2.849419	4.130943	4.028491	3.796521
protein_co	CD70_mole	526	479	371	13	8	28	30.50051	32.73135	28.3485	0.65212	0.521147	1.613574
protein_co	complemer	115	82	74	3	12	24	1.156795	0.97203	0.980901	0.026106	0.135609	0.239927
protein_co	SH2_domai	13	18	5	633	339	575	0.197032	0.321494	0.099862	8.299658	5.772212	8.661059
protein_co	thyroid_ho	1022	812	698	1114	932	1263	24.05767	22.52505	21.65174	22.68563	24.6472	29.54715
protein_co	G_protein-	713	563	430	829	565	757	18.35048	17.07549	14.58348	18.4576	16.33636	19.36258
protein_co	FBJ_murine	8	7	8	3	5	5	0.112193	0.115686	0.147843	0.036396	0.078776	0.069687
protein_co	optic_atrop	692	580	520	1152	946	1120	4.680016	4.622494	4.63425	6.739951	7.18756	7.527815
protein_co	small_nucl	2501	2113	1400	4319	2706	4054	146.9539	146.31	108.4002	219.5399	178.6258	236.734
protein_co	reticulon_2	268	229	168	341	245	321	6.019595	6.06143	4.972521	6.625977	6.182265	7.165511
protein_co	echinoderm	377	316	322	549	453	863	7.151112	7.063605	8.048648	9.008814	9.653382	16.26869

protein_co	vasodilator	1769	1465	1196	3271	2867	3732	40.6302	39.65207	36.19821	64.99272	73.9772	85.18683
protein_co	symplekin	1899	1538	1267	3180	2335	2953	15.37937	14.67834	13.52151	22.27941	21.24465	23.76767
protein_co	glycerophо	185	181	139	408	329	311	1.473016	1.698327	1.458429	2.81034	2.942935	2.460967
protein_co	syndecan_b	27	23	17	29	28	33	0.941018	0.944646	0.780761	0.87437	1.09633	1.143031
protein_co	pantothena	641	562	553	1150	930	1174	7.047804	7.281808	8.012273	10.93847	11.48756	12.82843
protein_co	transglutan	0	0	2	11	3	1	0	0	0.052811	0.190684	0.067535	0.019914
protein_co	gonadotrop	2	4	12	7	3	10	0.139686	0.329223	1.104432	0.422945	0.235393	0.694117
protein_co	forkhead_b	0	1	0	0	0	0	0	0.025759	0	0	0	0
processed_	family_with	1	0	0	0	0	0	0.010442	0	0	0	0	0
protein_co	CD93_mole	0	0	0	3	0	1	0	0	0	0.020483	0	0.007843
protein_co	GDNF-indu	321	242	295	511	453	351	3.5148	3.122612	4.256498	4.840381	5.572408	3.819552
protein_co	paired_box	0	0	0	2	0	0	0	0	0	0.032275	0	0
protein_co	N-ethylmal	146	160	124	280	197	192	2.014434	2.601521	2.254534	3.342115	3.053624	2.632759
protein_co	centromere	2362	1839	1496	1874	1755	2040	44.0305	40.39825	36.74855	30.22083	36.7536	37.79319
protein_co	proteasom	1804	1576	1274	2780	1866	2084	22.26237	22.91913	20.71758	29.67854	25.86994	25.5589
protein_co	NK2_home	0	0	0	1	1	0	0	0	0	0.021892	0.02843	0
protein_co	D-tyrosyl-tI	641	611	440	1140	793	935	14.23455	15.98947	12.87577	21.90048	19.78373	20.63512
protein_co	RanBP-type	1963	1633	1253	1455	1126	1261	37.46329	36.72645	31.51168	24.02214	24.14199	23.9172
protein_co	thioredoxir	997	832	901	1114	1091	994	8.556034	8.414101	10.18913	8.270381	10.51844	8.477608
protein_co	serine/thre	908	731	694	1322	1227	1309	7.190789	6.822054	7.242441	9.057016	10.91652	10.30244
protein_co	small_nucl	1342	1151	902	5491	2833	4121	48.9978	49.52295	43.39757	173.4357	116.2036	149.5328
protein_co	neurensin_	1414	1157	1038	1364	974	1165	35.8518	34.57021	34.68117	29.91844	27.74403	29.35602
protein_co	adaptor-rel	333	204	233	274	166	246	9.539692	6.886957	8.795912	6.79053	5.342534	7.003818
protein_co	ribosome_b	16788	13955	12259	8840	11469	14435	176.3089	172.7079	169.6544	80.31389	135.3163	150.6613
protein_co	bone_morp	1535	1187	1117	756	634	682	22.56718	20.56491	21.63999	9.615099	10.47146	9.964672
protein_co	zinc_finger_	341	320	275	280	208	324	4.446522	4.917259	4.725345	3.158545	3.047042	4.198757
protein_co	fibronectin	175	134	123	1902	1838	1595	1.93984	1.750409	1.796667	18.23901	22.88876	17.57107
protein_co	ovo-like_2_	0	0	0	209	135	190	0	0	0	6.155608	5.163504	6.428726
protein_co	proprotein	0	0	0	535	351	409	0	0	0	5.169286	4.404229	4.539904
protein_co	McKusick-K	534	434	379	973	641	913	10.61603	10.16758	9.928759	16.73388	14.31621	18.03854
protein_co	beaded_fila	148	147	118	106	96	102	3.550189	4.155413	3.729981	2.199676	2.587081	2.431642
protein_co	destrin_(ac	7295	6417	5812	20196	13979	15542	199.0745	206.3619	209.0022	476.7808	428.5638	421.5091
protein_co	lysosomal-a	1	0	0	24	0	4	0.025964	0	0	0.539075	0	0.103215
protein_co	small_nucl	1008	935	707	2234	1493	1930	32.05076	35.03455	29.62321	61.4503	53.33186	60.98806
protein_co	mitochond	381	383	333	1079	798	857	8.63464	10.22881	9.944851	21.15455	20.31754	19.30233
protein_co	leucine_ric	8	0	1	1615	1776	1801	0.157328	0	0.025915	27.47594	39.2382	35.19982
protein_co	TBC1_dom	1399	1102	1027	1089	947	983	14.25687	13.23412	13.79151	9.600579	10.8419	9.955652
protein_co	inosine_tri	1377	1091	876	1378	925	1198	61.51878	57.43883	51.57184	53.25814	46.42635	53.19125
protein_co	transcriptic	0	0	0	19	11	20	0	0	0	0.559601	0.42073	0.676708
protein_co	minichrom	135	111	101	1010	685	752	1.923832	1.864075	1.89666	12.45138	10.96662	10.65027
protein_co	transmemb	28	8	7	8	3	6	0.856848	0.288498	0.282279	0.211787	0.103137	0.182476
protein_co	family_with	34	51	24	231	123	152	0.969824	1.714318	0.902111	5.700187	3.941561	4.308909
protein_co	mitochond	408	325	277	1051	742	1094	19.16586	17.99114	17.14679	42.71043	39.15806	51.07344
protein_co	sphingosin	2	2	1	0	4	0	0.066425	0.078278	0.043766	0	0.149249	0

protein_co	nicalin	3088	2363	1923	5361	3850	5026	40.81942	36.80954	33.49683	61.30535	57.1741	66.02702
protein_co	Cbp/p300-i	40	35	18	13	5	8	1.72026	1.773818	1.020097	0.48366	0.241576	0.341927
protein_co	heterogene	2508	2121	2140	5273	5139	5472	17.36542	17.30635	19.52569	31.58483	39.97472	37.65421
protein_co	zinc_finger_	383	342	361	212	192	201	4.980693	5.241121	6.186329	2.385008	2.805054	2.597746
protein_co	MYC_associ	798	776	610	1021	758	1054	13.39046	15.34481	13.4883	14.82114	14.2893	17.57693
protein_co	armadillo_	207	164	145	245	177	226	2.361807	2.205084	2.180103	2.418261	2.268801	2.562667
protein_co	growth_dif	175	160	147	4	1	2	3.602128	3.881041	3.987248	0.071227	0.023124	0.040913
protein_co	matrix_me	173	120	89	75	66	107	2.075882	1.696856	1.407283	0.77854	0.889712	1.275998
protein_co	N-terminal_	382	358	233	272	193	312	9.441391	10.42708	7.58863	5.815734	5.358941	7.663671
protein_co	inhibitor_c	3061	2381	1957	10849	6989	8330	132.6124	121.5591	111.724	406.6058	340.1614	358.6539
protein_co	RNA_bindir	3960	3183	2592	6191	5041	5961	115.3805	109.2901	99.51922	156.049	165.0072	172.61
protein_co	dynein_ligh	1584	1191	1051	2454	1292	1840	57.28042	50.75395	50.08279	76.76948	52.48831	66.12695
protein_co	eukaryotic_	2564	2347	2067	5767	3666	4654	51.10719	55.12952	54.29243	99.44363	82.09289	92.19344
protein_co	ERGIC_and_	6193	5348	4279	4703	2863	3581	115.1206	117.1522	104.8164	75.6293	59.78917	66.15552
protein_co	reactive_ox	560	546	433	771	596	866	59.53204	68.401	60.65763	70.90553	71.18001	91.49351
pseudogen	BPI_fold_c	2	0	4	3	0	0	0.089883	0	0.236887	0.116636	0	0
protein_co	family_with	1	0	0	3	0	0	0.016833	0	0	0.043687	0	0
protein_co	BPI_fold_c	1	0	0	0	0	0	0.027388	0	0	0	0	0
protein_co	centrosom	1468	1207	1080	593	1125	997	9.254272	8.966657	8.971701	3.233955	7.967422	6.246274
protein_co	pleiomorph	588	468	544	1510	1306	1242	5.456495	5.117872	6.652274	12.12206	13.61535	11.45428
antisense	MMP24_an	1211	1059	748	891	542	623	42.31785	43.60964	34.44418	26.9352	21.27785	21.63601
protein_co	gastrin-rele	0	1	0	19	13	22	0	0.032342	0	0.451104	0.400823	0.600057
protein_co	lysine_(K)-s	1990	1855	1769	1733	2116	2481	17.28225	18.98446	20.24463	13.01993	20.64486	21.4133
protein_co	angiomotir	412	408	394	4894	6392	5064	3.140632	3.665111	3.957773	32.27356	54.74011	38.36394
protein_co	transmemb	1209	1063	794	947	867	1007	29.13321	30.18578	25.21258	19.74127	23.47092	24.11577
protein_co	proteasom	1814	1554	1254	6717	3956	4917	35.55534	35.89431	32.38917	113.8953	87.11097	95.78056
protein_co	argonaute_	167	164	176	296	171	226	2.422896	2.803943	3.36485	3.715121	2.78717	3.258639
protein_co	uroporphyr	1449	1348	1027	1408	1075	1255	41.51055	45.50793	38.76996	34.8944	34.59773	35.73086
protein_co	ST3_beta-g	305	272	239	227	170	184	6.593305	6.929139	6.808258	4.245141	4.128586	3.953036
protein_co	transmemb	200	108	130	224	104	128	4.583636	2.916829	3.926072	4.441106	2.677704	2.915411
protein_co	HECT_dom	1009	933	726	932	836	816	14.79708	16.12403	14.02996	11.82398	13.77337	11.89282
protein_co	kinesin_ligh	586	507	367	681	831	926	9.545668	9.732486	7.877884	9.596632	15.20753	14.99096
protein_co	X-ray_repai	499	430	269	1439	918	1369	7.202169	7.31372	5.116228	17.96745	14.88519	19.63703
protein_co	tubulin_ga	226	169	190	819	713	731	3.073379	2.708329	3.404835	9.635064	10.89297	9.879494
protein_co	MCF.2_cell	6	5	7	23	21	23	0.048274	0.047407	0.074216	0.160087	0.189817	0.183909
protein_co	coagulation	23	17	12	1	5	11	0.802665	0.699137	0.551852	0.03019	0.196031	0.381513
protein_co	PCI_domai	478	442	428	1168	684	856	6.022322	6.562441	7.105827	12.7304	9.681468	10.71814
protein_co	protein_Z_	9	0	1	27	20	38	0.307201	0	0.04498	0.797273	0.766936	1.289061
protein_co	leucine_ric	584	440	386	534	287	409	8.381009	7.441204	7.299709	6.629606	4.627159	5.833328
protein_co	IGF-like_far	1	0	0	6	1	0	0.044302	0	0	0.229953	0.049771	0
protein_co	calpain_sm	7558	6080	4693	10170	6282	7611	208.6173	197.7672	170.6982	242.844	194.8007	208.7829
protein_co	programme	5	22	11	78	38	53	0.190985	0.990281	0.553677	2.577428	1.630653	2.011937
protein_co	RNA_bindir	1846	1499	1221	3203	2351	2819	58.17207	55.66619	50.70296	87.31779	83.23088	88.28512
protein_co	kin_of_IRR	0	0	4	0	4	1	0	0	0.094852	0	0.080865	0.017884

protein_co ubiquitin-li	1114	963	1013	3914	2904	3070	21.04792	21.44161	25.22134	63.97463	61.64099	57.64637
protein_co hematopoi	5	9	6	2	5	7	0.431819	0.91597	0.682838	0.149425	0.485122	0.600813
protein_co cytochrom	2814	2231	1613	2704	2114	2846	223.3523	208.6762	168.7079	185.6675	188.5039	224.4971
protein_co keratin_36	3	0	1	0	0	0	0.093042	0	0.040869	0	0	0
protein_co thyroid_ho	681	598	510	206	138	197	7.365233	7.621627	7.268493	1.92739	1.676747	2.11746
protein_co chemokine_	2	4	0	2	4	3	0.048726	0.114842	0	0.042153	0.109482	0.072638
protein_co nuclear_rec	81	84	57	77	63	60	1.546977	1.890537	1.434526	1.272192	1.351725	1.138832
protein_co FERM_dom	1647	1299	1094	1021	713	998	23.42031	21.76784	20.49987	12.55995	11.39037	14.1039
protein_co peroxiredo	4833	4109	3009	2465	2023	3507	286.5216	287.0674	235.0702	126.4214	134.7366	206.6265
protein_co BCL2-like_1	336	246	212	2302	1265	2133	12.43059	10.72493	10.3353	73.67511	52.57654	78.42472
protein_co interferon_	807	733	602	1566	1163	1717	14.86548	15.91169	14.61291	24.95514	24.06767	31.43296
protein_co protein_arg	3664	2922	2246	11411	6334	8262	115.0509	108.1239	92.93495	309.9711	223.4404	257.8276
protein_co related_RA	816	714	455	764	438	541	41.37917	42.66747	30.4045	33.51567	24.95254	27.26456
protein_co proline_ric	10	2	5	116	98	117	0.334435	0.078822	0.220351	3.356079	3.682021	3.88872
protein_co SR-related_	2937	2382	1788	5737	4512	5623	36.10954	34.51174	28.96813	61.01912	62.32126	68.70618
protein_co proline_ric	1478	1151	968	1603	2017	2299	11.25044	10.3247	9.709685	10.55581	17.24844	17.39176
protein_co testis-speci	2	0	1	0	0	0	0.05623	0	0.037049	0	0	0
protein_co fibronectin	53	24	22	10	14	15	0.710527	0.379161	0.388653	0.115976	0.210854	0.199851
protein_co argininosuc	236	176	169	330	281	303	5.830179	5.123771	5.501631	7.052561	7.798755	7.439131
protein_co Shwachmar	604	527	489	1756	992	1246	19.60537	20.15839	20.91615	49.30894	36.17419	40.19442
protein_co signal_tran	16	24	22	54	28	35	0.196944	0.34813	0.356845	0.575015	0.387195	0.428154
protein_co WNK_lysin	156	99	80	128	124	125	2.064183	1.54371	1.394917	1.465199	1.843293	1.643778
protein_co beclin_1_a	578	398	447	625	570	522	12.22041	9.916261	12.45375	11.43144	13.53885	10.96826
protein_co protein_kir	0	0	0	3	6	10	0	0	0	0.043855	0.113902	0.167935
protein_co TNF_recept	440	395	350	1199	876	895	10.08837	10.67265	10.57477	23.78211	22.56427	20.39393
protein_co GLIS_family	480	424	309	217	207	228	5.686211	5.919086	4.823642	2.223845	2.75487	2.68427
protein_co nuclear_sp	523	458	415	761	442	580	10.89655	11.24501	11.39385	13.71624	10.34567	12.0095
protein_co DnaJ_(Hsp4	1436	1187	1091	2897	2099	2316	47.51454	46.2839	47.56984	82.92464	78.02497	76.15884
protein_co AT_hook_D	2056	1596	1391	2278	2739	2750	16.90691	15.46611	15.07312	16.20533	25.30359	22.47416
protein_co interferon_	525	403	297	172	122	181	33.04878	29.89567	24.63697	9.36672	8.627898	11.32359
protein_co dachshund_	0	0	0	3	15	8	0	0	0	0.024614	0.159824	0.075405
protein_co zinc_finger_	724	708	592	869	820	900	11.66442	13.44203	12.56843	12.11176	14.84183	14.41042
processed_ EMG1_nucl	27	27	19	69	49	79	0.90756	1.069504	0.841589	2.006428	1.850362	2.639054
protein_co synovial_sa	0	0	0	2	1	0	0	0	0	0.070568	0.045821	0
protein_co ubiquitous	345	292	183	421	243	320	20.43025	20.3772	14.2804	21.56749	16.16627	18.83277
protein_co complemer	15	15	6	18	2	8	0.196563	0.231638	0.103609	0.204055	0.029444	0.104186
protein_co ELK1_mem	921	791	758	827	677	697	18.09227	18.3112	19.62173	14.05406	14.9407	13.60742
protein_co translocase	507	464	325	1361	964	1267	17.56615	18.94496	14.83839	40.7934	37.52276	43.62696
protein_co pecanex-lik	945	915	915	1140	932	854	10.72208	12.2342	13.68054	11.18962	11.87989	9.629747
protein_co autophagy_	340	356	368	477	413	394	3.795854	4.683684	5.413937	4.606933	5.179999	4.37156
protein_co kinectin_1_	2534	2039	2188	4149	3751	3485	21.49535	20.38272	24.45795	30.44699	35.74654	29.3799
protein_co SIX_homeo	2464	1968	1968	36	19	25	32.63613	30.7178	34.3493	0.4125	0.282723	0.329085
protein_co ras_homolo	251	213	237	170	121	141	4.024285	4.024405	5.007237	2.357909	2.179463	2.246693
protein_co discs_large_	405	345	362	2255	1715	1721	7.211942	7.239747	8.494554	34.73815	34.30918	30.45704

protein_co	L-3-hydrox	317	270	228	119	117	114	10.99037	11.03123	10.41652	3.569135	4.557094	3.927964
protein_co	heat_shock	56	36	48	577	459	492	1.071448	0.811694	1.210205	9.550404	9.866081	9.355299
protein_co	zinc_finger_	740	669	654	1238	1062	994	9.511128	10.13289	11.07676	13.76525	15.33465	12.69686
protein_co	tRNA_meth	257	250	264	432	301	310	2.441384	2.79866	3.304774	3.550175	3.212319	2.926674
protein_co	sphingosin	294	263	236	691	562	533	4.699472	4.954098	4.971055	9.555267	10.09223	8.467177
protein_co	pleckstrin_	578	452	444	2346	2698	3124	4.378294	4.034805	4.43195	15.37333	22.9598	23.51786
protein_co	pregnancy-	0	0	0	3	7	13	0	0	0	0.029804	0.090311	0.148369
protein_co	ras_homol	254	261	241	503	326	362	4.07856	4.938792	5.09947	6.987215	5.880846	5.776854
protein_co	ecotropic_	8	2	9	5	3	3	0.227703	0.067084	0.337564	0.123115	0.095929	0.084861
protein_co	oligodendr	23	28	29	15	5	4	0.410672	0.589159	0.682339	0.231698	0.100297	0.07098
protein_co	WD_repeat	525	421	391	358	342	284	5.137527	4.854942	5.042041	3.030685	3.759845	2.761995
protein_co	allograft_in	11	4	3	1261	1297	1550	0.165676	0.070996	0.059542	16.43028	21.94602	23.20107
protein_co	family_with	12	6	5	15	22	16	0.139318	0.082089	0.076495	0.150654	0.286945	0.184611
protein_co	nucleopori	850	695	750	1737	1447	1223	5.921032	5.705194	6.884534	10.46746	11.3239	8.466708
protein_co	cancer/test	0	0	0	1	0	0	0	0	0	0.046122	0	0
protein_co	arginine_va	0	0	0	0	1	0	0	0	0	0	0.033736	0
protein_co	solute_carr	483	422	330	834	549	714	12.02186	12.37782	10.82364	17.95782	15.35133	17.6617
protein_co	mitogen-ac	5713	4562	3566	6416	3793	4670	103.367	97.27027	85.02251	100.4258	77.09916	83.97389
protein_co	heterogene	1190	1023	1038	1660	1438	1797	28.33998	28.71014	32.57503	34.19981	38.4734	42.53147
protein_co	armadillo_	579	489	429	396	289	365	14.31706	14.24923	13.97872	8.470979	8.028277	8.9697
protein_co	transmemb	277	241	223	9	11	13	6.680936	6.84986	7.087568	0.187786	0.298057	0.311609
protein_co	translocase	170	126	110	347	334	389	5.408635	4.724071	4.611755	9.550613	11.93807	12.2998
protein_co	zinc_finger_	415	333	257	456	331	331	5.297929	5.009673	4.323406	5.036002	4.747174	4.199482
protein_co	calnexin	16150	13521	13889	15272	12689	11878	200.7035	198.0151	227.4512	164.188	177.1573	146.7018
protein_co	cleavage_ar	2025	1745	1197	3128	2253	2950	34.81829	35.35777	27.12135	46.52776	43.52038	50.40969
protein_co	inositol_13	95	68	69	106	77	68	1.142784	0.963955	1.093767	1.103087	1.040592	0.812941
protein_co	zinc_finger_	66	49	77	63	65	76	1.098775	0.96132	1.689237	0.907337	1.215703	1.257443
protein_co	osteomodu	3	4	6	1	1	4	0.064852	0.101899	0.170919	0.018701	0.024286	0.085936
protein_co	FYVE_RhoG	0	0	0	75	67	60	0	0	0	0.7313	0.84839	0.672098
protein_co	human_imi	70	61	62	142	169	178	0.300826	0.308925	0.35111	0.52792	0.815929	0.760232
protein_co	phosphopa	458	373	286	749	578	666	14.99504	14.39123	12.33908	21.21421	21.25979	21.67035
protein_co	endothelin	0	0	0	9	0	10	0	0	0	0.332144	0	0.423965
protein_co	B-cell_CLL/	0	4	5	3	1	15	0	0.032823	0.045879	0.018071	0.007823	0.103803
protein_co	cytochrom	3230	2844	2295	3781	2865	4613	107.9542	112.0143	101.0775	109.3218	107.5748	153.2251
protein_co	TNF_recept	195	184	127	1033	862	1029	4.278282	4.757291	3.671752	19.60641	21.24668	22.43674
protein_co	abhydrolas	226	143	95	359	305	328	5.72472	4.268634	3.171058	7.866893	8.6795	8.257133
protein_co	mannan-bi	24	39	29	3	14	12	0.212401	0.40674	0.338204	0.022968	0.139195	0.105545
protein_co	ATPase_typ	1	2	0	0	3	0	0.012581	0.029652	0	0	0.042402	0
protein_co	HRAS-like_s	8	4	2	143	52	113	0.397306	0.2341	0.130888	6.143756	2.901264	5.577287
protein_co	helicase_(D	25	45	34	13	27	30	0.369081	0.782891	0.661448	0.166031	0.447811	0.440162
protein_co	RAP1B_me	2290	2027	2036	2482	1827	2029	56.94452	59.39874	66.71585	53.39262	51.03922	50.14275
protein_co	tetraspanin	1	2	3	0	0	2	0.034921	0.082306	0.138054	0	0	0.069412
protein_co	bestrophin	0	0	0	7	9	3	0	0	0	0.090768	0.151552	0.044689
protein_co	RAB3A_inte	21	18	3	525	419	383	0.115256	0.116419	0.021697	2.492684	2.583497	2.089071

protein_co	protein_tyr	4	0	4	40	34	19	0.018687	0	0.024625	0.161662	0.178449	0.088216
protein_co	dual-specifi	530	558	543	710	739	675	3.148421	3.906234	4.250613	3.648701	4.931856	3.985018
protein_co	YEATS_dom	95	75	54	569	410	420	3.507249	3.262957	2.627069	18.17265	17.00497	15.40997
protein_co	taste_recep	3	2	5	2	8	6	0.144253	0.113329	0.316818	0.083195	0.432159	0.286725
protein_co	taste_recep	2	7	10	4	4	6	0.106521	0.43935	0.701844	0.184301	0.23934	0.31759
protein_co	taste_recep	25	2	6	16	24	3	1.150891	0.1085	0.363982	0.637202	1.241237	0.137254
protein_co	crystallin_g	0	0	2	9	4	25	0	0	0.058947	0.17414	0.100509	0.555704
protein_co	leucine_ric	0	0	0	10	13	11	0	0	0	0.244001	0.411927	0.30834
protein_co	iduronidase	335	270	177	53	14	19	7.878824	7.483202	5.485607	1.078339	0.369908	0.444099
protein_co	fibroblast_g	1375	1059	879	239	228	272	20.00381	18.1557	16.85131	3.007952	3.726438	3.93268
protein_co	transmemb	435	336	299	351	246	270	10.29934	9.3749	9.328811	7.189363	6.543415	6.353217
protein_co	aurora_kina	28	28	26	435	328	390	0.700542	0.825547	0.857205	9.415181	9.219329	9.697297
protein_co	peptidylpro	1195	940	740	2386	1864	2683	15.72961	14.58092	12.83561	27.16961	27.56417	35.09784
protein_co	F-box_and_	618	488	405	1066	729	838	17.04038	15.85688	14.71569	25.42793	22.58226	22.96384
protein_co	ER_membra	3123	2487	2438	3678	2672	2922	24.81013	23.28306	25.52264	25.27737	23.84749	23.06997
protein_co	ubiquitin_p	3120	2653	3213	3047	2974	2635	10.3591	10.38035	14.05766	8.751914	11.09322	8.694765
protein_co	heterochro	2700	2222	2452	2328	2459	2256	29.64344	28.74856	35.47482	22.11113	30.33	24.61578
protein_co	egf-like_mo	0	3	2	117	144	129	0	0.027658	0.020619	0.791853	1.265632	1.002987
protein_co	SIN3_transc	1953	1749	1345	2475	2094	2443	20.15866	21.27435	18.29433	22.10027	24.28204	25.06066
protein_co	solute_carr	1891	1469	1304	1205	878	1013	19.63354	17.97364	17.84101	10.82324	10.2412	10.45264
protein_co	epidermal_	707	734	529	1012	758	807	9.560481	11.6967	9.426507	11.8387	11.51539	10.84535
protein_co	Kruppel-lik	38	52	22	35	12	11	0.996907	1.607612	0.760551	0.794332	0.353672	0.286796
protein_co	olfactory_r	0	0	0	0	0	1	0	0	0	0	0	0.049357
protein_co	coagulation	1	3	4	2	0	0	0.015244	0.053891	0.080349	0.026374	0	0
protein_co	ubiquinol-c	21	12	10	28	16	39	0.845446	0.569318	0.530519	0.975186	0.723661	1.560417
protein_co	growth_fac	239	242	202	369	272	498	5.395692	6.438307	6.00946	7.206736	6.898699	11.17347
protein_co	synaptogyr	34	15	5	29	9	12	0.877618	0.456273	0.170071	0.647571	0.260986	0.307835
protein_co	protein_kir	108	69	75	1751	1201	1698	2.477308	1.865144	2.267004	34.74605	30.94912	38.70826
protein_co	WAP_follist	17	7	3	20	25	24	0.184501	0.089527	0.042905	0.187777	0.304817	0.258864
protein_co	WD_repeat	240	234	189	469	320	423	3.915513	4.498838	4.063254	6.619318	5.865114	6.858472
protein_co	F-box_and_	259	225	177	73	58	60	3.865722	3.957496	3.48128	0.942577	0.972541	0.890004
protein_co	CTF18_chro	310	250	202	1413	1112	1577	3.651915	3.470612	3.135777	14.40006	14.71678	18.46292
protein_co	guanine_nu	2	5	18	2	27	35	0.107604	0.317011	1.276158	0.093087	1.631961	1.871435
pseudogen	tubulin_be	7	10	6	29	6	16	0.225144	0.379026	0.254301	0.806907	0.216802	0.511437
protein_co	microtubul	4902	3867	5116	4410	4706	3903	10.45258	9.716987	14.37526	8.134895	11.27331	8.27101
protein_co	SWI/SNF_re	3975	3112	3054	5988	5815	5890	36.3455	33.53206	36.79742	47.36509	59.73272	53.52276
protein_co	lysine_(K)-s	2282	2182	1633	1217	1377	1550	21.60046	24.33936	20.36893	9.96554	14.64301	14.58104
protein_co	toll-like_re	0	0	1	292	189	260	0	0	0.02607	4.997489	4.200653	5.111978
protein_co	gigaxonin	39	41	54	147	108	92	0.439765	0.544813	0.802389	1.433959	1.368136	1.030989
protein_co	methyltran	49	41	36	108	67	74	1.239421	1.22212	1.199942	2.36325	1.903911	1.86022
protein_co	interleukin	2	1	0	0	0	5	0.152129	0.089638	0	0	0	0.377974
protein_co	ER_membra	4	0	8	5	5	5	0.277905	0	0.732423	0.300518	0.390262	0.345237
protein_co	methyltran	450	410	356	806	631	729	5.577955	5.988988	5.814968	8.642921	8.787006	8.980483
protein_co	tubulin_alp	61	68	60	87	36	41	1.292277	1.697625	1.674989	1.59444	0.856796	0.863216

protein_co	villin_1	1	3	1	44	40	33	0.008106	0.028658	0.010682	0.308552	0.364268	0.26585
protein_co	angio-assoc	1951	1663	1363	3280	2367	3451	45.50127	45.7052	41.8887	66.17639	62.0174	79.98726
protein_co	paroxysmal	945	695	654	1071	801	1065	16.56049	14.35269	15.10268	16.23655	15.76968	18.54815
protein_co	tumor_nec	962	830	751	1014	1000	891	12.26915	12.47454	12.62159	11.18769	14.32809	11.29345
protein_co	ring_finger_	403	336	409	645	653	617	5.517254	5.420811	7.378635	7.639073	10.04339	8.394846
protein_co	enoyl_CoA_	1985	1717	1407	3093	1876	2428	64.98941	66.24597	60.70312	87.60421	69.00236	79.00242
protein_co	A_kinase_(I	616	476	685	622	540	470	2.614161	2.380486	3.830689	2.283521	2.574509	1.982253
protein_co	guanine_nu	646	511	492	313	207	363	35.47706	33.07067	35.60533	14.87039	12.77128	19.81214
protein_co	split_hand/	1076	876	745	1324	1205	2031	20.54256	19.70849	18.74275	21.8672	25.84511	38.53557
protein_co	huntingtin_	295	207	235	708	614	577	1.949032	1.611664	2.045972	4.046627	4.557371	3.788632
protein_co	protein_tyr	698	578	717	1784	1144	1317	10.84933	10.58723	14.68593	23.98862	19.97664	20.34431
protein_co	P450_(cytc	1586	1241	1025	1643	937	1083	33.1613	30.57787	28.24146	29.71864	22.00985	22.50435
protein_co	fibrinogen-	21	29	36	1	1	1	0.260915	0.424606	0.589411	0.010748	0.013958	0.012348
protein_co	serine/thre	306	278	199	773	365	584	10.31844	11.047	8.842607	22.5494	13.8272	19.57109
protein_co	STEAP_fami	28	29	32	3	2	3	0.333037	0.40648	0.501556	0.030869	0.026725	0.035462
protein_co	guanine_nu	957	769	790	796	703	667	15.1373	14.33408	16.46639	10.89212	12.49225	10.48508
pseudogen	postmeioti	176	140	108	143	159	209	6.253433	5.861934	5.056667	4.395465	6.346759	7.380092
protein_co	peroxisoma	186	156	143	244	216	240	1.846433	1.824955	1.870645	2.095431	2.408925	2.36778
protein_co	mitochond	130	121	83	230	126	171	1.772882	1.944594	1.49159	2.713485	1.930439	2.31762
protein_co	sarcoglycar	727	645	574	899	576	782	20.57087	21.50726	21.40252	22.00599	18.31006	21.99048
protein_co	RNA_bindir	208	196	123	396	264	285	2.69038	2.987538	2.096478	4.431069	3.836218	3.663573
protein_co	CAS1_dom	192	187	229	704	473	497	2.578557	2.95954	4.052712	8.179206	7.136507	6.633481
protein_co	zinc_finger_	330	280	253	278	280	227	2.016218	2.015991	2.036943	1.469371	1.921899	1.378348
protein_co	leucine_ric	68	43	39	12	2	2	1.06477	0.793455	0.804723	0.162552	0.035182	0.031123
protein_co	ZFP36_ring	682	547	439	449	422	447	20.21599	19.10755	17.14786	11.51383	14.0531	13.16824
protein_co	steroid_5_a	327	281	249	318	225	234	4.131672	4.183998	4.145837	3.475907	3.193814	2.93835
protein_co	serine_pept	0	0	0	3	5	4	0	0	0	0.180074	0.38975	0.275827
protein_co	RAS-like_fa	50	64	41	215	170	208	1.328173	2.003419	1.43517	4.940675	5.073209	5.49108
protein_co	phosphorib	5275	4577	3784	16704	10231	11299	83.6119	85.4936	79.0372	229.0494	182.1851	177.9899
protein_co	kinase_inse	1878	1515	1777	639	692	597	17.0508	16.20947	21.26039	5.018951	7.058366	5.386827
protein_co	phosphorib	355	337	368	1634	1072	1067	4.648541	5.200263	6.34996	18.50987	15.77002	13.88553
protein_co	tubulin_ga	667	605	532	642	570	745	5.833742	6.235681	6.131516	4.857574	5.600739	6.475709
protein_co	adrenomed	235	215	127	274	174	213	2.909526	3.136895	2.072015	2.934729	2.420208	2.620859
protein_co	DiGeorge_s	757	629	517	859	488	617	34.72819	34.0051	31.25443	34.09121	25.15099	28.13074
protein_co	DiGeorge_s	515	457	403	990	998	930	5.807159	6.072671	5.988201	9.657277	12.64259	10.42195
protein_co	aspartate_b	41	26	23	160	105	159	0.646583	0.483194	0.477973	2.182849	1.860283	2.491997
protein_co	pre-B_lymp	0	2	0	2	4	1	0	0.20455	0	0.15016	0.390006	0.086253
protein_co	stromal_ce	629	544	398	1257	835	1228	38.49698	39.23575	32.09917	66.55402	57.41317	74.6937
protein_co	galactose-3	0	0	0	18	5	1	0	0	0	0.432065	0.155859	0.027575
protein_co	tyrosine_3-	934	749	738	6392	4121	4456	26.31553	24.86876	27.40037	155.7992	130.4419	124.7729
protein_co	chromoson	4	0	2	4	15	13	0.169819	0	0.11189	0.146909	0.715428	0.548503
pseudogen	POM121_tr	18	18	12	0	1	0	0.189904	0.22379	0.166831	0	0.011853	0
protein_co	guanine_nu	84	96	98	81	75	65	1.33145	1.79318	2.046947	1.110692	1.335537	1.023926
protein_co	mannosyl_(	88	85	90	83	133	145	0.920349	1.047601	1.240359	0.75095	1.562682	1.507119

protein_co	adenosine_	12	7	6	0	11	11	0.247292	0.169994	0.162935	0	0.254665	0.225284
protein_co	activating_	7745	6943	5134	10717	7200	8826	203.0847	214.5409	177.3971	243.1039	212.0984	230.0008
protein_co	alpha_14-g	196	160	126	213	124	165	4.470674	4.300748	3.787235	4.203002	3.177516	3.740335
protein_co	ret_finger_	0	0	0	0	1	1	0	0	0	0	0.03997	0.035359
protein_co	CDC42_effe	1852	1527	1108	2524	1567	1813	44.95494	43.67999	35.44141	53.00158	42.73212	43.73648
protein_co	apolipopro	11	15	16	0	0	2	0.160251	0.257517	0.307158	0	0	0.028957
protein_co	melanin-co	31	17	13	133	141	166	0.575647	0.372007	0.318107	2.136533	2.941461	3.063463
protein_co	tyrosylprot	414	323	323	434	286	284	10.01717	9.209889	10.29869	9.084426	7.774274	6.829246
protein_co	BAI1-associ	4	8	1	39	18	39	0.098678	0.232573	0.032509	0.832319	0.498866	0.956173
protein_co	mercaptop	1406	1189	782	2745	1778	1974	12.67627	12.63267	9.290682	21.40974	18.00889	17.68735
protein_co	galanin_rec	0	0	0	3	1	6	0	0	0	0.118753	0.051405	0.272847
protein_co	thiosulfate_	224	176	170	494	280	390	6.599211	6.110317	6.599754	12.59024	9.267255	11.41874
protein_co	apolipopro	0	9	1	5	0	0	0	0.390466	0.048514	0.159245	0	0
protein_co	apolipopro	415	404	300	98	66	83	8.182686	9.387204	7.79478	1.671617	1.461978	1.626431
protein_co	ras-related_	118	88	86	2	3	3	4.215275	3.704535	4.048342	0.061807	0.120397	0.106506
protein_co	leukemia_i	475	433	406	168	174	241	6.335846	6.80622	7.136279	1.938578	2.60741	3.194756
protein_co	chromoson	363	358	259	946	658	944	12.31896	14.31718	11.58249	27.77293	25.08664	31.83825
protein_co	apolipopro	23	26	25	73	49	67	0.451983	0.602109	0.647395	1.241025	1.081782	1.308516
protein_co	RIB43A_do	1	1	10	18	11	26	0.035819	0.042211	0.472011	0.557767	0.442649	0.925552
protein_co	keratin_17	0	0	0	19	9	10	0	0	0	0.474471	0.291867	0.286881
protein_co	ER_membr	1249	1105	914	1660	1230	1638	32.75052	34.14484	31.58179	37.65537	36.23347	42.6854
protein_co	ring_finger_	53	35	28	3	0	3	0.873559	0.679816	0.608148	0.042776	0	0.049141
protein_co	sperm_anti	314	266	271	2360	2057	2144	2.043953	2.040469	2.324585	13.28974	15.04266	13.86998
protein_co	carboxypep	1862	1739	1514	61	49	46	35.24352	38.7888	37.76246	0.998832	1.041945	0.865301
protein_co	dedicator_(	897	832	873	147	159	157	5.938236	6.490758	7.615774	0.841871	1.182527	1.032938
protein_co	protection_	194	186	137	437	280	290	2.517292	2.844146	2.342542	4.905422	4.081681	3.739724
protein_co	ATPase_H+_	931	680	506	1111	543	556	69.32217	59.66759	49.64869	71.56482	45.42254	41.14404
protein_co	N(alpha)-ac	462	404	379	795	774	933	6.069166	6.254254	6.560864	9.034772	11.42292	12.18087
protein_co	cadherin-re	154	117	126	172	133	134	1.254294	1.122979	1.352334	1.211909	1.216969	1.084659
protein_co	PRKR_inter	596	500	350	643	526	790	9.199077	9.094421	7.118702	8.585626	9.120797	12.1181
protein_co	VGF_nerve_	148	142	107	5631	3478	4303	3.042822	3.440411	2.898901	100.1529	80.33291	87.92165
protein_co	podocalyxi	52	21	47	9770	10976	10223	0.44618	0.212341	0.531422	72.52112	105.8035	87.1756
protein_co	forkhead_b	170	153	168	6	6	18	1.084203	1.1499	1.411906	0.033104	0.042989	0.114089
protein_co	striatin_int	32	46	46	41	36	77	0.331205	0.561063	0.627392	0.367108	0.418599	0.792039
protein_co	RAB_memb	387	340	305	738	426	605	11.47796	11.88338	11.92034	18.93535	14.19425	17.83277
protein_co	muskelin_1	964	719	860	1043	728	766	4.574679	4.020866	5.377951	4.281845	3.881182	3.612618
protein_co	DnaJ_(Hsp4	263	229	222	492	346	400	5.128354	5.262169	5.704401	8.29947	7.57962	7.75161
protein_co	filamin_C_g	11656	10118	9447	7593	7507	8797	67.16154	68.70255	71.72984	37.8484	48.59444	50.37503
protein_co	leucine_ric	817	635	636	1077	984	1139	11.29906	10.34906	11.59076	12.88543	15.28848	15.65502
protein_co	calumenin	12008	10228	10605	9316	7389	7175	143.8921	144.4323	167.4603	96.5737	99.47206	85.44722
protein_co	coiled-coil_	187	162	151	40	40	49	2.374662	2.424277	2.526806	0.439423	0.570649	0.618395
protein_co	smoothene	1039	911	729	1096	967	969	14.71527	15.20471	13.60552	13.42846	15.38609	13.63912
protein_co	interferon_	0	2	1	6	3	3	0	0.044787	0.025041	0.098634	0.064044	0.056655
protein_co	leucine_ric	1424	1272	1044	39	30	23	37.65633	39.63896	36.38005	0.892186	0.891248	0.604457

protein_co	kelch_dom	601	499	653	313	355	292	7.113243	6.959865	10.18453	3.204797	4.720311	3.434675
protein_co	NADH_deh	615	628	508	1142	797	868	5.805762	6.986358	6.319498	9.326382	8.452622	8.143544
protein_co	FEZ_family_	0	0	0	2	0	0	0	0	0	0.043639	0	0
protein_co	opsin_1_(c	136	116	84	150	80	96	6.56932	6.603081	5.346821	6.268098	4.341308	4.60853
protein_co	mitochond	912	796	618	1726	1139	1508	39.57556	40.70544	35.33911	64.79419	55.52711	65.03442
protein_co	myosin_IB	3165	2677	3007	3086	2768	2301	32.97093	32.86343	41.27867	27.81098	32.3946	23.8223
protein_co	homeobox_	132	94	93	4	14	17	1.659119	1.392319	1.540357	0.043494	0.197688	0.212355
protein_co	metaxin_2	392	278	292	710	442	685	13.03572	10.89434	12.79578	20.42539	16.51279	22.63858
protein_co	phosphodi	0	0	1	1	0	0	0	0	0.015649	0.010273	0	0
protein_co	chimerin_1	987	912	734	514	363	397	21.35381	23.25199	20.92613	9.620203	8.82295	8.536076
protein_co	glutamate_	6	13	4	81	53	44	0.07965	0.20337	0.069973	0.930218	0.790427	0.580496
pseudogen	eukaryotic_	8	6	10	25	19	20	0.315595	0.278932	0.519846	0.853184	0.842058	0.784114
protein_co	O-sialoglyc	96	109	90	191	144	163	2.293473	3.068711	2.833346	3.947469	3.864861	3.870077
protein_co	ORM1-like_	673	595	549	1077	675	855	13.23525	13.78926	14.22736	18.32296	14.91317	16.71063
protein_co	histone_ac	450	423	361	2206	1498	1673	6.195955	6.863462	6.549947	26.2763	23.17163	22.89293
protein_co	homeobox_	393	336	245	0	0	0	8.604554	8.669263	7.068653	0	0	0
protein_co	homeobox_	529	454	420	0	0	0	14.08033	14.24034	14.73131	0	0	0
protein_co	homeobox_	321	267	309	0	0	0	8.764342	8.590781	11.11751	0	0	0
protein_co	homeobox_	35	52	29	3	0	1	0.827203	1.448287	0.903185	0.061338	0	0.023488
protein_co	HECT_and_	1634	1305	1604	1439	1650	1567	5.64032	5.308469	7.296101	4.2971	6.398596	5.375642
protein_co	small_nucl	27	19	25	118	103	110	0.750739	0.622567	0.916009	2.838378	3.217447	3.039677
protein_co	proteasom	7	7	4	36	14	12	0.219802	0.259024	0.165512	0.977913	0.493869	0.374477
protein_co	twisted_ga	1043	967	1108	1484	1110	1162	14.70113	16.06202	20.5798	18.0952	17.57675	16.2773
protein_co	Rho_GTPas	2	12	7	19	2	14	0.038308	0.270858	0.17668	0.314826	0.043036	0.266497
protein_co	eukaryotic_	1291	1160	1218	2441	1668	1566	12.42895	13.16053	15.45221	20.33008	18.0407	14.98338
protein_co	myosin_VC	3	1	4	406	370	318	0.022783	0.00895	0.040031	2.667387	3.156805	2.400125
protein_co	cingulin-lik	13	14	12	406	487	527	0.09527	0.120906	0.115886	2.573969	4.00952	3.838262
protein_co	tropomodu	280	156	259	176	166	179	1.612825	1.058915	1.965911	0.877011	1.074203	1.024689
protein_co	tau_tubulin	156	119	204	91	98	73	0.75734	0.680801	1.305063	0.382183	0.534492	0.352208
protein_co	elongation_	0	0	0	2	0	0	0	0	0	0.038945	0	0
protein_co	chromoson	153	98	90	67	54	65	1.32115	0.997227	1.02409	0.500494	0.523846	0.557807
protein_co	INO80_hon	474	446	452	620	629	754	3.897194	4.321312	4.89719	4.409896	5.809963	6.161049
protein_co	NMDA_rece	493	444	449	811	576	592	3.620462	3.84244	4.345084	5.152297	4.752133	4.320643
protein_co	delta-like_4	0	1	2	8	3	4	0	0.018685	0.041787	0.109731	0.053437	0.06303
protein_co	aldehyde_d	3	9	8	4	1	1	0.038756	0.137016	0.13619	0.044704	0.014513	0.012839
protein_co	family_with	755	560	726	934	875	783	4.326743	3.781893	5.482587	4.630459	5.633408	4.459494
protein_co	isovaleryl-C	920	799	694	1024	847	1003	10.44067	10.68549	10.3785	10.05318	10.79874	11.3123
protein_co	kinetochor	274	220	219	1424	935	1107	7.638669	7.227646	8.045371	34.34315	29.28382	30.67075
protein_co	deoxyuridi	619	494	408	2354	1915	2387	15.26338	14.3547	13.2573	50.21454	53.04908	58.49545
protein_co	ChaC_catio	188	147	120	317	194	210	5.403315	4.978825	4.544839	7.881788	6.264022	5.998344
protein_co	ceroid-lipo	726	629	488	2097	1571	1972	17.14325	17.50307	15.18487	42.83689	41.67559	46.27784
protein_co	cAMP-regul	2695	2302	2433	5479	4122	4396	26.60872	26.78414	31.65499	46.79825	45.7217	43.13528
protein_co	vacuolar_p	682	581	673	707	827	623	2.69446	2.70502	3.503783	2.416405	3.670641	2.446161
protein_co	calmodulin	101	73	102	232	159	196	1.286893	1.096102	1.7126	2.557243	2.275974	2.481914

protein_co immunoglc	1724	1442	1102	8	6	13	38.49442	37.94311	32.42477	0.15453	0.150508	0.288479
protein_co THAP_dom	29	36	33	204	73	111	0.63997	0.936206	0.959645	3.89453	1.809813	2.434414
protein_co lysyl_oxida	2734	2269	1754	119	104	107	51.95286	50.81039	43.92132	1.956235	2.220207	2.020712
protein_co chemokine	9	6	8	8	9	1	0.248939	0.195573	0.291592	0.191427	0.279667	0.027489
protein_co anaphase_p	608	604	496	1456	664	995	17.49355	20.47945	18.80575	36.24087	21.46305	28.45162
protein_co methyl-CpG	333	319	315	718	508	569	7.114347	8.03135	8.868214	13.27022	12.1928	12.08127
protein_co coatomer_	2670	2331	2325	3948	2416	2634	40.60685	41.77702	46.5957	51.94314	41.27946	39.81195
protein_co proteasom	66	65	38	136	101	135	2.288216	2.655666	1.736087	4.079012	3.933902	4.651537
protein_co sulfatase_m	3509	3152	2099	2152	1754	2234	90.53116	95.83144	71.36117	48.03082	50.83858	57.2806
protein_co palladin_cy	6856	6220	6254	5304	4620	4025	56.40458	60.30329	67.80102	37.7494	42.70066	32.90933
protein_co signal_pept	1497	1283	1298	3036	2385	2549	17.33815	17.51115	19.81027	30.41905	31.03261	29.34002
protein_co butyrobeta	15	2	2	6	5	1	0.421058	0.066159	0.07398	0.145702	0.157677	0.027897
protein_co myogenic_	0	1	0	0	0	0	0	0.034641	0	0	0	0
protein_co secretion_r	81	91	52	69	33	49	2.738327	3.625341	2.316533	2.017959	1.253324	1.646289
protein_co potassium_	283	248	232	27	20	25	2.214351	2.286751	2.39212	0.182762	0.175808	0.194406
protein_co tryptophan	1	4	3	7	8	20	0.009942	0.046864	0.039303	0.060205	0.089353	0.197611
protein_co cysteine_ar	1	2	1	0	0	0	0.036361	0.085697	0.047914	0	0	0
protein_co E2F_transcr	15	11	21	181	88	106	0.231385	0.199961	0.426873	2.415385	1.525024	1.625026
protein_co dCMP_dear	1837	1571	1469	2123	1363	1802	49.31674	49.70138	51.96869	49.30582	41.10835	48.07836
protein_co SRY_(sex_d	43	24	25	1637	922	1366	1.630704	1.072568	1.249342	53.70545	39.28137	51.48338
protein_co family_witl	204	152	152	1053	689	882	5.544129	4.868036	5.443542	24.7568	21.0364	23.82217
protein_co RPA_intera	418	379	285	618	550	692	5.797573	6.194642	5.208943	7.415175	8.570017	9.538623
protein_co ubiquitin_s	6	1	1	14	7	8	0.037529	0.007371	0.008242	0.075754	0.049188	0.04973
protein_co sex_hormo	6	3	4	16	14	13	0.229845	0.135429	0.20192	0.530233	0.602506	0.494922
protein_co phospholip	864	624	596	1099	921	1213	13.05767	11.11332	11.86952	14.36854	15.63726	18.21891
protein_co CD68_mole	2	1	0	0	0	1	0.05644	0.033256	0	0	0	0.028046
protein_co thioredoxir	523	472	470	837	663	1109	12.47776	13.2704	14.77636	17.27521	17.77041	26.29517
protein_co ATPase_Na-	67	66	40	6	6	4	1.124975	1.305928	0.88504	0.087153	0.11318	0.066748
protein_co fragile_X_m	1086	880	866	1770	1283	1736	19.44333	18.56652	20.43118	27.41429	25.80575	30.88874
protein_co kinesin_fan	4291	3467	3179	5395	4818	5735	28.68668	27.31383	28.00574	31.20155	36.18575	38.1035
protein_co mannose-P	1135	1049	740	1918	1031	1238	36.52768	39.78403	31.38287	53.39957	37.2764	39.59647
protein_co matrix_met	10	3	6	20	12	15	0.215295	0.076114	0.170224	0.3725	0.290244	0.320948
protein_co chemokine	0	0	0	0	1	0	0	0	0	0	0.033526	0
protein_co mitochond	112	96	68	315	239	340	3.192995	3.225214	2.554606	7.768797	7.654682	9.633159
protein_co PHD_finger	828	686	912	760	705	570	5.613413	5.480597	8.147537	4.457314	5.369512	3.840442
protein_co leucine_ric	6	8	7	62	59	59	0.183187	0.287833	0.281628	1.637562	2.02369	1.790213
protein_co cyclin_T1	661	557	610	868	699	750	5.0185	4.983503	6.102912	5.701054	5.962092	5.659047
protein_co pseudourid	66	73	86	169	179	152	0.800666	1.043608	1.374803	1.773606	2.439548	1.83257
protein_co KRI1_homc	595	511	364	690	608	737	8.413433	8.514992	6.782541	8.440503	9.658482	10.35699
protein_co interleukin	7021	6038	5541	13049	12281	14264	60.74501	61.56187	63.17345	97.66791	119.3698	122.6486
protein_co solute_carr	1854	1589	1420	4584	3099	3714	25.93885	26.19823	26.17967	55.48155	48.70927	51.64075
protein_co adaptor-rel	16	10	0	1044	844	1033	0.482104	0.355081	0	27.21346	28.5701	30.93359
protein_co cyclin-depe	93	101	74	86	49	71	3.462386	4.431196	3.630438	2.769835	2.049451	2.627003
protein_co microtubul	158	143	146	157	112	130	1.337065	1.426062	1.628107	1.149365	1.064786	1.093323

protein_co kallikrein-r	1	3	1	16	15	30	0.046726	0.165193	0.061574	0.646763	0.787413	1.393135
protein_co neuroguidi	311	232	206	813	476	622	5.958975	5.238492	5.201316	13.47612	10.2463	11.84435
protein_co receptor-in	1	0	2	6	2	0	0.027431	0	0.072294	0.14238	0.061633	0
protein_co adenylate_	8	2	4	1	2	4	0.080274	0.02365	0.052891	0.008681	0.022546	0.039889
protein_co RAB2B_mer	474	425	323	561	350	417	8.570366	9.055596	7.695881	8.774995	7.109485	7.49319
protein_co BCL2-like_2	756	642	615	762	641	891	11.10219	11.11038	11.90136	9.680656	10.57533	13.00392
protein_co ajuba_LIM_	852	660	556	2892	2051	2550	10.58323	9.661169	9.100982	31.07706	28.62156	31.47955
protein_co D-tyrosyl-tF	371	335	297	438	241	333	7.228969	7.692267	7.625946	7.383114	5.27556	6.448465
protein_co poly_(ADP-	164	177	164	738	423	521	4.385012	5.577085	5.778373	17.0705	12.70622	13.8444
protein_co HEAT_repea	236	220	241	356	254	278	1.593632	1.750676	2.144509	2.079644	1.926898	1.865651
protein_co forkhead_b	0	0	1	4	4	4	0	0	0.024376	0.06401	0.083125	0.073535
protein_co sorting_nex	1863	1583	1510	2047	1495	1413	29.02562	29.06409	31.00134	27.58986	26.1673	21.87865
protein_co E2F-associa	320	252	207	418	287	373	12.82446	11.90137	10.93187	14.49201	12.92172	14.8562
protein_co egl_nine_h	23	18	21	102	56	26	0.427393	0.394166	0.514226	1.639694	1.16906	0.480156
protein_co MIS18_bin	260	181	254	682	606	429	2.881444	2.363864	3.709415	6.538592	7.544988	4.725021
protein_co neural_reti	1	11	5	30	10	19	0.025174	0.326327	0.165866	0.653337	0.282815	0.475353
protein_co ribonuclea	0	0	0	33	16	18	0	0	0	1.12119	0.705946	0.702562
protein_co neural_pre	297	257	208	424	243	414	6.836294	6.971151	6.309027	8.442929	6.28376	9.470529
protein_co defender_a	3169	2553	1962	3529	2490	3031	229.5075	217.8877	187.2443	221.1003	202.5924	218.1576
protein_co telomerase	573	453	488	580	564	634	2.83639	2.64251	3.183215	2.483718	3.136458	3.118963
protein_co erythrocyte	5	5	2	159	197	155	0.056236	0.066271	0.029642	1.547063	2.489219	1.732564
protein_co cysteine_di	91	92	73	157	67	105	2.590124	3.085845	2.738021	3.865822	2.142412	2.970148
protein_co receptor_a	1368	1128	1094	2473	1629	1851	21.82739	21.20957	23.00212	34.13523	29.2002	29.3516
protein_co integrin_al	679	476	580	694	584	596	10.57263	8.734282	11.9008	9.348365	10.21586	9.222933
protein_co glutamine_	92	75	59	179	150	190	0.908858	0.873126	0.76806	1.529764	1.664749	1.865398
protein_co forkhead_b	0	0	0	0	1	1	0	0	0	0	0.02252	0.019922
protein_co SEC14-like_	3683	3207	3334	1503	1234	1407	35.862	36.79924	42.77925	12.66061	13.49886	13.61559
protein_co rhomboid_	231	182	174	652	543	540	3.397991	3.154923	3.372829	8.296995	8.973443	7.8943
protein_co aralkylamir	5	1	3	0	8	2	0.138372	0.032613	0.109404	0	0.248723	0.055007
protein_co Rac/Cdc42_	285	218	201	24	19	26	2.506759	2.259599	2.329693	0.182617	0.187746	0.227275
protein_co MAP7_dom	471	380	336	437	289	274	5.459866	5.191009	5.132573	4.382334	3.763639	3.156613
protein_co fibroblast_	25	26	32	51	48	45	0.494591	0.606159	0.83424	0.872849	1.066833	0.884765
protein_co ash2_(absei	762	658	590	1045	896	885	13.05535	13.28515	13.3205	15.48863	17.24609	15.06907
protein_co TELO2_inte	130	98	80	321	194	200	2.912539	2.587388	2.361855	6.221519	4.882915	4.453157
protein_co ADP-ribosy	0	0	0	0	0	1	0	0	0	0	0	0.040102
protein_co cholinergic	18	14	13	43	41	33	0.489942	0.449063	0.466284	1.012521	1.253734	0.892681
protein_co cyclin-depe	768	687	435	386	305	313	19.82383	20.8973	14.79621	8.619394	8.844542	8.02935
protein_co shugoshin-l	45	36	27	433	293	321	0.920891	0.868171	0.728105	7.665607	6.736159	6.528454
protein_co ribosomal_	5081	4594	3048	3771	2625	3313	269.5323	287.1836	213.0646	173.0538	156.4372	174.6597
protein_co cadherin_1	1	0	0	0	2	0	0.018595	0	0	0	0.041781	0
protein_co Kruppel-lik	835	733	576	1070	928	1198	15.30669	15.83456	13.91401	16.96843	19.11138	21.82536
protein_co transmemb	1191	973	768	1767	1117	1352	17.08283	16.44629	14.5159	21.9254	17.99908	19.27234
protein_co deoxyhypu	433	371	314	1134	818	1163	11.28678	11.39628	10.78566	25.57162	23.95436	30.12808
protein_co MAU2_chro	969	913	768	987	797	934	10.27229	11.40569	10.72851	9.051566	9.491851	9.840113

protein_co	SHC_(Src_h	340	387	239	513	419	468	6.792429	9.110963	6.291858	8.865977	9.403928	9.29184
protein_co	hsa-mir-31	462	305	266	229	207	188	10.37706	8.073083	7.873158	4.449703	5.223383	4.196623
protein_co	abhydrolas	2536	1999	1395	3065	1998	2791	23.87664	22.1791	17.30745	24.96419	21.13336	26.11521
protein_co	lipopolysac	0	0	1	0	0	1	0	0	0.035575	0	0	0.02683
protein_co	synaptotag	4	0	2	7	0	0	0.055845	0	0.036795	0.084544	0	0
protein_co	troponin_I	1	0	0	0	0	0	0.053368	0	0	0	0	0
protein_co	core-bindir	0	1	1	1	3	10	0	0.013935	0.015583	0.01023	0.039854	0.117521
protein_co	guanidinoa	730	725	456	782	554	664	29.12353	34.08523	23.97291	26.98926	24.83019	26.32685
protein_co	haloacid_d	205	187	157	865	651	639	5.07145	5.451638	5.118147	18.51217	18.09291	15.71046
protein_co	chromoson	264	195	224	284	200	228	6.33564	5.514781	7.083851	5.896142	5.392196	5.437898
protein_co	PHD_finger	429	359	362	932	693	747	5.300277	5.226883	5.893654	9.961396	9.618859	9.172158
protein_co	proline_ric	0	0	0	3	0	1	0	0	0	0.022988	0	0.008803
protein_co	UDP-N-acet	0	0	0	5	0	2	0	0	0	0.096216	0	0.044213
protein_co	EF-hand_ca	13	6	8	11	9	7	0.091108	0.049553	0.073882	0.066692	0.070861	0.048755
protein_co	nucleoredc	12	13	3	11	7	13	0.436027	0.556651	0.143644	0.345771	0.285746	0.469446
protein_co	StAR-relate	101	63	90	284	310	257	1.099309	0.808065	1.29085	2.674114	3.790612	2.779978
protein_co	family_witl	1	0	0	92	60	82	0.013192	0	0	1.049962	0.889249	1.075094
protein_co	glycerophо	4	4	3	3	10	9	0.08686	0.102359	0.085845	0.056356	0.243954	0.194227
protein_co	spermidine	1702	1585	1394	926	606	788	79.38817	87.12295	85.68283	37.36545	31.75542	36.52852
protein_co	guanine_nu	554	387	405	1010	682	853	12.44349	10.24355	11.98733	19.62533	17.20941	19.04106
protein_co	SH3-domai	2095	1649	1882	1959	1655	1489	21.20271	19.66686	25.09931	17.15161	18.81718	14.97655
protein_co	motile_spe	194	171	200	286	246	217	2.467104	2.562648	3.351587	3.146406	3.514551	2.742553
protein_co	dedicator_(	274	366	196	215	162	234	2.281509	3.591367	2.150614	1.54872	1.515429	1.936409
protein_co	ECSIT_hom	776	641	481	903	529	719	24.16601	23.52384	19.73891	24.3273	18.50751	22.25265
protein_co	low_densit	1209	1040	912	2279	1497	1613	11.99282	12.15725	11.92133	19.557	16.68268	15.90153
protein_co	elongation_	1070	889	640	1392	1155	1616	26.29845	25.7487	20.72818	29.59706	31.89168	39.47275
protein_co	tetraspanin	1	0	0	0	1	0	0.050905	0	0	0	0.057188	0
protein_co	chromoson	4	2	0	2	1	1	0.242849	0.143091	0	0.105043	0.068206	0.060337
protein_co	protein_kir	14714	12092	9279	10308	7797	9731	344.3739	333.5068	286.1775	208.7069	205.0105	226.3428
protein_co	calponin_1	131	88	83	1224	858	935	3.752852	2.970844	3.133308	30.33434	27.61382	26.6202
protein_co	cell_divisio	962	965	862	1948	1254	1442	23.03448	27.22938	27.19853	40.35109	33.73261	34.31455
protein_co	thioesteras	198	136	117	639	361	451	4.599525	3.723006	3.581529	12.84138	9.421152	10.412
protein_co	exocyst_co	2	5	2	29	20	25	0.061595	0.181465	0.081167	0.77264	0.691983	0.765184
protein_co	poliovirus_	1465	1281	1039	6714	4570	5599	31.45116	32.40822	29.39337	124.6934	110.221	119.4591
protein_co	apolipopro	1236	1049	680	20713	15550	22162	54.1681	54.1761	39.27072	785.292	765.6047	965.2588
protein_co	translocase	1745	1469	1123	7926	5503	6889	27.05184	26.83677	22.94119	106.2964	95.84069	106.1371
protein_co	apolipopro	36	24	17	61	62	99	2.766148	2.173157	1.7213	4.054765	5.351969	7.559929
protein_co	growth_arr	37	26	27	301	284	335	1.839265	1.523081	1.768647	12.9441	15.86024	16.54996
protein_co	leucine-rich	122	116	144	56	48	45	1.311965	1.470034	2.040608	0.520971	0.579899	0.480933
protein_co	dipeptidyl-	0	0	0	13	25	18	0	0	0	0.12409	0.3099	0.197385
protein_co	exportin_7	1171	846	983	1848	1666	1578	12.68028	10.79567	14.02686	17.31159	20.26731	16.98199
protein_co	angiotensir	0	2	0	18	24	8	0	0.035579	0	0.235067	0.407021	0.120021
protein_co	family_witl	209	199	116	108	107	117	2.677152	3.00391	1.958031	1.196778	1.539783	1.489437
protein_co	scaffold_at	1263	1030	912	1759	1816	2163	19.8352	19.0624	18.87396	23.89803	32.04042	33.75977

protein_co ribosomal_	10131	9027	6232	6595	6079	9424	591.3398	620.9196	479.3437	333.0141	398.6264	546.6756
protein_co ATPase_am	57	67	38	42	5	19	0.576215	0.798163	0.506207	0.367301	0.056784	0.190885
protein_co neurocan	0	0	0	0	0	3	0	0	0	0	0	0.022866
protein_co kinesin_fan	0	0	2	1850	2137	2144	0	0	0.015229	9.24776	13.87252	12.31222
protein_co GTP_bindir	280	276	206	910	609	901	5.081755	5.902987	4.926718	14.28763	12.41715	16.25137
protein_co plasmalem	0	0	0	2	0	0	0	0	0	0.039739	0	0
protein_co bone_marr	2	1	1	0	0	0	0.103908	0.061224	0.068462	0	0	0
protein_co solute_carr	763	717	401	193	139	186	9.300939	10.29979	6.441417	2.035273	1.903558	2.25333
protein_co NOP2/Sun_	162	113	88	1432	886	1075	3.751724	3.083908	2.685551	28.68943	23.05147	24.74195
protein_co Usher_synd	1	4	6	10	9	19	0.014714	0.069358	0.116337	0.12729	0.148772	0.27784
protein_co collagen_b	4195	3391	2544	4463	2833	3514	59.95882	57.11576	47.91517	55.18372	45.49008	49.91517
protein_co DET1_and_	1257	1084	878	2525	1829	2299	16.3185	16.58369	15.02015	28.35759	26.6752	29.66153
protein_co mitochond	423	375	233	583	409	654	23.13434	24.1688	16.79219	27.58343	25.1298	35.5471
protein_co 6-phospho	834	770	559	1454	659	888	27.57826	30.00534	24.35832	41.59376	24.48134	29.18256
protein_co LSM7_hom	1337	1015	799	1747	1750	2500	99.69311	89.18809	78.50826	112.6911	146.5956	185.2607
protein_co tubby_like_	619	517	517	700	755	684	2.94619	2.899798	3.242616	2.882247	4.037069	3.235459
protein_co sorting_nex	1374	1100	1187	1156	875	1042	17.32752	16.34743	19.72583	12.61161	12.39672	13.05951
protein_co reticulon_4	65	58	55	164	130	191	1.518608	1.596862	1.693284	3.31466	3.412122	4.434812
protein_co glutaminyl-	244	227	211	705	495	630	3.146031	3.449102	3.58501	7.86367	7.170136	8.072784
protein_co chromoson	226	188	108	279	241	300	7.887056	7.731637	4.966667	8.423134	9.448712	10.40489
protein_co radial_spok	133	134	120	127	101	98	2.233868	2.65227	2.655963	1.845324	1.905796	1.635843
protein_co acyl-CoA_sy	6	13	3	6	6	1	0.115131	0.293962	0.075857	0.099599	0.129342	0.01907
protein_co myeloid/ly	1076	850	735	769	953	1098	29.5	27.46223	26.55412	18.23892	29.35295	29.91726
protein_co myeloid/ly	716	674	690	2427	2698	2143	4.920269	5.458117	6.248269	14.42808	20.82892	14.6355
protein_co actinin_alp	13238	10871	9743	23146	21471	26057	141.2115	136.6546	136.9542	213.5929	257.3055	276.237
protein_co serine/thre	30	36	28	32	25	23	0.339583	0.480213	0.417655	0.313356	0.317917	0.258739
protein_co NADH_deh	1814	1650	1343	1937	1537	1696	19.53916	20.944	19.06248	18.04933	18.59908	18.15533
protein_co erythropoi	0	0	0	32	17	19	0	0	0	1.101929	0.760218	0.751629
protein_co actin_relat	412	386	290	1043	599	725	12.71819	14.04179	11.79671	27.85321	20.77322	22.24209
protein_co zinc_finger_	665	535	589	531	515	418	6.399884	6.067521	7.469655	4.420872	5.568096	3.997941
protein_co FCH_domai	8	10	1	20	9	20	0.131776	0.194112	0.021706	0.284996	0.166547	0.327405
protein_co unc-13_ho	268	229	206	1	15	11	1.404632	1.414394	1.422754	0.004534	0.088322	0.057297
protein_co microtubul	609	454	450	1077	875	910	9.429969	8.284302	9.182064	14.42686	15.22124	14.00374
protein_co kelch_dom	0	0	0	0	0	2	0	0	0	0	0	0.035193
protein_co SCO2_cyto	376	264	235	776	452	574	18.93988	15.67113	15.59883	33.81537	25.57861	28.73498
protein_co peroxidasir	10016	8056	8960	10701	10848	10030	77.88734	73.82426	91.81537	71.98797	94.77009	77.51453
protein_co single_stra	2764	2255	1639	1850	1216	1786	86.3807	83.0486	67.49824	50.01651	42.69346	55.47148
protein_co growth_dif	329	244	165	599	350	469	10.1265	8.850352	6.692408	15.94974	12.10266	14.34651
protein_co pyroglutam	1262	1080	907	539	583	669	9.42069	9.500669	8.922067	3.480768	4.889236	4.96317
protein_co KIAA1683	43	31	30	12	13	14	0.412328	0.350302	0.37908	0.099545	0.140045	0.133417
protein_co LSM4_hom	1978	1595	1200	6504	5123	6810	54.88327	52.15326	43.87628	156.1195	159.6935	187.7891
protein_co jun_D_prot	2043	1554	1305	3182	2370	2369	57.83874	51.8452	48.68507	77.93161	75.37857	66.65384
protein_co histidine_ri	3	0	0	0	0	2	0.066592	0	0	0	0	0.044121
protein_co transient_r	405	328	272	246	192	230	5.218083	4.980086	4.618061	2.741915	2.779113	2.945055

protein_co	sulfotransfe	120	110	41	44	36	58	2.48064	2.679676	1.116866	0.786861	0.836054	1.191572
protein_co	zinc_finger_	197	127	105	229	164	178	1.741131	1.322745	1.222896	1.75091	1.628389	1.563489
protein_co	crumbs_ho	0	0	2	201	199	254	0	0	0.096692	6.379473	8.202154	9.26124
protein_co	olfactomed	4	2	4	35	18	23	0.080703	0.047552	0.106346	0.610885	0.40799	0.461175
protein_co	calmodulin	1149	890	940	1256	1440	1274	7.904002	7.214797	8.520983	7.474458	11.12855	8.709758
protein_co	UBA_doma	817	702	539	1548	1127	1299	23.167	23.45805	20.14055	37.9736	35.90217	36.6072
protein_co	S-antigen;_	0	0	0	0	1	3	0	0	0	0	0.008932	0.023704
protein_co	zinc_finger_	184	102	133	262	267	273	1.878716	1.2273	1.789492	2.314236	3.062694	2.770229
protein_co	helicase_wi	482	330	338	152	110	149	3.16438	2.553069	2.924106	0.863273	0.811303	0.972159
protein_co	sterile_alph	27	27	12	205	124	183	0.655391	0.772338	0.383842	4.304803	3.381483	4.414659
protein_co	lymphocyt	210	178	118	1	6	1	4.211215	4.206445	3.118207	0.017348	0.135173	0.01993
protein_co	troponin_T	6	1	1	0	0	0	0.254933	0.05007	0.05599	0	0	0
protein_co	troponin_I_	3	3	4	0	0	0	0.213185	0.251226	0.374568	0	0	0
processed_	H19_imprii	1	0	0	2712	1962	3383	0.022547	0	0	52.89891	49.69836	75.80636
pseudogen	cytochrom	3	1	2	0	0	0	0.063251	0.024846	0.055566	0	0	0
protein_co	collagen_ty	44902	40094	32748	6110	6795	7057	280.7223	295.3913	269.7931	33.04574	47.72542	43.84711
protein_co	ataxin_10	1636	1342	1269	2918	1880	2163	26.01726	25.14999	26.59345	40.14455	33.58808	34.1857
protein_co	tubulin_ga	1703	1367	1230	2270	1568	1729	25.37532	24.00338	24.15109	29.26077	26.24775	25.60363
protein_co	calcyon_ne	4	0	0	0	0	1	0.230178	0	0	0	0	0.057189
protein_co	cytochrom	18	14	7	9	8	7	0.120351	0.110309	0.061675	0.052057	0.060092	0.046514
protein_co	patatin-like	49	55	41	25	39	34	0.488717	0.646444	0.538865	0.215707	0.436993	0.337015
protein_co	p21_protei	968	734	637	1854	1470	1872	8.935812	7.984759	7.748773	14.80578	15.24492	17.17411
protein_co	motor_neu	0	0	0	8	10	3	0	0	0	0.168533	0.273578	0.072604
protein_co	zinc_finger_	30	42	30	14	26	17	0.439588	0.725238	0.579269	0.177466	0.428003	0.247561
protein_co	centrosom	176	161	155	803	616	743	2.367882	2.552586	2.747982	9.346003	9.310588	9.934495
protein_co	TAF4_RNA_	246	188	218	538	419	431	2.812848	2.533238	3.284751	5.321773	5.382378	4.897766
protein_co	GATA_bind	0	0	0	18	13	8	0	0	0	0.31768	0.297953	0.162201
protein_co	RBBP8_N-t	0	0	0	161	187	229	0	0	0	2.640037	3.982097	4.313862
protein_co	laminin_alp	3365	2891	2434	8284	10200	11138	15.59132	15.78531	14.86118	33.20481	53.0942	51.28788
protein_co	oxysterol_b	483	428	335	625	576	523	6.440932	6.725932	5.886826	7.210155	8.629251	6.931272
protein_co	adhesion_r	439	293	275	901	690	880	16.95193	13.33305	13.99336	30.09833	29.93317	33.77124
protein_co	argininosuc	2403	1831	1606	333	248	248	64.47907	57.89758	56.78653	7.729871	7.475939	6.613423
protein_co	PR_domain	2	0	2	0	0	5	0.042763	0	0.056352	0	0	0.106248
protein_co	exosome_c	623	568	449	1718	1065	1417	11.92416	12.81136	11.32455	28.44632	22.90016	26.95376
protein_co	protein-O-r	418	355	259	499	381	476	6.470566	6.475919	5.283243	6.682355	6.625826	7.322891
protein_co	uridine-cyt	505	342	309	836	615	807	11.95136	9.538044	9.636502	17.11573	16.35122	18.98057
protein_co	fibrinogen_	17	5	7	14	11	19	0.276667	0.095893	0.150121	0.197106	0.201117	0.307306
protein_co	proline-rich	6355	5152	5357	4323	5666	5477	30.46912	29.109	33.84549	17.93051	30.51898	26.09737
protein_co	charged_m	1244	1045	731	1066	765	935	55.90713	55.34395	43.29114	41.44451	38.624	41.76073
protein_co	ubiquitin-c	2084	1570	1372	3317	2619	3170	73.16249	64.95274	63.47163	100.7394	103.294	110.6012
protein_co	tripartite_r	7759	5954	5003	24492	15989	18364	138.7734	125.4921	117.9141	378.955	321.2704	326.4204
protein_co	chromoson	809	759	420	1203	786	940	25.04635	27.6914	17.13484	32.21993	27.33805	28.92234
protein_co	Yip1_doma	1246	1004	812	922	712	974	42.55773	40.41115	36.54696	27.24296	27.32055	33.06199
protein_co	autophagy_	212	154	137	500	320	374	5.758589	4.929559	4.903833	11.74933	9.765158	10.09628

protein_co eukaryotic_	3762	3265	2803	5150	4014	4200	69.6865	71.2722	68.42074	82.52777	83.53266	77.31946
protein_co transmemb	281	266	192	542	396	658	22.43804	25.03037	20.20294	37.44043	35.52408	52.21726
protein_co zinc_finger_	1047	943	847	1401	1736	1732	9.058542	9.614582	9.656725	10.48607	16.8737	14.89255
protein_co neuronal_P	94	92	50	181	122	173	2.35071	2.711229	1.647692	3.915731	3.427521	4.299589
protein_co glia_matur	0	1	0	9	3	12	0	0.060688	0	0.400963	0.173568	0.614172
protein_co mitogen-ac	213	161	171	184	141	203	3.281849	2.92329	3.471921	2.452561	2.440659	3.108455
protein_co Rho_guanir	1	0	0	400	306	451	0.017295	0	0	5.984829	5.945649	7.752021
protein_co leucine_ric	1148	949	807	2097	1587	1730	22.95176	22.35874	21.26094	36.269	35.64512	34.37398
protein_co sestrin_2	1417	1135	1071	1804	1482	1478	21.72528	20.50683	21.63813	23.92737	25.52659	22.52058
protein_co sphingomy	0	0	0	37	26	32	0	0	0	0.885813	0.80835	0.88011
protein_co ATPase_inh	1261	1107	1000	1199	1084	1979	35.98846	37.23084	37.60824	29.60263	34.75574	56.13111
protein_co mediator_c	320	248	234	652	461	579	9.252386	8.450113	8.915679	16.30851	14.97455	16.63765
protein_co thymocyte_	36	25	17	28	22	18	0.666157	0.545157	0.414532	0.448224	0.457347	0.331022
protein_co CAP-GLY_d	422	357	479	1330	1344	1151	3.799507	3.787826	5.683097	10.35928	13.5945	10.29911
protein_co coiled-coil_	24	12	13	9	7	12	0.358315	0.211126	0.255759	0.116241	0.117409	0.178051
protein_co huntingtin_	266	226	217	524	473	650	3.102513	3.106329	3.335235	5.287206	6.197865	7.534508
protein_co zinc_finger_	525	347	391	654	577	535	6.639757	5.171654	6.516351	7.155395	8.198185	6.724443
protein_co peter_pan_	54	52	42	67	45	45	1.185246	1.345009	1.214784	1.272192	1.109625	0.981605
protein_co eukaryotic_	2908	2275	1963	3165	2567	3210	101.1514	93.25367	89.97722	95.23885	100.3119	110.9666
protein_co angiopoieti	7	4	3	0	0	1	0.195046	0.131343	0.110153	0	0	0.027692
protein_co chromoson	151	115	101	7	8	8	3.735556	3.352612	3.292566	0.14981	0.22234	0.196688
protein_co DNA_(cytos	1830	1419	1508	5736	5230	5232	17.91457	16.36986	19.45322	48.57665	57.51831	50.90176
protein_co zinc_finger_	202	151	158	194	164	133	4.452157	3.92196	4.588925	3.698996	4.060804	2.913268
protein_co solute_carr	1506	1232	1078	376	265	347	21.18765	20.42564	19.98534	4.576239	4.188445	4.851734
protein_co pregnancy_	1	5	0	9	1	3	0.024704	0.145562	0	0.192343	0.027754	0.073655
protein_co dyskeratosi	1041	805	781	2549	2049	2301	21.38594	19.4886	21.14285	45.30128	47.28993	46.97902
protein_co plexin_A3	2269	1996	1595	651	693	818	17.79075	18.44282	16.47992	4.415742	6.104385	6.374155
protein_co dual_specif	3	5	4	63	65	98	0.065279	0.128212	0.114695	1.185915	1.588958	2.119267
protein_co membrane_	485	430	377	426	285	310	10.79747	11.28121	11.06003	8.204514	7.128106	6.858854
protein_co zinc_finger_	126	161	124	726	569	561	1.323	1.992151	1.715717	6.594606	6.711979	5.854122
protein_co zinc_finger_	178	177	196	221	220	182	1.148367	1.345677	1.666293	1.233434	1.594529	1.166921
protein_co solute_carr	4	8	3	17	19	26	0.108876	0.256608	0.107604	0.400299	0.580999	0.703324
protein_co low_densit	1160	919	689	1176	791	893	18.73446	17.49064	14.66348	16.4306	14.35188	14.33324
protein_co chromoson	400	264	231	778	490	676	5.672756	4.412098	4.316989	9.545017	7.806911	9.527752
protein_co nucleolar_p	595	631	538	2400	1440	1652	10.6888	13.35821	12.73588	37.29806	29.06187	29.49386
protein_co ubiquitinat	1361	1100	1234	1422	1255	1190	13.0483	12.42783	15.58998	11.79392	13.51725	11.33841
protein_co castor_zinc	4	1	8	108	78	119	0.026684	0.007861	0.070326	0.623271	0.584567	0.788946
protein_co polycystic_	10	10	8	4	4	3	0.069114	0.081446	0.07286	0.023916	0.031058	0.020606
protein_co hydroxyste	0	1	0	0	0	0	0	0.054967	0	0	0	0
protein_co NUT_family	5	4	2	5	7	7	0.0631	0.059488	0.03326	0.054587	0.099245	0.087795
protein_co hyaluronan	423	320	305	443	423	430	7.109219	6.337801	6.754857	6.440925	7.986766	7.182235
protein_co fructose-16	0	0	0	1	1	1	0	0	0	0.035095	0.045575	0.040317
protein_co solute_carr	261	208	178	795	615	700	8.566398	8.045039	7.698614	22.57293	22.67681	22.83313
protein_co proline_ric	517	421	409	484	495	469	5.950107	5.709833	6.202866	4.818841	6.400126	5.364346

protein_co	ubiquitin-li	8785	7521	6673	9828	8115	8782	130.679	131.8399	130.8037	126.4714	135.6131	129.8276
protein_co	regucalcin	1	0	0	0	0	1	0.023687	0	0	0	0	0.023541
protein_co	polymerase	68	37	46	15	17	22	0.904974	0.580278	0.806715	0.172696	0.254171	0.290978
pseudogen	taxilin_gam	648	581	650	939	672	688	4.700064	4.96606	6.21265	5.891927	5.475793	4.959373
protein_co	peptidylpro	578	508	482	1004	766	779	13.70963	14.19936	15.06537	20.6013	20.41154	18.36306
protein_co	UL16_bind	33	21	30	13	8	3	1.295072	0.971195	1.551444	0.441353	0.352711	0.117007
protein_co	A_kinase_(I	5306	4233	5222	4514	4381	3641	33.31415	31.31965	43.20492	24.51806	30.9018	22.71914
protein_co	spectrin_re	679	526	657	144	115	93	1.295478	1.182642	1.651812	0.237676	0.246495	0.176341
protein_co	UL16_bind	47	46	32	34	53	33	2.575804	2.970844	2.310999	1.61197	3.263171	1.797374
protein_co	large_tumo	540	482	495	683	630	616	3.803131	4.000384	4.593964	4.161321	4.984678	4.311594
protein_co	EPS8-like_1	24	26	18	241	212	220	0.501019	0.639622	0.495165	4.352341	4.971962	4.56431
protein_co	AAR2_splic	747	665	560	1185	790	940	14.70693	15.42872	14.52861	20.18286	17.4734	18.39242
protein_co	tubulin_tyr	0	1	5	3	7	8	0	0.023785	0.132984	0.052382	0.158723	0.16047
protein_co	RNA_bindir	2900	2502	2381	4398	3044	3369	33.52159	34.08168	36.26777	43.97895	39.52941	38.70234
protein_co	cytochrom	0	0	0	2	4	0	0	0	0	0.132176	0.343295	0
protein_co	zinc_finger_	73	81	43	209	150	170	1.049618	1.372462	0.814726	2.599666	2.422973	2.42922
protein_co	gamma-glu	1072	985	786	401	390	531	21.48098	23.25962	20.75471	6.95131	8.779564	10.57459
protein_co	acyl-CoA_sy	698	610	586	564	442	467	12.05638	12.41648	13.3381	8.427596	8.576951	8.016562
protein_co	ectodyspla	737	560	635	638	614	626	11.41531	10.22151	12.9607	8.548772	10.68409	9.63616
protein_co	Cdc42_gua	288	257	319	837	793	727	2.816739	2.962063	4.111304	7.081782	8.713172	7.066398
protein_co	complemer	43	63	20	2	2	4	1.757886	3.035079	1.077425	0.070732	0.091855	0.162514
protein_co	glial_fibrill	12	19	24	1	1	4	0.205863	0.384111	0.542553	0.014841	0.019273	0.068197
protein_co	peptide_YY	2	0	1	0	0	0	0.100553	0	0.066252	0	0	0
protein_co	HIG1_hypo	2	10	0	7	5	13	0.166743	0.982484	0	0.50487	0.468314	1.077138
protein_co	ATPase_H+_	1607	1182	1107	3756	2106	2419	60.68201	52.59793	55.08413	122.6966	89.34114	90.77988
protein_co	zinc_finger_	137	119	125	92	103	117	2.383476	2.439744	2.865728	1.384653	2.013151	2.022952
protein_co	zinc_finger_	614	552	430	381	315	511	23.02108	24.38954	21.24519	12.35792	13.26835	19.04092
protein_co	testis_expr	0	0	0	1	0	0	0	0	0	0.031673	0	0
protein_co	zinc_finger_	116	90	94	228	175	195	2.067729	1.890537	2.207996	3.515876	3.504473	3.454458
protein_co	cytochrom	5901	4778	3457	6470	4649	5904	79.17	75.54196	61.11801	75.09349	70.07185	78.72107
protein_co	ER_membr	477	391	316	1211	765	958	12.87098	12.43303	11.23608	28.26834	23.19015	25.69024
protein_co	Gse1_coile	478	458	449	1459	1786	1478	3.376357	3.812352	4.179281	8.915357	14.17265	10.37539
protein_co	GINS_comp	120	71	90	1559	993	1331	2.3767	1.657138	2.348932	26.71174	22.09487	26.19877
protein_co	charged_m	1762	1403	1298	3351	2508	3008	37.56828	35.25171	36.46909	61.80915	60.07475	63.73865
protein_co	SH3_domai	2188	2015	1777	1915	1023	1249	60.23655	65.37248	64.46664	45.60837	31.64007	34.17314
protein_co	cytochrom	958	888	565	1473	922	1026	20.52508	22.4202	15.95154	27.30141	22.19215	21.84622
protein_co	solute_carr	2	0	3	5	4	5	0.036311	0	0.071773	0.07853	0.081586	0.090216
protein_co	coagulatior	27	23	16	32	30	51	0.697612	0.700302	0.54476	0.715259	0.870804	1.309574
protein_co	proline_ric	628	531	359	460	219	268	22.52503	22.44437	16.96817	14.27337	8.824679	9.553229
protein_co	nuclear_fac	104	95	60	203	128	132	1.186097	1.276785	0.901723	2.002839	1.640008	1.496134
protein_co	indoleamir	3	2	1	2	0	0	0.075738	0.059502	0.033268	0.04368	0	0
protein_co	gap_junctic	1	0	1	5	3	5	0.022272	0	0.029349	0.096338	0.075064	0.110673
protein_co	CAP_adeny	5711	4566	4779	14285	11011	10864	97.37392	91.74312	107.3748	210.7045	210.9144	184.0899
protein_co	palmitoyl-p	844	685	720	1968	1413	1430	16.30737	15.59693	18.33196	32.89498	30.67134	27.45916

protein_co	RAB11_fam	118	154	135	720	779	913	0.723958	1.113421	1.091441	3.821441	5.369306	5.566882
protein_co	ring_finger_	1277	986	1169	1364	1162	1059	8.12861	7.396213	9.805612	7.511087	8.309609	6.699324
protein_co	ATP-bindin	313	276	255	419	371	384	6.971195	7.244011	7.484071	8.073093	9.282947	8.499704
protein_co	TNF_recept	564	432	454	616	598	667	3.90821	3.527683	4.145619	3.692687	4.655314	4.593399
protein_co	HAUS_augn	88	62	46	577	438	552	1.466879	1.217896	1.010425	8.320519	8.202283	9.144507
protein_co	mitochond	768	688	640	1037	866	965	8.865827	9.35952	9.735827	10.35619	11.23117	11.07121
protein_co	SH3-domai	241	191	219	79	116	76	4.521183	4.222557	5.413947	1.28211	2.444793	1.416962
protein_co	2-hydroxya	84	65	44	317	226	259	1.962508	1.789586	1.354627	6.406996	5.931843	6.013698
protein_co	TBC1_dom	494	426	509	431	473	380	3.957157	4.021361	5.372902	2.986734	4.256636	3.025169
protein_co	calpain_7	392	379	322	624	508	482	4.767487	5.431874	5.160528	6.565246	6.940906	5.825861
protein_co	raftlin_lipi	1255	1142	923	658	508	516	22.28067	23.89228	21.5934	10.10586	10.13205	9.104242
protein_co	chromoson	1	2	6	6	5	3	0.015917	0.037515	0.125851	0.08262	0.089411	0.047457
protein_co	zinc_finger_	633	663	547	695	638	661	5.018216	6.19393	5.714363	4.766433	5.682186	5.20783
protein_co	UDP-N-acet	0	0	4	0	0	0	0	0	0.059767	0	0	0
protein_co	solute_carr	1337	958	1225	3283	4137	3701	10.83289	9.147145	13.07928	23.0116	37.65716	29.80174
protein_co	potassium_	25	15	14	23	23	35	0.242982	0.171804	0.179307	0.193386	0.251138	0.338074
protein_co	napsin_A_a	1	0	0	14	5	9	0.016101	0	0	0.195008	0.090444	0.144017
protein_co	nuclear_rec	1090	939	718	881	620	789	24.24609	24.61432	21.04623	16.95329	15.49373	17.44222
protein_co	leucine_ric	0	2	1	11	3	17	0	0.04133	0.023108	0.166872	0.059102	0.29627
protein_co	PDZ_and_L	1943	1462	1029	194	134	128	45.0764	39.9697	31.45768	3.893509	3.492451	2.951182
protein_co	kinesin_fam	354	310	310	564	511	566	2.963022	3.057739	3.419228	4.083887	4.80509	4.70823
protein_co	mannosyl_	3399	2739	2130	3327	2512	3639	56.67604	53.82047	46.80182	47.99148	47.05622	60.30316
protein_co	glutamine-f	3064	2912	2530	94	82	81	52.44462	58.73685	57.0647	1.391884	1.576794	1.377866
protein_co	tubulin_ga	458	360	323	2347	1334	1520	15.05088	13.94139	13.9873	66.72255	49.24946	49.64206
protein_co	proteasom	1572	1205	1301	6431	4322	4666	26.4705	23.91133	28.86833	93.6809	81.76047	78.08434
protein_co	ribosomal_	14276	12638	8227	14130	9717	12949	403.7316	421.1838	306.5932	345.6937	308.7219	363.942
protein_co	PSMC3_int	62	40	63	269	237	245	2.318038	1.762365	3.103875	8.700498	9.954656	9.10342
protein_co	amine_oxic	10	7	4	20	37	44	0.131498	0.108473	0.069313	0.227516	0.546599	0.575017
protein_co	ATP_citrate	6279	5112	5574	6838	5917	5749	76.61132	73.50221	89.61985	72.17629	81.10602	69.71149
protein_co	vacuolar_p	517	464	407	1859	1214	1673	24.85967	26.29238	25.78897	77.32985	65.58017	79.94851
protein_co	receptor_(	6	5	12	13	4	11	0.370217	0.363565	0.97571	0.693923	0.277277	0.674539
protein_co	amine_oxic	35	25	23	97	64	70	0.697379	0.587013	0.603897	1.671996	1.432615	1.386144
antisense	-	0	3	0	1	5	5	0	0.342163	0	0.083727	0.543656	0.480933
protein_co	NADH_deh	79	86	46	84	102	96	5.201914	6.673314	3.991432	4.78496	7.545452	6.282275
protein_co	ankyrin_rep	36	36	11	30	22	37	0.229099	0.269979	0.092246	0.16516	0.157287	0.234009
protein_co	diaphanous	1944	1551	1596	4439	4169	4247	17.76887	16.70638	19.22345	35.10037	42.80993	38.5794
protein_co	Nedd4_fam	1810	1541	1503	1987	1727	1628	23.0123	23.08825	25.18113	21.85457	24.66737	20.57053
protein_co	ubiquitin-c	1621	1330	1185	3627	2687	3178	29.96416	28.97196	28.86505	58.00022	55.80021	58.38249
protein_co	exocyst_co	1217	995	1009	930	922	787	15.39527	14.83292	16.81987	10.17753	13.10318	9.894207
protein_co	ArfGAP_wit	2074	1858	1264	1002	823	1211	20.64291	21.79289	16.57845	8.627656	9.202609	11.97887
protein_co	chromoson	202	197	126	738	566	674	3.225967	3.707506	2.651636	10.19596	10.15486	10.6974
protein_co	anoctamin_	21	13	21	1	0	0	0.2321	0.16932	0.305852	0.009561	0	0
protein_co	protein_tyr	500	531	581	1074	855	900	5.057412	6.329363	7.744071	9.397788	9.715688	9.047124
protein_co	transmemb	95	94	64	10	10	20	2.595147	3.02603	2.303844	0.23632	0.306893	0.542973

protein_co	kringle_cor	4	1	8	133	90	123	0.090536	0.026673	0.238609	2.604213	2.288513	2.766793
protein_co	THO_comp	323	312	217	973	571	782	12.0507	13.71739	10.66852	31.40404	23.93287	28.9952
protein_co	TNF_recept	2425	1844	1566	2859	2055	2519	34.69781	31.0927	29.52684	35.38894	33.03325	35.82021
protein_co	BARX_hom	6	1	2	0	0	0	0.207341	0.040723	0.091075	0	0	0
protein_co	ninjurin_1	213	207	132	266	132	219	5.56586	6.374265	4.545288	6.013084	3.875035	5.687304
protein_co	nephronop	741	713	533	223	331	291	7.070886	8.017745	6.702204	1.840872	3.548401	2.759677
protein_co	microtubul	8007	7014	7988	4770	4048	3509	35.22507	36.3626	46.30789	18.15363	20.00652	15.34176
protein_co	interleukin	939	767	914	807	627	686	12.31704	11.85614	15.79872	9.157512	9.239693	8.942824
protein_co	WD_repeat	242	259	267	239	198	193	3.116449	3.930533	4.530965	2.662598	2.864566	2.470083
protein_co	creatine_ki	11	19	11	26	62	34	0.355743	0.724109	0.468782	0.727411	2.2526	1.092778
protein_co	zinc_finger_	142	167	121	439	304	338	1.632137	2.261995	1.832687	4.365115	3.925462	3.860953
protein_co	keratin_34	64	56	67	0	0	1	1.935022	1.995267	2.669412	0	0	0.030048
protein_co	keratin_33I	0	0	1	4	0	0	0	0	0.043412	0.113999	0	0
protein_co	tensin_4	23	10	3	35	23	21	0.299396	0.1534	0.05146	0.394139	0.336353	0.271673
protein_co	topoisomer	1347	1082	1345	4042	3524	3521	12.38477	11.72343	16.29587	32.14991	36.40034	32.17334
protein_co	StAR-relate	999	810	643	841	666	946	15.32543	14.64331	12.99849	11.16108	11.47811	14.42274
protein_co	retinoic_ac	717	645	429	426	323	351	15.7244	16.66946	12.39787	8.08216	7.958045	7.650179
protein_co	protein_ph	1031	702	623	4	2	4	18.95872	15.21229	15.0964	0.063632	0.041317	0.0731
protein_co	KH_domair	53	55	44	414	317	316	0.513332	0.627758	0.561578	3.468852	3.449299	3.04172
protein_co	chromodor	688	623	560	1400	1033	1199	12.27617	13.09995	13.16732	21.61054	20.70732	21.26196
protein_co	peroxisoma	537	429	366	393	223	288	16.33869	15.3818	14.67435	10.34424	7.622488	8.708532
protein_co	flavin_cont	37	37	46	9	37	17	0.744231	0.877031	1.219267	0.156607	0.836098	0.339832
protein_co	protein_inh	1331	1185	1003	487	362	368	24.28971	25.48413	24.12016	7.688406	7.421676	6.67424
protein_co	protein_kir	545	453	470	745	614	590	5.326351	5.217213	6.052934	6.298723	6.741409	5.730532
protein_co	RNA_bindir	650	573	551	1049	861	1047	12.1725	12.64527	13.5973	16.99436	18.11417	19.486
pseudogen	clustered_r	44	27	34	101	137	101	1.221502	0.883308	1.243813	2.425637	4.272785	2.786586
protein_co	follicle_stir	1	0	0	0	0	0	0.028011	0	0	0	0	0
protein_co	pyruvate_d	1414	1095	903	2027	1659	1877	21.48639	19.60808	18.08159	26.64592	28.32105	28.34574
protein_co	retinoic_ac	52	77	56	11	7	10	1.137105	1.984244	1.61369	0.208091	0.171967	0.217324
protein_co	methylcrot	714	569	571	2057	1329	1333	10.31374	9.685844	10.86899	25.70487	21.56712	19.1363
protein_co	zinc_finger_	197	180	157	294	180	258	2.418126	2.603708	2.539493	3.121929	2.482185	3.147328
protein_co	zinc_finger_	70	74	36	130	124	111	1.5126	1.884364	1.025093	2.430146	3.01021	2.383739
protein_co	zinc_finger_	37	54	17	17	12	17	0.646261	1.111494	0.391282	0.256873	0.23547	0.295097
protein_co	VCP-interac	1130	901	779	1066	729	915	24.47763	22.99973	22.23633	19.97612	17.74057	19.69798
protein_co	chondroitii	4707	3884	4031	1189	1124	1027	54.76775	53.25581	61.80567	11.96811	14.69251	11.87574
protein_co	small_nucl	395	331	344	1537	1057	1410	8.570366	8.463253	9.835479	28.84956	25.76477	30.40402
pseudogen	keratin_17_	0	0	0	4	1	6	0	0	0	0.118497	0.038471	0.204194
protein_co	lethal_gian	2228	1868	1440	2320	1761	2174	19.64566	19.41044	16.73203	17.69711	17.44455	19.05112
protein_co	nuclear_rec	1	0	2	0	0	0	0.045797	0	0.120698	0	0	0
protein_co	lin-28_hom	0	2	0	19662	18581	20554	0	0.031132	0	224.6752	275.729	269.8177
protein_co	THAP_dom	136	130	112	261	214	174	3.331779	3.75308	3.615681	5.531474	5.889795	4.236393
protein_co	rhophilin_F	87	64	75	728	668	678	1.214307	1.05268	1.379448	8.790299	10.47454	9.404779
protein_co	chromoson	594	495	439	741	510	638	12.76256	12.53325	12.42942	13.77313	12.31036	13.62328
protein_co	chromoson	60	52	43	168	120	156	1.382271	1.411733	1.305405	3.348223	3.105792	3.571711

protein_co	leucine_ric	4	2	6	3	1	1	0.043085	0.025387	0.085164	0.027955	0.012101	0.010705
protein_co	actin-relate	995	803	738	1266	1024	1082	29.02275	27.60184	28.36656	31.94568	33.55556	31.36551
protein_co	abhydrolas	7	5	4	20	14	21	0.12944	0.108955	0.097469	0.319936	0.290836	0.385922
protein_co	GTP_cyclol	12	16	7	178	134	132	0.215865	0.339179	0.165934	2.770032	2.708044	2.359855
protein_co	lectin_gala	3143	2533	1860	530	386	508	96.23687	91.39856	75.04899	14.03899	13.27802	15.45861
protein_co	podocan-lil	15	22	10	14	5	12	0.2894	0.500193	0.254239	0.233668	0.108374	0.230091
protein_co	DnaJ_(Hsp4	2407	2053	1897	4414	3262	3877	56.28488	56.57333	58.45448	89.29168	85.69366	90.09924
protein_co	zinc_finger_	71	71	52	194	196	186	0.866285	1.020864	0.836066	2.047704	2.686628	2.255408
protein_co	F-box_and_	274	208	167	487	240	278	8.045387	7.197253	6.461713	12.37053	7.916927	8.112427
protein_co	regulatory_	614	456	408	703	528	606	7.50364	6.567129	6.570503	7.432278	7.249142	7.360137
protein_co	zinc_finger_	9	0	3	11	1	8	0.155658	0	0.068373	0.164583	0.01943	0.137508
protein_co	chromoson	17	15	6	27	36	39	0.358136	0.37239	0.166566	0.492069	0.852023	0.816533
protein_co	DDB1_and_	418	334	231	1712	1132	1536	9.744313	9.175474	7.096133	34.52564	29.6463	35.58572
protein_co	coiled-coil_	400	366	237	379	337	435	5.913543	6.376406	4.617118	4.847189	5.597147	6.391263
protein_co	retbindin	3	0	0	3	0	0	0.076504	0	0	0.066183	0	0
protein_co	matrilin_3	323	226	283	111	90	128	6.774937	5.586223	7.822111	2.014136	2.120774	2.668224
protein_co	tripartite_r	371	296	266	550	350	383	10.20848	9.598112	9.645028	13.0922	10.81942	10.47359
protein_co	spermatoge	53	73	63	90	67	65	0.564221	0.915806	0.88379	0.828856	0.801304	0.687696
protein_co	leucine_ric	2611	2139	1819	2417	1644	1976	31.02782	29.95451	28.48472	24.84758	21.94802	23.33678
protein_co	LIM_homeo	0	0	0	13	14	2	0	0	0	0.144476	0.202054	0.025535
protein_co	growth_arr	0	0	0	0	3	0	0	0	0	0	0.0592	0
protein_co	chaperonin	9	6	9	19	15	19	0.142102	0.111639	0.187256	0.259523	0.266072	0.298141
protein_co	acetyl-CoA_	1891	1610	1863	1754	1881	1671	10.04933	10.08274	13.04648	8.06377	11.23009	8.825344
protein_co	DEAH_(Asp	1640	1311	1183	3946	2597	3058	21.09921	19.87614	20.05588	43.91798	37.53559	39.09934
protein_co	v-raf-1_mu	1321	1056	1023	2358	1485	1721	21.19244	19.96407	21.62662	32.7254	26.76416	27.43902
protein_co	solute_carr	0	0	0	2	5	12	0	0	0	0.021322	0.069222	0.146967
protein_co	peroxisome	295	268	277	379	246	314	7.697187	8.240469	9.524115	8.554847	7.210979	8.142342
protein_co	nucleopori	79	41	68	1710	1769	1636	0.581607	0.355708	0.6597	10.89085	14.63119	11.97004
protein_co	Fc_recepto	0	0	0	3	3	8	0	0	0	0.047329	0.061463	0.144992
protein_co	hydroxyste	161	134	109	614	318	400	3.354388	3.290026	2.9926	11.06672	7.443267	8.282416
protein_co	enolase_su	662	588	364	776	532	653	8.504474	8.901719	6.162056	8.624108	7.678036	8.337048
lincRNA	long_interg	0	0	0	2	0	0	0	0	0	0.0451	0	0
protein_co	elastin_mic	1381	1217	1128	2457	2179	2293	12.37081	12.84702	13.31523	19.04026	21.9286	20.41354
protein_co	ADP-ribosy	1322	1036	928	1356	915	1214	27.52182	25.41631	25.45825	24.42128	21.4001	25.11736
protein_co	tripartite_r	966	794	727	1480	1194	1121	15.0459	14.57366	14.92142	19.94186	20.89269	17.35227
protein_co	cyclic_nucl	2	2	3	0	0	3	0.056834	0.066976	0.11234	0	0	0.084725
protein_co	tripartite_r	811	709	684	227	195	221	14.36438	14.79856	15.96457	3.478204	3.880162	3.890166
protein_co	ribosomal_	380	313	259	557	418	487	3.066704	2.976732	2.754373	3.888718	3.789776	3.905952
protein_co	translocase	519	414	345	842	593	587	9.67478	9.094549	8.474765	13.57841	12.41874	10.87481
protein_co	EFR3_homo	682	562	727	1512	1225	1106	6.639529	6.447573	9.326573	12.73408	13.39794	10.70083
protein_co	pentatricop	761	755	689	2079	1399	1516	5.982788	6.994763	7.137942	14.13958	12.35622	11.8448
protein_co	inner_mem	1453	1203	1147	3685	2105	2183	25.63254	25.00914	26.66394	56.23758	41.71836	38.27273
protein_co	mitochond	482	472	400	1354	862	988	6.846675	7.900995	7.487339	16.63851	13.7559	13.94759
protein_co	IQ_motif_c	2	1	0	53	64	61	0.031739	0.018701	0	0.72762	1.141025	0.962067

protein_co	integrin-lin	357	279	206	1066	632	796	7.129361	6.565891	5.421062	18.41631	14.17909	15.79811
protein_co	period_circ	154	124	141	174	138	170	1.276885	1.211602	1.540583	1.248083	1.285462	1.400844
protein_co	receptor_((	158	151	85	10	5	9	9.191953	10.35225	6.516351	0.503285	0.326791	0.520359
protein_co	selenocyste	58	34	20	108	102	119	0.541739	0.374238	0.246165	0.872668	1.070315	1.104635
protein_co	protein_tyr	0	1	0	57	66	62	0	0.010877	0	0.455115	0.684346	0.568701
protein_co	RAN_membi	6549	5791	4904	19253	11205	14282	130.2933	135.7713	128.5679	331.3665	250.4426	282.3878
protein_co	protein_kir	789	721	816	1250	955	852	8.2096	8.840714	11.18845	11.2517	11.16342	8.810372
protein_co	caspase_rec	44	26	30	25	26	22	0.551861	0.384288	0.49583	0.271256	0.366352	0.274226
protein_co	RAP1_GTPa	6	24	6	103	114	105	0.047687	0.224787	0.06284	0.708195	1.017903	0.829376
protein_co	clustered_r	1860	1532	1213	3524	3195	3914	18.78486	18.23312	16.14324	30.78889	36.25058	39.28489
protein_co	inositol_pc	221	147	160	468	292	344	3.663106	2.87132	3.494717	6.710672	5.437373	5.666635
protein_co	MYB_bindi	1313	1058	832	3391	3194	3393	14.46048	13.73127	12.07469	32.3079	39.51864	37.1374
protein_co	replication	1239	1001	943	3769	3133	2884	15.1138	14.38943	15.15824	39.77329	42.93503	34.96288
protein_co	serpin_pep	2921	2708	2067	210	149	184	99.89706	109.1382	93.15291	6.21303	5.724749	6.253866
protein_co	ubiquitin-c	889	892	833	2772	1979	2193	11.84312	14.00349	14.62325	31.94629	29.61823	29.03438
protein_co	eukaryotic_	248	222	158	504	287	316	5.892893	6.216372	4.947306	10.36026	7.661395	7.462316
protein_co	TBC1_dom	297	260	281	325	434	308	3.192584	3.293565	3.980402	3.022263	5.241127	3.290381
protein_co	transmemb	207	162	154	519	354	419	6.30903	5.818545	6.185115	13.6843	12.12117	12.69159
protein_co	coenzyme_	69	100	63	191	127	183	2.736276	4.673238	3.2922	6.552503	5.658009	7.212263
protein_co	PNN-intera	1397	1265	1212	1687	1319	1445	14.46764	15.43828	16.54012	15.114	15.346	14.87232
protein_co	popeye_do	39	32	22	49	29	21	1.535092	1.484318	1.141109	1.66851	1.28238	0.821483
protein_co	Sec61_gam	4050	3469	2293	3008	2535	3270	174.7441	176.3839	130.3726	112.2764	122.8781	140.2184
protein_co	LanC_lantib	334	339	308	569	421	362	4.062093	4.85859	4.936157	5.986579	5.752208	4.375439
protein_co	fidgetin-lik	40	23	39	669	478	430	0.572335	0.387816	0.735343	8.280937	7.683646	6.114606
protein_co	dopa_deca	0	0	0	0	1	0	0	0	0	0	0.029141	0
protein_co	G-rich_RNA	2719	2371	2257	3762	2749	2955	21.59414	22.19041	23.62072	25.84691	24.52735	23.32351
protein_co	enamelin	0	0	0	2	2	1	0	0	0	0.016129	0.020946	0.009265
protein_co	immunoglo	11	4	3	0	0	0	0.404973	0.17354	0.145542	0	0	0
protein_co	ankyrin_rep	1930	1690	1987	2257	2284	1745	9.474788	9.777009	12.8542	9.585324	12.59672	8.513679
protein_co	UTP3_smal	755	656	591	1209	1043	1239	19.29076	19.7521	19.8987	26.7234	29.93889	31.46178
protein_co	integrin_be	1827	1401	1133	5173	5741	5939	16.34114	14.76689	13.35391	40.02665	57.68732	52.79183
protein_co	WW_doma	1455	1116	978	1259	948	1077	20.7179	18.72639	18.35086	15.50856	15.16492	15.24081
protein_co	H3_histone	6715	5572	4976	13352	9694	12004	127.5561	124.7307	124.5576	219.4141	206.8746	226.6161
protein_co	unkempt_h	642	521	398	471	475	632	8.394201	8.027663	6.857443	5.327559	6.977293	8.212418
protein_co	tripartite_r	232	168	117	14	7	14	5.420261	4.625392	3.602076	0.282959	0.18373	0.325065
protein_co	zinc_finger_	1223	1093	1241	1824	1373	1369	17.6086	18.54495	23.54534	22.71885	22.20844	19.58897
protein_co	ankyrin_rep	0	0	0	0	5	1	0	0	0	0	0.07502	0.013273
protein_co	eukaryotic_	7447	5944	4897	16478	12143	17612	260.921	245.422	226.0958	499.4536	477.9722	613.2618
protein_co	lysine_(K)-s	1773	1601	1149	1270	1499	1584	13.98248	14.879	11.94071	8.664473	13.28086	12.41482
protein_co	C-type_lect	1	0	0	0	0	0	0.029412	0	0	0	0	0
protein_co	solute_carr	0	1	1	0	1	6	0	0.020872	0.02334	0	0.019898	0.105615
protein_co	guanylate_(	1	0	0	1	0	0	0.014316	0	0	0.012385	0	0
protein_co	G_protein_	5	1	2	2	1	1	0.133892	0.031557	0.070575	0.046332	0.030084	0.026613
protein_co	discs_large_	2111	1883	1238	515	399	590	28.11533	29.55373	21.72753	5.933695	5.970035	7.809381

protein_co	heat-respor	210	203	156	447	238	394	10.51808	11.98175	10.29619	19.36813	13.39193	19.61205
protein_co	vacuolar_p	739	613	782	345	353	349	2.762952	2.700825	3.852746	1.115863	1.482698	1.296773
protein_co	regulator_c	0	3	0	0	4	3	0	0.043567	0	0	0.055378	0.036742
protein_co	matrilin_2	700	542	677	827	689	732	9.018909	8.229289	11.49422	9.21774	9.972963	9.372958
protein_co	receptor_a	401	400	317	77	60	59	9.783105	11.50004	10.19123	1.625122	1.644495	1.43052
protein_co	pterin-4_al	79	91	67	227	176	177	0.744056	1.010013	0.83155	1.849556	1.86226	1.656767
protein_co	stromal_ce	781	677	603	1007	622	870	26.36921	26.93654	26.82861	29.41294	23.59313	29.19274
protein_co	flotillin_2	1598	1223	1086	3967	2729	3314	30.69656	27.68512	27.49018	65.92317	58.89324	63.26668
protein_co	Era_G-prot	552	453	415	1715	858	1137	15.181	14.68137	15.03988	40.80266	26.50927	31.07645
protein_co	protein_arg	584	522	332	1502	1157	1360	7.295314	7.684378	5.465175	16.2317	16.23729	16.88417
protein_co	NIP7_nucle	502	414	376	1683	1044	1352	11.06427	10.75292	10.92048	32.08974	25.85048	29.61457
protein_co	telomeric_	402	330	324	677	432	549	7.134522	6.90176	7.577373	10.39419	8.613341	9.683243
protein_co	vacuolar_p	1066	818	717	1854	1218	1613	24.23147	21.91205	21.47715	36.45821	31.10419	36.43901
protein_co	metastasis_	993	861	708	666	1007	908	10.53093	10.76038	9.894312	6.11019	11.99765	9.570024
protein_co	heat_shock	43	31	26	7	6	10	0.722457	0.61378	0.575641	0.101743	0.113252	0.166976
protein_co	ankyrin_rep	18	13	9	176	168	119	0.253306	0.215588	0.166898	2.142639	2.656022	1.664293
protein_co	SCP2_stero	0	0	0	0	3	0	0	0	0	0	0.268716	0
protein_co	PC-esterase	1057	988	735	424	285	383	27.75726	30.57494	25.43453	9.632309	8.408054	9.995626
protein_co	synaptoson	62	57	58	123	73	67	1.454939	1.576286	1.79356	2.497015	1.924531	1.562563
protein_co	BTB_(POZ)_	476	396	476	2458	2338	2224	4.90557	4.809332	6.464341	21.91429	27.06924	22.7786
protein_co	proliferatin	1320	1034	924	6347	4060	4708	51.42172	47.46793	47.43287	213.8967	177.6838	182.2715
protein_co	NTF2-like_e	215	205	122	519	323	415	10.13563	11.38868	7.578914	21.16619	17.10661	19.4433
protein_co	polymerase	214	175	156	558	341	453	4.68931	4.518979	4.504583	10.57773	8.394573	9.865134
protein_co	Ras_and_Ra	951	722	846	225	228	180	11.17578	9.998655	13.10094	2.287404	3.010102	2.102226
protein_co	protein_tyr	2389	2130	1825	1610	1156	1205	33.9533	35.67406	34.17933	19.79496	18.45749	17.02012
protein_co	death_asso	1375	1122	1019	2536	1645	2051	34.84627	33.50839	34.03005	55.59886	46.83479	51.65697
protein_co	Rh_family_	0	0	0	0	0	3	0	0	0	0	0	0.06509
protein_co	KIAA0907	669	680	509	1053	917	1092	7.872311	9.429575	7.892756	10.71933	12.12256	12.77051
protein_co	ATPase_Na-	0	0	3	4	0	3	0	0	0.053445	0.046781	0	0.040307
protein_co	nestin	254	258	208	6740	8655	11905	2.419398	2.896012	2.610789	55.53879	92.61678	112.6971
protein_co	brevican	5	16	5	24	18	22	0.076482	0.288415	0.100785	0.317588	0.309323	0.334444
protein_co	Rho_guanir	974	678	761	1200	1183	1323	7.485053	6.140061	7.706468	7.977745	10.21339	10.10428
protein_co	RAB25_mer	5	3	2	1843	1162	1557	0.240641	0.170148	0.126842	76.73398	62.8282	74.4728
protein_co	hyaluronan	0	0	0	0	1	0	0	0	0	0	0.033583	0
protein_co	DDB1_and_	506	397	390	688	544	631	6.524146	6.032131	6.626322	7.674049	7.879907	8.085598
protein_co	synaptotag	634	434	517	185	152	118	6.405456	5.167228	6.883133	1.616946	1.725256	1.18482
protein_co	immunoglo	338	292	212	405	387	509	4.51756	4.599146	3.733859	4.682796	5.810952	6.761058
protein_co	aldehyde_d	0	0	0	71	58	60	0	0	0	1.227528	1.302228	1.191711
protein_co	metallothio	24	23	3	166	125	111	0.363543	0.410563	0.059883	2.175284	2.127179	1.671004
protein_co	methylmal	120	124	95	217	184	231	2.131137	2.595129	2.223251	3.333902	3.671107	4.077104
protein_co	DPH2_hom	276	274	197	1301	999	1131	5.910888	6.915145	5.559614	24.10371	24.03578	24.0722
protein_co	target_of_E	138	91	102	456	375	508	3.058124	2.376427	2.978591	8.741859	9.335902	11.18792
protein_co	nuclear_au	1731	1486	1312	7616	6652	7456	25.04533	25.33702	25.01487	95.32781	108.1262	107.2125
protein_co	mutY_hom	154	146	88	380	239	344	4.226497	4.721933	3.182565	9.022076	7.368971	9.382703

protein_co	catenin_be	1893	1652	1295	1186	922	1023	33.51749	34.46974	30.2152	18.16639	18.34007	18.0014
protein_co	lipin_3	22	32	20	176	178	233	0.26695	0.457577	0.319795	1.847492	2.426476	2.809781
protein_co	zinc_finger_	46	25	45	71	70	72	0.878213	0.562457	1.132112	1.172637	1.501375	1.366106
protein_co	RNA_bindir	279	232	189	1525	1248	1388	6.200897	6.076387	5.535374	29.3213	31.16119	30.6584
protein_co	V-set_and_t	956	677	533	55	44	37	25.83542	21.56023	18.98103	1.285829	1.335855	0.993731
protein_co	chromoson	323	300	217	810	536	637	10.58165	11.58188	9.367965	22.95613	19.72716	20.73957
protein_co	serine_incc	2172	1923	1738	1353	1122	1212	25.86903	26.99024	27.27752	13.94059	15.01282	14.34606
protein_co	protein_ph	201	169	184	261	189	153	3.076363	3.048143	3.711027	3.455772	3.249768	2.327248
protein_co	dimethylgl	0	0	0	6	0	4	0	0	0	0.088729	0	0.067955
protein_co	adaptor-rel	1714	1503	1624	1622	1289	1177	15.54314	16.06179	19.40657	12.72453	13.13197	10.60753
protein_co	zinc_finger_	368	296	285	103	106	78	3.15656	2.992023	3.221409	0.764304	1.021459	0.664922
protein_co	InaD-like_(I	59	70	65	704	669	594	0.367257	0.513479	0.53317	3.790997	4.678353	3.674632
protein_co	KN_motif_a	12	7	12	285	318	281	0.136183	0.093615	0.179455	2.798004	4.054307	3.169249
protein_co	angiopoieti	2	0	2	3	2	0	0.037748	0	0.049742	0.048983	0.042407	0
protein_co	solute_carr	6	2	3	0	0	0	0.076229	0.029944	0.050226	0	0	0
protein_co	F-box_prot	553	483	356	242	135	186	8.818184	9.076287	7.480641	3.338354	2.418448	2.947655
protein_co	REM2_and_	60	68	42	58	67	78	2.055961	2.745868	1.896478	1.719312	2.579215	2.656243
protein_co	caspase_9_	191	123	107	210	167	190	2.26568	1.719402	1.672568	2.155001	2.225516	2.239899
protein_co	neuromedi	2	0	0	0	0	0	0.051077	0	0	0	0	0
protein_co	dynactin_4	1229	1052	1242	1008	909	855	15.46209	15.59693	20.59078	10.97084	12.84782	10.69035
protein_co	phosphodi	0	0	0	0	6	0	0	0	0	0	0.06254	0
protein_co	ATPase_am	4	1	6	12	2	15	0.022116	0.006516	0.043716	0.057398	0.012423	0.082424
protein_co	microtubul	19	11	14	18	6	4	0.211898	0.144568	0.205748	0.173663	0.075175	0.044335
protein_co	zinc_finger_	201	156	142	252	147	182	3.256163	2.978117	3.03133	3.531617	2.675324	2.930158
protein_co	ubiquitin_s	260	236	247	516	384	376	3.608982	3.860384	4.517968	6.196181	5.988136	5.186912
protein_co	exportin_4	510	415	521	1289	971	902	2.731678	2.619477	3.677324	5.972763	5.842889	4.801485
protein_co	proteasom	1674	1531	1227	3530	2298	3483	62.06108	66.88768	59.94366	113.2144	95.71124	128.3296
protein_co	cyclin-depe	305	258	231	546	497	419	5.285435	5.268751	5.275063	8.185336	9.675788	7.216133
protein_co	arachidona	0	3	0	14	17	9	0	0.208655	0	0.71481	1.127191	0.5279
pseudogen	high_mobil	77	65	67	180	174	331	4.138535	4.116957	4.74532	8.369343	10.50641	17.68046
protein_co	WAS_prote	499	475	471	366	328	303	5.49793	6.167361	6.838399	3.488533	4.059959	3.317806
protein_co	ring_finger_	1	0	0	0	5	2	0.010342	0	0	0	0.058093	0.020556
protein_co	G_protein-r	0	0	0	1	0	0	0	0	0	0.009451	0	0
protein_co	cholinergic	0	1	2	73	76	71	0	0.007107	0.015895	0.380875	0.514943	0.425564
protein_co	myosin_hea	0	0	0	0	0	2	0	0	0	0	0	0.017419
protein_co	myosin_hea	3400	2897	2980	4355	5125	4597	23.18982	23.28488	26.78364	25.69624	39.27004	31.16037
protein_co	phosphatid	192	191	150	319	124	180	9.680639	11.34863	9.966183	13.91414	7.023823	9.019551
protein_co	SCO1_cyto	280	215	173	694	501	532	8.475402	7.669161	6.900542	18.17292	17.03684	16.00382
protein_co	myosin_ph	5661	4726	4433	5902	5888	5880	27.3448	26.90186	28.21721	24.66288	31.95203	28.22725
protein_co	chitinase_3	1	2	1	0	0	0	0.027573	0.064987	0.036335	0	0	0
protein_co	myosin_bir	0	0	0	5	0	3	0	0	0	0.126867	0	0.087447
protein_co	phosphatid	338	319	271	351	431	469	2.328136	2.589342	2.459777	2.091519	3.33517	3.210511
protein_co	dual_serine	553	416	520	430	376	416	3.718106	3.296075	4.607176	2.501083	2.8401	2.779711
protein_co	chitinase_1	0	4	0	0	0	0	0	0.044507	0	0	0	0

protein_co solute_carr	598	550	430	526	576	613	6.335544	6.86677	6.003244	4.820937	6.855739	6.454355
protein_co leucine-rich	1	0	0	2	9	1	0.014842	0	0	0.025679	0.150065	0.01475
protein_co transmemb	48	54	53	153	111	149	0.67982	0.901267	0.989153	1.874594	1.766139	2.097243
protein_co doublecort	696	572	701	501	330	280	6.460973	6.25737	8.575147	4.023365	3.441531	2.58319
protein_co cyclin_A1	3	4	1	2	1	1	0.08095	0.127192	0.035557	0.046686	0.030314	0.026817
protein_co component	598	497	577	352	305	338	6.022202	5.898174	7.657107	3.066619	3.450667	3.382832
protein_co spastic_par	1502	1365	1240	1292	1213	1102	16.08361	17.22477	17.49726	11.96848	14.59229	11.72748
protein_co relaxin/insu	0	0	2	0	0	0	0	0	0.049778	0	0	0
protein_co epithelial_s	540	466	342	525	435	504	6.210762	6.316029	5.183368	5.223642	5.620687	5.760913
protein_co transient_r	3	5	1	123	64	49	0.039129	0.076851	0.017187	1.387846	0.937782	0.635154
protein_co periostin_o	1280	1183	1087	7299	5501	5372	20.09027	21.88102	22.48227	99.1065	96.99882	83.79564
protein_co regulatory_	97	82	78	177	193	183	2.228853	2.220397	2.361778	3.518405	4.982141	4.178981
protein_co tumor_pro	52390	46441	34519	38906	26806	30602	1498.422	1565.288	1301.004	962.643	861.3244	869.8515
protein_co KIAA1704	468	400	367	542	438	423	5.770001	5.811619	5.962535	5.780859	6.06671	5.182986
protein_co stomatin_(l	0	0	0	0	0	1	0	0	0	0	0	0.024806
protein_co klotho	6	1	0	132	156	151	0.063453	0.012463	0	1.207642	1.853425	1.58704
protein_co replication_	109	117	109	1796	1169	1274	2.402401	3.038869	3.165778	34.24431	28.94561	27.90604
protein_co StAR-relate	856	798	904	290	286	276	7.658863	8.413961	10.65844	2.244665	2.874787	2.454196
protein_co insulin_rec	0	0	4	1	0	2	0	0	0.070826	0.011624	0	0.026708
protein_co MORC_fam	399	380	371	430	342	371	5.509509	6.183447	6.750698	5.136549	5.305364	5.09124
protein_co brain_expr	0	2	1	99	119	133	0	0.115855	0.064776	4.209927	6.571619	6.497371
protein_co ring_finger_	17	9	17	34	38	38	0.319488	0.199322	0.421007	0.552773	0.802302	0.709739
protein_co TBC1_dom	471	537	498	51	33	32	4.36159	5.860103	6.076983	0.408561	0.34331	0.294499
protein_co transcriptic	2110	1810	1416	705	753	1027	71.10471	71.87892	62.88021	20.55266	28.50755	34.39505
protein_co testis_expr	0	0	0	0	0	1	0	0	0	0	0	0.038154
protein_co brain_expr	3	10	5	91	102	105	0.183823	0.72208	0.403723	4.823727	7.021462	6.394069
protein_co family_with	215	165	205	402	353	312	3.972884	3.593011	4.991788	6.426234	7.328097	5.729698
protein_co solute_carr	242	206	166	189	182	208	4.655422	4.670012	4.208105	3.145346	3.933364	3.976643
protein_co EPH_recept	230	164	204	54	37	46	2.623665	2.204608	3.066518	0.53289	0.474167	0.521492
protein_co serine/argi	1778	1376	1403	3730	3807	3334	23.46774	21.40252	24.40236	42.59036	56.45096	43.73354
protein_co BTB_(POZ)_	2590	2224	1512	2216	1471	1613	49.80646	50.39968	38.31532	36.86537	31.77954	30.8269
protein_co PML-RARA_	5	8	1	7	0	2	0.099252	0.18714	0.026158	0.120207	0	0.039456
protein_co suppressor_	93	84	54	242	195	281	2.133238	2.270611	1.632243	4.802138	5.025045	6.405783
protein_co zinc_finger_	233	182	144	496	245	311	8.810894	8.110405	7.175652	16.2259	10.40829	11.68784
protein_co phosphodi	2	1	0	31	36	29	0.032281	0.019021	0	0.432856	0.652784	0.465185
protein_co HSPA_(heat	1081	782	575	2395	1567	2017	32.36947	27.59457	22.68885	62.04094	52.71423	60.02406
protein_co casein_kina	2494	1906	1622	3089	2181	2709	45.87729	41.31724	39.3176	49.15664	45.07192	49.52448
protein_co ankyrin_rep	122	110	85	398	252	249	1.093785	1.162176	1.004213	3.086869	2.538176	2.218611
protein_co CNDP_dipe	1227	1103	949	4890	3668	4173	14.36184	15.21416	14.63749	49.51507	48.23296	48.54266
protein_co MACRO_do	125	128	96	127	93	116	5.491804	6.627078	5.557905	4.826939	4.590258	5.064921
protein_co WD_repeat	357	263	247	628	522	782	10.88706	9.451597	9.925997	16.56781	17.88389	23.70057
protein_co lectin_gala	2	1	0	0	0	0	0.058305	0.034354	0	0	0	0
protein_co reticulon_3	2135	1862	1656	3051	2239	2636	22.89427	23.52966	23.40044	28.30311	26.97318	28.09209
protein_co retinoic_ac	23	9	9	3	8	6	1.298127	0.598603	0.669371	0.146478	0.507257	0.33655

protein_co	HRAS-like_s	0	0	0	0	2	2	0	0	0	0	0.160312	0.141817
protein_co	myosin_hea	33	17	18	39	22	41	0.252428	0.153243	0.181439	0.258078	0.189058	0.311686
protein_co	FGFR1OP_N	486	477	397	1215	834	844	11.30959	13.08086	12.17408	24.45964	21.80348	19.51923
protein_co	mediator_c	692	544	464	1001	632	941	32.10795	29.74489	28.36999	40.17941	32.94372	43.3916
protein_co	PDZ_domai	41	36	37	43	45	41	0.185456	0.191897	0.220544	0.168263	0.228675	0.184311
protein_co	MORC_fam	1024	885	790	1068	1093	1019	12.13058	12.3547	12.33229	10.94501	14.54625	11.9968
protein_co	like-glycosy	368	373	327	644	660	503	4.418754	5.277982	5.174097	6.689611	8.903177	6.002465
protein_co	glutathione	0	0	0	1	0	3	0	0	0	0.041673	0	0.143623
protein_co	myosin_XV	0	0	0	0	1	1	0	0	0	0	0.006944	0.006143
protein_co	solute_carr	147	132	107	306	239	328	2.417622	2.558304	2.318941	4.35367	4.415888	5.361109
protein_co	C1q_and_tu	369	367	252	1269	896	1085	3.904703	4.576513	3.513961	11.61679	10.65169	11.4104
protein_co	gamma-glu	0	0	0	3	4	3	0	0	0	0.058071	0.100551	0.066713
protein_co	family_with	0	0	0	120	84	127	0	0	0	2.653727	2.41235	3.226453
pseudogen	zinc_finger_	0	3	0	614	449	542	0	0.078574	0	11.80543	11.21104	11.97179
protein_co	aarF_doma	123	103	97	337	255	282	2.739479	2.703381	2.846882	6.493156	6.380462	6.24197
protein_co	makorin_ri	1218	1023	1005	1087	1040	1301	18.59883	18.40861	20.2227	14.35922	17.84106	19.74355
protein_co	ArfGAP_wit	1307	1155	882	2286	1775	2272	18.44678	19.2103	16.40395	27.91157	28.14443	31.8686
protein_co	KRAB-A_do	334	365	231	337	252	300	4.399675	5.665967	4.009783	3.840316	3.729269	3.927399
pseudogen	zinc_finger_	189	181	168	234	204	212	2.84257	3.208005	3.329611	3.044586	3.4469	3.168801
protein_co	ARP3_actin	184	143	158	326	231	279	1.757377	1.609498	1.988562	2.693567	2.47861	2.648263
protein_co	neurotensi	0	2	1	557	467	549	0	0.100869	0.056397	20.62247	22.45372	23.35094
protein_co	B-cell_trans	1088	1070	784	782	566	680	23.52933	27.26915	22.34249	14.63021	13.75138	14.61501
protein_co	leucine-rich	7	6	9	42	32	30	0.068704	0.069397	0.116401	0.35661	0.352842	0.292625
protein_co	chromoson	239	196	214	419	296	321	4.109418	3.971418	4.848763	6.232459	5.717724	5.485258
protein_co	ATPase_typ	527	426	576	1257	1297	1059	3.613977	3.442639	5.205136	7.457153	9.992262	7.217394
protein_co	surfactant_	0	0	0	0	0	1	0	0	0	0	0	0.041073
protein_co	DPY30_dor	0	0	0	4	0	4	0	0	0	0.081276	0	0.09337
protein_co	transmemb	247	199	183	604	379	431	6.30493	5.986094	6.155584	13.33777	10.86855	10.93378
protein_co	transmemb	1118	869	1184	882	873	706	6.722093	6.15729	9.381002	4.587693	5.896931	4.218685
protein_co	v-Ki-ras2_K	787	597	752	1456	1401	1144	7.227157	6.46062	9.100085	11.5669	14.45373	10.44067
protein_co	importin_8	1033	808	1092	1488	1399	1280	10.27006	9.466532	14.30639	12.79789	15.62569	12.64713
protein_co	leucyl-tRNA	2227	1850	1761	3045	2437	2138	24.73764	24.21681	25.77699	29.26095	30.41184	23.60236
protein_co	serine_pept	59	59	56	77	54	78	0.854354	1.006804	1.068584	0.964583	0.878474	1.12251
protein_co	inositol(my	231	192	223	587	417	453	4.546234	4.452953	5.78335	9.994036	9.219873	8.860284
protein_co	leucine_ric	39	30	42	392	274	263	0.459537	0.416566	0.652138	3.995809	3.627065	3.07979
protein_co	E2F_transcr	150	116	116	1063	671	732	1.576876	1.437049	1.606938	9.667243	7.924611	7.647634
protein_co	carbonic_a	1	0	2	0	0	1	0.019009	0	0.050099	0	0	0.018892
protein_co	coiled-coil_	246	231	172	777	420	594	6.198708	6.859384	5.711225	16.93753	11.88952	14.87518
protein_co	SWAP_swit	514	416	494	1586	1538	1484	5.573878	5.31612	7.05921	14.87855	18.73698	15.99329
protein_co	aryl_hydro	114	81	123	129	124	157	1.562733	1.308495	2.221876	1.529793	1.909636	2.138893
protein_co	lymphatic_	707	584	521	17	39	15	11.43577	11.13182	11.105	0.23788	0.708696	0.241128
protein_co	adenosine_	145	109	106	56	75	45	1.921994	1.70262	1.851504	0.642148	1.116849	0.592797
protein_co	MICAL_C-te	4	2	4	4	19	18	0.069568	0.040991	0.091673	0.060183	0.371236	0.311121
protein_co	SET_bindin	539	544	655	485	469	358	3.835891	4.562297	6.14262	2.985948	3.749725	2.532038

protein_co	microtubul	894	664	846	871	568	575	7.504241	6.568171	9.357815	6.324853	5.356322	4.796746
protein_co	related_RA	409	401	382	2128	1365	1738	9.182725	10.60962	11.30177	41.33167	34.42944	38.77999
protein_co	hydroxyste	1209	981	1069	1630	1348	1475	11.55337	11.04736	13.46154	13.47513	14.47176	14.00825
protein_co	zinc_finger_	649	546	741	676	616	592	4.522668	4.483836	6.804606	4.075301	4.822583	4.099976
protein_co	testis_expr	23	12	20	69	37	25	0.119529	0.073491	0.136965	0.310211	0.216021	0.129121
protein_co	transmemb	2542	2041	2058	2190	1781	1748	62.47725	59.11484	66.65405	46.56435	49.1767	42.69701
protein_co	ring_finger_	273	212	176	111	98	104	7.737094	7.080406	6.572986	2.721455	3.120257	2.929262
protein_co	dual_specif	0	0	0	4	2	2	0	0	0	0.100162	0.065037	0.057533
protein_co	D4_zinc_an	1479	1327	1045	1550	1265	1364	16.17763	17.10507	15.06253	14.667	15.54484	14.8276
protein_co	multiple_e	985	946	697	1788	1469	1717	16.49174	18.66502	15.37793	25.89767	27.63128	28.56999
protein_co	chromoson	1871	1630	1559	1909	1111	1352	37.61967	38.6221	41.30686	33.20551	25.09599	27.01641
protein_co	goosecoid_	15	8	6	0	0	0	0.630751	0.396427	0.33247	0	0	0
protein_co	chromoson	65	54	53	87	103	104	1.119078	1.095589	1.202424	1.295774	1.992201	1.779467
protein_co	unc-79_ho	21	6	5	20	15	18	0.122172	0.041135	0.038331	0.100657	0.098037	0.104072
protein_co	numb_hom	749	653	716	1136	970	938	7.666822	7.876873	9.657871	10.05947	11.15461	9.542146
protein_co	catsper_ch	5	0	0	0	5	8	0.073062	0	0	0	0.082081	0.116178
protein_co	vertebrae_	0	0	0	0	1	0	0	0	0	0	0.01716	0
protein_co	COX16_cyt	102	98	71	164	101	101	3.14501	3.560861	2.884795	4.374502	3.498583	3.094944
protein_co	tetratricop	42	29	27	468	482	500	0.426207	0.346798	0.361052	4.10847	5.494996	5.042558
protein_co	mediator_c	244	162	171	799	483	544	6.474989	5.066071	5.97971	18.34252	14.39943	14.34689
protein_co	eukaryotic_	1293	1143	1193	3552	2538	2817	15.26259	15.89948	18.55688	36.27151	33.65661	33.04655
protein_co	ADAM_met	2	1	0	0	2	1	0.037883	0.022321	0	0	0.042559	0.018824
protein_co	lysyl_oxida	11743	9798	8331	4767	2970	3559	175.1722	172.2387	163.7638	61.51687	49.77275	52.7623
protein_co	elongator_	662	551	465	891	752	742	10.15265	9.95818	9.397429	11.82121	12.95651	11.30928
protein_co	CBP80/20-	1519	1246	1126	504	457	611	13.98563	13.51915	13.66147	4.014374	4.727042	5.590815
protein_co	maestro	14	14	17	4	1	4	0.348132	0.410253	0.557058	0.086048	0.027936	0.098852
protein_co	methyl-CpG	642	518	447	1224	700	750	8.330421	7.920795	7.643183	13.73967	10.2042	9.6717
protein_co	immediate_	346	316	266	605	376	618	12.36839	13.31163	12.53007	18.70921	15.0999	21.95509
protein_co	mitochond	210	216	187	334	261	420	8.645108	10.47881	10.14443	11.89489	12.07093	17.18344
protein_co	cyclin_B1	965	755	758	7129	4517	5353	23.55374	21.71634	24.38016	150.5304	123.8602	129.8492
protein_co	cyclin-depe	476	395	402	1067	787	1007	17.31953	16.93687	19.2748	33.58586	32.17014	36.41399
protein_co	CD180_mo	7	0	0	0	0	1	0.135945	0	0	0	0	0.019301
protein_co	interleukin	72	76	57	42	26	37	1.094387	1.361317	1.14169	0.552269	0.443978	0.55892
protein_co	calcium/ca	29	25	29	8	9	13	1.03178	1.048181	1.359634	0.246231	0.359733	0.459666
protein_co	THUMP_do	352	312	309	657	539	531	4.704678	4.914156	5.442276	7.596536	8.093289	7.053285
protein_co	von_Hippel	1274	1280	963	2316	1467	1871	18.04839	21.36909	17.97753	28.3838	23.34792	26.34222
protein_co	basic_helix	640	504	429	836	705	631	9.755899	9.053676	8.617463	11.02444	12.07329	9.559305
protein_co	ADP-ribosy	1412	1173	1182	1852	1362	1468	24.8761	24.35301	27.441	28.22615	26.95714	25.70297
protein_co	ER_degrada	1105	953	964	856	870	824	9.518353	9.673854	10.94237	6.378761	8.419142	7.054015
protein_co	contactin_	0	0	0	26	22	30	0	0	0	0.263854	0.289934	0.34975
protein_co	cell_adhesi	0	0	0	5	2	0	0	0	0	0.028578	0.014845	0
protein_co	Meis_home	1450	1220	1300	1295	1124	1103	15.93284	15.79764	18.82363	12.31	13.87525	12.0451
protein_co	ATP_bindin	12	14	25	131	92	94	0.184785	0.254051	0.507296	1.745101	1.59156	1.438546
protein_co	katanin_p8	435	380	338	785	633	672	8.457338	8.70633	8.659563	13.20314	13.82602	12.98444

protein_co	ER_membr	821	793	675	1202	581	962	37.63165	42.83417	40.77075	47.66258	29.91819	43.82227
protein_co	transient_r	0	0	1	3	4	0	0	0	0.012207	0.024041	0.041628	0
protein_co	guanine_nu	43	32	30	11	15	11	1.700122	1.490969	1.563031	0.376242	0.666272	0.432229
protein_co	glutathione	0	0	1	1	6	3	0	0	0.060089	0.039448	0.307369	0.135954
protein_co	PRP38_pre	792	705	668	1652	1480	1495	11.24712	11.79811	12.5005	20.29501	23.61168	21.09925
protein_co	tetraspanin	10	10	9	621	523	561	0.166638	0.196373	0.19763	8.952194	9.790968	9.290677
protein_co	glutathione	542	538	420	102	60	97	6.95107	8.130959	7.098008	1.131659	0.864476	1.236328
protein_co	synaptotag	95	120	121	76	79	59	1.12944	1.681232	1.895656	0.781657	1.055153	0.69711
protein_co	vav_3_guar	24	17	17	57	43	32	0.254626	0.212543	0.23767	0.523154	0.512518	0.337405
protein_co	proline/ser	184	168	144	1207	923	1189	5.209167	5.604887	5.372146	29.56111	29.35629	33.45353
protein_co	3-hydroxy-	2	0	1	0	0	6	0.043609	0	0.028733	0	0	0.130018
protein_co	protein_tyr	0	0	0	2	0	0	0	0	0	0.025068	0	0
protein_co	sortilin_1	322	213	344	2677	2566	2600	2.425583	1.890806	3.414708	17.44503	21.71531	19.4645
protein_co	wingless-ty	197	138	195	34	42	13	2.731633	2.254978	3.56308	0.407848	0.654266	0.179147
protein_co	prostaglanc	2249	2047	2053	1829	2033	1765	19.2723	20.67136	23.18291	13.55879	19.57179	15.03137
protein_co	late_endos	349	276	278	847	426	660	10.0964	9.409297	10.59792	21.19764	13.84521	18.97556
protein_co	notch_2	5152	4479	5404	1926	2518	1945	23.94872	24.53549	33.10218	7.745078	13.14956	8.985365
protein_co	tripartite_r	68	65	55	235	231	274	1.024179	1.153685	1.091602	3.061947	3.908659	4.101351
protein_co	choline/eth	415	402	345	811	635	682	4.14538	4.73205	4.541195	7.008097	7.125888	6.770336
protein_co	CD101_mo	21	6	5	51	21	23	0.313437	0.105533	0.098341	0.658513	0.352127	0.341168
protein_co	V-set_dom	0	0	0	1093	856	830	0	0	0	19.1647	19.49134	16.71886
protein_co	nerve_grow	12	23	15	160	90	131	0.606774	1.370504	0.999474	6.998878	5.112543	6.583038
protein_co	adaptor-rel	148	141	145	222	164	137	2.780435	3.1216	3.589665	3.608005	3.461338	2.557887
protein_co	N-ethylmal	466	448	400	671	541	517	6.391322	7.240856	7.229356	7.961416	8.335873	7.047011
protein_co	spire_homo	325	218	295	159	147	152	3.037215	2.400799	3.632863	1.285441	1.543329	1.41171
protein_co	periphilin_	750	700	660	1250	912	1047	6.645313	7.309023	7.70607	9.581361	9.078165	9.219567
protein_co	FK506_bin	1418	1284	921	452	346	364	15.14431	16.16015	12.96187	4.176136	4.151436	3.863529
protein_co	ADP-ribosy	4384	3734	3176	8154	6493	8418	56.53918	56.74928	53.9752	90.97303	94.07482	107.894
protein_co	transmemb	282	247	220	1382	980	1171	9.854363	10.17146	10.13064	41.77828	38.47287	40.66736
protein_co	solute_carr	5018	4224	4878	4742	4725	4611	54.349	53.9128	69.62056	44.43093	57.49258	49.63244
pseudogen	pleckstrin_	37	46	38	204	128	210	1.065153	1.560541	1.441547	5.080466	4.139705	6.00813
protein_co	tyrosine_3-	7435	6303	5843	13936	10476	12150	177.6247	177.4503	183.9471	288.0206	281.1686	288.475
protein_co	kinase_D-in	1876	1711	1949	985	978	755	13.49237	14.50148	18.47149	6.128505	7.902112	5.396496
protein_co	grainyhead	2	0	2	385	256	318	0.019608	0	0.025838	3.265292	2.819599	3.098383
protein_co	Rho-associa	885	750	1010	2585	2341	1968	5.650359	5.642884	8.497457	14.27764	16.79126	12.48727
protein_co	radical_S-a	2	1	0	2	0	0	0.030089	0.017729	0	0.02603	0	0
protein_co	v-myc_mye	13	3	13	462	334	392	0.264502	0.071931	0.348548	8.131858	7.634495	7.926483
protein_co	lipin_1	880	736	851	399	295	326	8.576597	8.453124	10.92941	3.364095	3.230007	3.157618
protein_co	cytidine_m	5	8	7	17	21	21	0.091784	0.173059	0.169328	0.269966	0.433077	0.383112
protein_co	isoamyl_ac	319	327	243	351	213	262	6.046608	7.304256	6.06963	5.755609	4.535757	4.935511
protein_co	lactate_deh	19838	17386	13714	18733	12589	14541	434.7034	448.9541	395.999	355.1121	309.9099	316.6643
protein_co	serum_amy	0	0	2	0	0	0	0	0	0.136523	0	0	0
protein_co	anoctamin_	0	0	0	1	2	0	0	0	0	0.006895	0.017909	0
protein_co	interleukin	2007	1977	2277	1338	1136	889	11.73154	13.61826	17.53903	6.76592	7.459936	5.164391

protein_co	follistatin	404	369	268	882	608	858	8.427172	9.070556	7.366651	15.91593	14.24797	17.78678
protein_co	complemer	0	0	0	0	1	0	0	0	0	0	0.027308	0
protein_co	neuron_na	2945	2534	2839	1008	1156	878	11.9098	12.07627	15.12932	3.526491	5.252017	3.528771
protein_co	cell_divisio	640	558	635	1078	889	833	6.818723	7.005907	8.915211	9.935846	10.64079	8.820186
protein_co	translocase	985	911	827	1940	1481	1765	20.6686	22.52684	22.86731	35.21596	34.91234	36.8069
protein_co	crumbs_ho	3	1	0	2	0	0	0.017602	0.006914	0	0.010152	0	0
protein_co	endoplasm	2	0	0	3	0	2	0.029834	0	0	0.038714	0	0.02965
protein_co	ribosomal_	526	520	348	629	402	526	7.274546	8.474822	6.342117	7.525473	6.245904	7.229621
protein_co	asparaginyl	1902	1660	1639	4811	3268	3429	32.49234	33.4184	36.89642	71.09988	62.71936	58.21671
protein_co	KIAA1468	305	246	356	604	494	482	2.894247	2.75092	4.451645	4.958333	5.266374	4.545613
protein_co	F-box_prot	1166	1063	991	1296	1295	1408	16.67455	17.91414	18.67515	16.03333	20.80532	20.01096
protein_co	RNA_bindir	850	687	672	2777	2229	2684	11.99676	11.42638	12.49825	33.90657	35.34306	37.64759
protein_co	ankyrin_rep	99	109	54	204	86	109	1.914229	2.483661	1.375901	3.412336	1.868126	2.09457
protein_co	enoyl_CoA_	19	25	10	67	25	46	0.569258	0.882679	0.394812	1.736574	0.841482	1.369692
protein_co	interleukin	0	1	0	7	3	6	0	0.036591	0	0.188031	0.10465	0.185152
protein_co	cyclin_H	326	298	309	712	449	517	7.21822	7.775635	9.015832	13.63815	11.16884	11.37661
protein_co	histamine_	8	0	0	4	0	1	0.115466	0	0	0.049944	0	0.014344
protein_co	transmemb	349	333	304	339	248	312	6.282355	7.063963	7.211165	5.279099	5.01531	5.581633
protein_co	potassium_	232	280	225	1237	1058	1084	2.675885	3.805787	3.419769	12.34276	13.70926	12.42563
protein_co	Cdk5_and_	243	191	192	282	210	218	2.571904	2.382258	2.677839	2.582025	2.49699	2.293055
protein_co	dedicator_	40	25	23	90	47	64	0.347325	0.255813	0.263171	0.676054	0.458483	0.552288
protein_co	epithelial_r	5187	4624	4185	3188	2588	2926	99.63895	104.6738	105.9359	52.97783	55.85039	55.85947
protein_co	SRY_(sex_d	63	56	42	171	149	139	0.478588	0.501322	0.420442	1.123779	1.271619	1.049412
protein_co	RAS-like_es	801	724	665	27	11	23	18.73045	19.95085	20.49142	0.546188	0.288973	0.534507
protein_co	solute_carr	0	0	0	3	0	0	0	0	0	0.061641	0	0
protein_co	killer_cell_l	2	0	0	4	10	2	0.066259	0	0	0.114641	0.37219	0.06585
protein_co	chromoson	7	1	13	94	37	29	0.20086	0.033814	0.491557	2.333386	1.192742	0.826996
protein_co	proline-rich	5	2	0	4	0	2	0.393321	0.185402	0	0.272207	0	0.156357
protein_co	low_densit	209	204	199	209	236	290	1.370068	1.575916	1.719031	1.185237	1.738028	1.889311
protein_co	myosin_bir	0	0	1	0	0	0	0	0	0.016543	0	0	0
protein_co	damage-spe	628	482	459	828	665	812	18.01026	16.28975	17.34634	20.54252	21.42551	23.14334
protein_co	acid_phosp	403	410	266	860	565	583	9.684621	11.61097	8.423528	17.87883	15.2537	13.92374
protein_co	family_with	7125	5322	4175	3487	2047	2208	305.1817	268.6307	235.6486	129.2078	98.50097	93.99015
protein_co	RAB33A_m	14	8	13	18	24	25	0.589168	0.396742	0.720924	0.65531	1.134676	1.045589
protein_co	SRY_(sex_d	0	0	0	46	14	11	0	0	0	1.015791	0.401477	0.279052
protein_co	RNA_bindir	612	536	437	558	453	496	21.20412	21.8847	19.95193	16.72499	17.63259	17.07891
protein_co	Serine/thre	304	248	306	2765	2166	1980	4.894788	4.705644	6.492568	38.51398	39.1803	31.68364
pseudogen	folate_hydr	0	0	0	3	0	0	0	0	0	0.063375	0	0
protein_co	piwi-like_R	6	19	12	54	36	34	0.084503	0.315341	0.222708	0.657925	0.569602	0.475892
protein_co	pumilio_ho	1626	1313	1458	2222	2058	1696	16.01527	15.24002	18.9237	18.93305	22.77236	16.60157
protein_co	SPOC_dom	374	280	285	602	319	365	4.999983	4.411254	5.020842	6.962359	4.791116	4.849527
protein_co	tyrosyl-tRN	2502	2294	1950	4347	2881	3637	40.90746	44.19934	42.01309	61.48482	52.9185	59.09738
protein_co	polyhomec	3390	2830	2496	3466	2747	3029	46.37467	45.62203	44.99461	41.01783	42.21714	41.18035
protein_co	cell_divisio	235	222	197	2708	1916	2150	5.038936	5.609589	5.56637	50.23225	46.15466	45.8162

protein_co guanine_nu	912	788	657	1796	1346	1533	20.04242	20.40744	19.02635	34.1448	33.23146	33.48167
protein_co argonaute_	217	197	197	268	263	209	1.614418	1.727148	1.931333	1.72486	2.198168	1.545297
protein_co hook_hom	0	0	0	211	268	219	0	0	0	1.649918	2.721452	1.9673
protein_co cytochrom	19	9	12	22	3	9	0.394617	0.220278	0.328427	0.395283	0.069999	0.185769
protein_co basic_trans	766	656	618	1593	1082	1210	8.622752	8.70218	9.167278	15.513	13.68338	13.53668
protein_co zinc_finger_	739	513	683	881	717	711	6.678627	5.463453	8.133889	6.887818	7.279657	6.385898
protein_co PRP38_pre	451	412	429	1478	896	1103	8.666566	9.329853	10.86332	24.57016	19.34317	21.06472
protein_co desmocolli	192	146	171	3213	3064	2789	1.983737	1.777636	2.328166	28.71817	35.56483	28.6379
protein_co desmoglein	0	0	0	52	48	58	0	0	0	0.431049	0.516714	0.552328
protein_co ring_finger_	202	140	167	907	646	658	2.995541	2.446578	3.263436	11.63574	10.76231	9.697492
protein_co elongator_	1292	1091	1059	1332	1054	1051	11.69427	11.63703	12.6311	10.42984	10.71766	9.454157
protein_co desmoglein	2	0	2	0	2	3	0.020988	0	0.027656	0	0.023578	0.031287
protein_co desmocolli	1138	880	1059	1014	1069	959	8.633828	7.867756	10.58746	6.655215	9.111458	7.23085
protein_co desmocolli	3	2	5	5	3	1	0.037186	0.029215	0.081671	0.053616	0.041777	0.012319
protein_co dystrobrevi	143	97	135	199	177	138	1.160773	0.927876	1.444042	1.397421	1.614112	1.113269
protein_co formin_hor	416	293	284	393	356	336	4.433955	3.68021	3.988881	3.62371	4.26282	3.559155
protein_co tubulin_po	2175	1866	1691	3654	2275	2515	28.57237	28.88722	29.27288	41.52586	33.57511	32.83482
protein_co diacylglyce	128	82	89	101	115	123	1.17708	0.888621	1.078501	0.80349	1.188072	1.124115
protein_co solute_carr	71	24	49	47	37	55	1.435208	0.571709	1.305231	0.821897	0.840248	1.104915
protein_co translocase	443	376	278	871	768	1121	34.4895	34.49674	28.52087	58.66301	67.1728	86.73581
protein_co gastric_intr	2	0	0	0	5	0	0.065238	0	0	0	0.183228	0
protein_co DEAH_(Asp-	518	498	377	1167	931	1111	6.272515	7.106379	6.015727	12.22491	12.66516	13.37013
protein_co apelin_rece	0	4	0	0	1	0	0	0.144583	0	0	0.034459	0
protein_co fatty_acid_	12278	10129	9063	8621	7286	8790	128.1312	124.5664	124.6333	77.83015	85.42116	91.1645
protein_co transmemb	27	21	22	11	18	27	0.844803	0.774316	0.907088	0.297747	0.632723	0.839586
protein_co transcobala	0	0	0	52	18	21	0	0	0	1.5054	0.676717	0.698417
protein_co complemer	1	1	2	0	0	0	0.019126	0.022539	0.050407	0	0	0
protein_co transmemb	2005	1727	1559	1925	1590	1553	55.05534	55.88361	56.41128	45.72764	49.04912	42.38051
protein_co clock_circa	511	393	530	429	431	357	2.62547	2.379501	3.588368	1.906806	2.487783	1.822905
protein_co platelet-der	2654	2422	2604	60	76	37	21.36639	22.97796	27.62524	0.417873	0.687374	0.296034
protein_co gamma-glu	57	46	36	41	46	42	2.108761	2.005476	1.755051	1.312198	1.911874	1.544228
protein_co collagen_ty	9995	8470	7419	14562	16089	20718	84.24538	84.13056	82.40309	106.1811	152.3496	173.5485
protein_co claudin_10	3	0	2	51	48	42	0.059798	0	0.052533	0.879422	1.074866	0.831999
protein_co DAZ_intera	1228	1047	906	729	588	505	9.198011	9.241646	8.942492	4.723741	4.947912	3.75921
protein_co UBA_doma	1148	841	729	1402	987	1153	24.06981	20.77944	20.14156	25.42973	23.24861	24.02535
protein_co arginine_ar	1318	1100	1193	2092	1690	1943	20.58296	20.24381	24.55091	28.26292	29.65024	30.15608
protein_co basic_immu	355	327	255	372	225	308	4.872713	5.289289	4.612299	4.417214	3.469557	4.201485
protein_co excision_re	176	175	137	197	137	148	1.835622	2.150877	1.882894	1.777459	1.60524	1.534058
protein_co tripeptidyl_	747	737	738	1662	1297	1249	8.486464	9.866901	11.04835	16.33429	16.5537	14.10192
protein_co KDEL_(Lys-A	396	348	318	541	405	421	10.06463	10.42291	10.65037	11.89496	11.56397	10.63395
protein_co cysteinyl-tF	1096	950	764	2206	1561	2105	16.50265	16.85675	15.15903	28.73504	26.40555	31.49959
protein_co Rho_GTPas	772	555	575	740	784	751	4.042177	3.424507	3.967351	3.351913	4.611722	3.907937
protein_co STT3A_subu	6373	4999	4805	5529	4486	4453	74.02215	68.42393	73.54378	55.55554	58.53641	51.40201
protein_co ADAM_met	3	0	4	8	0	7	0.039607	0	0.069589	0.091369	0	0.091845

protein_co acrosomal_	8	12	9	22	29	20	0.191468	0.338451	0.283847	0.455504	0.779748	0.475715
protein_co v-ets_eryth	762	693	745	2259	1991	1737	7.874495	8.439332	10.14516	20.19514	23.11469	17.83927
protein_co solute_carr	4	1	5	13	2	5	0.045501	0.013405	0.07495	0.12793	0.025559	0.056526
protein_co klotho_bet	6	4	8	11	21	21	0.052227	0.041031	0.091764	0.082833	0.205359	0.181666
protein_co transmemb	1277	1223	1144	1937	1355	1439	17.99458	20.30881	21.2428	23.61258	21.45059	20.15215
protein_co adenomatc	618	536	684	455	449	370	2.967577	3.033091	4.328171	1.890114	2.422194	1.765732
protein_co neuronal_r	2302	2244	1865	1243	1034	1021	34.19477	39.28116	36.50632	15.97308	17.25536	15.07266
protein_co WD_repeat	465	404	491	1008	737	760	3.492844	3.576141	4.86007	6.550127	6.219318	5.673479
protein_co osteoclast_	412	332	383	1271	981	1179	16.53653	15.70336	20.25727	44.13223	44.23493	47.02954
protein_co riboflavin_l	204	190	209	682	469	549	4.023831	4.416419	5.432387	11.63743	10.39277	10.76196
protein_co ubiquilin_1	1645	1365	1393	3205	2436	2418	14.38281	14.06429	16.04959	24.24203	23.92788	21.01086
protein_co N(alpha)-ac	345	320	285	954	688	678	6.89492	7.536457	7.505676	16.49383	15.44712	13.46634
protein_co chromosor	183	147	106	801	531	586	4.163387	3.941124	3.177872	15.7649	13.57186	13.24961
protein_co annexin_A1	3380	2981	2630	21749	11425	14696	81.00523	84.19096	83.05905	450.9191	307.6108	350.0299
protein_co cathepsin_l	2705	2322	1969	1004	859	1022	65.78107	66.54309	63.0978	21.12177	23.46799	24.69984
protein_co transmemb	2370	1946	2357	3912	4019	3832	19.23504	18.61207	25.20804	27.46671	36.64475	30.90864
protein_co ATP/GTP_b	341	349	298	603	545	472	4.109465	4.956366	4.732406	6.286533	7.378642	5.653046
protein_co golgi_mem	6390	5396	4826	3723	3172	3468	111.0614	110.5201	110.5311	55.97811	61.93618	59.90332
protein_co family_witl	0	1	0	137	76	84	0	0.025748	0	2.589538	1.865526	1.824012
protein_co phosphoser	1421	1196	989	6635	4784	5006	34.38261	34.10225	31.53377	138.8829	130.0424	120.3775
protein_co iron-sulfur_	626	579	449	1266	856	1034	16.92598	18.44867	15.99781	29.61257	26.00173	27.78495
protein_co ADAM_met	994	945	975	2161	2008	2103	8.119634	9.096807	10.49517	15.27101	18.42735	17.07257
protein_co hepatitis_A	3	0	4	9	4	3	0.054635	0	0.095994	0.141792	0.081838	0.054297
protein_co cyclin_J-lik	164	144	115	513	441	469	2.522465	2.610062	2.330848	6.825926	7.620244	7.169085
protein_co TAO_kinase	402	324	308	224	172	127	4.854535	4.610772	4.901252	2.34009	2.333453	1.524175
protein_co ubiquitin_s	182	191	188	236	125	180	2.574896	3.184408	3.504943	2.88844	1.986769	2.530874
protein_co serine_dehy	0	3	2	3	2	3	0	0.11654	0.086878	0.085552	0.074067	0.098283
protein_co musashi_RI	72	65	53	759	798	906	1.281261	1.363093	1.242842	11.68449	15.95354	16.02297
protein_co HNF1_hom	30	19	18	55	52	71	0.394493	0.294428	0.311907	0.625668	0.768194	0.927868
protein_co F-box_prot	564	579	491	719	684	595	6.37054	7.706954	7.308251	7.025691	8.679652	6.679189
protein_co T-box_3	260	200	157	3633	3758	4032	2.914389	2.641869	2.319042	35.22918	47.32384	44.91634
protein_co 2'-5'-oligoa	0	0	2	0	0	0	0	0	0.066919	0	0	0
protein_co harakiri_BC	1	5	8	168	147	156	0.009145	0.053885	0.096408	1.32911	1.510271	1.417826
protein_co ring_finger_	15	0	10	211	196	149	0.204563	0	0.17971	2.489327	3.002906	2.019447
protein_co purinergic_	160	126	100	299	170	267	1.818497	1.687603	1.497709	2.939861	2.170654	3.015876
protein_co coiled-coil_	3	7	3	70	77	111	0.051988	0.142951	0.068507	1.049402	1.499066	1.911673
protein_co deltex_hon	10	5	1	3	3	9	0.15323	0.090286	0.020192	0.039768	0.051643	0.137055
protein_co TRAF-type_	679	472	504	806	746	770	11.31118	9.265893	11.06378	11.61546	13.96131	12.7479
protein_co cyclin_D_b	779	719	719	971	682	775	9.246869	10.05757	11.24659	9.971017	9.094748	9.142576
protein_co transmemb	230	192	212	382	258	339	9.565144	9.409618	11.61808	13.74327	12.05404	14.01113
protein_co coiled-coil_	50	31	28	19	26	16	0.794194	0.580264	0.58607	0.26108	0.463959	0.252573
protein_co transmemb	179	186	139	289	176	255	9.26338	11.34322	9.479077	12.9383	10.23242	13.11494
protein_co POM121_tr	1626	1209	1300	2008	2152	1796	14.7426	12.91775	15.53216	15.74999	21.92022	16.18339
protein_co CD36_mole	263	199	269	63	48	48	2.253355	2.00925	3.037113	0.466958	0.462024	0.408719

protein_co	UDP_glucu	1	0	0	0	0	1	0.017855	0	0	0	0	0.017745
protein_co	patatin-like	280	266	309	249	226	191	3.473167	3.88827	5.050809	2.671961	3.149381	2.354565
protein_co	hypoxia_in	528	609	312	509	400	486	20.40354	27.73294	15.8877	17.0158	17.36523	18.66455
protein_co	family_with	0	2	3	12	9	6	0	0.068633	0.115121	0.302303	0.294435	0.173644
protein_co	RAD50_int	268	272	297	369	296	275	4.767536	5.702104	6.962263	5.678695	5.915615	4.861849
protein_co	SRSF_prote	597	567	632	618	549	498	8.542101	9.560498	11.91632	7.649655	8.82494	7.081567
processed_	kielin/chor	10	1	3	1	6	15	0.103643	0.012214	0.040973	0.008966	0.069862	0.154505
protein_co	testis_deriv	1005	879	732	4670	3380	3414	19.12498	19.71201	18.35612	76.88026	72.26046	64.56663
protein_co	MyoD_fami	1468	1262	1269	639	510	516	16.90243	17.12338	19.25394	6.364833	6.596937	5.904491
protein_co	mitochond	239	183	217	416	352	371	1.165414	1.051575	1.394366	1.754844	1.928297	1.797901
protein_co	brain-speci	9	8	6	9	13	1	0.079279	0.083045	0.069647	0.068584	0.12865	0.008754
protein_co	ankyrin_rep	45	48	44	209	195	194	0.45309	0.569534	0.583793	1.820459	2.205744	1.941256
protein_co	5-hydroxyt	2	3	2	30	22	16	0.068621	0.121298	0.090426	0.890452	0.848004	0.545577
protein_co	KH_homolo	39	71	38	59	31	31	1.005698	2.157588	1.291283	1.316189	0.898078	0.794464
protein_co	KIAA1009	133	128	124	185	135	170	1.365623	1.548803	1.677783	1.643289	1.557263	1.734753
protein_co	synaptotag	4036	3467	3471	7187	6332	6422	33.1631	33.57105	37.58317	51.0875	58.45127	52.44256
protein_co	sorting_nex	520	473	476	1235	762	802	7.615302	8.163042	9.185981	15.64638	12.53683	11.67261
protein_co	5'-nucleotic	2027	1654	1878	814	493	478	30.2456	29.08379	36.92656	10.50742	8.264269	7.088364
protein_co	melanocort	31	29	28	18	3	6	0.762272	0.840336	0.907279	0.382898	0.082874	0.146625
protein_co	EPH_recept	545	443	486	16	5	9	4.379606	4.195168	5.146472	0.11123	0.04514	0.071877
protein_co	akirin_2	497	407	363	1255	761	834	15.83133	15.27786	15.23711	34.58341	27.23296	26.402
protein_co	origin_recc	340	252	273	917	502	645	7.16558	6.258642	7.581758	16.71879	11.88571	13.50958
protein_co	Leber_cong	153	138	146	125	104	88	1.716459	1.824435	2.158389	1.213152	1.310764	0.981148
protein_co	mitogen-ac	1143	901	1036	1370	1047	1092	12.32164	11.44601	14.71691	12.77632	12.67996	11.69915
protein_co	glycoprotei	0	6	0	23	14	24	0	0.52722	0	1.483627	1.172765	1.778503
protein_co	proline_ric	190	159	137	411	288	308	2.559488	2.524084	2.431952	4.789657	4.358541	4.123442
protein_co	LIM_domai	60	29	45	29	48	34	1.384682	0.788685	1.368504	0.578975	1.244483	0.779807
protein_co	PHD_finger	1505	1348	1112	705	598	643	8.898391	9.392301	8.663923	3.606012	3.972146	3.778293
protein_co	N-acetyltra	1042	898	773	2153	1655	1675	13.78424	13.99905	13.47502	24.63894	24.59586	22.02112
protein_co	ets_homolo	1	0	0	0	0	0	0.016807	0	0	0	0	0
protein_co	E74-like_fa	0	5	0	1	0	0	0	0.127322	0	0.018693	0	0
protein_co	proline_ric	1	4	2	262	185	242	0.009573	0.045127	0.025231	2.169858	1.989701	2.302459
protein_co	cell_cycle_	4848	3875	4434	9885	7688	6940	62.47759	58.84918	75.29951	110.205	111.3074	88.88547
protein_co	ATP_syntha	3376	2917	1918	3373	2164	2559	90.4498	92.09768	67.71557	78.17799	65.13456	68.13733
protein_co	DnaJ_(Hsp4	281	237	227	190	273	250	4.354924	4.328423	4.635909	2.547363	4.753198	3.85056
protein_co	CD63_mole	22651	19416	14649	8490	7803	11026	972.56	982.417	828.8421	315.355	376.3914	470.4968
protein_co	advillin	118	107	73	39	42	59	2.125566	2.271346	1.732807	0.607743	0.849945	1.056219
protein_co	anti-Muller	0	0	1	0	0	0	0	0	0.032268	0	0	0
protein_co	growth_dif	1004	899	818	542	530	615	14.24625	15.03258	15.29519	6.653178	8.448737	8.672646
protein_co	glutaminas	50	55	47	106	102	94	0.982572	1.273692	1.217103	1.802036	2.251872	1.835828
protein_co	integrin_al	15	14	14	78	53	52	0.182639	0.20088	0.224629	0.821599	0.724982	0.629239
protein_co	thymocyte_	0	0	0	1	2	1	0	0	0	0.010936	0.028403	0.012563
protein_co	family_with	19	18	17	1	5	14	0.325738	0.363659	0.38406	0.014831	0.096302	0.238535
protein_co	retinol_deh	14	7	10	1	11	13	0.522321	0.307762	0.491637	0.032275	0.461054	0.482017

protein_co	ArfGAP_wit	25	11	21	1	0	0	0.296489	0.153733	0.328187	0.01026	0	0
protein_co	biogenesis_	5	7	6	18	12	6	0.215382	0.355341	0.340586	0.670773	0.580725	0.256863
protein_co	keratin_85	0	0	2	0	0	0	0	0	0.057019	0	0	0
protein_co	cyclin-depe	1704	1474	1363	2931	2388	2728	43.45446	44.29649	45.80316	64.66117	68.41449	69.13831
protein_co	protein_ph	0	0	0	7	0	1	0	0	0	0.1287	0	0.021122
protein_co	trophinin_	234	205	133	1258	869	1152	4.470658	4.615476	3.348436	20.79214	18.65196	21.87347
protein_co	tetraspanin	400	322	234	356	244	243	6.166685	5.849985	4.753817	4.747935	4.226012	3.723126
protein_co	beta-14-N-a	49	24	25	14	12	4	0.464894	0.268334	0.31256	0.114908	0.127905	0.037716
protein_co	transcriptic	596	478	448	1073	738	836	8.858179	8.372076	8.77427	13.79625	12.32264	12.3485
protein_co	coenzyme_	63	73	31	120	78	68	2.018936	2.756843	1.309117	3.326797	2.808185	2.165712
protein_co	Fas_apoptc	15	27	17	0	0	0	0.170631	0.36194	0.254829	0	0	0
protein_co	PAN2_poly	261	256	210	283	243	233	2.572152	2.973056	2.727157	2.412712	2.690366	2.282032
protein_co	extra_spinc	260	245	194	1546	1427	1502	2.066145	2.294355	2.031534	10.62821	12.73974	11.86225
pseudogen	keratin_12	0	0	0	0	5	2	0	0	0	0	0.168106	0.059485
protein_co	keratin_7	13	6	6	4369	3487	4086	0.392379	0.213413	0.238643	114.0795	118.2398	122.5661
protein_co	zinc_finger_	49	62	61	71	54	79	1.174868	1.751829	1.927337	1.4727	1.454574	1.882477
protein_co	heterogene	34727	29870	24120	37738	38553	46963	446.1252	452.2013	408.3209	419.4028	556.4123	599.5908
protein_co	solute_carr	14	8	7	0	0	1	0.294701	0.19845	0.194172	0	0	0.02092
protein_co	activin_A_r	503	458	458	606	706	705	5.835924	6.262016	7.002319	6.082432	9.202279	8.129061
protein_co	osteosarcor	6699	5204	4264	1927	1798	2000	91.64127	83.89296	76.8658	22.80478	27.63248	27.19072
protein_co	major_intri	2	0	0	5	0	5	0.04074	0	0	0.088109	0	0.10122
protein_co	potassium_	32	26	13	4	4	12	0.438095	0.419468	0.234529	0.047374	0.061522	0.163271
protein_co	LTV1_homc	331	280	242	1115	622	773	9.487531	9.457804	9.140614	27.64796	20.02925	22.01985
protein_co	microtubul	3	1	0	509	465	493	0.041349	0.016243	0	6.06916	7.200287	6.753118
protein_co	CD164_mo	3559	3010	3337	5052	3641	3775	37.96434	37.83741	46.90713	46.6202	43.63325	40.01975
protein_co	lactation_e	81	52	59	139	128	124	0.901834	0.682263	0.865622	1.338811	1.601034	1.372059
protein_co	NHS-like_1	749	590	697	903	1255	942	5.287041	4.907835	6.483334	5.514188	9.952303	6.608325
protein_co	Abelson_he	404	323	298	266	196	235	3.612255	3.40335	3.51114	2.057509	1.968803	2.088212
protein_co	hairy/enha	0	3	1	145	110	133	0	0.069889	0.026051	2.479776	2.442999	2.61302
protein_co	protein_kir	66	57	47	581	355	411	1.863523	1.896587	1.748733	14.19155	11.26077	11.533
protein_co	neuromedi	0	4	0	2	3	0	0	0.184306	0	0.06765	0.131778	0
protein_co	sphingomy	79	74	56	135	76	114	2.542455	2.8065	2.37492	3.758573	2.747824	3.646202
protein_co	microtubul	1731	1496	1260	1321	959	1438	20.9178	21.30382	20.06431	13.80971	13.01927	17.2698
protein_co	RALBP1_as	554	416	398	1861	1285	1357	4.832643	4.276371	4.575018	14.04379	12.59294	11.76426
protein_co	syntaxin_1	0	0	0	3	5	1	0	0	0	0.071338	0.154403	0.027318
protein_co	tec_proteir	17	19	19	11	26	7	0.2441	0.321499	0.359507	0.136639	0.419412	0.099891
protein_co	protease-as	291	235	187	331	237	263	14.22514	13.5375	12.04592	13.99763	13.01551	12.777
protein_co	sema_dom	148	145	121	62	72	92	1.817084	2.097918	1.957643	0.658519	0.993104	1.122563
protein_co	chaperonin	6338	5182	4287	11732	8878	9923	165.2093	159.1793	147.2551	264.5558	259.9838	257.0602
protein_co	early_grow	0	0	0	1	0	0	0	0	0	0.019308	0	0
protein_co	RAB11_fam	1668	1485	1247	352	362	281	20.33754	21.33712	20.03565	3.712855	4.958609	3.405009
protein_co	SMYD_fami	428	373	283	912	638	863	8.738429	8.974401	7.613964	16.10822	14.63387	17.51096
protein_co	dysferlin_li	17	10	19	1072	1015	1044	0.13243	0.091801	0.195042	7.224312	8.882881	8.082559
protein_co	coiled-coil_	233	147	145	165	159	211	3.621624	2.6926	2.969958	2.218679	2.776474	3.259414

protein_co	empty_spir	1	0	3	0	2	0	0.024196	0	0.095653	0	0.054366	0
protein_co	potassium_	90	93	63	407	299	357	1.007121	1.226392	0.928997	3.940003	3.758888	3.970242
protein_co	ubiquitin_s	403	390	422	990	677	646	4.493517	5.124519	6.200528	9.549477	8.480454	7.158525
protein_co	glucosamin	4312	3438	4006	2922	2301	2219	44.56883	41.87603	54.563	26.12737	26.71888	22.79394
protein_co	carboxypep	39	38	38	35	35	53	0.310248	0.356233	0.398348	0.240866	0.312796	0.419015
protein_co	MDM2_onc	2330	2145	2018	3910	3351	3421	16.71217	18.13056	19.07361	24.26144	27.00228	24.38595
protein_co	kelch-like_f	633	508	635	824	881	898	5.165174	4.884859	6.827941	5.81663	8.076184	7.282278
protein_co	beta-carote	0	0	0	0	0	2	0	0	0	0	0	0.039411
protein_co	M-phase_pl	480	409	326	791	431	644	23.03869	23.1338	20.61907	32.844	23.24036	30.71935
protein_co	carbohydra	0	1	0	1	0	1	0	0.019226	0	0.014114	0	0.016214
protein_co	KIAA0513	531	369	401	191	152	193	3.617044	2.962053	3.599469	1.125526	1.163193	1.306551
protein_co	dynein_cyt	1613	1403	1704	1131	1559	1364	18.91336	19.38649	26.32927	11.47255	20.53665	15.89492
protein_co	F-box_and_	51	43	33	20	14	26	1.628462	1.618017	1.388533	0.55246	0.502209	0.82507
protein_co	formin_hor	860	674	602	988	693	771	10.53674	9.731388	9.719393	10.47196	9.53872	9.387973
protein_co	coiled-coil_	523	424	320	387	389	405	11.24163	10.73991	9.063845	7.196174	9.393476	8.651519
protein_co	solute_carr	211	189	109	12	11	18	2.419439	2.553884	1.647	0.119035	0.141701	0.205123
protein_co	angiotensir	52	36	31	0	7	5	1.201629	0.98034	0.943982	0	0.181725	0.114828
protein_co	zinc_finger_	69	50	61	215	183	172	1.327855	1.13391	1.546914	3.57934	3.956413	3.289573
protein_co	pecanex-lik	619	413	494	569	457	425	4.80717	3.779688	5.055459	3.822734	3.987164	3.280178
protein_co	potassium_	63	55	46	422	321	320	1.543398	1.587841	1.485012	8.943609	8.834692	7.791067
protein_co	URB2_ribos	216	204	172	877	882	867	2.03728	2.267432	2.137767	7.155824	9.345761	8.126916
protein_co	egl_nine_h	1474	1291	1189	2006	1625	1757	10.99549	11.34882	11.68783	12.94527	13.6182	13.02563
protein_co	calpain_9	5	0	1	0	5	4	0.106564	0	0.028085	0	0.119718	0.084725
protein_co	componen	242	245	208	643	455	518	1.634982	1.950612	1.851807	3.758129	3.453489	3.47806
protein_co	ATP-bindin	178	125	166	525	481	482	2.443219	2.021899	3.002516	6.233971	7.417142	6.575051
protein_co	nucleoside-	266	230	208	550	409	572	1.617726	1.648383	1.666946	2.89367	2.794446	3.457236
protein_co	TAF5-like_R	338	263	273	777	665	652	4.405233	4.039383	4.68867	8.760647	9.736949	8.44519
protein_co	glutamate-a	3232	2823	2584	6475	5543	5575	27.90367	28.72155	29.39796	48.36072	53.76305	47.83485
protein_co	syntaxin_6	669	600	562	656	604	694	7.301077	7.716479	8.082244	6.193379	7.405371	7.527139
protein_co	regulator_c	3	0	0	0	0	0	0.11091	0	0	0	0	0
protein_co	ribonuclea	221	145	172	77	72	97	2.760727	2.134549	2.831355	0.832118	1.010445	1.204239
protein_co	DEAH_(Asp-	2974	2395	2721	6916	5822	5915	37.13361	35.24024	44.77026	74.70406	81.66717	73.39908
protein_co	KIAA1614	217	203	125	39	51	36	1.189993	1.311861	0.903295	0.185017	0.314198	0.196199
protein_co	centrosom	418	366	496	509	507	399	1.640304	1.692529	2.564865	1.72794	2.235141	1.556075
protein_co	N-acetylneu	45	41	62	42	29	28	0.985254	1.057856	1.788802	0.795514	0.713317	0.609261
protein_co	family_with	168	173	177	1019	821	794	1.283789	1.557892	1.782347	6.7363	7.048171	6.029959
protein_co	phosphatid	382	354	311	1119	740	822	7.689528	8.397436	8.249574	19.4863	16.73467	16.44439
protein_co	acyl-CoA_b	932	865	672	1152	942	992	29.54551	32.3146	28.07241	31.59302	33.54869	31.25338
protein_co	laminin_ga	10924	8783	9932	18463	17416	15275	73.30808	69.45765	87.82975	107.1853	131.3009	101.8734
protein_co	ring_finger_	533	489	449	901	801	761	2.505777	2.709138	2.78161	3.6644	4.230549	3.555572
protein_co	G_protein-r	4	3	1	6	10	19	0.05532	0.048893	0.018224	0.071785	0.155371	0.261146
protein_co	SP110_nuc	335	226	220	45	37	30	6.508342	5.174175	5.632265	0.756312	0.807563	0.579237
protein_co	mitochond	545	501	420	953	698	782	16.5062	17.88115	16.76234	24.96931	23.74954	23.53786
protein_co	cholinergic	7	0	1	0	0	0	0.12263	0	0.023085	0	0	0

protein_co	paired_box	10	4	16	679	560	463	0.146651	0.069128	0.3092	8.614254	9.226181	6.748007
protein_co	dedicator_	245	192	213	188	197	157	1.779712	1.643585	2.03891	1.181421	1.607678	1.133426
protein_co	tubulin_tyr	381	285	301	2112	1332	1405	4.060906	3.579727	4.227652	19.47399	15.94965	14.88277
protein_co	ubiquitin_s	84	55	91	137	203	123	0.553666	0.427207	0.790396	0.781182	1.503189	0.805718
protein_co	5-hydroxyt	11	14	4	4	5	10	0.259284	0.388882	0.124244	0.081565	0.132404	0.234257
protein_co	integral_m	17877	14909	13409	6548	5823	7322	455.4505	447.6124	450.1712	144.3172	166.6642	185.3898
protein_co	solute_carr	7	5	5	59	68	52	0.10537	0.088695	0.09918	0.768307	1.149947	0.777916
protein_co	serpin_pep	6122	5023	4745	10162	6030	6860	54.11667	52.32486	55.27246	77.71055	59.88308	60.26588
protein_co	DnaJ_(Hsp4	993	888	693	936	885	1209	11.71616	12.34685	10.77467	9.553772	11.73082	14.1766
protein_co	wingless-ty	0	0	0	14	27	11	0	0	0	0.251741	0.630487	0.22723
protein_co	transmemb	697	567	525	1357	1059	1261	12.56808	12.04831	12.4747	21.16795	21.45266	22.59752
protein_co	cytochrom	65	39	41	140	88	88	1.341062	0.948216	1.11469	2.498771	2.039704	1.804379
protein_co	eukaryotic_	1515	1370	1103	1935	1520	1906	22.75336	24.24715	21.82948	25.14068	25.64635	28.4489
protein_co	armadillo_	1191	1089	1054	737	710	717	10.95046	11.79928	12.77015	5.862069	7.333779	6.551628
protein_co	calcium_bi	786	629	718	1485	1239	1246	10.87601	10.25663	13.09201	17.7761	19.2605	17.13463
protein_co	cytochrom	1688	1405	1032	1722	1423	2323	121.09	118.7734	97.55516	106.8641	114.6805	165.6131
protein_co	REV1_polyr	382	345	326	677	518	551	4.256674	4.530366	4.786956	6.526175	6.48464	6.101945
protein_co	testis_speci	70	68	47	127	94	116	0.955614	1.093957	0.845507	1.499861	1.441655	1.573809
protein_co	major_facil	122	91	92	265	229	254	1.59516	1.402145	1.585138	2.997459	3.36379	3.30056
protein_co	transmemb	1185	979	967	1285	1071	1146	14.90853	14.51464	16.03163	13.98564	15.13753	14.32883
protein_co	ectodysplas	5	3	0	2	0	4	0.061232	0.043295	0	0.021188	0	0.048683
protein_co	transformir	275	283	230	883	692	637	2.434985	2.952957	2.683652	6.763745	6.883649	5.605477
protein_co	GRIP_and_(	428	425	425	405	378	310	3.345946	3.915355	4.378233	2.739007	3.319831	2.408499
protein_co	mitochond	242	164	197	697	413	537	8.541147	6.821058	9.162244	21.28122	16.3757	18.83583
protein_co	G_protein-(	0	0	0	1	0	1	0	0	0	0.02655	0	0.030501
protein_co	chromoson	433	393	356	524	375	402	4.807771	5.142277	5.208836	5.033269	4.677741	4.436
protein_co	ankyrin_rep	87	82	119	54	95	93	0.734705	0.816046	1.324267	0.394503	0.901294	0.780524
protein_co	enhancer_c	468	377	447	556	556	552	6.802961	6.458038	8.56238	6.991815	9.079794	7.974452
protein_co	Rho_guanir	218	163	136	64	91	87	2.41043	2.123893	1.98158	0.612183	1.13039	0.95602
protein_co	iron-sulfur_	1333	1087	1074	2213	1361	1718	19.1507	18.40311	20.33264	27.5042	21.96655	24.52943
protein_co	aldehyde_d	1402	1229	1308	386	266	218	9.834805	10.1596	12.09095	2.342438	2.096276	1.519791
protein_co	stabilin_2	13	12	14	13	16	10	0.083412	0.090735	0.118372	0.072159	0.115333	0.063767
protein_co	ubiquitin_s	0	4	4	17	8	4	0	0.062046	0.069382	0.193581	0.118301	0.052326
protein_co	SCY1-like_2	696	641	763	1483	1260	1136	6.376005	6.919975	9.21083	11.75286	12.96758	10.34254
protein_co	cytoskeletc	10079	8220	7405	5011	4035	4435	172.5161	165.8025	167.0214	74.19926	77.58982	75.44239
protein_co	plexin_C1	84	69	80	38	29	27	0.605369	0.586	0.759742	0.236912	0.234795	0.193381
protein_co	adaptor_pr	1220	1026	1099	528	351	456	19.94073	19.76221	23.67084	7.46583	6.445214	7.407227
protein_co	PWP1_hon	1205	978	883	1939	1305	1403	24.33953	23.27936	23.50285	33.88175	29.61315	28.16387
protein_co	DNA-damag	438	355	327	1075	852	906	6.589416	6.293732	6.482692	13.99086	14.39997	13.54599
protein_co	KIAA1033	836	680	830	985	900	761	7.605889	7.290541	9.950769	7.752521	9.198887	6.880786
protein_co	solute_carr	54	41	26	85	54	67	0.642574	0.574937	0.407697	0.875007	0.721892	0.792345
protein_co	villin-like	186	128	107	113	88	135	2.218298	1.79897	1.681611	1.165865	1.179068	1.600112
protein_co	filamin_B_b	1048	901	869	8911	9977	9607	5.81757	5.894028	6.356747	42.79271	62.2199	53.00023
protein_co	NIMA-relat	185	157	119	240	170	146	3.008935	3.009178	2.550486	3.376878	3.106269	2.359954

protein_co	protocadhe	0	0	0	33	24	39	0	0	0	0.377558	0.356588	0.512603
protein_co	vacuolar_p	574	505	575	873	775	704	6.879812	7.132851	9.081704	9.051946	10.43555	8.385848
protein_co	ribonuclea	275	236	238	507	351	400	8.937246	9.03837	10.19255	14.25417	12.81525	12.91935
protein_co	cytoskeletc	753	635	740	2581	2040	1955	10.985	10.91656	14.22563	32.57288	33.43369	28.34403
protein_co	leukocyte_	2	4	0	23	13	7	0.073325	0.172819	0	0.729484	0.535448	0.255054
protein_co	TBC1_dom	851	808	876	628	582	535	7.079319	7.921006	9.602865	4.519439	5.439187	4.423086
protein_co	thrombosp	88	56	61	12	9	11	1.462275	1.096583	1.335706	0.172501	0.168011	0.181656
protein_co	bora_auror	80	81	66	427	400	330	1.535078	1.831608	1.668857	7.088123	8.622822	6.29309
protein_co	leucine-rich	483	395	385	636	580	582	5.428981	5.232092	5.702519	6.184311	7.323998	6.501354
protein_co	succinate-C	641	519	494	1077	760	970	15.68169	14.96268	15.92563	22.79363	20.88803	23.58393
protein_co	regulator_c	253	242	276	413	331	359	3.32772	3.751014	4.783768	4.699366	4.891063	4.692781
protein_co	mediator_c	325	266	272	381	415	474	8.509309	8.207288	9.384576	8.629764	12.20698	12.33386
protein_co	PHD_finger	129	129	123	203	125	158	4.200116	4.94958	5.277296	5.717822	4.572257	5.112558
pseudogen	ribosomal_	37	33	40	45	18	25	3.200681	3.364044	4.559692	3.367567	1.749292	2.149267
protein_co	componen	454	439	464	386	317	292	5.343533	6.088976	7.196568	3.930275	4.191611	3.415585
protein_co	LIM_domai	977	698	951	1458	1223	1107	6.363601	5.357608	8.16251	8.215404	8.949194	7.165816
protein_co	sciellin	6	0	0	0	0	3	0.102599	0	0	0	0	0.050983
protein_co	integral_m	5738	4878	4010	8789	5629	6076	161.9272	162.2214	149.1209	214.5664	178.4595	170.4067
protein_co	sprouty_hc	262	217	227	1304	1072	1045	5.122061	4.999312	5.847956	22.05383	23.54438	20.30343
protein_co	nudix_(nuc	381	275	247	1864	1161	1471	9.614165	8.17761	8.213313	40.69073	32.91303	36.89002
protein_co	endothelin	3	0	0	468	395	481	0.035523	0	0	4.793981	5.254526	5.660335
protein_co	regulator_c	383	406	359	225	201	124	6.273639	7.837072	7.749077	3.188352	3.698843	2.018608
protein_co	lymphocyt	9	12	19	4940	3877	3792	0.120809	0.189821	0.336081	57.36475	58.46555	50.58633
protein_co	SET_domai	82	81	108	131	109	95	0.702112	0.817306	1.218573	0.970347	1.0485	0.8084
protein_co	secernin_1	2458	1980	2272	3781	3387	3104	24.669	23.41757	30.04781	32.82761	38.18861	30.96
protein_co	chromoson	3	2	11	4	12	10	0.064799	0.050908	0.313095	0.074743	0.291192	0.214664
protein_co	tensin_3	410	281	384	2974	3156	2889	2.846663	2.299141	3.513325	17.86307	24.61718	19.93469
protein_co	speedy_hor	20	33	19	15	17	25	0.399706	0.777197	0.500378	0.259337	0.381688	0.496546
protein_co	carbohydra	352	295	205	495	254	364	8.86126	8.751488	6.80051	10.78006	7.183492	9.106759
protein_co	insulin-like	644	596	749	1029	1616	1036	8.022118	8.748962	12.29475	11.08872	22.61484	12.82545
protein_co	glycoprotei	640	548	566	30	23	17	11.83866	11.94566	13.79665	0.480072	0.477969	0.312522
protein_co	Rap_guanir	21	20	22	100	58	64	0.167914	0.188454	0.231807	0.691722	0.521009	0.508579
protein_co	ras-related_	5432	4475	4206	10283	6819	6881	123.7949	120.183	126.3127	202.7336	174.5873	155.849
protein_co	KDEL_(Lys-A	6892	6092	5446	5331	3736	4270	126.515	131.7843	131.7375	84.6581	77.04647	77.89944
protein_co	nucleopori	231	232	224	716	531	659	4.835654	5.723192	6.179112	12.9664	12.48783	13.71003
protein_co	interleukin	2	5	3	2	4	0	0.06934	0.204282	0.137059	0.059985	0.155798	0
protein_co	zinc_finger_	280	252	198	466	331	328	7.633099	8.095627	7.112837	10.98985	10.13724	8.88641
protein_co	acyloxyacyl	98	75	63	6	8	8	2.165366	1.952871	1.834343	0.114688	0.198584	0.175673
protein_co	basic_leuci	1294	1067	1015	3198	2425	2342	32.60621	31.68382	33.70287	69.71199	68.64783	58.64926
protein_co	diacylglyce	1	5	3	0	0	0	0.007654	0.045097	0.030257	0	0	0
protein_co	transformir	1085	765	621	3022	2062	2341	16.8498	14.00018	12.70842	40.59967	35.97517	36.13068
protein_co	DEAD_(Asp-	1323	1251	867	3304	2008	2316	23.13109	25.77512	19.97515	49.97344	39.4411	40.24245
protein_co	HUS1_chec	223	211	180	518	375	374	4.022433	4.485114	4.278498	8.083078	7.599138	6.704482
protein_co	NAC_alpha_	386	368	234	160	128	134	4.275151	4.803072	3.41519	1.533018	1.592661	1.474955

protein_co drebrin-like	2554	2244	1719	2241	1818	2439	14.05815	14.55584	12.46861	10.67117	11.24217	13.34224
protein_co cerebral_ca	939	790	636	1566	1003	1260	9.372472	9.29229	8.36528	13.52207	11.24705	12.49881
protein_co myosin_IG	2	3	5	3	0	3	0.018667	0.032998	0.061498	0.024224	0	0.027828
protein_co tweety_hor	16501	13527	11866	7093	7192	7736	180.4916	174.3634	171.0354	67.11811	88.37826	84.09551
protein_co tetratricop	282	275	243	398	281	318	2.977535	3.421744	3.381029	3.635414	3.333214	3.33691
protein_co NK2_home	0	0	0	0	1	1	0	0	0	0	0.047166	0.041724
protein_co zinc_finger_	45	42	41	163	224	210	0.269039	0.29591	0.323015	0.843052	1.504529	1.247764
protein_co 510-methe	3	3	2	5	0	2	0.175108	0.206354	0.153833	0.252475	0	0.116018
protein_co ADAM_met	836	643	548	459	444	569	8.061689	7.306978	6.963621	3.829089	4.810074	5.453077
protein_co abhydrolas	227	145	155	562	427	359	4.935362	3.71508	4.440784	10.57042	10.42966	7.757061
protein_co iron-respor	1391	1211	1227	1669	1656	1464	11.5897	11.89039	13.47176	12.02996	15.50081	12.1226
protein_co alpha-kinas	26	6	7	7	10	22	0.126085	0.034288	0.044732	0.029366	0.05448	0.106028
protein_co transmemb	33	26	31	109	56	57	0.842359	0.782103	1.042749	2.406982	1.605907	1.445998
protein_co calcium_an	57	46	45	188	139	165	1.888383	1.795892	1.964548	5.388107	5.173437	5.432615
protein_co calcium_bi	1188	1066	881	579	398	366	17.08145	18.06228	16.69241	7.201946	6.428956	5.229968
protein_co radical_S-ad	517	467	349	548	358	492	10.82694	11.52495	9.631086	9.927927	8.422618	10.23976
protein_co N-myristoy	1875	1519	1416	3973	2957	3287	19.85684	18.95718	19.76091	36.39909	35.18109	34.5954
protein_co MYCBP_ass	4	2	6	0	1	2	0.066467	0.039164	0.131381	0	0.018668	0.033028
protein_co serine/argir	2674	2355	2352	5938	5331	5809	47.457	49.25347	55.00611	91.16792	106.291	102.4589
protein_co vascular_er	690	622	620	1196	944	1002	9.257295	9.834052	10.96129	13.88127	14.2284	13.36018
protein_co chondroad	14	17	8	7	25	28	0.414295	0.59284	0.311965	0.179202	0.831134	0.823473
protein_co translation	280	284	204	672	521	582	6.433801	7.690154	6.176957	13.35801	13.4492	13.29053
protein_co testis_expr	430	382	376	661	644	556	4.351037	4.555067	5.013569	5.786138	7.320812	5.591248
protein_co DDB1_and_	1477	1280	1249	2218	2184	2063	12.31205	12.57381	13.71978	15.99464	20.45275	17.09066
protein_co growth_ho	0	0	0	1	0	0	0	0	0	0.040245	0	0
protein_co LIM_domai	564	400	336	1286	1066	1278	9.351306	7.815563	7.341203	18.44579	19.85635	21.0588
protein_co BRCA1_inte	106	131	96	802	751	691	0.927868	1.351322	1.107354	6.073201	7.38532	6.011294
protein_co K(lysine)_ac	409	392	386	1270	914	927	5.418635	6.120118	6.738896	14.55571	13.60385	12.20551
protein_co actin-like_6	413	375	361	1619	1131	1492	11.50165	12.30689	13.24805	39.00496	35.3852	41.29414
protein_co NADH_dehy	808	710	583	1239	853	1158	10.5725	10.94792	10.0524	14.02492	12.53904	15.05859
protein_co mitochond	525	478	309	1066	760	902	20.28761	21.7674	15.73493	35.63623	32.99394	34.64078
protein_co transforme	1898	1645	1660	5008	3819	4379	22.40401	22.88246	25.82097	51.13956	50.64404	51.37055
protein_co sodium_ch	213	202	200	1	10	17	1.282579	1.433385	1.586972	0.005209	0.067648	0.101733
protein_co membrane-	1041	979	1034	1750	1377	1322	14.7239	16.31782	19.27204	21.41279	21.8804	18.58289
protein_co UDP-N-acet	635	542	759	2	8	5	5.447663	5.479525	8.580511	0.014843	0.077104	0.04263
protein_co TRAF_famil	466	388	414	431	297	311	11.36366	11.1499	13.30355	9.092275	8.136503	7.537066
protein_co B_lymphoi	0	4	0	2	6	2	0	0.09576	0	0.035149	0.136936	0.040379
protein_co GATA_bind	48	75	63	8	6	10	0.744337	1.370556	1.287372	0.10732	0.104527	0.154113
protein_co SKI-like_on	180	176	179	467	402	388	1.326842	1.528856	1.73874	2.978013	3.329061	2.842419
protein_co glutamyl-pr	2514	1964	2092	3924	3080	2972	26.54441	24.43748	29.10746	35.84262	36.53487	31.18647
protein_co H2.0-like_h	495	413	256	1	3	2	7.886185	7.753877	5.374481	0.013782	0.053695	0.031667
protein_co vacuolar_p	462	386	403	740	538	646	8.766573	8.631421	10.07692	12.14738	11.46883	12.18232
protein_co interleukin	15	12	15	19	2	9	0.487187	0.459296	0.641993	0.533852	0.072977	0.290507
protein_co potassium_	619	652	573	1042	850	767	8.336422	10.3477	10.16901	12.14003	12.86048	10.26583

protein_co ribosomal_	437	378	427	402	286	286	4.214065	4.295549	5.426033	3.353581	3.098381	2.740914
protein_co Ras_associa	59	28	44	17	13	11	0.69427	0.388277	0.682281	0.173057	0.171858	0.128641
protein_co COBW_don	258	279	242	496	405	500	4.132761	5.266619	5.108234	6.8733	7.288274	7.959766
protein_co interleukin	0	0	3	0	0	0	0	0	0.175138	0	0	0
protein_co interleukin	0	2	0	0	0	0	0	0.06492	0	0	0	0
protein_co interleukin	0	0	0	36	16	15	0	0	0	0.610652	0.35245	0.2923
protein_co interleukin	0	0	0	1	0	0	0	0	0	0.038616	0	0
protein_co interleukin	0	0	0	0	2	3	0	0	0	0	0.08708	0.115551
protein_co sphingomy	1595	1246	1071	3566	2681	2953	17.24691	15.87727	15.26072	33.35762	32.56841	31.73392
protein_co WD_repeat	1038	879	840	1877	1672	1969	5.802212	5.790182	6.187431	9.076607	10.49981	10.93834
protein_co coiled-coil_	492	401	312	261	211	259	7.312456	7.023436	6.110652	3.355843	3.523138	3.825671
protein_co Sin3A-assoc	494	366	465	1329	1079	929	6.267158	5.471821	7.773766	14.58585	15.37851	11.71302
protein_co bridging_in	1616	1276	997	723	576	718	16.64125	15.48468	13.52927	6.440889	6.663709	7.34816
protein_co IMP4_U3_s	1110	970	846	2084	1444	1498	24.70135	25.43762	24.80863	40.11976	36.10056	33.12982
protein_co heparan_su	1842	1696	1340	1418	1421	1669	24.80094	26.90986	23.77487	16.51649	21.49422	22.33287
protein_co UDP-glucos	3420	2876	2908	4430	3471	3926	16.56525	16.41602	18.56099	18.56259	18.88755	18.8987
protein_co glycophorii	1495	1311	938	1638	1231	1472	43.84863	45.31319	36.25372	41.56156	40.56225	42.90741
protein_co signal_tran	337	303	351	967	641	658	6.003067	6.360526	8.239203	14.9016	12.82775	11.64874
protein_co abl-interact	756	663	714	1519	1288	1391	10.73589	11.09524	13.36132	18.66109	20.54855	19.63148
protein_co YME1-like_	2906	2285	2200	4155	3377	3229	38.51941	35.69253	38.42745	47.64508	50.28798	42.5365
protein_co DnaJ_(Hsp4	817	682	596	1033	715	738	20.53789	20.20343	19.74308	22.46452	20.19244	18.4374
protein_co nipsnap_ho	294	257	256	391	339	479	9.531324	9.818522	10.93656	10.96594	12.34681	15.43303
protein_co leucine_ric	872	591	533	2370	1954	2108	9.994489	7.982496	8.05019	23.49933	25.16041	24.01178
protein_co ferric-chela	8	5	6	0	1	0	0.26421	0.194597	0.261123	0	0.037103	0
protein_co cyclin-depe	1056	799	784	1533	1184	1392	20.70581	18.46215	20.25719	26.0036	26.08129	27.12547
protein_co thioredoxir	4459	3952	2870	6302	4004	5164	271.65	283.7242	230.4035	332.1343	274.0409	312.657
protein_co outer_dens	1226	1031	884	1305	1149	1092	17.50894	17.35143	16.63629	16.12289	18.43481	15.49893
protein_co KIAA0368	1962	1724	1812	2618	1985	1930	14.05361	14.55235	17.10338	16.22264	15.97344	13.73902
protein_co torsin_fami	867	657	684	715	603	585	16.57632	14.80272	17.23297	11.82601	12.95196	11.11564
protein_co chromoson	580	483	378	1381	843	1134	12.84761	12.60806	11.03369	26.46372	20.97833	24.96416
protein_co structural_	375	275	349	1295	1039	914	3.322101	2.870921	4.074194	9.924629	10.34061	8.047062
protein_co Kruppel-lik	961	860	650	287	210	224	18.08613	19.07339	16.1202	4.672693	4.440079	4.189672
protein_co torsin_fami	631	622	521	1676	971	1179	16.09141	18.69228	17.50803	36.97445	27.81846	29.88052
protein_co Ral_GEF_wi	17	20	13	142	114	125	0.142045	0.196931	0.143138	1.026427	1.070116	1.037998
protein_co family_witl	11726	9341	7847	14058	10870	14918	156.883	147.2741	138.3453	162.7094	163.3822	198.3564
protein_co ST6_(alpha-	995	795	590	37	37	48	31.15097	29.33072	24.34083	1.002105	1.301365	1.49348
protein_co tropomodu	1	0	4	39	24	20	0.016245	0	0.085625	0.548069	0.437994	0.322885
protein_co DAB2_inter	1430	1169	1111	1320	1503	1655	11.15944	10.75048	11.42497	8.911344	13.17693	12.83553
protein_co syntaxin_bi	830	626	633	470	362	345	11.24099	9.990974	11.29705	5.506648	5.507875	4.643604
protein_co solute_carr	162	116	117	1651	1348	1513	3.948638	3.331941	3.757967	34.81307	36.91231	36.65058
protein_co angiopoieti	455	398	291	244	199	228	6.498018	6.698224	5.476427	3.014549	3.192799	3.236041
protein_co CDK5_regu	704	554	506	1425	1331	1452	5.97762	5.543352	5.661623	10.46727	12.69646	12.2527
protein_co ZFP37_zinc	134	108	99	27	35	48	1.132157	1.075307	1.102229	0.197346	0.332215	0.403044
protein_co solute_carr	0	0	2	0	3	0	0	0	0.078166	0	0.09996	0

protein_co	solute_carr	1068	843	841	1257	980	1176	11.91842	11.08618	12.36739	12.13517	12.28634	13.04261
protein_co	toll-like_re	173	126	180	144	127	127	1.89075	1.622802	2.59236	1.361487	1.55934	1.379435
protein_co	zinc_finger_	430	372	356	361	320	284	7.263761	7.405308	7.92461	5.275496	6.072844	4.767834
protein_co	aldolase_B_	13	8	3	2	0	0	0.280797	0.203632	0.08539	0.037372	0	0
protein_co	syntaxin_1	142	96	107	193	205	185	2.776079	2.211677	2.756526	3.264102	4.502424	3.594387
protein_co	PRP4_pre-r	726	621	549	1861	1443	1595	11.96612	12.06189	11.92405	26.53542	26.71972	26.12684
protein_co	folylpolyglu	1164	999	711	1661	1071	1260	26.34601	26.64615	21.20637	32.52329	27.23331	28.34275
protein_co	ubiquitin_s	452	373	373	362	335	369	5.367728	5.219969	5.83708	3.718978	4.469366	4.354999
protein_co	bile_acid_C	9	2	3	25	1	5	0.141092	0.036949	0.061975	0.33905	0.017612	0.077901
protein_co	ATPase_H+_	1257	1015	932	2173	1844	2337	61.61743	58.63291	60.20313	92.14909	101.5496	113.851
protein_co	testis_expr	567	498	484	1518	1226	1219	6.734921	6.970852	7.57582	15.59855	16.36021	14.39007
protein_co	GTPase_act	35	49	47	69	95	91	0.384746	0.634759	0.680829	0.656172	1.173217	0.994161
protein_co	mitochond	284	305	231	789	525	676	4.512378	5.710762	4.83653	10.84494	9.371205	10.6744
protein_co	dolichyl-ph	1074	967	712	1242	886	1269	34.21097	36.299	29.88656	34.22517	31.70617	40.17282
protein_co	WD_repeat	1	2	1	5	0	4	0.042285	0.099661	0.055721	0.182903	0	0.168096
protein_co	thiosulfate_	116	94	176	82	153	98	1.421564	1.357511	2.842208	0.869331	2.106439	1.193559
protein_co	gamma-am	4	3	1	6	4	2	0.036758	0.032488	0.01211	0.047699	0.041296	0.018266
protein_co	proteasom	2342	1876	1662	3453	2452	3244	125.4937	118.4609	117.3548	160.0644	147.6062	172.753
protein_co	nuclear_rec	0	0	0	5	3	9	0	0	0	0.073774	0.057483	0.152554
protein_co	chromoson	105	111	88	193	134	152	1.871021	2.330878	2.066364	2.975156	2.682522	2.691799
protein_co	Rab9_effect	795	620	518	1045	775	940	17.17881	15.78792	14.74995	19.53464	18.81381	20.18662
protein_co	golgin_A1	264	230	208	339	300	266	2.911148	2.988789	3.022446	3.233874	3.716471	2.915088
protein_co	xeroderma_	211	214	173	153	108	138	7.052115	8.428645	7.619348	4.423758	4.055176	4.5838
protein_co	nuclear_ca	912	807	840	2217	1701	1797	9.324486	9.723232	11.31733	19.60915	19.53815	18.25945
protein_co	acidic_(leu	2822	2406	1916	6548	5189	6185	102.1186	102.6007	91.36463	204.9838	210.9505	222.4319
protein_co	olfactory_r	0	1	0	0	0	0	0	0.066654	0	0	0	0
protein_co	phosducin-	460	355	396	491	498	481	8.657255	7.873318	9.820924	7.99405	10.52933	8.996572
protein_co	ribosomal_	14725	12842	8287	15126	11109	17160	993.0651	1020.616	736.4692	882.4895	841.6789	1150.136
protein_co	cathepsin_	16	13	8	2654	2106	2805	0.547902	0.524606	0.361	78.62244	81.01959	95.46081
protein_co	LIM_homeo	0	0	1	178	237	253	0	0	0.01201	1.403375	2.426544	2.291505
protein_co	actin_relat	911	684	571	2292	1608	2104	19.30714	17.08295	15.94669	42.02205	38.28554	44.31544
protein_co	ectonucleo	1161	1108	959	310	187	185	16.85344	18.9541	18.34466	3.89297	3.049629	2.668933
protein_co	defective_i	79	66	56	813	555	567	1.807406	1.779425	1.688308	16.09097	14.26497	12.89203
protein_co	derlin_1	1112	975	948	1276	984	1138	10.67847	11.03356	11.9963	10.60029	10.61569	10.86065
protein_co	v-myc_mye	1894	1567	1305	1256	773	779	42.75917	41.68937	38.82349	24.53025	19.60549	17.47819
protein_co	nephroblas	98	84	65	34	20	10	2.057184	2.077942	1.798023	0.617432	0.471657	0.20862
protein_co	interleukin	1	4	3	0	0	0	0.020046	0.094491	0.079246	0	0	0
protein_co	chromoson	552	572	417	1092	686	1015	10.60742	12.9531	10.55945	18.15332	14.80961	19.38412
protein_co	RAN_bindi	355	362	384	637	571	513	4.107092	4.935393	5.854261	6.375416	7.421492	5.898385
protein_co	polymerase	1524	1260	962	1496	985	1311	36.19653	35.26628	30.10869	30.73807	26.28254	30.94528
protein_co	phospholip	482	429	454	1340	942	851	6.026821	6.321289	7.480522	14.49469	13.23248	10.575
protein_co	interleukin	142	125	103	62	37	56	2.499209	2.592575	2.388836	0.943993	0.731585	0.979517
protein_co	ubiquitin_a	1096	919	861	3275	2485	2282	12.69102	12.54032	13.13784	32.80652	32.3267	26.26099
protein_co	aprataxin	527	509	358	987	654	897	13.24782	15.07852	11.8591	21.46416	18.46973	22.40969

protein_co	ring_finger_	448	341	395	1210	1100	1038	4.514192	4.049147	5.24486	10.54752	12.45213	10.39463
protein_co	talin_1	11988	9574	9881	10971	11715	11913	71.93207	67.69808	78.12887	56.94886	78.97091	71.0406
protein_co	chemokine_	0	1	0	0	0	0	0	0.073225	0	0	0	0
protein_co	signaling_t	0	0	0	0	1	4	0	0	0	0	0.048315	0.170964
protein_co	doublesex_	0	0	0	5	8	10	0	0	0	0.103058	0.214135	0.236787
protein_co	DnaJ_(Hsp4	200	161	173	171	165	191	2.025287	1.921275	2.30854	1.498013	1.877109	1.922204
protein_co	sperm_assc	2	17	7	8	4	10	0.042677	0.427485	0.196833	0.147679	0.09589	0.212068
protein_co	dynactin_3	1346	1144	900	894	713	795	18.37982	18.40897	16.19473	10.5608	10.93792	10.7888
protein_co	CD72_mole	7	6	5	2	3	1	0.182107	0.183944	0.171409	0.045011	0.087679	0.025855
protein_co	transmemb	629	478	379	147	71	123	8.968458	8.031601	7.121003	1.813207	1.137299	1.742938
protein_co	glyoxylate_	1522	1014	986	1465	1135	1406	16.92066	13.28458	14.4449	14.08975	14.1758	15.53451
protein_co	aldehyde_d	748	550	462	1069	754	756	12.91581	11.19154	10.51228	15.96837	14.6265	12.97333
protein_co	histidine_t	92	90	63	290	161	226	2.24761	2.591092	2.02819	6.129064	4.418838	5.487206
protein_co	Rho_guanir	26	33	23	443	315	371	0.306017	0.457713	0.356726	4.510653	4.165165	4.339665
protein_co	insulin-like	22	16	28	125	152	119	1.065601	0.91327	1.787166	5.237752	8.271125	5.728337
protein_co	DENN/MAD	638	558	658	466	405	383	4.716709	4.861382	6.410311	2.98035	3.363741	2.814018
protein_co	ribosomal_	32258	28600	18706	35310	22662	26966	1231.269	1286.438	940.8738	1165.94	971.7687	1022.92
protein_co	canopy_3_l	891	779	560	1423	1041	1588	27.68217	28.52115	22.9269	38.24639	36.33476	49.03234
protein_co	forkhead_b	412	313	283	1623	1125	1388	3.667063	3.283013	3.319268	12.49691	11.24923	12.27779
protein_co	peptidylpro	295	206	257	1865	998	1328	8.98079	7.390381	10.31004	49.11728	34.13282	40.1791
protein_co	kinesin_ligl	183	192	164	172	127	147	2.68818	3.323653	3.174578	2.185741	2.095849	2.146023
protein_co	kinesin_fan	856	732	951	636	625	584	6.544987	6.595583	9.581872	4.206832	5.368638	4.437696
protein_co	zinc_finger_	280	217	178	306	261	299	7.188884	6.565537	6.022243	6.79654	7.528232	7.629292
protein_co	pim-1_onc	201	134	116	489	439	485	4.015524	3.1547	3.053789	8.451194	9.852803	9.629364
protein_co	guanosine_	21	15	16	531	509	631	0.733836	0.6177	0.736774	16.05229	19.98234	21.91384
protein_co	FtsJ_methy	640	520	515	766	635	772	8.401249	8.044041	8.908527	8.698726	9.364544	10.07142
protein_co	transcriptic	36	20	13	6736	6233	5807	0.574578	0.37617	0.273417	93.00616	111.7616	92.11028
protein_co	Yip1_doma	2745	2386	1948	2115	1216	1500	86.81184	88.92301	81.18212	57.86421	43.20353	47.14521
protein_co	transmemb	294	260	217	1032	498	698	9.79525	10.20819	9.527144	29.74479	18.64003	23.11177
protein_co	transmemb	1147	943	861	1134	831	976	18.30118	17.73105	18.10313	15.65279	14.89587	15.47659
protein_co	fibroblast_	60	62	46	104	70	60	1.461113	1.779227	1.476132	2.190932	1.915048	1.45209
protein_co	tight_junct	807	625	481	964	801	885	12.31931	11.24346	9.675934	12.73072	13.73708	13.4266
protein_co	calpain_11	0	0	0	0	2	0	0	0	0	0	0.043604	0
protein_co	tubulointer	3	3	2	0	0	0	0.090549	0.106706	0.079548	0	0	0
protein_co	hypocretin	5	3	2	10	4	5	0.144096	0.101885	0.075953	0.249314	0.129507	0.143206
protein_co	histone_clu	0	0	0	2	0	1	0	0	0	0.192029	0	0.110302
protein_co	KIAA0319	0	4	0	6	4	4	0	0.036188	0	0.039848	0.034499	0.030519
protein_co	interferon_	3	0	0	10	12	14	0.029792	0	0	0.085911	0.133879	0.138172
protein_co	solute_carr	658	631	650	339	432	341	5.245471	5.927821	6.828209	2.337875	3.868935	2.70161
protein_co	tubulin_be	802	576	569	3763	3112	3996	26.61986	22.52999	24.88734	108.051	116.0433	131.8155
protein_co	leucine_ric	131	102	96	294	252	324	2.180903	2.001116	2.106061	4.234238	4.713186	5.360677
protein_co	glial_cells_	0	1	0	13	9	9	0	0.022563	0	0.215329	0.193592	0.171257
protein_co	forkhead_b	16	14	2	274	161	219	0.387314	0.399373	0.063798	5.737952	4.378428	5.268622
protein_co	biphenyl_h	232	153	177	259	220	323	3.299036	2.563879	3.316707	3.186118	3.514559	4.564689

protein_co receptor_(T	603	457	474	793	655	619	7.673899	6.853652	7.948989	8.730416	9.364598	7.828869
protein_co tubulin_be	2155	1851	1498	12844	10942	13922	56.47913	57.16816	51.73534	291.2085	322.171	362.6202
protein_co mitochond	303	248	190	298	315	537	31.63929	30.51707	26.14403	26.91928	36.95249	55.72731
protein_co high_mobil	12385	9427	8287	35223	26837	30116	303.6935	272.4081	267.776	747.1861	739.303	733.916
protein_co transcriptic	74	84	59	190	213	178	1.19077	1.592878	1.251074	2.644922	3.850569	2.846596
protein_co flotillin_1	3241	2716	2306	2721	1936	2632	89.73942	88.6219	84.13919	65.17721	60.22248	72.42687
protein_co immediate_	674	519	417	1545	753	1026	26.43128	23.98462	21.5491	52.4143	33.17434	39.98668
protein_co mediator_c	490	443	424	1360	1531	1262	3.424114	3.648068	3.904386	8.221556	12.01922	8.764378
protein_co piggyBac_tr	197	138	144	315	239	260	3.349189	2.764774	3.226048	4.632837	4.564786	4.392952
protein_co alpha_tubu	512	524	383	650	420	544	10.24406	12.35494	10.09801	11.25068	9.440622	10.8171
protein_co thiopurine_	557	445	363	587	380	503	9.270083	8.727614	7.961041	8.451417	7.104951	8.319669
protein_co ring_finger_	3	8	13	61	62	62	0.031538	0.099107	0.180088	0.554752	0.732229	0.64775
protein_co nurim_(nuc	455	334	274	989	627	632	13.72544	11.87322	10.89182	25.80918	21.24866	18.94705
protein_co mitochond	5312	4396	3834	7546	5322	6833	136.7149	133.3284	130.0303	168.011	153.8798	174.7748
protein_co valyl-tRNA_	481	494	320	733	582	878	4.206247	5.090773	3.687521	5.545193	5.717705	7.630515
protein_co TAF8_RNA_	437	407	300	707	502	654	3.463355	3.801169	3.133082	4.847279	4.469597	5.151136
protein_co family_with	564	474	482	418	318	238	6.384161	6.32281	7.189631	4.09321	4.043905	2.677388
protein_co chromoson	7	4	15	65	21	31	0.543383	0.36591	1.534383	4.364998	1.83137	2.391548
protein_co fibroblast_g	0	0	0	1106	600	746	0	0	0	37.27269	26.25868	28.88159
protein_co fibroblast_g	2	9	3	16	17	23	0.090652	0.480727	0.179187	0.627382	0.86566	1.036064
protein_co cytoplasmi	1132	987	1178	179	295	215	8.713173	8.952703	11.94841	1.191917	2.550944	1.644667
protein_co FH2_domai	17	19	15	260	253	254	0.136715	0.180065	0.158962	1.808858	2.285798	2.030073
protein_co toll-like_re	19	11	9	24	10	7	0.239495	0.163396	0.149493	0.261708	0.141609	0.08769
protein_co mitochond	6	8	9	0	0	1	0.237226	0.372742	0.468909	0	0	0.039294
protein_co tetratricop	29	7	19	16	28	14	0.689707	0.196188	0.595464	0.329192	0.748125	0.330906
protein_co myosin_VII	0	1	3	13	6	6	0	0.008361	0.028047	0.079789	0.047823	0.042306
protein_co FCH_and_d	297	261	288	361	360	260	3.487131	3.611266	4.455938	3.666756	4.748576	3.033855
protein_co arrestin_be	153	163	173	566	702	645	2.428049	3.048321	3.61782	7.770438	12.51562	10.17268
protein_co solute_carr	1	4	3	4	0	0	0.009011	0.042477	0.035624	0.031182	0	0
protein_co protein-kin	442	386	404	1185	1015	985	3.443697	3.544027	4.14781	7.987006	8.884188	7.626908
protein_co ankyrin_rep	249	183	154	189	151	152	3.242083	2.807908	2.642289	2.128872	2.208771	1.96688
protein_co interleukin_	80	106	71	91	139	110	1.038059	1.620858	1.214018	1.021495	2.026263	1.418516
protein_co nuclear_mi	3813	3031	2757	2310	2344	2432	27.49067	25.75204	26.1933	14.40766	18.98564	17.42576
protein_co coiled-coil_	711	685	526	1284	827	984	9.377441	10.64664	9.141875	14.65017	12.25376	12.89791
protein_co synaptotag	243	251	230	379	371	322	2.037482	2.480095	2.541266	2.749095	3.494705	2.6832
protein_co RAB30_mer	366	326	352	145	151	92	1.951496	2.048384	2.473227	0.668833	0.904508	0.487511
protein_co CREB/ATF_b	821	777	817	941	862	863	10.04032	11.1978	13.16623	9.955364	11.84298	10.48878
protein_co leucine_ric	817	650	617	103	100	79	10.03312	9.40664	9.984678	1.094244	1.379632	0.964164
protein_co prolylcarbo	1794	1650	1389	1403	1075	1116	13.42988	14.55596	13.70209	9.085954	9.04081	8.302783
protein_co asparaginyl	162	155	143	660	389	568	3.404701	3.838864	3.960361	11.99971	9.184649	11.86375
protein_co ring_finger_	411	320	325	512	366	528	8.289047	7.605361	8.637359	8.932967	8.292642	10.58294
protein_co mitochond	668	616	491	1972	1147	1611	30.83224	33.50553	29.86379	78.74058	59.47592	73.8982
protein_co peptidase_i	124	82	178	97	105	67	0.975146	0.759922	1.844603	0.659907	0.927655	0.52364
protein_co tocopherol	0	0	0	78	49	58	0	0	0	1.527936	1.246501	1.305225

protein_co	gamma-glu	642	652	492	2454	1809	2009	21.15004	25.31226	21.35876	69.93809	66.95204	65.77575
protein_co	solute_carr	10	13	11	1	4	1	0.139686	0.213995	0.202479	0.012084	0.062771	0.013882
protein_co	sulfatase_1	1787	1649	1467	824	720	647	16.5684	18.01705	17.92342	6.609159	7.49959	5.961697
protein_co	trimethylgu	321	277	316	905	683	638	4.493405	4.569382	5.828979	10.95928	10.74089	8.875665
protein_co	syndecan_b	4244	3740	3840	4671	3423	3816	62.60284	65.01257	74.64224	59.60621	56.72501	55.94183
protein_co	NIMA-relat	368	310	340	298	246	217	3.446362	3.421227	4.195916	2.414306	2.588197	2.01968
protein_co	DEAD_(Asp	57	57	79	28	45	13	0.497058	0.585752	0.907807	0.211229	0.440853	0.112664
protein_co	neurexophi	0	2	0	2	0	0	0	0.068483	0	0.050273	0	0
protein_co	sortilin-rel	5	4	6	484	583	414	0.024276	0.022886	0.038388	2.032893	3.179976	1.997635
protein_co	transmemb	0	0	0	6	4	2	0	0	0	0.049512	0.042866	0.01896
protein_co	BUD13_hor	189	117	129	586	519	481	4.556397	3.323936	4.098116	12.22138	14.05647	11.5243
protein_co	transient_r	18	15	7	12	10	7	0.206621	0.202909	0.105885	0.119165	0.128959	0.079857
protein_co	matrix_met	2	7	4	2	4	1	0.080032	0.330094	0.210925	0.069235	0.179821	0.039769
protein_co	matrix_met	0	0	0	24	11	7	0	0	0	0.56195	0.334476	0.188292
protein_co	chromoson	68	60	89	31	24	22	1.641581	1.706915	2.83125	0.647408	0.650899	0.52782
protein_co	DCN1_defe	744	568	514	1965	1249	1671	25.66	23.08549	23.36047	58.62857	48.39441	57.27562
protein_co	Yes-associat	2238	1990	2123	4050	4144	3890	21.99813	23.05079	27.4986	34.43846	45.7609	38.00012
protein_co	tripartite_r	11	6	6	58	50	59	0.174985	0.112478	0.125775	0.798178	0.893568	0.932761
processed_	solute_carr	203	122	134	484	429	419	1.833337	1.298414	1.594725	3.781418	4.352639	3.760711
protein_co	B-cell_trans	1	1	0	0	3	5	0.037978	0.044754	0	0	0.127997	0.188716
protein_co	POU_class_	23	12	4	4	0	4	0.40413	0.248474	0.092616	0.060802	0	0.069849
protein_co	radixin	1755	1379	1678	3112	3126	2922	20.68836	19.15669	26.06608	31.73596	41.39873	34.23252
protein_co	protein_ph	562	495	549	1527	1280	1227	5.325369	5.527461	6.855207	12.51744	13.62613	11.55494
protein_co	ferredoxin_	277	280	224	716	505	561	4.574128	5.44871	4.87429	10.22833	9.368477	9.206638
protein_co	chromoson	94	82	73	240	145	244	1.724941	1.773239	1.765241	3.809961	2.989258	4.449854
protein_co	FXYD_dom	53	49	34	86	52	58	1.292433	1.408106	1.092562	1.814236	1.424573	1.405626
protein_co	Rho_GTPas	99	71	74	0	4	1	0.846851	0.71571	0.834138	0	0.03844	0.008501
protein_co	FXYD_dom	0	0	1	0	0	0	0	0	0.04452	0	0	0
protein_co	matrix_met	289	286	232	0	0	1	5.633265	6.569547	5.959161	0	0	0.019372
protein_co	transmemb	3	0	0	49	28	43	0.048585	0	0	0.686493	0.50943	0.692078
protein_co	caspase_1_	8	2	6	0	0	0	0.211658	0.062357	0.209185	0	0	0
protein_co	alkB_alkyla	76	65	90	211	193	163	0.986398	0.994166	1.539273	2.369102	2.814134	2.102498
protein_co	mitogen-ac	354	327	263	241	220	253	7.985135	8.692283	7.81753	4.702828	5.575075	5.671647
protein_co	unc-13_hor	0	0	0	3	3	5	0	0	0	0.016879	0.02192	0.032318
protein_co	sulfide_qui	21	28	16	61	35	30	0.555048	0.87212	0.55727	1.394774	1.03927	0.788029
protein_co	CTD_(carbo	408	434	421	962	832	680	3.163434	3.965477	4.301456	6.452628	7.247212	5.239829
protein_co	SAFB-like_t	1202	966	930	1630	1606	1526	15.34485	14.53256	15.64501	18.0015	23.03311	19.36075
protein_co	thrombosp	8696	7000	8552	12053	10778	9816	59.2122	56.16902	76.73512	70.99861	82.44777	66.42566
protein_co	mitogen-ac	1031	799	779	422	569	596	7.547313	6.892671	7.514601	2.672447	4.679452	4.336003
protein_co	nucleolar_a	474	412	364	2329	1627	1837	10.41678	10.66988	10.54123	44.27798	40.16908	40.12122
protein_co	NADH_dehy	255	276	176	339	275	382	8.517321	10.86373	7.746585	9.795476	10.31917	12.68048
protein_co	kinesin_fam	282	207	269	2618	1678	1807	4.135557	3.577357	5.198427	33.21372	27.64559	26.33617
protein_co	integrin_al	1334	1201	1132	3	10	3	14.08803	14.94667	15.75345	0.027408	0.118643	0.031487
protein_co	cancer_sus	211	126	212	876	701	596	1.166881	0.821148	1.544951	4.190937	4.35523	3.275668

protein_co	HAUS_augn	376	332	280	1342	913	1135	5.040723	5.245056	4.946498	15.56397	13.7507	15.12204
protein_co	Rtf1_Paf1/I	1421	1128	1172	2188	1778	2017	14.9829	14.01581	16.28412	19.95778	21.06118	21.13574
protein_co	poly_(ADP-	402	334	297	650	408	520	5.819601	5.697977	5.665763	8.140358	6.635541	7.481352
protein_co	ribosomal_	21659	19419	14813	29532	16763	29552	584.4286	617.4859	526.7092	689.3646	508.1523	792.4824
protein_co	progestin_a	32	31	44	83	61	68	0.309144	0.352923	0.560143	0.69367	0.662049	0.652875
protein_co	leucine_ric	134	114	97	182	139	131	2.317574	2.323489	2.210728	2.723097	2.700801	2.251696
protein_co	tubulin_ga	466	375	246	655	524	605	5.633821	5.342635	3.919107	6.850487	7.117009	7.269125
protein_co	regulator_c	464	409	370	835	659	771	7.828114	8.131479	8.225753	12.18677	12.49032	12.92716
protein_co	inositol-tris	69	50	45	98	66	83	2.0049	1.712067	1.723023	2.463388	2.154451	2.396798
protein_co	uveal_auto	807	578	637	731	557	588	6.156994	5.19673	6.404267	4.824759	4.774187	4.458432
protein_co	SMAD_fami	403	333	286	1114	789	890	7.142692	6.955177	6.679712	17.08068	15.71024	15.67677
protein_co	phospholip	66	70	37	154	125	128	0.752553	0.940586	0.555943	1.519068	1.601225	1.450484
protein_co	transmemb	29	4	4	212	201	227	0.554056	0.090058	0.100705	3.503922	4.314204	4.310137
protein_co	p21_protei	7	9	1	230	142	144	0.087921	0.133212	0.016551	2.49911	2.003696	1.797491
protein_co	ADAM_met	2499	2106	2594	2739	2852	2315	26.2812	26.10023	35.94874	24.91919	33.69593	24.19577
protein_co	dual_oxida	34	22	24	27	29	35	0.313697	0.2392	0.291795	0.215505	0.300593	0.320929
protein_co	solute_carr	7	8	5	5	9	1	0.150401	0.202558	0.141565	0.092936	0.217242	0.021353
protein_co	stimulated_	144	131	83	681	578	584	2.640631	2.830895	2.005664	10.80327	11.90754	10.64309
protein_co	cytochrom	32	10	11	20	18	17	0.383544	0.141245	0.173737	0.207376	0.242374	0.202499
protein_co	zinc_finger_	402	304	321	276	208	193	4.34155	3.869006	4.568342	2.578641	2.523662	2.071504
protein_co	sema_dom	7	4	8	42	45	34	0.060762	0.040917	0.091508	0.315388	0.438829	0.293307
protein_co	BCL2-like_1	4	5	0	4	2	0	0.169547	0.249751	0	0.146674	0.095238	0
protein_co	ribosomal_	1445	1373	1054	2559	1571	1962	37.96513	42.51035	36.49156	58.16347	46.37055	51.23016
protein_co	spectrin_be	16	38	9	76	106	175	0.072262	0.202247	0.053563	0.296939	0.53783	0.785485
protein_co	GRINL1A_c	8	0	2	0	0	0	0.134198	0	0.04421	0	0	0
protein_co	GTP_cyclol	42	60	47	102	105	141	2.832512	4.768489	4.17691	5.950941	7.955377	9.450422
protein_co	breast_can	547	400	439	642	508	543	9.001779	7.757256	9.520075	9.13985	9.391907	8.880768
protein_co	tubulin_tyr	441	457	467	583	512	463	2.762302	3.373307	3.854644	3.159106	3.602895	2.882194
protein_co	formin_bin	1340	1130	1278	2270	2090	1841	13.28233	13.19943	16.69303	19.46518	23.27367	18.13564
protein_co	cysteine_cc	223	213	180	654	328	425	5.703305	6.419607	6.066372	14.4698	9.424203	10.8024
protein_co	general_tra	290	232	215	608	333	429	11.36409	10.71351	11.10222	20.6112	14.65987	16.7072
protein_co	bromodom	0	0	1	0	0	0	0	0	0.018875	0	0	0
protein_co	Rab_gerany	1013	896	780	2118	1590	1868	13.88279	14.47046	14.0863	25.11056	24.48012	25.44216
protein_co	interferon-i	138	173	155	0	0	0	1.418062	2.09493	2.098857	0	0	0
protein_co	GIPC_PDZ_	6	8	23	13	21	21	0.08257	0.129738	0.417093	0.154766	0.324667	0.28721
protein_co	Rho_GTPas	2248	1878	2278	3376	3278	2910	14.03436	13.81653	18.74066	18.23315	22.99081	18.05506
protein_co	interferon-i	178	154	154	0	0	0	5.58595	5.695145	6.368432	0	0	0
protein_co	solute_carr	36	29	15	111	54	47	0.432564	0.410632	0.237505	1.153808	0.728938	0.561248
pseudogen	-	148	137	107	173	109	181	10.48898	11.44193	9.992866	10.60671	8.678547	12.74852
protein_co	chloride_cl	42	61	31	303	270	219	0.552428	0.945503	0.537307	3.447719	3.989689	2.862727
protein_co	dihydrolipo	365	272	239	411	339	397	5.461691	4.796343	4.712669	5.320336	5.698795	5.903838
protein_co	RNA_3'-terr	942	851	746	1529	1209	1462	19.67275	20.94357	20.52994	27.62388	28.36544	30.34388
protein_co	intraflagell	522	462	414	304	321	309	4.965894	5.179359	5.189937	2.501863	3.430686	2.921427
protein_co	ethanolami	633	476	655	1751	1510	1431	4.13673	3.665789	5.640655	9.899257	11.08612	9.294001

protein_co	cell_growth	47	28	28	1	3	3	1.308216	0.918431	1.027009	0.024079	0.093811	0.082987
protein_co	hydroxyacy	2066	1869	1544	1734	1330	1429	37.93829	40.44491	37.36195	27.54606	27.43773	26.0789
protein_co	ketohexoki	4	8	4	82	69	90	0.087832	0.20701	0.115742	1.557657	1.702131	1.964025
protein_co	adenylate_	579	490	494	459	500	535	6.069868	6.053463	6.824369	4.162712	5.888705	5.573964
protein_co	protein_ph	334	318	301	759	664	741	4.560818	5.117178	5.416236	8.966048	10.18623	10.05597
protein_co	polyribonu	312	255	282	1598	1050	1171	3.744636	3.606636	4.460042	16.59185	14.15772	13.96759
protein_co	dynein_cyt	268	251	184	215	120	209	4.887422	5.394185	4.421786	3.391927	2.458529	3.787922
protein_co	luteinizing_	0	0	0	12	15	11	0	0	0	0.180548	0.293081	0.19013
protein_co	SMEK_hom	938	780	814	1421	1194	1082	9.473226	9.28318	10.83314	12.41516	13.54717	10.86005
protein_co	THUMP_do	138	139	106	277	158	172	2.320793	2.754731	2.349081	4.029955	2.985132	2.874719
protein_co	cytochrom	4698	3945	4507	6814	5954	5213	47.40171	46.90673	59.92436	59.4766	67.48992	52.27312
protein_co	RAB1A_mer	3812	3195	3079	5366	3921	5103	82.47285	81.45844	87.78142	100.4319	95.30244	109.7219
protein_co	ARP2_actin	7279	6413	7013	7182	7683	7207	99.80769	103.6241	126.7158	85.19237	118.3511	98.21017
protein_co	prolactin_r	896	707	659	1567	1064	1211	15.51689	14.42857	15.03893	23.47625	20.70081	20.84253
protein_co	solute_carr	657	503	400	5015	3599	4159	10.76516	9.712482	8.636742	71.08682	66.25002	67.72573
protein_co	ATP-bindin	0	0	0	2	3	1	0	0	0	0.0302	0.058829	0.017347
protein_co	prolyl_end	687	570	664	776	509	469	5.797938	5.668899	7.384476	5.665543	4.825959	3.933682
protein_co	solute_carr	1	2	4	0	0	6	0.017712	0.041745	0.09336	0	0	0.105615
protein_co	elastin_mic	8125	7024	5116	127	144	252	109.2295	111.2777	90.63203	1.477009	2.174843	3.366872
protein_co	F-box_prot	902	769	849	1182	1197	1001	11.77627	11.83136	14.60642	13.35001	17.55676	12.98808
protein_co	all-trans_re	541	562	405	797	430	592	23.09764	28.27573	22.78559	29.43688	20.62471	25.11897
protein_co	centromere	211	174	192	792	671	720	2.546865	2.475026	3.053933	8.270117	9.099029	8.637053
protein_co	leucine-rich	2634	2269	2504	5696	4062	4229	22.01209	22.34534	27.57494	41.17925	38.13594	35.1231
protein_co	tripartite_r	0	2	0	0	0	1	0	0.061557	0	0	0	0.025957
protein_co	dystrobrevi	82	70	64	161	127	101	1.754714	1.765215	1.804709	2.980446	3.053129	2.147946
protein_co	ARP1_actin	2984	2392	2233	4486	3379	3829	44.89228	42.40735	44.26866	58.38417	57.10973	57.24899
protein_co	cytochrom	0	0	0	2	0	0	0	0	0	0.049593	0	0
protein_co	transmemb	17	19	10	86	55	61	0.317571	0.418266	0.246165	1.389804	1.154261	1.132483
protein_co	cytochrom	0	0	0	16	22	12	0	0	0	0.346142	0.618078	0.298237
protein_co	myoferlin	5721	4650	5658	6316	5611	4824	44.26709	42.40031	57.69083	42.27797	48.77512	37.0959
protein_co	lysyl_oxida	148	132	86	14	13	5	2.144886	2.254361	1.642388	0.175523	0.211658	0.072015
protein_co	STAM_bind	114	97	76	94	66	79	1.442465	1.446369	1.267211	1.028943	0.938196	0.99343
protein_co	cholesterol	79	96	48	20	3	5	3.035079	4.346315	2.430071	0.664716	0.129483	0.190907
protein_co	ladybird_h	0	0	0	5	2	0	0	0	0	0.108067	0.056136	0
protein_co	ATPase_fam	708	613	592	1336	962	951	8.078065	8.242172	8.900833	13.18693	12.331	10.78361
protein_co	BTB_(POZ)_	0	1	2	0	0	0	0	0.033705	0.075379	0	0	0
protein_co	kinesin_fam	466	396	457	2122	1788	1764	5.078325	5.085537	6.562746	20.0052	21.89027	19.10481
protein_co	CUB_and_z	15	13	23	22	16	15	0.27355	0.27938	0.552723	0.347081	0.327804	0.27186
protein_co	transformir	421	290	324	588	658	648	2.304162	1.870406	2.336742	2.784013	4.045813	3.524646
protein_co	dual_specif	878	809	796	688	392	474	18.17841	19.73863	21.71747	12.3229	9.117935	9.75325
protein_co	calcium_ho	82	45	53	88	93	96	2.142725	1.38571	1.825002	1.989291	2.730138	2.493065
protein_co	ADP-ribosy	686	689	511	779	573	843	35.71044	42.26661	35.05313	35.08097	33.51003	43.61224
protein_co	centrosom	207	224	205	1563	1145	1164	4.154202	5.297518	5.421332	27.13559	25.81498	23.2156
protein_co	kinesin_fam	186	147	163	1003	897	891	1.51028	1.406595	1.744082	7.045445	8.1825	7.190049

protein_co	ectonucleo	193	175	209	366	379	356	0.81163	0.867253	1.158196	1.331512	1.790561	1.487855
protein_co	exocyst_co	19	10	13	282	181	255	0.281996	0.174903	0.254254	3.620771	3.017982	3.761307
protein_co	phospholip	430	339	403	76	83	37	2.848427	2.646326	3.517843	0.435525	0.61768	0.243584
protein_co	retinol_bin	22	17	6	25	6	11	0.886379	0.807147	0.318554	0.871364	0.27158	0.440452
protein_co	debranchin	312	252	194	692	497	616	6.195645	5.897115	5.076548	11.88779	11.0876	12.15688
protein_co	DnaJ_(Hsp4	1401	1035	1322	1114	1045	884	9.595127	8.353338	11.93106	6.600256	8.040405	6.016924
protein_co	G_protein-	1	0	0	468	264	349	0.032924	0	0	13.32953	9.764703	11.41934
protein_co	annexin_A7	637	540	601	1486	1070	1094	15.51215	15.49649	19.28599	31.30505	29.27288	26.47644
protein_co	family_with	303	309	264	534	378	347	2.966184	3.564684	3.405604	4.522303	4.157155	3.375938
protein_co	nuclear_rec	2498	2066	2224	4115	3098	2843	35.40739	34.50952	41.54044	50.4585	49.33237	40.04866
protein_co	microsemi	0	0	0	1	0	0	0	0	0	0.060984	0	0
protein_co	translocase	479	457	290	1783	1028	1310	15.07654	16.95077	12.02815	48.54902	36.35032	40.97765
protein_co	activating_	487	446	385	855	539	645	10.64503	11.48841	11.08954	16.16766	13.23597	14.01159
protein_co	phospholip	0	2	0	0	2	0	0	0.110617	0	0	0.105454	0
protein_co	zinc_finger_	58	44	38	43	21	28	0.73582	0.657815	0.635276	0.471927	0.299304	0.35303
protein_co	oncoprotei	0	0	3	0	0	4	0	0	0.088495	0	0	0.088988
protein_co	ADAM_met	3065	2519	2258	5	5	5	30.796	29.82628	29.89666	0.043461	0.056439	0.049928
protein_co	ribosomal_	19095	17557	11359	18745	12688	17186	359.2425	389.2471	281.6067	305.0819	268.17	321.3309
protein_co	tet_methyl	74	64	61	273	302	239	0.421795	0.42989	0.458178	1.346156	1.933864	1.353871
protein_co	DNA_replic	130	91	103	758	511	461	1.558498	1.285617	1.627178	7.861316	6.88229	5.492545
protein_co	myopalladi	13	2	9	2	1	5	0.114457	0.020751	0.104419	0.015233	0.009891	0.04375
protein_co	aldehyde_d	69	48	79	17	11	6	0.720499	0.590653	1.087041	0.153566	0.12904	0.062265
protein_co	5-aminoim	1067	926	824	4059	2537	2833	24.82991	25.39386	25.26811	81.7133	66.32545	65.51895
protein_co	SWI/SNF_re	468	353	307	845	633	640	7.57456	6.732763	6.547639	11.83127	11.50971	10.2944
protein_co	BRCA1_assc	71	64	70	514	456	466	0.683544	0.726098	0.888058	4.280894	4.931991	4.458656
protein_co	signal_tran	13	11	16	5	7	0	0.243881	0.243184	0.39554	0.081146	0.147531	0
protein_co	myostatin	1	0	0	0	0	1	0.01876	0	0	0	0	0.018644
protein_co	amyotroph	83	99	81	61	37	52	0.740496	1.040847	0.952279	0.470801	0.370847	0.46106
protein_co	asparagine_	684	560	573	1356	953	1005	14.78026	14.26005	16.31607	25.34829	23.13492	21.5825
protein_co	methyltran	289	282	213	819	494	559	11.16784	12.84185	10.84641	27.37905	21.44606	21.46807
protein_co	Sjogren_syr	1416	1196	1119	2432	1948	2025	30.43624	30.29465	31.69513	45.22247	47.03982	43.25759
protein_co	NGFI-A_bin	171	191	182	859	734	691	2.077308	2.734295	2.913473	9.027366	10.01728	8.34243
protein_co	cyclin-depe	34	24	35	1	0	5	0.491936	0.409212	0.667318	0.012517	0	0.071897
protein_co	peptidylpro	743	581	585	1628	1273	1245	6.177004	5.692097	6.408844	11.70864	11.88958	10.28651
protein_co	FAST_kinas	155	206	137	554	462	394	2.765707	4.331605	3.221291	8.551599	9.261164	6.986834
protein_co	malate_deh	18	19	21	41	25	29	0.373262	0.464304	0.573846	0.735509	0.582412	0.597653
protein_co	HECT_C2_a	299	238	314	99	115	80	2.285498	2.143846	3.162817	0.654648	0.987544	0.607728
protein_co	isocitrate_d	1776	1595	1572	3409	2413	2538	38.51831	40.76544	44.92744	63.96086	58.79369	54.70482
protein_co	Obg-like_A7	2086	1808	1428	3680	2461	2660	25.00224	25.53702	22.55421	38.15711	33.13793	31.68516
protein_co	corepresso	482	375	307	462	363	412	13.28348	12.17876	11.14905	11.01462	11.23881	11.28422
protein_co	sperm_spec	1123	955	1107	7530	6912	6140	9.184727	9.204431	11.93078	53.27758	63.50958	49.90735
protein_co	cholinergic	26	15	26	0	0	1	0.693783	0.471681	0.914237	0	0	0.026519
protein_co	family_with	53	50	81	186	153	170	0.486118	0.540434	0.979007	1.475848	1.576545	1.549617
protein_co	WD_repeat	532	398	346	1190	785	938	12.34207	10.88094	10.57761	23.88286	20.45951	21.62663

protein_co abl-interact	921	758	866	1123	906	902	7.322219	7.101652	9.072684	7.723708	8.092083	7.126877
protein_co integrin_al	2647	2239	3331	6686	7139	5814	19.93383	19.87	33.05569	43.55782	60.39809	43.51324
protein_co solute_carr	96	118	135	243	263	277	1.476565	2.138801	2.736212	3.233334	4.544499	4.234193
protein_co solute_carr	490	498	451	698	512	521	5.897042	7.062762	7.152362	7.267023	6.922407	6.231398
protein_co disrupted_i	117	97	89	264	163	168	1.722496	1.682873	1.726622	3.362322	2.695933	2.458054
protein_co SUMO1/ser	350	255	391	285	278	282	3.747088	3.217163	5.516166	2.639573	3.343641	3.000437
protein_co coiled-coil_	0	0	0	6	0	4	0	0	0	0.21236	0	0.16264
protein_co cytochrom	182	148	146	446	325	537	14.08664	13.4991	14.89099	29.86303	28.25976	41.30664
protein_co poly_(ADP-	81	60	74	41	35	41	0.633509	0.553001	0.762666	0.277405	0.307528	0.318685
protein_co meiosis-spe	66	53	76	144	97	100	1.72719	1.634478	2.620865	3.260031	2.851786	2.600793
protein_co ubiquitin_s	631	549	620	682	664	612	5.71234	5.856851	7.396244	5.341117	6.75308	5.506122
protein_co SECIS_bind	710	611	783	1043	1088	869	5.23803	5.311999	7.612131	6.656669	9.01753	6.371462
protein_co tropomodu	2287	1946	2073	1700	1467	1425	25.93746	26.00825	30.98099	16.67912	18.69134	16.06149
protein_co signal_pept	400	289	328	597	483	501	9.092485	7.741543	9.824971	11.73978	12.33442	11.31801
protein_co glucuronic_	353	295	357	938	783	749	3.710179	3.653838	4.944509	8.528762	9.245512	7.823689
protein_co Src_homol	212	159	141	405	330	427	4.489396	3.96786	3.934649	7.419423	7.850821	8.98648
protein_co anterior_pl	405	340	320	183	153	186	5.11843	5.063697	5.329255	2.000764	2.172312	2.336169
protein_co von_Willeb	383	302	301	1185	869	826	7.753882	7.205007	8.030114	20.754	19.76465	16.6192
protein_co cartilage_in	701	581	584	1	1	0	8.332204	8.138139	9.147229	0.010283	0.013353	0
protein_co poly_(ADP-	164	135	111	95	44	81	3.179174	3.083978	2.83549	1.593151	0.958235	1.560505
protein_co phosphopa	114	112	85	281	189	279	2.682344	3.105523	2.635502	5.719774	4.995977	6.524142
protein_co hyperpolar	0	0	0	52	86	71	0	0	0	0.329489	0.707655	0.516823
protein_co semaphorin	335	264	249	263	256	364	4.565054	4.239475	4.471315	3.100415	3.919134	4.929605
protein_co ubiquitin-li	535	471	381	1466	768	1001	16.46711	17.08408	15.45338	39.03558	26.55669	30.62015
protein_co Rho_GTPas	620	513	555	39	36	38	7.04214	6.866532	8.306934	0.383213	0.459372	0.42895
protein_co family_with	347	325	296	270	245	230	3.135972	3.461252	3.525082	2.110909	2.48747	2.065762
protein_co HECT_and_	190	193	207	80	67	72	2.022274	2.420754	2.903297	0.736613	0.801143	0.761603
protein_co HECT_and_	13	7	9	101	145	124	0.182024	0.115502	0.166059	1.223404	2.28088	1.725507
protein_co HECT_and_	1	6	3	127	101	102	0.01507	0.106555	0.059576	1.655696	1.709954	1.52765
protein_co protocadhe	192	131	176	441	506	424	1.894273	1.52307	2.288173	3.763943	5.608426	4.157353
protein_co N-deacetyla	4	3	5	3	0	1	0.063194	0.055853	0.104093	0.041002	0	0.015701
protein_co chromoson	79	55	70	346	283	284	0.628734	0.515834	0.73413	2.382204	2.530319	2.2463
protein_co adaptor-rel	258	310	227	753	631	622	4.706677	6.664437	5.457018	11.88373	12.93222	11.27703
protein_co COP9_signa	561	454	504	1155	817	862	13.06639	12.46108	15.46885	23.27221	21.37784	19.95306
protein_co heterogene	4506	4001	3419	10440	9381	13532	51.893	54.29917	51.88616	104.0114	121.3712	154.8778
protein_co protein_kir	0	0	2	10	9	11	0	0	0.040666	0.133486	0.156014	0.168684
protein_co RasGEF_do	0	0	0	229	219	202	0	0	0	1.658698	2.059976	1.680854
protein_co SEC31_hon	6999	6028	6054	4711	3397	3263	86.61384	87.90866	98.72532	50.43447	47.2276	40.13082
protein_co fibroblast_	180	167	229	0	0	2	1.820668	1.990591	3.05231	0	0	0.020105
protein_co 1-acylglyce	29	8	15	1164	873	899	0.583538	0.1897	0.397738	20.26223	19.73488	17.97797
protein_co fibroblast_	134	89	115	237	298	207	1.047099	0.819558	1.184174	1.602117	2.616062	1.607544
protein_co Bardet-Biec	310	336	276	533	447	402	4.374123	5.586961	5.131841	6.506081	7.08575	5.63722
protein_co KIAA1109	650	603	847	523	465	442	2.164799	2.366621	3.717256	1.506846	1.739828	1.462972
protein_co bone_morp	76	44	70	33	22	14	0.722744	0.493095	0.87721	0.271486	0.23504	0.132315

protein_co	RAP1_GTP-	826	649	687	1740	960	1155	11.87972	10.99963	13.02021	21.64903	15.51124	16.50889
protein_co	La_ribonuc	179	125	161	446	291	381	1.937526	1.594452	2.29644	4.176306	3.538641	4.098539
protein_co	multimerin	0	0	1	11	8	17	0	0	0.013372	0.096567	0.091203	0.171447
protein_co	phosphodi	60	62	92	263	309	231	0.444012	0.540682	0.897152	1.683689	2.568921	1.698888
protein_co	PR_domain	55	54	84	207	207	213	0.546295	0.632071	1.099459	1.778682	2.309853	2.102588
protein_co	transient_r	10	1	13	4	10	5	0.144057	0.016976	0.246782	0.049849	0.161839	0.071584
protein_co	N-acylethar	196	164	158	82	57	62	5.469918	5.393562	5.810542	1.97971	1.787099	1.719595
protein_co	nucleopori	538	372	378	1352	904	886	12.03306	9.804916	11.1409	26.15975	22.71493	19.69415
protein_co	BMP2_indu	175	134	217	199	211	196	1.342317	1.211237	2.193369	1.320484	1.818229	1.494111
protein_co	GTPase_act	2533	2087	2584	3956	3514	3389	27.46253	26.66459	36.91753	37.10434	42.80122	36.51628
protein_co	septin_11	7470	6427	7228	7503	6637	6299	70.70789	71.69067	90.15716	61.43915	70.5778	59.25548
protein_co	Fraser_sync	738	641	721	959	1172	800	3.130896	3.204627	4.030718	3.519605	5.585846	3.372966
protein_co	scavenger_	3645	3220	3055	1454	1317	1204	40.51437	42.17688	44.74634	13.98102	16.44547	13.29988
protein_co	cyclin_G2	1042	936	853	398	333	343	9.982721	10.5673	10.76874	3.298582	3.584054	3.265765
protein_co	CCR4-NOT_	260	201	220	371	355	313	1.55656	1.418063	1.735601	1.921451	2.387646	1.862286
protein_co	USO1_vesic	2101	1954	2022	1719	1369	1189	30.99165	33.96646	39.30381	21.936	22.68669	17.43051
protein_co	cyclin-depe	4	1	1	26	38	26	0.062597	0.018442	0.020622	0.351987	0.668071	0.404365
protein_co	shroom_fa	164	121	168	1984	2283	2183	0.78787	0.68502	1.063542	8.245465	12.32155	10.42255
protein_co	annexin_A3	15	15	11	7158	4307	5147	0.271585	0.320046	0.262447	112.1165	87.60697	92.6144
protein_co	pyrophospl	711	624	581	965	746	907	22.35217	23.11754	24.06916	26.24462	26.34741	28.33785
protein_co	centromere	311	308	338	1163	810	914	1.911826	2.231238	2.738039	6.184873	5.593996	5.583981
protein_co	glutathione	129	111	110	758	706	691	1.598265	1.62065	1.795919	8.124402	9.826819	8.50838
protein_co	integrator_	88	111	89	169	108	106	2.35889	3.506348	3.143763	3.918995	3.252354	2.823843
protein_co	glutamyl_a	35	32	28	180	167	157	0.266878	0.287542	0.281344	1.187355	1.430574	1.189746
protein_co	caspase_6_	186	147	104	858	663	794	6.361127	5.924416	4.686939	25.38466	25.47321	26.98679
protein_co	lymphoid_	368	301	243	2307	1776	1652	5.603188	5.400836	4.875605	30.38771	30.37942	24.9981
protein_co	hydroxyacy	482	372	334	1414	807	1002	12.48413	11.35432	11.39968	31.6828	23.48193	25.79221
protein_co	epidermal_	14	3	6	150	81	85	0.15188	0.038353	0.085775	1.407753	0.987203	0.916433
protein_co	3'-phospho	1859	1480	1603	2552	2050	2323	36.0371	33.80953	40.94857	42.79707	44.64505	44.75373
protein_co	SEC24_fam	683	555	657	1015	866	840	7.113653	6.811959	9.01721	9.145365	10.13302	8.694826
protein_co	protein_ph	1838	1626	1701	1090	892	890	20.76959	21.6526	25.32921	10.65546	11.32391	9.994985
protein_co	solute_carr	84	91	78	1598	1269	1226	1.102937	1.408056	1.349587	18.15145	18.71898	15.99822
protein_co	microsoma	7	1	0	2	3	0	0.090564	0.015246	0	0.022385	0.043604	0
protein_co	fibrillin_2	9577	8107	10098	7986	9492	7463	45.5458	45.43454	63.28329	32.85574	50.71374	35.27297
protein_co	mitogen-ac	4004	3640	2479	1130	1200	1638	37.44493	40.11506	30.54993	9.141983	12.60751	15.22378
protein_co	regulator_c	1635	1286	1190	1092	843	990	18.85396	17.47563	18.08284	10.89358	10.92098	11.34566
protein_co	guanylyl_cy	1682	1521	1137	1882	1761	1906	24.64621	26.26397	21.95429	23.8565	28.98895	27.75599
protein_co	ring_finger_	604	474	505	747	496	452	10.10312	9.343376	11.13127	10.80941	9.320712	7.513918
protein_co	KIAA1644	19	13	13	33	56	47	0.148997	0.120136	0.134339	0.223873	0.493357	0.366295
protein_co	parvin_gam	5	5	0	0	0	0	0.05222	0.061538	0	0	0	0
protein_co	beta-14-N-a	4	2	2	48	44	65	0.041785	0.02462	0.027531	0.43377	0.516366	0.674805
protein_co	phosphodi	0	0	1	0	1	0	0	0	0.093391	0	0.07962	0
protein_co	endoplasm	4	1	0	420	192	256	0.101032	0.029765	0	9.177262	5.448176	6.426144
protein_co	ets_variant	119	93	101	196	152	162	2.84938	2.624179	3.186835	4.059966	4.088801	3.855032

protein_co	GABA(A)_re	380	317	376	730	595	679	6.259358	6.153363	8.161479	10.40236	11.01063	11.11541
protein_co	kinesin_fan	50	45	56	458	422	369	0.398472	0.422617	0.588099	3.157594	3.778238	2.922563
protein_co	copine_VIII	113	112	104	398	309	280	1.714627	2.002702	2.079502	5.224409	5.267429	4.222394
protein_co	tyrosyl-tRN	400	359	334	1029	645	723	9.979452	10.55476	10.98065	22.2088	18.07821	17.92646
protein_co	FYVE_RhoG	112	55	103	237	197	181	0.719412	0.416322	0.871829	1.316955	1.421591	1.155441
protein_co	ALG10_alp	18	19	13	105	64	94	0.398219	0.495348	0.37899	2.009563	1.590664	2.066745
protein_co	phosphatid	0	0	0	49	30	27	0	0	0	0.463667	0.368652	0.293508
protein_co	family_witl	461	458	402	5199	4379	4733	7.716029	9.033696	8.866532	75.27933	82.34115	78.72978
protein_co	AE_binding	715	648	622	584	689	770	10.45658	11.16775	11.98695	7.388553	11.32014	11.19139
protein_co	solute_carr	0	0	2	2	0	1	0	0	0.040256	0.026428	0	0.01518
protein_co	methyltran	70	40	45	27	36	43	0.604744	0.407231	0.512296	0.20179	0.349402	0.369191
protein_co	ethanolami	756	772	803	1108	895	972	5.59064	6.727661	7.825103	7.088307	7.435528	7.143575
protein_co	zinc_finger_	811	852	587	770	507	645	23.50035	29.09379	22.41437	19.30222	16.50481	18.57475
protein_co	transmemb	74	53	73	147	119	105	1.420462	1.198894	1.846526	2.441058	2.56622	2.003073
protein_co	prickle_hor	108	84	88	114	156	107	1.344375	1.232205	1.443491	1.227622	2.181576	1.323702
protein_co	complemer	489	444	352	325	299	303	7.627621	8.161506	7.23532	4.385576	5.239629	4.697129
protein_co	NADH_dehy	158	129	130	267	228	219	2.508901	2.413922	2.720224	3.667759	4.067339	3.456052
protein_co	calsyntenin	505	467	351	786	656	902	6.223278	6.781906	5.699933	8.379409	9.081984	11.04699
protein_co	killer_cell_l	34	23	25	25	22	38	1.34831	1.074845	1.306429	0.857657	0.980127	1.497628
protein_co	vesicle-assc	197	137	121	203	137	157	3.023884	2.478144	2.44748	2.695615	2.362482	2.395015
protein_co	TAP_bindin	40	55	30	25	26	18	0.90343	1.463876	0.892875	0.48847	0.659716	0.404033
protein_co	CD27_mole	0	1	0	0	0	0	0	0.046628	0	0	0	0
protein_co	retinol_bin	33	45	30	10	48	38	1.726337	2.774158	2.068081	0.452558	2.820992	1.975626
protein_co	peroxisoma	859	802	578	592	480	528	13.98411	15.3859	12.3995	8.337316	8.778733	8.542503
protein_co	PILR_alpha_	265	224	177	5	11	19	5.205701	5.185474	4.581856	0.08497	0.242759	0.370934
protein_co	solute_carr	15	24	12	218	251	251	0.209584	0.395172	0.220945	2.635039	3.939946	3.485386
protein_co	adhesion_n	92	52	73	301	271	249	1.294332	0.862121	1.353367	3.663426	4.283278	3.481504
protein_co	SR-related_	732	678	844	1322	1376	1072	7.317373	7.986949	11.11786	11.43243	15.45296	10.64997
protein_co	collagen_ty	2	11	11	1745	1551	1789	0.02088	0.135331	0.15133	15.76003	18.19112	18.56173
protein_co	protein_tyr	3	5	6	7	12	6	0.029384	0.057713	0.077443	0.059314	0.132046	0.058406
protein_co	acidic_(leu	0	0	0	0	0	1	0	0	0	0	0	0.132864
protein_co	LLP_homol	123	133	78	444	294	446	5.255643	6.696988	4.391877	16.4122	14.11293	18.93936
pseudogen	ribosomal_	71	59	54	51	49	110	5.610165	5.493845	5.622712	3.486185	4.349731	8.638128
protein_co	leucine-rich	509	485	489	641	415	482	6.620876	7.43441	8.381878	7.213046	6.064498	6.230951
protein_co	membrane-	178	158	95	189	113	177	3.160126	3.305587	2.222506	2.902748	2.253782	3.122967
protein_co	inhibin_bet	97	92	52	14	4	13	2.114152	2.362977	1.493491	0.263971	0.097943	0.28159
protein_co	GLI_pathog	10545	8897	9389	484	285	274	94.99111	94.44676	111.4527	3.771766	2.884233	2.452995
protein_co	tryptophan	0	0	0	1	3	6	0	0	0	0.015307	0.059635	0.105509
protein_co	pleckstrin_	10243	8924	9059	3238	2440	2463	67.20468	68.9984	78.32266	18.37859	17.98503	16.06003
protein_co	transmemb	203	181	150	480	383	456	2.303262	2.420098	2.242712	4.711418	4.881971	5.141879
protein_co	leucine-rich	40	34	31	2	5	0	0.459258	0.460027	0.469022	0.019865	0.064494	0
protein_co	protein_tyr	13	9	16	0	2	0	0.095575	0.077974	0.155008	0	0.016519	0
protein_co	dual_specif	517	490	435	1143	806	959	6.220567	6.947724	6.897052	11.89731	10.89491	11.46747
protein_co	POC1_cent	100	116	113	300	224	221	0.906524	1.239208	1.349872	2.352683	2.281268	1.991045

protein_co transmemb	646	616	806	786	803	799	4.748005	5.335394	7.806359	4.997631	6.630454	5.836266
protein_co lumican	1934	1984	1374	5268	3272	4082	34.03852	41.14935	31.86661	80.20899	64.69588	71.39978
protein_co keratocan	0	4	0	7	1	2	0	0.115426	0	0.148285	0.02751	0.048672
protein_co small_nucl	845	770	593	2409	1969	2851	32.20672	34.58499	29.78375	79.43093	84.31107	107.9933
protein_co amidohydr	3	1	2	14	11	14	0.074355	0.029208	0.065321	0.30018	0.30629	0.344849
protein_co neural_pre	168	152	159	831	620	715	2.45693	2.619595	3.064188	10.51351	10.18648	10.392
protein_co synaptoner	14	10	8	21	16	10	0.20086	0.169072	0.151248	0.260644	0.25789	0.142586
protein_co achaete-scu	0	0	0	0	1	2	0	0	0	0	0.02406	0.042568
protein_co growth_arr	157	101	161	426	441	359	2.105303	1.596039	2.844957	4.941827	6.643587	4.784307
protein_co transmemb	1275	1200	1274	138	140	138	6.189232	6.864595	8.149498	0.57952	0.763491	0.665756
protein_co solute_carr	374	369	299	532	345	464	7.13254	8.292893	7.514129	8.777024	7.39164	8.794279
protein_co thymine-DI	491	472	549	1665	1479	1313	7.995702	9.057831	11.781	23.45591	27.05779	21.24954
protein_co chromoson	393	339	285	657	420	507	10.13435	10.30172	9.684625	14.65654	12.1675	12.99334
protein_co serine_deh	6	20	8	108	61	88	0.219217	0.861114	0.385166	3.413583	2.503817	3.195332
protein_co methylmal	350	346	353	591	450	467	6.799761	7.921525	9.037225	9.9329	9.821711	9.016793
protein_co glycolipid_	903	659	558	591	400	376	20.29105	17.45056	16.52288	11.4886	10.09778	8.396809
protein_co G_protein-	393	347	374	208	162	150	3.802926	3.956963	4.769049	1.741212	1.761122	1.442535
protein_co trichoplein	252	235	198	434	402	406	3.891812	4.276872	4.029501	5.798344	6.974714	6.231419
protein_co family_witl	82	75	57	127	95	132	1.3179	1.420486	1.207197	1.765774	1.715304	2.108395
protein_co forkhead_b	0	0	0	0	0	3	0	0	0	0	0	0.047117
protein_co nucleopori	892	749	796	1738	1367	1408	7.425058	7.347234	8.731379	12.51549	12.78358	11.64789
protein_co myotubula	512	512	619	587	460	535	4.789855	5.644552	7.630937	4.750655	4.834586	4.974115
protein_co solute_carr	287	207	312	22	20	14	4.781015	4.063644	6.849007	0.317047	0.374298	0.23178
protein_co solute_carr	1575	1286	1412	3689	3349	2952	11.34913	10.92019	13.40762	22.99607	27.11104	21.14015
protein_co pancreatic_	0	0	0	3	3	10	0	0	0	0.054937	0.071343	0.210372
protein_co ligand_of_r	86	118	127	305	342	262	0.984416	1.59173	1.915662	3.020252	4.398003	2.980515
protein_co sulfite_oxic	257	236	168	415	301	326	4.757285	5.148078	4.097983	6.645645	6.259528	5.997266
protein_co coiled-coil_	106	118	71	159	84	127	2.692776	3.532511	2.376772	3.494254	2.397302	3.206326
protein_co solute_carr	2	4	5	3	9	9	0.052133	0.122871	0.171746	0.06765	0.263557	0.233149
protein_co TAR_(HIV-1	483	414	349	1542	1065	1423	13.69604	13.83424	13.04091	37.82641	33.92708	40.10166
protein_co retinol_deh	3	4	3	3	6	8	0.049663	0.078033	0.065444	0.042963	0.111587	0.131617
protein_co desert_hed	0	0	0	2	0	0	0	0	0	0.047313	0	0
protein_co activin_A_r	1	0	3	12	10	14	0.012847	0	0.050786	0.133363	0.144324	0.178742
protein_co G_protein-	2	0	0	7	0	1	0.051878	0	0	0.157076	0	0.025779
protein_co neuropepti	20	17	17	23	14	25	0.753072	0.754332	0.843511	0.7492	0.592221	0.935527
protein_co nucleic_aci	846	731	551	1227	753	979	25.23272	25.6932	21.65609	31.6593	25.23119	29.01924
protein_co NEDD4_bin	8	7	7	16	3	8	0.139044	0.143373	0.160323	0.240572	0.058578	0.138185
protein_co SWI/SNF_re	1847	1663	1562	1100	1054	1150	22.89441	24.29192	25.51399	11.79555	14.6775	14.16674
protein_co breast_can	87	50	73	563	418	368	0.419325	0.283994	0.463649	2.347486	2.263377	1.762743
protein_co KAT8_regul	347	326	335	783	504	596	6.768801	7.493883	8.611164	13.21317	11.0449	11.55415
protein_co ceramide_s	1180	959	815	1669	1071	1133	20.83735	19.95658	18.965	25.49646	21.24707	19.88383
protein_co mitogen-ac	571	556	447	314	247	327	5.372189	6.164489	5.541885	2.555688	2.610725	3.057543
protein_co integrin_be	6	0	9	37	13	21	0.110794	0	0.218999	0.591057	0.269685	0.385384
protein_co UDP-N-acet	4	2	5	1108	962	1024	0.040669	0.023963	0.06699	9.745571	10.98825	10.34699

protein_co cysteine_su	553	491	371	317	242	335	11.06857	11.58124	9.785322	5.488943	5.441653	6.663783
protein_co limb_regio	559	505	429	268	302	318	10.56929	11.25207	10.68873	4.38361	6.414903	5.975453
protein_co chromoson	584	505	344	685	404	591	22.58403	23.01374	17.53	22.91618	17.5517	22.71359
protein_co extended_s	3786	2968	2686	5076	3687	3945	45.67789	42.19845	42.70378	52.97977	49.97441	47.30229
protein_co transmemb	9098	7832	7146	16450	12568	13573	148.02	150.16	153.2048	231.528	229.7152	219.4624
protein_co ankyrin_rep	3887	3293	3423	3578	5480	5752	23.68573	23.64673	27.48615	18.86147	37.51474	34.8338
protein_co zinc_finger_	505	433	465	456	559	600	6.292116	6.357705	7.63472	4.91511	7.824674	7.429614
protein_co WD_repeat	178	165	239	433	388	414	2.582488	2.82104	4.569313	5.434619	6.324104	5.969366
protein_co heterogene	137	106	82	141	127	163	3.066772	2.796236	2.418854	2.730506	3.193844	3.626254
protein_co lysophosph	229	191	201	161	118	110	4.035781	3.96673	4.667916	2.454602	2.336271	1.926613
protein_co esterase_D	2166	1924	1540	2331	1514	1858	96.19983	100.6997	90.13041	89.56145	75.5424	82.01083
protein_co retinoblast	441	325	521	1100	880	870	4.823756	4.189259	7.509643	10.40884	10.8138	9.457484
protein_co strawberry_	1020	790	969	1170	1054	910	4.917568	4.488326	6.156144	4.879767	5.708735	4.360148
protein_co MORN_rep	13	5	4	39	19	59	0.482294	0.218598	0.195552	1.251687	0.791901	2.175353
protein_co SET_domai	826	734	610	765	1082	966	5.33609	5.58787	5.192874	4.27531	7.852708	6.201973
protein_co vacuolar_p	217	173	169	566	439	466	2.505058	2.353484	2.570867	5.65246	5.693399	5.346303
protein_co vacuolar_p	603	512	432	1124	869	1046	10.56717	10.57349	9.97608	17.04004	17.10843	18.21724
protein_co ras_homol	7	3	1	5	11	2	0.123323	0.062284	0.023216	0.076205	0.217716	0.035018
protein_co density-reg	1670	1571	1326	3220	2370	2658	31.92902	35.39586	33.40777	53.25839	50.90571	50.50493
protein_co diaphanou	128	170	159	1712	1520	1411	1.410584	2.207726	2.308985	16.32134	18.81836	15.45346
protein_co SLAIN_mot	3	1	0	135	126	100	0.060229	0.023659	0	2.344654	2.841853	1.995224
protein_co RNA_bindi	953	829	849	1553	1394	1369	12.21025	12.5168	14.33423	17.21338	20.06521	17.43191
protein_co serine/argi	0	0	0	31	29	23	0	0	0	0.167484	0.203468	0.142754
protein_co methyltran	0	3	2	0	1	1	0	0.172025	0.128241	0	0.054665	0.048359
protein_co muscleblin	589	588	646	536	475	452	6.67857	7.856925	9.652405	5.257703	6.050773	5.0935
protein_co ring_finger_	0	4	3	1	4	0	0	0.18136	0.1521	0.033284	0.172895	0
protein_co Zic_family_	0	0	0	5	0	0	0	0	0	0.049363	0	0
protein_co abhydrolas	156	122	167	453	351	357	1.54717	1.425872	2.182553	3.886644	3.910837	3.518774
protein_co RAB20_me	151	120	110	417	314	530	5.280112	4.944866	5.068666	12.61436	12.33516	18.41839
protein_co growth_ho	20	15	28	188	109	194	0.732241	0.647176	1.35088	5.954491	4.483316	7.05887
protein_co cullin_4A	1554	1239	1309	2521	1822	1901	22.09192	20.75682	24.52206	31.00404	29.09912	26.85803
protein_co tetratricop	4	11	4	0	0	0	0.036304	0.117652	0.04784	0	0	0
protein_co somatostat	6	1	7	0	0	0	0.073957	0.014526	0.1137	0	0	0
protein_co cadherin_2	405	367	293	1195	954	1227	6.036346	6.446029	5.754685	15.40813	15.97411	18.17495
protein_co RAS_(RAD_	1	1	0	8	5	4	0.02753	0.032443	0	0.190531	0.154644	0.109442
protein_co cerebellin_	64	80	51	3	1	2	1.444256	2.127459	1.516593	0.058566	0.025352	0.044854
protein_co testis-speci	61	65	57	41	43	51	2.316643	2.90904	2.852588	1.347027	1.834623	1.924904
protein_co neuro-oncc	1	1	1	16	10	13	0.008052	0.009489	0.01061	0.11145	0.090458	0.104028
protein_co fat_storage	0	0	0	4	2	8	0	0	0	0.15343	0.099625	0.352523
protein_co MAM_dom	2	0	0	21	28	14	0.02021	0	0	0.18358	0.317871	0.140599
protein_co thioredoxir	593	608	632	1467	1171	1208	12.60804	15.23363	17.70699	26.98273	27.9704	25.52521
protein_co FERM_dom	1535	1303	1667	1468	1477	1326	15.86266	15.86789	22.70064	13.12372	17.14736	13.61824
protein_co pellino_E3_	125	117	88	35	43	36	1.119923	1.235296	1.038952	0.271275	0.432808	0.320546
protein_co reticulon_1	1	1	3	46	15	20	0.015412	0.018162	0.060929	0.613319	0.25972	0.306341

protein_co	chromoson	407	400	432	34	44	33	3.317473	3.8422	4.640144	0.239748	0.402916	0.267323
protein_co	synaptotag	0	4	1	8	9	19	0	0.077524	0.021672	0.113821	0.166289	0.310552
protein_co	solute_carr	224	228	194	135	100	61	4.255035	5.10384	4.856145	2.218462	2.134048	1.151581
protein_co	N(alpha)-ac	492	416	425	1016	840	924	3.407505	3.395251	3.87878	6.087348	6.535815	6.35994
protein_co	ADAM_met	8	2	8	15	15	13	0.159341	0.046943	0.209972	0.258459	0.335643	0.25733
protein_co	retinol_det	2	0	0	0	0	0	0.05635	0	0	0	0	0
protein_co	DDB1_and_	1095	844	957	753	735	707	9.738012	8.845161	11.2151	5.793142	7.343323	6.248637
protein_co	RAB15_mer	634	498	489	815	753	734	9.548959	8.839001	9.705333	10.61909	12.74121	10.98683
protein_co	WD_repeat	122	102	94	259	239	251	2.157969	2.126144	2.191029	3.96322	4.74933	4.412338
protein_co	estrogen_re	2	1	2	14	11	19	0.019399	0.011431	0.025564	0.117476	0.119867	0.183156
protein_co	potassium_	1	0	0	2	1	1	0.01268	0	0	0.02194	0.014246	0.012602
protein_co	stonin_2	277	297	201	900	860	790	3.408799	4.307103	3.259512	9.581361	11.88965	9.661808
protein_co	EF-hand_ca	31	29	16	159	104	136	0.530265	0.58457	0.36065	2.352836	1.998545	2.311958
protein_co	G_protein-r	0	0	0	5	0	1	0	0	0	0.128216	0	0.029459
protein_co	prostaglanc	94	83	51	107	104	119	1.024172	1.065689	0.732234	1.008537	1.272998	1.288552
protein_co	Jun_dimeri	305	325	239	660	513	728	2.989632	3.754122	3.0871	5.596608	5.649166	7.09184
protein_co	adenylate_l	18	19	17	36	34	25	0.288769	0.359202	0.359387	0.499624	0.612782	0.398591
protein_co	solute_carr	0	0	0	0	0	3	0	0	0	0	0	0.033251
protein_co	fibulin_5	896	808	687	63	32	43	19.57702	20.80449	19.78018	1.190809	0.785485	0.93372
protein_co	serpin_pep	0	0	0	0	2	0	0	0	0	0	0.047091	0
protein_co	chromoson	283	230	203	244	188	228	5.985738	5.732792	5.657989	4.464616	4.467228	4.79265
protein_co	tryptophan	1850	1640	1439	5425	3292	3505	31.67556	33.09052	32.46745	80.35545	63.323	59.64174
protein_co	solute_carr	2	1	0	0	1	2	0.060922	0.035896	0	0	0.034221	0.060546
protein_co	WD_repeat	392	314	370	539	539	619	6.781984	6.401878	8.43543	8.067193	10.47631	10.64317
protein_co	non_impri	726	624	617	1278	1076	1074	11.88839	12.04143	13.31393	18.10424	19.79464	17.47835
pseudogen	hect_doma	1124	1064	921	871	664	771	9.96745	11.11902	10.76248	6.681884	6.615077	6.79488
protein_co	solute_carr	113	80	114	102	108	89	1.106405	0.923066	1.470874	0.86397	1.187978	0.866035
protein_co	dual_oxida	0	0	0	0	0	1	0	0	0	0	0	0.019603
protein_co	microfibril	686	524	446	1090	938	916	16.85268	15.16992	14.43825	23.16511	25.88789	22.36402
protein_co	transcriptic	2601	2173	2510	1793	1559	1431	22.71894	22.36735	28.89059	13.5485	15.29829	12.42216
protein_co	sorbitol_de	744	649	646	545	382	442	8.02365	8.248042	9.180501	5.084621	4.628193	4.737301
protein_co	small_EDRK	11385	9433	6675	8022	6055	8804	215.8787	210.782	166.7872	131.5898	128.9852	165.9076
protein_co	zinc_finger_	336	283	272	607	641	641	3.179298	3.155626	3.39153	4.968711	6.813952	6.027812
protein_co	dual_oxida	0	0	0	0	2	0	0	0	0	0	0.017912	0
protein_co	LysM_putat	47	29	45	70	65	49	1.414569	1.028564	1.784734	1.822583	2.197803	1.465656
protein_co	solute_carr	0	0	0	384	235	303	0	0	0	7.34619	5.838279	6.659172
protein_co	fibroblast_	1	0	4	4	0	0	0.009684	0	0.051043	0.033509	0	0
protein_co	glucosamin	4	1	2	4	2	4	0.069797	0.020563	0.045988	0.060381	0.039206	0.069366
protein_co	BCL2/aden	986	855	835	1092	781	750	8.252936	8.43344	9.209856	7.9071	7.343983	6.23882
protein_co	general_tra	662	516	509	1672	1104	1635	22.15356	20.34897	22.44596	48.40441	41.50532	54.37672
protein_co	signal_reco	4489	3917	2830	5653	3590	4505	220.6612	226.9013	183.3148	240.3911	198.2531	220.0801
protein_co	bromo_adj	879	655	685	709	823	953	9.905307	8.698162	10.17196	6.911755	10.41905	10.67288
protein_co	dispatched	51	41	20	12	24	27	0.536671	0.508427	0.277334	0.10924	0.283725	0.282365
protein_co	codanin_1	337	306	229	556	473	531	3.847556	4.117025	3.445286	5.491523	6.066877	6.025029

protein_co transducin-	704	515	501	1176	1457	1488	4.772757	4.114442	4.475785	6.897108	11.09699	10.02557
protein_co acidic_(leu	2463	2277	1814	5523	4942	6030	35.13707	38.27994	34.10148	68.16151	79.20506	85.49251
protein_co COMM_dor	715	473	492	1863	1181	1613	9.003999	7.019362	8.164494	20.29576	16.70815	20.18707
protein_co ubiquitin-c	814	630	711	974	855	802	13.76804	12.55727	15.84719	14.2518	16.24662	13.4813
protein_co proline-seri	10	7	4	0	6	9	0.269832	0.222586	0.142229	0	0.181884	0.241349
protein_co electron-tr	1759	1441	1257	2837	1953	2483	40.7185	39.30945	38.34388	56.81307	50.78988	57.12317
protein_co high_mobil	745	623	587	816	737	702	9.591693	9.452227	9.958912	9.088499	10.65996	8.982262
protein_co S-phase_cy	107	98	70	166	119	119	1.041686	1.12431	0.898019	1.398054	1.301514	1.151356
protein_co tetraspanin	3258	2580	2381	2642	1741	2136	44.75396	41.76449	43.09973	31.39614	26.86756	29.16025
protein_co WD_repeat	445	354	358	822	485	587	6.4918	6.085769	6.882131	10.37385	7.948697	8.510457
protein_co nuclear_rec	358	277	436	460	604	376	2.24374	2.045863	3.600899	2.49408	4.252806	2.342001
protein_co nei_endonu	82	101	51	115	81	145	1.327166	1.926371	1.087719	1.610172	1.472806	2.332326
protein_co mannosida	866	796	555	966	673	902	9.511805	10.30304	8.032909	9.178785	8.304417	9.846032
protein_co DnaJ_(Hsp4	7	13	3	52	30	59	0.114202	0.249935	0.064496	0.733912	0.549854	0.956619
protein_co mesoderm_	696	556	464	2139	1756	1821	12.08889	11.38044	10.62013	32.14037	34.265	31.43379
protein_co tropomyos	2223	1894	1766	21851	17065	18295	41.22166	41.38787	43.15305	350.5261	355.5014	337.1538
protein_co insulin-like	1053	842	907	1761	2006	1695	4.72311	4.450603	5.36095	6.833167	10.10834	7.555775
protein_co arrestin_do	370	265	288	193	192	193	4.810454	4.060105	4.934142	2.170724	2.804365	2.493741
protein_co PIF1_5'-to-3	144	102	105	504	405	554	2.83718	2.368273	2.726142	8.590491	8.96455	10.84785
protein_co ubiquitin_s	391	364	300	242	229	232	3.764308	4.129684	3.805962	2.015518	2.476811	2.21976
protein_co cytochrom	1	3	0	22	11	10	0.026457	0.093535	0	0.503536	0.326954	0.262939
protein_co Bardet-Biec	371	270	339	168	132	181	7.887995	6.764935	9.497893	3.090047	3.15294	3.824555
protein_co promyelocy	2695	2105	1810	924	785	824	26.45577	24.35123	23.41397	7.846873	8.657258	8.038935
protein_co cytochrom	1	1	0	695	651	591	0.019717	0.023236	0	11.85484	14.42042	11.58097
protein_co ADAM_met	29	18	17	54	62	51	0.247348	0.180921	0.191071	0.398444	0.594088	0.432305
protein_co lines_homo	137	135	107	247	196	221	1.504442	1.747012	1.548366	2.34647	2.418021	2.411887
protein_co unc-51-like	216	163	158	450	373	466	3.875044	3.446018	3.735208	6.983906	7.517627	8.30842
protein_co proprotein	5	9	4	113	94	76	0.060065	0.127409	0.06332	1.174331	1.268604	0.907345
protein_co secretory_c	1385	1239	1047	2254	1726	1940	23.18889	24.44605	23.09999	32.64729	32.46535	32.2806
protein_co cytochrom	0	0	0	2	7	4	0	0	0	0.033577	0.152614	0.077147
protein_co hyaluronan	147	131	84	2056	1727	2564	2.534134	2.661281	1.908211	30.66185	33.44673	43.92785
protein_co Rh_family_	0	0	0	7	5	1	0	0	0	0.161752	0.15004	0.026546
protein_co polymerase	996	823	769	1096	1224	1290	11.7124	11.40495	11.91647	11.14962	16.17026	15.07599
protein_co retinaldehy	0	0	0	5	0	0	0	0	0	0.126516	0	0
protein_co Fanconi_an	238	179	213	1608	1422	1277	2.656537	2.354502	3.132949	15.52702	17.83149	14.16575
protein_co abhydrolas	1134	932	1094	696	1147	1014	6.872935	6.656596	8.737382	3.649232	7.809831	6.107687
protein_co WD_repeat	1	4	7	2	15	2	0.021976	0.103591	0.202716	0.038023	0.370336	0.043681
protein_co TOPBP1-int	200	140	115	716	610	536	1.563757	1.289955	1.184873	4.843009	5.358191	4.164988
protein_co neurotroph	11	2	0	209	182	158	0.029141	0.006244	0	0.478982	0.541664	0.415984
protein_co de-etiolate	131	112	109	161	104	120	2.995797	3.018326	3.284751	3.185151	2.67192	2.727294
protein_co milk_fat_gl	4297	3592	2860	13948	10354	13069	114.4879	112.7814	100.4142	321.4913	309.9213	346.0559
protein_co zinc_finger_	312	265	228	485	556	528	3.577559	3.580842	3.4451	4.811018	7.162359	6.016941
protein_co unc-45_hor	1629	1333	1097	1738	1311	1745	21.54945	20.78032	19.12302	19.88968	19.48349	22.94141
protein_co ST8_alpha-h	167	119	130	248	198	167	1.548904	1.300655	1.588862	1.989861	2.06311	1.539339

protein_co multiple_C	16	28	21	40	31	20	0.188528	0.388795	0.326069	0.407736	0.410361	0.234205
protein_co furin_(paire	1256	1075	928	3567	3250	4187	15.66774	15.80274	15.25455	38.4931	45.54588	51.90741
protein_co IQ_motif_c	2704	2270	2980	6204	5729	4797	19.79157	19.57972	28.74251	39.28334	47.10874	34.89418
protein_co CREB_regul	509	355	444	407	336	363	5.173155	4.251803	5.946419	3.578452	3.836419	3.66652
protein_co elongation_	86	78	85	613	549	483	1.238891	1.324148	1.613573	7.639382	8.884974	6.914989
protein_co SH3-domai	2	1	0	74	40	48	0.052625	0.031008	0	1.684453	1.182424	1.255206
protein_co SEC11_hon	3607	3112	2525	4247	3181	3900	52.66359	53.54402	48.58033	53.64257	52.17675	56.58985
protein_co glyoxylate_	1025	867	809	2539	1916	2002	14.38614	14.33992	14.96249	30.82805	30.21099	27.92506
protein_co phosphom	298	296	227	321	283	270	2.916697	3.414082	2.927762	2.717961	3.111792	2.626325
protein_co solute_carr	4	3	2	1	2	2	0.085839	0.075867	0.056557	0.018565	0.048217	0.042654
protein_co transformir	2602	2156	1533	1479	934	1124	27.70007	27.04765	21.50555	13.62087	11.17042	11.89185
protein_co chromoson	778	626	512	365	391	394	14.7469	13.98307	12.78869	5.985177	8.326203	7.422104
protein_co armadillo_	358	290	224	430	276	366	3.91265	3.735021	3.226048	4.065551	3.388801	3.97538
protein_co poly(A)-spe	338	283	318	859	659	684	5.813533	5.736104	7.207513	12.78144	12.7338	11.69201
protein_co fat_mass_a	539	382	408	322	420	303	2.425225	2.025507	2.419125	1.253378	2.123057	1.354926
protein_co ubiquinol-c	2454	2054	1675	3602	2550	2616	49.68153	49.00359	44.68585	63.08515	57.99755	52.63417
protein_co cerebellar_	402	338	374	716	604	609	7.876491	7.804239	9.656354	12.1362	13.29513	11.85861
protein_co immunoglc	11	5	1	6	10	10	0.49185	0.263462	0.058922	0.232089	0.50233	0.444375
protein_co Rho_GTPas	842	599	647	836	727	711	8.976302	7.525221	9.089175	7.710005	8.707006	7.532942
protein_co myosin_ligl	4	6	1	12	5	10	0.064151	0.113398	0.021134	0.166491	0.090088	0.159388
protein_co naked_cuti	926	758	855	274	349	371	10.67582	10.29832	12.98946	2.732774	4.520273	4.25083
protein_co DEAH_(Asp-	1195	980	990	1512	1526	1297	13.72927	13.26822	14.98821	15.02777	19.69623	14.80912
protein_co thioredoxir	283	229	235	349	229	214	5.86162	5.589511	6.414073	6.25345	5.328633	4.405089
protein_co MARVEL_d	45	35	48	604	459	634	0.818113	0.749853	1.149944	9.499498	9.37481	11.45512
protein_co carbohydra	0	0	0	6	3	2	0	0	0	0.113928	0.073975	0.043627
protein_co zinc_finger_	1439	1308	1494	1140	2206	1585	4.742411	5.079877	6.488194	3.250171	8.167572	5.191314
protein_co C-type_lect	6	14	1	23	3	12	0.17032	0.468326	0.037407	0.564812	0.095672	0.338535
protein_co copine_II	546	405	368	2345	1548	1704	8.388213	7.332278	7.450054	31.16612	26.71756	26.01693
protein_co NLR_family	120	98	81	4	2	1	0.922585	0.887888	0.820625	0.026604	0.017274	0.007641
protein_co katanin_p8	301	259	152	795	463	606	4.134727	4.192637	2.751432	9.447361	7.145135	8.272993
protein_co kinesin_fan	855	678	603	1310	909	1306	13.20821	12.34283	12.27524	17.50702	15.77578	20.05076
protein_co ADAM_met	0	3	0	612	681	590	0	0.031653	0	4.740222	6.849839	5.249838
protein_co nudix_(nuc	6	3	5	2	2	7	0.289823	0.170769	0.318263	0.083575	0.108533	0.336039
protein_co glycine_cle	256	134	116	331	327	352	8.732535	5.386569	5.214266	9.767679	12.53133	11.93308
protein_co CKLF-like_M	754	697	517	2812	1815	2274	17.13198	18.66277	15.47966	55.27319	46.32995	51.34951
protein_co CKLF-like_M	0	0	0	2	5	3	0	0	0	0.086905	0.282144	0.149755
protein_co cadherin_1	9503	8474	8133	3295	3197	2685	73.18858	76.90917	82.5407	21.95336	27.66141	20.55117
protein_co nucleolar_p	246	173	134	161	79	166	6.90901	5.72577	4.9593	3.911737	2.492625	4.633386
protein_co microtubul	1709	1539	1445	2548	1402	1725	29.32777	31.12308	32.6768	37.82678	27.02925	29.41953
protein_co membrane-	1743	1535	1341	1798	1368	1422	21.27159	22.07588	21.56583	18.98258	18.75589	17.24693
protein_co cadherin_1	1987	1708	1912	758	612	550	26.29187	26.6329	33.33851	8.676723	9.097541	7.232624
protein_co zinc_finger_	1066	847	943	943	909	745	7.946367	7.440497	9.263134	6.081156	7.612448	5.519215
protein_co TBC/LysM-a	476	396	374	615	476	608	7.42922	7.283473	7.69206	8.303752	8.346267	9.43082
protein_co oxidative_s	60	36	38	297	166	240	1.328507	0.939338	1.108743	5.688948	4.129236	5.28121

protein_co	interferon_	0	0	0	1	0	0	0	0	0	0.015115	0	0
protein_co	ras_homol	1813	1530	1137	2763	2058	2882	22.00918	21.88792	18.18868	29.01683	28.06729	34.77039
protein_co	ribosomal_	3	0	6	2	0	0	0.072788	0	0.191833	0.041979	0	0
protein_co	zinc_finger_	203	140	144	268	205	175	3.391298	2.756163	3.170058	3.87318	3.847448	2.905478
protein_co	ribosomal_	70630	60762	42046	58943	43618	61088	2415.518	2448.839	1894.875	1743.879	1675.853	2076.284
protein_co	NADH_deh	1155	1032	821	1777	1276	1497	63.82761	67.20682	59.7867	84.95267	79.21845	82.21632
protein_co	3-phosphoi	613	516	561	828	699	744	4.481816	4.445804	5.404944	5.237052	5.741426	5.406001
protein_co	tigger_tran	12	9	28	13	12	11	0.175884	0.155451	0.540801	0.164835	0.197594	0.160231
protein_co	differential	879	585	528	1556	1171	1390	10.45733	8.201533	8.277531	16.01418	15.65085	16.4345
protein_co	transcriptic	2900	2379	2027	1960	1417	1691	68.75454	66.46682	63.32744	40.19967	37.74177	39.84342
protein_co	galactosam	954	768	506	667	492	661	8.88872	8.432555	6.21264	5.376253	5.149974	6.120712
protein_co	growth_arr	6	3	6	44	41	47	0.082377	0.048538	0.108553	0.522602	0.632394	0.641302
protein_co	mediator_c	236	192	194	429	298	321	3.728462	3.574588	4.038817	5.863244	5.289115	5.040021
protein_co	nuclear_rec	1432	1161	1334	2607	2278	1886	7.071969	6.756731	8.681364	11.13785	12.63863	9.256539
pseudogen	CMT1A_du	11	16	14	16	17	17	0.758269	1.299744	1.271726	0.954144	1.316524	1.164634
protein_co	COP9_signa	882	712	661	2903	1684	1971	27.5969	26.25299	27.25386	78.57815	59.19471	61.28977
protein_co	GID_compl	268	212	251	248	256	257	3.34864	3.121595	4.132779	2.680701	3.593541	3.191364
protein_co	zinc_finger_	81	104	104	72	36	26	1.271337	1.923606	2.151017	0.977623	0.634786	0.405563
protein_co	myocardin	0	1	5	11	37	27	0	0.007369	0.041202	0.059507	0.259935	0.167798
protein_co	kinase_sup	619	520	475	399	407	319	4.530063	4.484603	4.580807	2.526094	3.34624	2.320139
protein_co	cirrhosis_a	733	667	546	2108	1334	1477	9.277014	9.948031	9.106085	23.08011	18.96746	18.5778
protein_co	RAN_bindi	545	501	426	635	608	647	5.438801	5.891848	5.602103	5.482056	6.816467	6.416831
protein_co	dipeptidase	0	0	0	0	1	0	0	0	0	0	0.029473	0
protein_co	glucose-fru	725	636	513	899	739	879	13.00651	13.44581	12.12761	13.95229	14.89417	15.67189
protein_co	NIN1/RPN1	804	748	699	865	588	594	24.54704	26.91235	28.12257	22.84663	20.1683	18.0235
protein_co	phosphorib	288	265	272	833	609	732	7.982726	8.655889	9.934876	19.97408	18.96379	20.16413
protein_co	myosin_XI>	651	552	444	1803	1512	1623	5.980321	5.975712	5.374787	14.32855	15.6043	14.81739
protein_co	DEAD_(Asp	505	440	388	1713	1039	1101	4.204309	4.316811	4.256668	12.3374	9.717798	9.109619
protein_co	RAS-like_fa	1425	1110	1085	509	480	503	23.53851	21.60698	23.61721	7.273524	8.90747	8.257369
protein_co	phosphatid	170	172	140	699	630	672	2.288904	2.729066	2.483942	8.141769	9.529458	8.992025
protein_co	target_of_r	120	83	88	584	405	414	2.541168	2.071273	2.455668	10.69862	9.635099	8.712887
protein_co	chromoson	180	214	211	394	301	305	2.621562	3.672895	4.049533	4.964173	4.924966	4.414659
protein_co	transducer_	611	546	529	839	729	712	14.51187	15.28205	16.55665	17.2388	19.45175	16.80628
protein_co	vacuolar_p	982	749	825	1229	1165	1222	3.966737	3.565421	4.391478	4.294739	5.286849	4.90572
protein_co	spermatoge	0	0	0	0	0	1	0	0	0	0	0	0.030877
protein_co	small_G_pr	1041	936	720	798	826	1059	11.33283	12.008	10.32893	7.515428	10.10222	11.45759
protein_co	aminopept	2076	1668	1810	2978	2631	2518	21.66052	20.50901	24.886	26.88	30.8398	26.11001
protein_co	src_kinase_	3	1	1	0	13	3	0.094145	0.036981	0.041353	0	0.458321	0.093564
protein_co	leucine_ric	26	18	15	30	22	33	0.614768	0.501554	0.467373	0.613652	0.584399	0.775464
protein_co	secernin_2	167	175	112	248	240	315	4.969728	6.137073	4.392067	6.384558	8.023733	9.316147
protein_co	slingshot_p	278	279	324	711	711	633	1.577956	1.866214	2.423427	3.491264	4.533867	3.570783
protein_co	rhomboid_	22	24	11	1	1	5	0.249882	0.321241	0.164642	0.009826	0.01276	0.056441
protein_co	sperm_acro	1	0	0	0	0	0	0.055786	0	0	0	0	0
protein_co	arylsulfatas	115	82	77	121	99	103	1.31155	1.102067	1.157211	1.19381	1.268444	1.167438

protein_co	ATP-bindin	332	312	335	0	0	0	3.096074	3.428743	4.116734	0	0	0
protein_co	glucose_6_	1869	1595	1240	1631	1149	1523	32.68805	32.87361	28.57829	24.67724	22.57609	26.47215
protein_co	clathrin_he	8436	6892	8212	9470	8241	7124	57.55286	55.40931	73.82681	55.89119	63.1625	48.30187
protein_co	breast_carc	225	209	213	134	100	127	2.614514	2.861948	3.261541	1.347027	1.305442	1.466634
protein_co	peptidyl-tR	552	439	384	860	524	754	7.10341	6.65732	6.511692	9.573908	7.575445	9.642925
protein_co	synovial_sa	1390	1296	1252	2760	2469	2283	24.1035	26.48362	28.60912	41.40353	48.09893	39.34421
protein_co	TAF4b_RNA	21	20	8	96	80	97	0.211361	0.237216	0.106104	0.835874	0.904577	0.970259
protein_co	AFG3_ATPa	539	457	430	781	825	708	8.474962	8.467833	8.909478	10.62339	14.5731	11.06348
protein_co	slowmo_ho	70	46	23	57	37	57	1.852009	1.434201	0.801877	1.304616	1.099755	1.498751
protein_co	inositol(my	514	362	288	662	448	522	16.83891	13.97547	12.43306	18.76168	16.48837	16.99538
protein_co	guanine_nu	17	7	13	43	36	23	0.137719	0.066827	0.138779	0.301355	0.327641	0.185176
protein_co	solute_carr	1675	1503	1609	1646	1263	1322	25.02855	26.46592	31.68194	21.27717	21.20183	19.63189
protein_co	regulation_	491	435	528	1177	931	917	5.857149	6.115066	8.299913	12.14631	12.47681	10.87136
protein_co	chromoson	290	321	195	522	317	426	9.710872	12.66696	8.604579	15.12146	11.92528	14.17684
protein_co	UDP-N-acet	2115	1806	2107	3525	2911	2830	29.10585	29.28834	38.20932	41.96546	45.00504	38.7049
protein_co	additional_	43	81	54	60	69	47	0.200675	0.44547	0.332089	0.242237	0.361763	0.217988
protein_co	adenylate_(	0	0	0	22	32	18	0	0	0	0.301128	0.568807	0.28304
protein_co	meprin_A_l	0	0	0	2	10	0	0	0	0	0.039618	0.257249	0
protein_co	solute_carr	0	0	1	0	0	0	0	0	0.052891	0	0	0
protein_co	GRB2_asso	76	82	51	172	185	162	0.572091	0.727399	0.50589	1.120064	1.564488	1.211926
protein_co	establishm	190	179	228	365	330	257	2.107435	2.339703	3.332501	3.502326	4.1121	2.832979
protein_co	oxysterol_b	931	729	763	759	705	637	11.74924	10.84163	12.68877	8.286381	9.995357	7.989309
protein_co	GATA_bind	13	9	16	47	47	50	0.182555	0.148936	0.296078	0.570968	0.741477	0.697799
protein_co	growth_reg	10	8	17	414	785	473	0.083794	0.078997	0.187714	3.001068	7.389774	3.938975
protein_co	chromoson	121	111	98	385	225	235	2.962933	3.20307	3.162258	8.155679	6.189677	5.718918
protein_co	proline_glu	1323	1151	928	2955	2609	3160	17.06235	17.49288	15.77109	32.96852	37.80089	40.50192
protein_co	Niemann-P	596	447	490	921	747	741	6.118447	5.407662	6.628662	8.179327	8.615185	7.560018
protein_co	solute_carr	23	30	19	0	0	0	0.306634	0.471325	0.333796	0	0	0
protein_co	arrestin_be	167	118	91	441	306	372	4.665512	3.88483	3.35011	10.65821	9.604027	10.32846
protein_co	zinc_finger_	0	0	1	1	0	3	0	0	0.028935	0.018996	0	0.065468
protein_co	WD_repeat	276	227	165	1092	767	948	3.642911	3.530794	2.869843	12.46881	11.37323	12.43533
protein_co	misshapen-	2040	1610	1539	2215	2598	3045	20.38113	18.95532	20.2615	19.1441	29.15992	30.23397
protein_co	spermidine	1246	887	689	370	272	389	42.20376	35.40494	30.75298	10.84171	10.35026	13.0946
protein_co	asialoglyco	57	32	18	68	41	44	1.448697	0.958429	0.602851	1.495115	1.170673	1.111387
protein_co	phosphoin	0	0	1	1	0	1	0	0	0.015544	0.010205	0	0.011723
protein_co	tumor_pro	1200	911	756	2512	1653	2064	23.94617	21.423	19.87977	43.36481	37.05755	40.93306
protein_co	coiled-coil_	131	135	111	97	94	114	1.615107	1.961421	1.803382	1.034582	1.301988	1.396833
protein_co	Rho_GDP_(	4175	3571	2569	6562	5342	6197	115.9647	116.887	94.03036	157.677	166.6948	171.0647
protein_co	transmemb	36	28	35	1217	1083	1470	0.361784	0.331598	0.463499	10.58035	12.22711	14.6816
protein_co	solute_carr	2699	2363	1509	304	292	371	29.58338	30.5222	21.79561	2.882581	3.595646	4.041369
protein_co	caspase_rec	10	9	2	15	13	27	0.116687	0.123758	0.030753	0.151418	0.170418	0.31311
protein_co	tweety_hor	140	127	100	30	37	28	2.024512	2.164229	1.90558	0.375298	0.601095	0.402402
protein_co	RAB40B_m	280	301	196	74	57	84	3.841275	4.866211	3.543302	0.878238	0.878499	1.145266
protein_co	eukaryotic_	1654	1425	1186	3625	2781	3394	24.37083	24.74325	23.0279	46.2068	46.03466	49.7

protein_co casein_kina	2845	2454	2142	3479	2949	3604	24.71564	25.12299	24.52132	26.14611	28.7815	31.11602
protein_co anaphase_p	1050	727	609	2014	1203	1754	26.02437	21.23403	19.89037	43.18305	33.49697	43.20461
protein_co tubulin_fol	1863	1617	1321	2337	2261	2083	24.09113	24.64117	22.51033	26.14364	32.84686	26.76968
protein_co fructosamii	517	434	322	786	689	916	14.80286	14.64374	12.14915	19.46887	22.16274	26.06515
protein_co nuclear_pr	921	654	627	845	553	658	18.76777	15.70499	16.83664	14.8961	12.65981	13.32565
protein_co regulatory_	833	632	595	1109	949	1009	6.881999	6.153097	6.477708	7.926184	8.808153	8.284578
protein_co forkhead_b	1042	679	766	1836	1669	1532	10.47759	8.045825	10.1498	15.9709	18.85381	15.30954
protein_co tripartite_r	451	427	333	334	234	335	6.942829	7.74631	6.755212	4.448047	4.046922	5.125242
protein_co chromobox	228	144	162	154	126	230	3.184001	2.369779	2.98118	1.860467	1.976778	3.192095
protein_co secreted_ar	1450	1237	890	20	20	25	34.34651	34.52958	27.78046	0.409834	0.532223	0.588524
protein_co ring_finger_	15	11	16	16	18	25	0.160265	0.1385	0.22527	0.147887	0.216058	0.265459
protein_co 5-azacytidi	415	283	262	556	577	842	5.981626	4.806896	4.976308	6.932805	9.343208	12.06127
protein_co zinc_finger_	9	3	13	60	46	39	0.128325	0.050408	0.244256	0.740085	0.736841	0.552639
protein_co WD_repeat	1401	1213	1142	3048	2274	2781	28.6704	29.25254	30.79616	53.96021	52.27995	56.5596
protein_co chromobox	471	396	322	224	195	224	9.360063	9.273852	8.432349	3.850959	4.35353	4.424004
protein_co ring_finger_	2	9	4	47	76	88	0.013939	0.073919	0.036737	0.283379	0.595072	0.609536
protein_co dymeclin	695	571	609	735	405	467	13.61228	13.17921	15.71803	12.45364	8.911486	9.090182
protein_co mitogen-ac	0	0	0	102	67	68	0	0	0	0.979348	0.835406	0.750054
protein_co elaC_homo	48	25	27	111	59	85	1.136988	0.697849	0.842778	2.274577	1.570058	2.000982
protein_co methyl-CpG	1070	952	848	1377	1061	1189	11.5488	12.10869	12.06101	12.85731	12.86523	12.75395
protein_co SMAD_fami	968	948	904	973	875	891	5.844096	6.744619	7.191927	5.081804	5.934705	5.346005
protein_co tumor_nec	3	0	0	25	43	55	0.019516	0	0	0.140695	0.314262	0.355588
protein_co zinc_finger_	98	88	79	282	348	251	0.870652	0.921316	0.92487	2.167359	3.473338	2.216165
protein_co F-box_prot	2	7	1	8	3	11	0.033223	0.13703	0.02189	0.114964	0.055986	0.181599
protein_co cerebellin_	3	0	0	9	0	1	0.047609	0	0	0.123558	0	0.015772
protein_co phorbol-12	784	810	753	1013	732	828	21.30685	25.94151	26.96702	23.81637	22.34927	22.36367
protein_co leprecan-lik	1673	1427	1070	1155	904	1149	31.73425	31.89799	26.74551	18.95297	19.26415	21.66017
protein_co 5'-nucleotic	1314	1132	901	1968	1387	1690	40.23393	40.8461	36.35438	52.1297	47.71145	51.42727
protein_co family_with	729	695	446	663	684	763	9.301997	10.45058	7.499259	7.318552	9.80514	9.67571
protein_co phosphatid	2710	2349	2014	2160	2224	2298	25.02094	25.55786	24.50353	17.25247	23.06844	21.08599
protein_co v-erb-b2_er	538	470	441	1762	1502	1699	5.777334	5.947715	6.240488	16.3687	18.12025	18.1321
protein_co growth_fac	0	0	0	107	71	78	0	0	0	2.18479	1.882653	1.829646
protein_co migration_	195	164	119	265	157	244	5.164329	5.118353	4.152992	6.071391	4.671195	6.422125
protein_co phenyletha	2	2	5	18	18	14	0.084503	0.099581	0.278385	0.657925	0.854403	0.587866
protein_co ADP-ribosy	1	0	2	1	0	0	0.019064	0	0.050244	0.016492	0	0
protein_co SH3_and_c	28	12	12	1	0	2	0.440913	0.222681	0.249006	0.013623	0	0.031299
protein_co insulin-like_	31946	25742	22894	5121	3348	4142	768.7514	729.9931	725.9821	106.6074	90.51153	99.05791
protein_co FK506_bin	22023	19600	14478	5871	5345	7038	412.5688	432.6962	357.4072	95.14698	112.4907	131.0324
protein_co thioredoxir	1328	971	754	3359	2031	2559	48.55362	41.83597	36.32701	106.2421	83.42237	92.98298
protein_co calcium_ch	10	8	5	2	2	6	0.063085	0.059474	0.041565	0.010915	0.014174	0.037617
protein_co Uncharacte	6	19	5	7	4	14	0.145243	0.542006	0.159495	0.14659	0.108781	0.336807
protein_co sterile_alph	614	488	350	1283	900	1114	15.02115	14.06895	11.28334	27.15342	24.73583	27.08505
protein_co bromodom	2480	1835	1679	3226	3877	3983	22.43569	19.5628	20.01582	25.24731	39.4033	35.81028
protein_co solute_carr	245	186	160	705	479	539	4.411749	3.946979	3.796641	10.98239	9.690124	9.645909

protein_co	nuclear_fac	2501	2026	1946	242	227	263	16.41118	15.66653	16.82689	1.37374	1.673405	1.715108
protein_co	tubulin_po	474	266	186	305	182	166	8.734435	5.776239	4.516523	4.862049	3.767705	3.040004
protein_co	phosphatid	47	40	25	233	188	212	1.971654	1.977424	1.381998	8.455741	8.860121	8.838493
protein_co	PR_domain	201	161	172	246	255	312	1.504686	1.420309	1.696731	1.593118	2.144564	2.321208
protein_co	phosphofru	6660	5653	4019	5395	4388	5523	58.69602	58.71114	46.67532	41.13286	43.44603	48.3748
protein_co	fem-1_hom	0	1	0	0	0	1	0	0.01623	0	0	0	0.013687
protein_co	multivesicu	979	710	503	650	422	674	23.38864	19.98885	15.83526	13.43379	11.32619	16.00265
protein_co	calcium_an	0	0	0	1	0	0	0	0	0	0.064415	0	0
protein_co	Uncharacte	0	0	0	2	0	0	0	0	0	0.035683	0	0
protein_co	SH3-domai	3008	2514	1927	3164	2391	2970	63.29353	62.33814	53.43158	57.59449	56.52103	62.108
protein_co	dihydrouri	349	259	190	791	649	745	8.029729	7.022348	5.760549	15.744	16.77526	17.03497
protein_co	dipeptidyl-	973	797	663	1847	1588	1910	11.99338	11.57695	10.76905	19.69513	21.99016	23.39763
protein_co	coiled-coil_	855	709	593	1077	951	917	13.62569	13.31514	12.45323	14.84811	17.02637	14.52351
protein_co	transmemb	54	45	28	24	28	25	1.551174	1.523303	1.059887	0.596405	0.903595	0.713701
protein_co	ZFP14_zinc	85	62	90	103	109	70	0.791972	0.680753	1.105015	0.830216	1.140949	0.648184
protein_co	sirtuin_3	324	332	265	288	233	312	6.529456	7.884555	7.037408	5.020969	5.275177	6.248795
protein_co	interferon_	15097	13311	9627	1336	890	1013	989.171	1027.776	831.2019	75.7269	65.51184	65.96291
protein_co	ATH1_acid_	451	464	211	35	42	61	5.404343	6.552265	3.331836	0.362825	0.565412	0.72645
protein_co	hormonally	292	184	192	776	750	765	2.093266	1.554413	1.813751	4.812451	6.040208	5.450203
protein_co	collagen_ty	259417	221020	180237	1163	1054	1254	3240.631	3253.642	2966.948	12.56822	14.79179	15.5682
protein_co	interferon_	1045	898	771	842	608	676	9.011783	9.125946	8.761605	6.28159	5.890431	5.793631
protein_co	superoxide	2438	2063	1697	2997	2193	2859	73.92334	73.71471	67.80544	78.61358	74.70257	86.15325
protein_co	collagen_ty	185869	159743	113564	1269	1151	1532	2843.135	2879.515	2289.106	16.79249	19.77948	23.28943
protein_co	salt-inducil	43	43	22	426	386	451	0.48312	0.569328	0.32572	4.140563	4.872178	5.035852
protein_co	DNA_(cytos	0	0	0	0	2	1	0	0	0	0	0.069726	0.030841
protein_co	SCY1-like_1	2513	2003	1716	2080	1343	1602	49.00211	46.02675	44.09348	35.08719	29.42032	31.0452
protein_co	transmemb	453	425	351	549	490	499	7.832224	8.659303	7.997032	8.211495	9.517701	8.574269
protein_co	amyloid_be	18247	15390	16366	13642	12261	12955	269.9872	268.3474	319.1017	174.6195	203.8106	190.5017
protein_co	dopey_fam	127	90	106	535	512	420	0.874887	0.730631	0.962252	3.188343	3.962481	2.875459
protein_co	URB1_ribos	1497	1157	1275	1238	1275	1134	7.316531	6.66383	8.211612	5.234402	7.00072	5.508155
protein_co	v-akt_murii	1957	1550	1311	3336	2393	2910	12.33987	11.51751	10.89324	18.19737	16.95163	18.23569
protein_co	interleukin	9	5	0	0	0	0	0.323468	0.211771	0	0	0	0
protein_co	epithelial_r	3903	3219	2406	1650	998	1305	235.8775	229.2535	191.6101	86.26506	67.75909	78.38052
protein_co	SUMO1_act	2078	1686	1683	6694	4553	5465	47.70659	45.61393	50.9157	132.9479	117.4301	124.6903
protein_co	netrin_5	10	10	12	2	1	1	0.218223	0.257163	0.345078	0.037757	0.024516	0.021688
protein_co	lemur_tyro	29	26	11	149	154	213	0.300272	0.317246	0.150087	1.334644	1.791373	2.191823
protein_co	gem_(nucle	89	90	85	355	205	284	2.843542	3.388591	3.578684	9.812077	7.358215	9.017737
protein_co	Cbl_proto-(	0	0	0	9	26	19	0	0	0	0.261045	0.979337	0.633101
protein_co	Wilms_tum	431	315	324	1025	731	1034	2.957942	2.547593	2.930166	6.085543	5.636103	7.052493
protein_co	ADAM_met	177	174	102	33	36	71	2.215261	2.566304	1.682235	0.357296	0.506178	0.88312
protein_co	solute_carr	0	7	0	0	0	0	0	0.111067	0	0	0	0
protein_co	arginyl_am	574	404	303	1251	988	984	7.704901	6.390629	5.359603	14.52699	14.89914	13.12683
protein_co	calpain_10	459	332	307	845	563	834	5.515188	4.701027	4.860946	8.783494	7.599851	9.959173
protein_co	myosin_IF	0	1	0	3	6	6	0	0.014499	0	0.03193	0.082932	0.073364

processed_ endogenou	68	58	102	121	150	89	0.925685	0.930442	1.829739	1.42496	2.294006	1.204076
protein_co NLR_family	0	0	0	6	0	0	0	0	0	0.072295	0	0
protein_co calcium_ch	0	0	0	0	7	6	0	0	0	0	0.047597	0.036091
protein_co zinc_finger_	950	789	594	1958	1399	1740	26.08607	25.53108	21.49346	46.51154	43.15706	47.48363
protein_co chromoson	298	272	238	575	425	561	11.07117	11.90839	11.65169	18.48026	17.73843	20.71332
protein_co fibrillin_3	0	0	0	148	189	208	0	0	0	0.724016	1.200699	1.168951
protein_co coactivator	2973	2386	1825	4092	3360	3951	51.91081	49.09536	41.99142	61.8104	65.90999	68.56138
protein_co ecotropic_\	769	642	503	271	262	294	10.56073	10.38986	9.102706	3.219586	4.042202	4.012589
protein_co transmemb	0	0	0	0	1	0	0	0	0	0	0.063953	0
protein_co solute_carr	3	10	6	2	2	0	0.048422	0.190206	0.127616	0.027926	0.036266	0
protein_co proteasom	1215	968	762	2386	1727	2343	76.21245	71.5537	62.98533	129.4742	121.7001	146.0601
protein_co G_protein-r	0	0	0	0	0	2	0	0	0	0	0	0.082922
protein_co sialic_acid_	0	1	0	0	2	3	0	0.020067	0	0	0.03826	0.050769
protein_co acid_phosp	18	12	16	32	16	31	0.707452	0.555793	0.828666	1.088022	0.70647	1.210865
protein_co zinc_finger_	170	141	159	376	299	233	1.86412	1.822011	2.297507	3.566775	3.683368	2.539162
protein_co family_with	10	6	11	57	41	49	0.413279	0.292214	0.59906	2.03789	1.903601	2.012559
protein_co ribosomal_	29769	25462	16884	17956	15020	21386	1390.998	1402.044	1039.615	725.8298	788.4627	993.1192
protein_co ribosomal_	56998	50287	36811	43448	27286	36859	1305.16	1356.96	1110.751	860.6708	701.929	838.7981
protein_co cytosolic_t	264	224	155	399	237	318	6.696896	6.696143	5.181269	8.755996	6.754093	8.016899
protein_co nitric_oxid	1411	1083	869	1823	1070	1412	28.56587	25.83782	23.18329	31.92788	24.33623	28.40958
protein_co IgLON_fami	0	0	0	22	16	15	0	0	0	0.386637	0.365163	0.302844
protein_co reticulocall	4577	3523	2497	32	24	49	130.3448	118.2313	93.70571	0.788362	0.767844	1.386815
protein_co zinc_finger_	170	136	177	296	239	246	1.867989	1.761048	2.56291	2.813714	2.950341	2.686396
protein_co solute_carr	215	203	128	2	0	3	2.732848	3.040746	2.143986	0.021992	0	0.037897
protein_co arginine-glu	2206	1666	1568	1868	2312	2172	14.55119	12.95016	13.62931	10.6594	17.13286	14.23844
protein_co membrane_	0	0	0	0	0	2	0	0	0	0	0	0.036261
protein_co chromoson	2	0	0	0	2	0	0.02248	0	0	0	0.025255	0
protein_co PR_domain	16	15	8	0	0	0	0.097128	0.107306	0.063996	0	0	0
protein_co chymotryp	0	1	0	0	1	0	0	0.067887	0	0	0.064718	0
protein_co peptidyl_ar	0	0	0	1	0	3	0	0	0	0.014362	0	0.049496
protein_co forkhead-as	34	18	28	4	3	3	0.353633	0.220625	0.383767	0.035991	0.035055	0.03101
protein_co peptidyl_ar	0	0	0	0	2	1	0	0	0	0	0.030929	0.01368
protein_co EPH_recept	1506	1199	1246	7083	4767	5553	20.1133	18.87056	21.92862	81.83493	71.52414	73.7048
protein_co Rho_guanir	128	132	86	407	323	431	2.23719	2.718779	1.980734	6.153897	6.342265	7.486516
protein_co EF-hand_dc	1518	1290	1059	1468	950	1217	33.22217	33.27002	30.54126	27.79363	23.35764	26.47015
protein_co peroxisoma	501	398	354	877	544	731	13.36193	12.50898	12.44141	20.23458	16.2997	19.37575
protein_co phosphoglu	7807	6528	6072	8919	6730	7381	210.9803	207.8954	216.2341	208.5148	204.3251	198.236
protein_co myomesin_	2	0	3	0	1	0	0.018227	0	0.036029	0	0.010239	0
protein_co SH3_domai	5672	4685	3357	2912	1875	2162	181.4389	176.6082	141.5078	80.58393	67.38208	68.73207
protein_co connector_	1	6	5	297	195	263	0.019806	0.14004	0.130496	5.088767	4.338872	5.176766
protein_co ribosomal_	22637	19659	15272	16557	13489	18259	1205.659	1233.884	1071.856	762.8697	807.1133	966.4788
protein_co interleukin	4	0	0	5	13	0	0.075684	0	0	0.081842	0.276336	0
protein_co zinc_finger_	1	0	0	0	3	0	0.028085	0	0	0	0.094657	0
protein_co chromoson	478	433	526	297	242	274	7.863827	8.39462	11.4032	4.226934	4.472707	4.479879

protein_co	KIAA0319-l	1189	1001	1007	1586	1318	1329	13.14405	13.04033	14.66937	15.16748	16.36861	14.60098
protein_co	eva-1_hom	1334	1090	733	185	277	312	67.00502	64.51862	48.51659	8.038707	15.63077	15.57456
protein_co	chromoson	4	0	0	0	0	0	0.092595	0	0	0	0	0
protein_co	DMRT-like_	0	0	0	5	10	12	0	0	0	0.072998	0.189595	0.201265
protein_co	polo-like_k	123	94	102	780	555	573	1.695325	1.526802	1.852605	9.300481	8.593891	7.848959
protein_co	mitogen-ac	609	483	408	565	610	581	7.482262	6.993101	6.605574	6.005194	8.419659	7.094166
protein_co	ficolin_(col	0	0	0	0	0	1	0	0	0	0	0	0.051082
protein_co	GPN-loop_(	417	395	343	744	480	579	14.43845	16.11717	15.64997	22.28541	18.67131	19.92383
protein_co	synaptotag	31	44	22	486	358	503	0.612149	1.023894	0.57247	8.302226	7.941954	9.871267
protein_co	WD_and_te	841	714	574	555	557	513	8.646995	8.651163	7.777068	4.936569	6.433887	5.24199
protein_co	neuroblast(	128	111	99	80	74	53	1.539752	1.573515	1.569317	0.832518	1.00005	0.633616
protein_co	heparan_su	5880	4962	4676	2555	5418	4865	21.72772	21.60731	22.76911	8.16753	22.49183	17.86608
protein_co	integrin_be	183	187	95	581	300	434	7.539457	9.078993	5.157597	20.70752	13.88543	17.77004
protein_co	SERPINE1_r	8378	6864	6533	13379	11742	12178	66.43793	64.1446	68.26895	91.78304	104.6085	95.97572
protein_co	B-cell_CLL/	354	371	280	548	405	337	6.648142	8.210659	6.929308	8.903086	8.544784	6.289796
protein_co	cysteine-ric	1826	1347	1321	8270	6022	7092	42.21409	36.69706	40.24336	165.396	156.4035	162.9427
protein_co	protein_kir	422	388	447	623	502	423	4.950388	5.363713	6.909858	6.322339	6.615757	4.931474
protein_co	phosphatid	441	357	451	846	612	666	5.079847	4.846044	6.845788	8.430347	7.91977	7.624229
protein_co	tubulointer	20	12	15	3815	2514	3381	0.222488	0.157313	0.219888	36.71419	31.41888	37.3793
protein_co	arginine_de	190	154	128	35	33	46	1.720039	1.642905	1.526967	0.274104	0.33562	0.413859
protein_co	ribosomal_	24505	22211	14278	23838	15221	20134	1163.515	1242.775	893.3454	979.1518	811.9129	950.0729
protein_co	kinesin_fam	431	330	314	1942	1398	1481	7.721681	6.967158	7.413086	30.09864	28.13785	26.36934
protein_co	protein_tyr	647	511	476	7136	8871	9337	4.432875	4.125809	4.29757	42.29597	68.28146	63.57673
protein_co	bestrophin	2	1	5	4	3	3	0.051725	0.030478	0.170404	0.089495	0.087165	0.077109
protein_co	MOB_kinas	241	179	175	67	71	55	2.228608	1.950638	2.132502	0.535987	0.737605	0.505462
protein_co	cytochrom	0	0	0	0	1	0	0	0	0	0	0.027396	0
protein_co	transmemb	0	0	0	0	3	0	0	0	0	0	0.162651	0
protein_co	LIM_domai	1169	900	790	1787	1462	1835	17.25342	15.65346	15.36465	22.81646	24.24137	26.91575
protein_co	synaptophy	30	11	19	41	16	14	0.438253	0.189367	0.365757	0.518144	0.262587	0.203255
protein_co	metal_resp	331	296	284	1195	911	958	4.248114	4.476792	4.803096	13.2678	13.13517	12.21921
protein_co	solute_carr	24	27	26	257	162	179	0.53207	0.705389	0.759567	4.928944	4.034798	3.94385
protein_co	immunoglo	286	225	260	1538	1873	1576	2.087279	1.935103	2.500476	9.710328	15.35682	11.4309
protein_co	zinc_finger_	721	581	634	680	732	629	7.572001	7.190492	8.774037	6.177992	8.636455	6.565014
protein_co	CTTNBP2_N	407	370	358	604	469	394	3.653889	3.914441	4.235248	4.690951	4.730237	3.515336
protein_co	striatin_int	105	76	87	67	84	122	1.65293	1.409892	1.804759	0.912437	1.485572	1.908687
protein_co	proteasom(	1089	974	852	2758	1797	2313	15.46064	16.29543	15.93948	33.87326	28.66136	32.6351
protein_co	fibronectin	0	0	0	0	2	0	0	0	0	0	0.0357	0
protein_co	chromoson	15	16	6	12	10	11	0.344071	0.432497	0.18136	0.238123	0.257695	0.25076
protein_co	CD53_mole	0	0	0	4	2	0	0	0	0	0.121725	0.079038	0
protein_co	prokinetici	1	0	4	0	0	0	0.039567	0	0.20856	0	0	0
protein_co	cadherin_E	29	14	39	245	295	282	0.145746	0.082915	0.258284	1.065192	1.665597	1.408502
protein_co	integrin_al	4423	4066	3723	49	53	61	44.44069	48.14358	49.29374	0.425915	0.598258	0.609121
protein_co	gap_junctio	0	0	0	28	28	20	0	0	0	0.403642	0.524182	0.331218
protein_co	G_protein-(	320	247	294	386	411	414	6.330762	5.758509	7.664576	6.60627	9.134754	8.139842

protein_co aldehyde_d	1712	1502	1294	1451	1050	1097	33.61832	34.75756	33.48431	24.64919	23.16384	21.40861
protein_co ATPase_Na-	154	106	98	2793	2409	2579	3.126117	2.535698	2.621473	49.04768	54.93769	52.029
protein_co TIP41_TOR_	477	462	449	866	729	736	15.49255	17.6829	19.217	24.33242	26.59997	23.75702
protein_co NME/NM23	225	209	174	237	166	241	2.771457	3.033745	2.824293	2.52544	2.297115	2.950206
protein_co pogo_trans	764	644	701	1746	1398	1329	6.467368	6.42432	7.819645	12.7862	13.29506	11.1807
protein_co mitochond	179	151	118	671	457	592	4.35298	4.327307	3.781381	14.11625	12.4853	14.30754
protein_co cellular_rep	198	157	193	555	383	415	5.310191	4.961942	6.820827	12.87659	11.53965	11.06121
protein_co DDB1_and_	989	937	775	1059	749	766	15.63411	17.45515	16.14409	14.48225	13.30172	12.03415
protein_co glycoprotei	0	0	0	3	3	6	0	0	0	0.049035	0.063679	0.112664
protein_co T-box_19	65	44	37	64	18	27	1.219406	0.972736	0.914685	1.038671	0.379364	0.503395
protein_co uridine-cyt	480	408	441	1430	1047	1236	5.442638	5.451744	6.589335	14.02708	13.33718	13.92824
protein_co transmemb	1541	1400	1181	2351	1448	1913	36.68259	39.27285	37.04606	48.41422	38.72353	45.2566
protein_co chemokine	0	0	6	1	1	0	0	0	0.306203	0.033503	0.043508	0
protein_co POU_class_	228	181	179	1464	1450	1250	0.84221	0.7879	0.871311	4.678314	6.01731	4.588861
protein_co maelstrom_	0	0	0	0	0	2	0	0	0	0	0	0.044683
protein_co immunoglo	0	2	0	5	2	1	0	0.048513	0	0.089034	0.046249	0.020456
protein_co dermatopo	1	1	0	0	0	0	0.029642	0.034932	0	0	0	0
protein_co microsoma	2003	1473	1224	2473	1718	2413	43.17623	37.4174	34.76802	46.11592	41.60408	51.69288
protein_co adenylate_(	3	5	1	35	30	29	0.031419	0.061709	0.013801	0.317104	0.352973	0.301841
protein_co ring_finger_	505	447	370	1013	799	879	8.814772	9.194631	8.510522	15.2965	15.66807	15.24819
protein_co poliovirus_	3	8	2	101	82	73	0.045352	0.142519	0.039842	1.320871	1.39264	1.096752
protein_co ubiquitin-fo	914	761	629	1031	770	822	43.43633	42.61855	39.39058	42.3866	41.10992	38.82293
protein_co protoporph	172	138	92	217	144	184	3.685087	3.48422	2.597419	4.022	3.466019	3.917841
protein_co Fc_fragmen	0	0	1	16	7	6	0	0	0.028923	0.303807	0.172608	0.130881
protein_co NUF2_NDC	135	85	95	1017	660	663	3.629779	2.693223	3.365928	23.6554	19.93606	17.71616
protein_co regulator_c	488	441	510	1955	1231	1272	4.407234	4.693447	6.069477	15.27411	12.48974	11.41676
protein_co succinate_c	1330	1053	1034	1772	1354	1947	49.58558	46.26358	50.79946	57.15187	56.71154	72.14053
protein_co prefoldin_s	789	666	531	1627	1478	2176	61.69933	61.37404	54.71832	110.0662	129.8455	169.111
protein_co nuclear_rec	9	3	11	13	5	7	0.323468	0.127063	0.520975	0.404199	0.201887	0.250033
protein_co ubiquitin_s	345	195	241	491	304	432	7.265172	4.839144	6.687729	8.944814	7.191996	9.041078
protein_co coagulation	0	0	0	1	0	0	0	0	0	0.020658	0	0
protein_co papillary_r	1221	992	915	2552	1596	1962	30.7375	29.42873	30.3535	55.57718	45.13722	49.08643
protein_co ribosomal_	182	156	90	330	244	321	4.274739	4.317873	2.785579	6.705252	6.438387	7.49295
protein_co mitochond	948	768	619	883	947	1350	50.69501	48.39775	43.61967	40.84892	56.89262	71.74643
protein_co phosphatid	190	179	184	312	259	307	2.327346	2.583851	2.970024	3.306168	3.564151	3.737278
protein_co calsequestr	7	2	2	7	3	9	0.189462	0.063791	0.071333	0.163902	0.091221	0.242089
protein_co interferon_	553	495	434	1543	1050	1200	8.863569	9.34966	9.166595	21.39501	18.90697	19.115
protein_co cellular_ret	1931	1753	1164	5645	4336	5232	103.0535	110.2477	81.85933	260.6198	259.9673	277.4967
protein_co hepatoma-(	4033	3496	2795	7973	7478	8462	89.71052	91.64181	81.92789	153.4263	186.8743	187.0673
protein_co v-abl_Abels	861	676	792	1215	1029	1025	3.753475	3.472835	4.549779	4.582153	5.039585	4.440827
protein_co xenotropic_	792	682	813	1114	994	900	4.94799	5.021056	6.693126	6.020767	6.976524	5.587992
protein_co regulator_c	131	102	110	134	106	99	2.857549	2.621981	3.161912	2.528658	2.59763	2.146185
protein_co torsin_A_in	685	576	641	602	537	499	11.91346	11.8053	14.69063	9.057471	10.4923	8.624971
protein_co family_with	0	3	0	1	0	1	0	0.064339	0	0.015744	0	0.018087

protein_co	hemicentin	208	152	205	202	205	145	0.604774	0.520811	0.78545	0.508094	0.669627	0.418994
protein_co	ral_guanine	1174	963	1081	439	463	369	12.15582	11.75032	14.74948	3.932274	5.385752	3.797102
protein_co	lysophosph	78	75	73	206	158	163	1.903826	2.157252	2.347957	4.349735	4.332501	3.953937
protein_co	LIM_homec	509	456	454	4	0	0	3.635096	3.837691	4.272566	0.024713	0	0
protein_co	prune_exop	190	137	161	264	246	183	3.356286	2.851892	3.747711	4.034338	4.881907	3.21267
protein_co	tuftelin_1	171	173	134	1121	841	987	2.909968	3.469327	3.004912	16.50292	16.07819	16.6924
protein_co	splicing_fac	1311	1157	980	4272	2594	2944	33.28808	34.61995	32.79042	93.83833	73.99546	74.29053
protein_co	extracellula	1053	890	679	215	188	175	18.18228	18.10994	15.44986	3.2116	3.646925	3.003085
protein_co	zinc_finger_	647	618	423	789	720	877	6.369063	7.169137	5.487145	6.719103	7.962562	8.579866
protein_co	threonyl-tR	360	298	204	606	530	666	6.983788	6.812585	5.214991	10.17008	11.55084	12.84022
protein_co	cingulin	11	17	5	1273	1666	1824	0.114388	0.208327	0.068516	11.45198	19.46315	18.85053
protein_co	sorting_nex	1016	850	688	1681	1446	1571	7.473677	7.368288	6.669048	10.69723	11.94973	11.48488
protein_co	SET_domai	399	368	311	335	499	314	4.760752	5.174371	4.889876	3.457884	6.688862	3.723419
protein_co	ADAMTS-lik	286	275	186	831	566	732	3.607606	4.087831	3.091725	9.068118	8.020817	9.176432
protein_co	myeloid_ce	3243	2828	2999	4771	4146	4418	43.6642	44.87093	53.20958	55.57136	62.71291	59.11721
protein_co	cathepsin_l	463	375	323	61	57	61	14.48681	13.82707	13.3177	1.651143	2.003621	1.896842
protein_co	regulatory_	567	463	478	430	387	438	8.394168	8.077606	9.325181	5.507139	6.436572	6.444338
protein_co	phosphatid	1763	1579	1361	1213	995	1198	23.43333	24.73267	23.83827	13.9478	14.85778	15.82516
protein_co	phosphatid	1274	1081	1003	1852	1617	1649	17.90465	17.90314	18.57515	22.51648	25.53028	23.03174
protein_co	acidic_(leu	907	856	863	2973	2501	2543	13.90602	15.46594	17.43577	39.43242	43.07827	38.7482
protein_co	family_with	301	224	257	182	146	161	5.656812	4.960899	6.36463	2.958964	3.082529	3.007051
protein_co	annexin_A9	81	95	43	108	136	135	2.348423	3.245802	1.642837	2.708807	4.429751	3.889867
protein_co	selenium_b	553	430	320	177	132	174	10.30858	9.446029	7.860651	2.854368	2.764374	3.223537
protein_co	ceramide_s	1365	1030	979	1152	870	887	28.84809	25.65244	27.26477	21.06201	20.65631	18.6302
protein_co	endosulfine	2049	1791	1436	4294	4112	5465	38.494	39.65097	35.55006	69.78726	86.78672	102.0354
pseudogen	-	365	343	264	242	149	204	17.50314	19.38314	16.68252	10.03925	8.027094	9.722161
protein_co	sema_dom	517	544	398	69	44	69	5.201538	6.449815	5.27666	0.600556	0.497328	0.689922
protein_co	mitochond	292	297	231	896	437	522	11.92806	14.29719	12.43466	31.66344	20.05477	21.19177
protein_co	aryl_hydro	837	813	661	491	560	486	9.067242	10.37881	9.435959	4.601445	6.815329	5.232336
protein_co	pogo_trans	1192	1139	1056	1580	1529	1461	9.523946	10.72436	11.11833	10.92096	13.72452	11.60114
protein_co	chromoson	79	76	38	64	61	83	1.995391	2.26215	1.264792	1.39844	1.730931	2.083476
protein_co	ornithine_c	3	8	0	9	1	2	0.041906	0.131689	0	0.108757	0.015693	0.027765
protein_co	HORMA_do	1	0	0	0	0	0	0.028175	0	0	0	0	0
protein_co	golgi_phos	376	306	281	398	366	393	6.637484	6.36567	6.536673	6.078014	7.258481	6.894739
protein_co	GA_binding	275	211	187	218	154	208	1.624138	1.46852	1.455347	1.113806	1.021786	1.220853
protein_co	inhibitor_c	174	141	137	295	236	276	2.817905	2.690936	2.923698	4.132969	4.293765	4.442177
protein_co	synaptotag	49	45	48	57	62	29	0.499925	0.541038	0.645334	0.503091	0.710639	0.294047
protein_co	potassium_	2	0	0	16	16	21	0.034133	0	0	0.236229	0.306775	0.356188
protein_co	denticleless	104	90	90	1464	1108	954	1.203994	1.227836	1.372993	14.66206	14.41052	10.97612
protein_co	dual-specifi	353	234	249	38	33	46	8.024118	6.268239	7.45859	0.747256	0.842724	1.039178
protein_co	eukaryotic_	1360	1108	838	1305	891	892	34.38384	33.01127	27.91864	28.5423	25.30709	22.41248
protein_co	integrator_	320	247	281	888	579	608	3.809561	3.465206	4.408249	9.145363	7.743772	7.193466
protein_co	vasohibin_	132	120	108	35	62	41	1.654406	1.772379	1.78372	0.379489	0.872989	0.510695
protein_co	TATA_box_l	63	44	49	276	232	242	1.745307	1.436452	1.788802	6.614599	7.22052	6.662794

protein_co	SET_and_M	284	290	194	2003	1479	1745	3.177355	3.823424	2.860118	19.38614	18.58937	19.40226
protein_co	sushi_dom	0	4	1	25	18	32	0	0.07171	0.020047	0.329015	0.307634	0.483807
protein_co	dual_specif	77	56	55	1361	852	1050	1.52334	1.305573	1.433849	23.29309	18.93628	20.64453
protein_co	HHIP-like_2	64	40	40	84	57	71	1.315815	0.96913	1.083701	1.494023	1.316554	1.450717
protein_co	tumor_pro	782	671	719	1826	1379	1431	8.732305	8.829818	10.58	17.63949	17.29958	15.88076
protein_co	ATPase_am	2349	2000	1691	730	692	814	21.21795	21.28911	20.12792	5.704351	7.022238	7.307258
protein_co	filaggrin_fa	0	0	0	2	2	6	0	0	0	0.010041	0.01304	0.034607
protein_co	ADAM_met	3549	2905	2288	2787	1738	1951	41.6787	40.20327	35.40781	28.31445	22.93016	22.77063
protein_co	jumping_tr	1853	1528	1167	2402	1756	2304	76.22351	74.07028	63.25855	85.47706	81.14974	94.19019
protein_co	RAB13_mer	9026	7574	5773	1698	1643	2219	225.0803	222.574	189.7049	36.6305	46.0287	54.99321
protein_co	tropomyos	7572	6379	5633	18863	13643	15443	99.2005	98.48338	97.24736	213.7849	200.7993	201.0687
protein_co	nucleopori	7	5	9	12	17	15	0.062929	0.05297	0.106617	0.093324	0.171691	0.134014
protein_co	SNAP-assoc	369	361	321	558	441	560	16.21181	18.69043	18.58424	21.20812	21.7667	24.45134
protein_co	solute_carr	323	247	184	271	253	319	3.796612	3.421352	2.85001	2.755662	3.340899	3.726439
protein_co	S100_calci	0	0	0	1	0	2	0	0	0	0.095614	0	0.219683
protein_co	ubiquitin_a	3816	3253	3103	5876	4921	5064	50.65768	50.88949	54.28171	67.48104	73.39042	66.80982
protein_co	solute_carr	2940	2260	2075	6285	4686	5458	57.15994	51.77975	53.16152	105.7092	102.3519	105.46
protein_co	HCLS1_assc	1005	874	670	1877	1047	1420	41.43746	42.46641	36.40296	66.95058	48.49789	58.18688
protein_co	cAMP_resp	56	40	22	113	112	98	1.692178	1.424377	0.876023	2.953925	3.802113	2.943023
protein_co	ephrin-A3	48	33	27	7	7	1	1.42602	1.155328	1.057019	0.179906	0.233632	0.029525
protein_co	chromoson	3236	2820	2368	2459	1792	2061	100.3027	103.0055	96.72099	65.93648	62.40096	63.48803
protein_co	GATA_zinc_	579	523	461	619	616	661	4.099069	4.363303	4.300732	3.791057	4.899327	4.650694
protein_co	interleukin	2433	2202	1852	8758	5851	6829	77.64041	82.80758	77.8792	241.7763	209.7611	216.5771
protein_co	Ras-like_wi	494	418	397	862	662	718	7.591539	7.569832	8.039484	11.4597	11.42904	10.96571
protein_co	integrator_	1320	1211	1065	1722	1316	1374	12.17246	13.16	12.94163	13.73728	13.63357	12.59218
protein_co	pyruvate_k	1	1	0	0	0	2	0.021356	0.025166	0	0	0	0.042448
protein_co	hyperpolar	106	92	60	90	100	99	1.509345	1.543752	1.12582	1.108634	1.599675	1.400966
protein_co	filaggrin	0	0	1	28	39	28	0	0	0.005473	0.100602	0.181969	0.115572
protein_co	actin_alpha	10	1	3	67	37	49	0.35507	0.041843	0.140369	2.058033	1.475928	1.7291
protein_co	chromoson	193	195	139	487	273	397	3.845545	4.578701	3.649641	8.394455	6.110999	7.861414
protein_co	UDP-N-acet	2922	2513	2395	2225	2549	2569	34.73138	35.1999	37.51304	22.87889	34.03774	30.34699
protein_co	tetratricop	106	127	127	415	324	366	1.725098	2.435672	2.72362	5.842775	5.923823	5.919687
protein_co	saccharopi	658	572	485	383	268	258	13.91737	14.2572	13.51786	7.007983	6.368177	5.423262
protein_co	lysosomal_	364	283	423	146	143	123	1.429564	1.309772	2.189159	0.496042	0.630939	0.480084
protein_co	Mitogen-ac	15	22	11	156	108	107	0.136704	0.236276	0.132105	1.229924	1.105767	0.969135
protein_co	centrosom	1217	977	1323	1222	1016	863	9.436027	8.926891	13.5174	8.196582	8.849961	6.64996
protein_co	acid_phosp	1426	1320	924	3053	2235	2499	48.64295	53.06173	41.53433	90.09282	85.64992	84.71811
protein_co	synaptoson	586	582	407	756	566	728	12.91029	15.11014	11.81592	14.40864	14.00889	15.93967
protein_co	signal_reco	2277	1995	1897	6313	4404	4753	75.53048	77.98466	82.92039	181.1582	164.1178	156.6883
protein_co	nuclear_VC	309	266	267	728	592	581	5.238158	5.313844	5.964392	10.67615	11.27433	9.788269
protein_co	SDE2_telon	508	472	411	642	600	626	6.765792	7.408052	7.21326	7.396955	8.977497	8.285886
protein_co	delta(4)-des	1400	1207	1119	5386	3596	4334	35.2772	35.84102	37.15617	117.4074	101.797	108.5337
protein_co	F-box_prot	545	392	495	917	716	806	5.293128	4.486514	6.335136	7.704567	7.812283	7.77966
protein_co	ADP-ribosy	9168	7394	6167	12572	7575	8429	241.9556	229.9576	214.4717	287.0308	224.5913	221.0787

protein_co	cornichon_	605	539	505	1223	1027	1290	7.764679	8.151997	8.540717	13.57868	14.8077	16.45385
protein_co	inositol-tris	834	689	756	306	340	310	7.179315	6.989455	8.575779	2.278775	3.288099	2.65209
protein_co	guanylate_l	4529	3675	2615	3390	2104	2678	94.06425	89.947	71.56963	60.90949	49.09271	55.27675
protein_co	CDC42_bin	1141	902	1320	729	729	599	5.564779	5.18413	8.483421	3.075763	3.994283	2.903346
protein_co	cornichon_	124	62	108	76	79	82	2.566334	1.512134	2.94544	1.360718	1.836825	1.686611
protein_co	chromoson	313	279	164	758	614	1046	4.662502	4.89763	3.21924	9.768028	10.27524	15.48517
protein_co	membrane_	463	497	436	1032	840	765	3.162389	4.000349	3.924241	6.097855	6.44559	5.192846
protein_co	poly_(ADP-	2429	1824	2050	5806	5116	4921	32.48956	28.75069	36.13308	67.18253	76.87691	65.4153
protein_co	presenilin_	133	117	99	387	261	312	2.856451	2.961203	2.801852	7.190335	6.29745	6.659466
protein_co	pyrroline-5	205	165	152	304	189	263	3.44646	3.268966	3.367424	4.421361	3.569688	4.394251
protein_co	lamin_B_re	703	594	695	3210	2711	2745	9.861558	9.819372	12.84724	38.95455	42.72369	38.26857
protein_co	wingless-ty	50	51	29	360	350	444	0.666595	0.801253	0.509478	4.152004	5.242148	5.88281
protein_co	epoxide_hy	2342	2005	1498	573	497	534	69.81295	70.43209	58.84313	14.77634	16.64388	15.81977
protein_co	renin	0	0	0	12	2	2	0	0	0	0.377464	0.081698	0.072272
protein_co	SRY_(sex_d	125	88	89	1135	1017	1101	1.849015	1.533982	1.734823	14.5241	16.90053	16.18555
protein_co	ethanolami	91	84	70	67	64	48	1.937904	2.108033	1.964372	1.234323	1.531158	1.015879
protein_co	protein_tyr	444	575	293	8	10	2	3.653373	5.575528	3.176973	0.056946	0.09244	0.016355
protein_co	pleckstrin_	7	9	9	150	100	114	0.072793	0.110291	0.123329	1.349408	1.168256	1.178158
protein_co	protein_tyr	1	0	0	0	2	0	0.014061	0	0	0	0.031594	0
protein_co	synaptotag	20	10	19	74	100	87	0.139062	0.081938	0.174088	0.445117	0.781139	0.601185
protein_co	ADP-ribosy	584	516	430	1147	824	1154	17.24347	17.9543	16.73074	29.29802	27.33305	33.86314
protein_co	odd-skippe	1802	1610	1372	68	63	78	22.85022	24.0585	22.9258	0.745946	0.897481	0.982969
protein_co	growth_dif	3	7	3	2	0	1	0.03816	0.104929	0.050286	0.022008	0	0.012642
protein_co	protein_dis	5953	4873	4203	6233	4697	4938	117.5085	113.354	109.327	106.4372	104.1605	96.87106
protein_co	ras_homolo	3062	2637	2176	2884	2381	2523	68.51451	69.53358	64.16099	55.82588	59.85298	56.10535
protein_co	ATPase_H+_	13	14	7	41	22	23	0.221867	0.281569	0.157428	0.605337	0.421815	0.390111
protein_co	heterogene	841	763	704	1448	1080	1199	10.66939	11.4071	11.76931	15.89188	15.39276	15.11724
protein_co	galactose_r	258	213	189	145	132	200	5.498702	5.349672	5.308076	2.673447	3.160556	4.236236
protein_co	calmodulin	87	71	94	123	80	106	3.080847	2.962896	4.386454	3.76807	3.182658	3.730495
protein_co	ATP-bindin	0	0	0	1	0	1	0	0	0	0.017185	0	0.019743
protein_co	echinoderm	1838	1651	1892	1912	1764	1626	17.53569	18.56229	23.78665	15.78077	18.9071	15.41727
protein_co	calmodulin	3220	2695	2277	15086	9663	12079	37.86539	37.34672	35.28454	153.4701	127.6579	141.1651
protein_co	ChaC_catio	34	43	14	240	118	180	1.362599	2.030789	0.739353	8.32077	5.312762	7.169212
protein_co	ribosomal_	13752	12442	8081	18998	11985	16725	628.1661	669.7395	486.4168	750.7227	615.0292	759.2493
protein_co	WD_repeat	50	46	55	92	60	81	0.489469	0.530665	0.709501	0.779123	0.659866	0.788043
protein_co	vacuolar_p	224	220	292	472	409	368	3.299606	3.818948	5.668024	6.01477	6.768406	5.387304
protein_co	additional_	365	248	363	558	771	586	2.160736	1.730086	2.83172	2.85763	5.127578	3.447594
protein_co	Ewing_tum	150	160	144	342	240	263	2.323332	2.920432	2.93912	4.58257	4.176191	4.048419
protein_co	small_nucl	666	570	418	2246	1727	2464	32.25865	32.53523	26.67983	94.11193	93.97521	118.6103
protein_co	abhydrolas	0	1	10	1	5	5	0	0.044563	0.498309	0.032714	0.212414	0.187907
protein_co	Meis_home	125	120	107	368	275	398	1.294781	1.464787	1.460511	3.297593	3.200133	4.097122
pseudogen	tripartite_r	0	0	1	0	1	4	0	0	0.041825	0	0.035657	0.126173
protein_co	tripartite_r	0	0	4	4	0	0	0	0	0.165906	0.108915	0	0
protein_co	cytosolic_i	913	826	732	1908	1266	1462	13.47133	14.36239	14.23264	24.3546	20.98565	21.43861

protein_co	zinc_finger_	293	206	199	186	186	203	2.773415	2.297849	2.482191	1.523082	1.977923	1.909646
protein_co	small_nucl	3501	3034	3034	7123	6313	5505	25.86831	26.41792	29.54107	45.53044	52.40355	40.42433
protein_co	mitochond	897	849	664	1139	852	933	12.90437	14.39326	12.58772	14.17526	13.76997	13.33938
protein_co	ankyrin_rep	22	14	14	13	23	8	0.533777	0.400288	0.44761	0.272862	0.626923	0.192902
protein_co	TP53RK_bi	199	190	121	644	396	611	12.86356	14.47334	10.30691	36.01281	28.75759	39.25175
protein_co	N-acetyltra	0	1	1	0	0	0	0	0.065879	0.073668	0	0	0
protein_co	exocyst_co	547	485	560	704	859	682	4.893329	5.112884	6.60146	5.448197	8.632953	6.063329
protein_co	sideroflexir	633	556	449	388	406	442	8.094601	8.378642	7.566114	4.292265	5.832662	5.617249
protein_co	testis_expr	1493	1262	1216	2362	1404	1557	22.08463	21.99869	23.70275	30.22549	23.33171	22.8891
protein_co	DEAQ_box_	4	2	0	9	5	8	0.078752	0.046402	0	0.153288	0.110591	0.156531
protein_co	dual_specif	471	413	333	578	337	424	11.46446	11.8465	10.681	12.17093	9.215349	10.25672
protein_co	ST6_beta-g	196	151	162	117	133	135	1.426314	1.294921	1.553492	0.73656	1.087326	0.976343
protein_co	nephronop	82	82	67	94	63	90	0.433856	0.511273	0.467134	0.430252	0.374474	0.473243
protein_co	mal_T-cell_	106	82	67	1	5	0	1.833305	1.671282	1.526998	0.014962	0.097151	0
protein_co	threonine_	44	20	17	125	104	120	0.638368	0.341944	0.325014	1.568885	1.695121	1.730251
protein_co	v-ral_simia	979	960	839	1805	1568	1516	22.11145	25.55129	24.97073	35.2675	39.78594	34.02854
protein_co	complemer	0	0	0	51	45	35	0	0	0	1.143291	1.310042	0.901366
protein_co	transmemb	140	107	129	504	320	445	4.264522	3.840902	5.178057	13.28116	10.95069	13.47138
protein_co	5'-nucleoti	0	1	0	0	0	0	0	0.025485	0	0	0	0
protein_co	RAB_memb	254	207	132	299	243	271	4.630514	4.447059	3.171058	4.715521	4.976807	4.90992
protein_co	solute_carr	1142	901	1079	2197	1692	1644	17.88187	16.62566	22.264	29.76048	29.76435	25.58341
protein_co	fibulin_7	41	12	34	62	39	38	0.472071	0.162821	0.515866	0.617558	0.504472	0.434827
pseudogen	-	0	0	1	2	0	11	0	0	0.090838	0.119268	0	0.753587
protein_co	zinc_finger_	154	113	115	384	202	220	4.496918	3.88848	4.425139	9.700375	6.62666	6.384496
protein_co	lipoyltrans	22	29	13	47	38	40	0.754829	1.17255	0.587766	1.395041	1.464734	1.363942
pseudogen	tripartite_r	0	0	0	1	0	0	0	0	0	0.044551	0	0
protein_co	cyclic_nucl	2	3	0	2	2	4	0.027566	0.048728	0	0.023847	0.030969	0.054792
protein_co	fumarylace	68	86	60	297	170	169	2.593651	3.865522	3.015704	9.79991	7.284514	6.406178
protein_co	lysozyme_G	15	30	29	43	17	14	0.765043	1.803114	1.94907	1.897257	0.974076	0.709631
protein_co	AF4/FMR2_	669	490	585	122	98	85	4.353722	3.757835	5.016782	0.686843	0.716489	0.549747
protein_co	UBX_doma	1442	1274	1293	1589	1483	1170	19.05664	19.84073	22.51721	18.16637	22.01767	15.36656
protein_co	neurexophi	0	0	0	113	94	93	0	0	0	4.919464	5.314388	4.651242
protein_co	speckle-typ	151	143	166	501	439	399	1.32682	1.480738	1.922109	3.808341	4.333598	3.484316
protein_co	thrombosp	0	0	0	0	10	2	0	0	0	0	0.097326	0.017219
protein_co	G_protein-	4	0	2	7	12	19	0.08151	0	0.053705	0.1234	0.274716	0.384783
protein_co	polymerase	498	399	300	1085	919	1138	11.32987	10.69734	8.993977	21.35445	23.48877	25.73046
protein_co	AMMECR1-	695	561	601	1025	1008	874	7.899096	7.513851	9.001231	10.07812	12.8707	9.872194
protein_co	UDP-N-acet	7	8	16	308	175	219	0.066941	0.090156	0.201628	2.54806	1.880109	2.081372
protein_co	plakophilin	456	426	451	1871	1552	1571	4.178829	4.600515	5.446294	14.83292	15.9783	14.30789
protein_co	secernin_3	245	188	204	343	237	256	4.270841	3.862	4.686108	5.172547	4.641354	4.435034
protein_co	KIAA1715	1016	802	791	744	578	540	7.068075	6.574896	7.251348	4.47758	4.517356	3.733454
protein_co	zinc_finger_	9	6	3	90	79	94	0.144911	0.113846	0.063653	1.25362	1.429014	1.504173
protein_co	transmemb	250	207	203	152	166	127	3.934378	3.83896	4.209853	2.069392	2.9349	1.986321
protein_co	cell_divisio	237	191	165	2076	1561	1526	3.950572	3.751907	3.624352	29.93656	29.23234	25.27992

protein_co distal-less_	188	136	168	498	460	447	3.77004	3.213913	4.439482	8.639339	10.36323	8.908515
protein_co ubiquitin_p	609	534	660	484	491	377	4.027616	4.16178	5.751876	2.769103	3.648054	2.477888
protein_co phosphatas	14	10	6	51	24	40	0.658821	0.554558	0.372071	2.076217	1.26882	1.870722
protein_co GULP_engu	846	708	859	1006	915	834	6.03044	5.947289	8.068757	6.203541	7.327382	5.908189
protein_co family_witl	404	332	514	156	220	136	3.675573	3.559499	6.162283	1.22781	2.248617	1.22968
protein_co heat_shock	8400	7040	6366	20815	18317	18389	181.1423	178.9041	180.9014	388.3113	443.7558	394.1017
protein_co coiled-coil_	108	75	92	262	208	236	1.551595	1.269764	1.741716	3.256259	3.357121	3.369584
protein_co methyltran	104	67	70	355	303	302	1.145861	0.869923	1.016323	3.383686	3.75051	3.306856
protein_co unc-80_hor	4	8	1	2	6	5	0.015615	0.036801	0.005144	0.006754	0.026313	0.019398
protein_co parathyroic	0	0	6	28	36	25	0	0	0.154287	0.472676	0.789212	0.484833
protein_co carboxypep	4	5	2	1	0	5	0.175156	0.258014	0.115407	0.037882	0	0.217593
protein_co neurobeach	182	160	275	108	200	135	0.880898	0.912602	1.753968	0.452211	1.08751	0.649378
protein_co KAT8_regul	211	252	223	342	245	271	2.349716	3.307048	3.272447	3.294747	3.065124	2.999244
protein_co sperm_assc	201	184	149	588	437	492	2.239768	2.416195	2.187903	5.668229	5.470633	5.448561
protein_co ATP-bindin	27	11	44	55	57	53	0.157078	0.075414	0.337317	0.276807	0.372541	0.306433
protein_co sulfatase_m	552	432	428	672	522	526	9.277279	8.556031	9.478948	9.770433	9.856009	8.785711
protein_co neuronal_t	0	0	0	0	4	1	0	0	0	0	0.049276	0.010898
protein_co rhomboid_	442	410	424	535	428	457	4.542792	4.965826	5.742503	4.756827	4.941893	4.667952
protein_co chemokine	7	6	6	697	511	645	0.168219	0.169917	0.190004	14.49017	13.79582	15.40448
protein_co transient_r	1	4	0	1	1	0	0.009418	0.044396	0	0.008148	0.010581	0
protein_co hairy_and_	65	44	44	119	73	66	2.150728	1.715663	1.91849	3.406294	2.713589	2.17033
protein_co espin-like	4	1	1	1	1	0	0.043789	0.012901	0.014426	0.00947	0.012299	0
protein_co ankyrin_rep	187	143	128	139	154	148	2.133613	1.922725	1.924504	1.371993	1.973985	1.678207
protein_co COP9_signa	604	512	463	1457	1166	1273	9.692743	9.682485	9.790967	20.22704	21.02119	20.30242
protein_co DIS3_mitot	305	246	274	659	509	487	3.456862	3.285674	4.092301	6.46146	6.481105	5.485558
protein_co copine_fam	4	3	1	11	3	11	0.1024	0.090504	0.033735	0.243611	0.08628	0.279862
protein_co Fanconi_an	96	97	104	1062	963	1124	0.973814	1.159534	1.390186	9.319494	10.97438	11.33133
protein_co TAM41_mit	248	229	217	533	289	381	4.743268	5.161413	5.469159	8.818937	6.209733	7.242035
protein_co vestigial_lik	2496	2154	1950	656	1056	1029	35.47402	36.07602	36.52038	8.065525	16.86082	14.53419
protein_co RAB5A_mer	734	663	642	1210	1081	1079	15.32283	16.31036	17.66089	21.852	25.35231	22.38587
protein_co family_witl	1911	1471	1266	1326	1008	1245	21.9078	19.87275	19.12523	13.15057	12.98218	14.1846
protein_co CTD_(carbo	2132	1656	1248	1366	1094	1427	42.78628	39.16379	33.00401	23.71543	24.66515	28.46105
protein_co RCD1_requ	559	504	561	1988	1559	1842	7.255213	7.708609	9.594803	22.32121	22.73179	23.75952
protein_co membrane-	36	20	29	1153	950	949	0.428576	0.280583	0.454944	11.87455	12.70567	11.22796
protein_co serine/thre	472	463	327	851	742	809	6.912351	7.990462	6.310538	10.78143	12.20778	11.77449
protein_co GDP-mann	1209	1100	803	837	682	813	12.95137	13.88638	11.33547	7.756715	8.207725	8.655448
processed_ glutamate_	16	13	5	60	88	73	0.109283	0.104637	0.045003	0.354526	0.675252	0.495526
protein_co ELL_associa	216	187	185	549	373	419	2.438221	2.487528	2.751857	5.361109	4.730174	4.700488
protein_co contactin_-	10	1	9	278	260	211	0.101849	0.012002	0.120791	2.449422	2.97494	2.135738
protein_co dynein_cyt	642	616	616	1595	1139	1146	7.094159	8.021466	8.969773	15.24718	14.13965	12.5852
protein_co RNA_bindir	410	367	362	347	291	269	2.64447	2.78951	3.076792	1.936187	2.108613	1.724315
protein_co glutamate_	2	0	1	5	2	4	0.023482	0	0.015472	0.050786	0.026381	0.046675
protein_co oxysterol_b	136	65	87	737	636	592	0.932277	0.525081	0.785887	4.370555	4.897926	4.033085
protein_co glycosyltra	190	202	135	565	306	422	3.953926	4.953743	3.702061	10.17153	7.153943	8.727645

protein_co chemokine	0	3	0	37	36	23	0	0.051918	0	0.470058	0.593934	0.335679
protein_co family_with	1	0	0	10	12	9	0.016963	0	0	0.146744	0.22868	0.151723
protein_co cysteine-se	134	86	85	466	281	476	2.253524	1.704366	1.883697	6.779635	5.309	7.955619
protein_co solute_carr	986	751	621	943	706	728	24.58776	22.06933	20.4065	20.34308	19.77861	18.04194
protein_co integrin_al	32	27	25	404	576	507	0.214744	0.213521	0.221078	2.345387	4.342518	3.381331
protein_co solute_carr	13	9	4	2	0	7	0.302254	0.246592	0.122553	0.040227	0	0.161747
protein_co golgin_A4	1185	967	1186	1426	1343	1217	8.071935	7.762344	10.64581	8.403144	10.27743	8.238716
protein_co CTD_(carbo	374	389	356	2274	1820	1720	4.267227	5.230351	5.352528	22.44541	23.32892	19.50348
protein_co SH3_and_c	150	138	109	286	183	204	2.460846	2.66796	2.356429	4.059029	3.372821	3.326082
protein_co IQ_motif_a	1198	924	1041	361	301	371	12.01427	10.91992	13.75707	3.13192	3.39122	3.697635
protein_co cullin-assoc	65	42	36	57	52	43	0.752496	0.57299	0.549197	0.570859	0.676306	0.494731
protein_co ribosomal_	16729	14810	10344	16991	10180	13597	418.3514	436.4489	340.8745	367.5811	286.0013	337.9278
protein_co protein_tyr	3311	2867	3281	962	963	812	19.43106	19.82769	25.37339	4.883998	6.349109	4.735906
protein_co interleukin	1093	1008	997	2153	1950	1784	6.635838	7.211793	7.976375	11.30792	13.30023	10.76416
protein_co SHQ1_H/AC	333	311	297	543	405	454	4.381051	4.821716	5.14903	6.180121	5.98602	5.936078
protein_co solute_carr	284	237	169	424	353	435	3.88608	3.821631	3.047298	5.019058	5.426466	5.915511
protein_co ubiquitin-li	668	640	652	1384	1119	1244	16.4181	18.53674	21.11683	29.42697	30.89766	30.3862
protein_co ADP-ribosy	2914	2524	2343	1821	1434	1551	73.42697	74.94842	77.79884	39.69529	40.59422	38.84074
protein_co TATA_elem	640	608	715	588	463	483	4.920453	5.50853	7.243791	3.910798	3.999034	3.690471
protein_co leucine-rich	567	495	613	77	68	55	5.681912	5.845528	8.094812	0.667521	0.765543	0.547752
protein_co leucine-rich	1	0	0	0	2	0	0.037204	0	0	0	0.083592	0
protein_co LIM_domai	955	844	823	525	555	473	4.461976	4.647008	5.067089	2.122004	2.91317	2.196315
protein_co zinc_finger_	165	163	145	197	220	187	1.497303	1.743092	1.733918	1.546518	2.242835	1.686463
protein_co nuclear_fac	214	188	184	227	134	158	2.887936	2.989776	3.272099	2.650102	2.031551	2.119047
protein_co collagen_ty	2176	1834	2131	345	233	213	20.19274	20.05593	26.05882	2.76961	2.429078	1.964381
protein_co neurexophi	910	696	740	416	381	333	5.909753	5.326528	6.332781	2.337137	2.779726	2.149225
protein_co G_protein-r	2	0	0	0	0	0	0.03372	0	0	0	0	0
protein_co myosin_hea	406	267	300	34	40	34	3.038457	2.354753	2.958579	0.220125	0.336307	0.252881
protein_co pleckstrin_	2813	2346	2767	2028	2358	1877	24.30603	23.88797	31.50563	15.15916	22.88954	16.11826
protein_co abhydrolas	539	442	431	587	421	511	11.01745	10.64686	11.60926	10.37991	9.667707	10.38061
protein_co transgelin_	7	16	7	14	20	22	0.24905	0.670836	0.328187	0.430904	0.799407	0.777896
protein_co phospholip	3	2	7	0	0	2	0.088927	0.069863	0.273428	0	0	0.058918
protein_co RAB_memb	411	251	357	551	474	403	5.603592	4.032789	6.413982	6.498892	7.260259	5.460588
protein_co ADP-ribosy	34	11	41	124	90	126	0.395951	0.15096	0.629189	1.249244	1.177482	1.458286
protein_co immunoglo	3	3	4	37	42	27	0.044638	0.052603	0.07843	0.476267	0.702077	0.399263
protein_co autophagy_	491	480	414	1105	599	737	8.63589	9.948874	9.595348	16.81322	11.83591	12.88258
protein_co nuclear_rec	0	0	0	2	0	2	0	0	0	0.020738	0	0.023823
protein_co BOC_cell_a	919	724	602	604	682	721	8.461352	7.855429	7.303912	4.810876	7.054361	6.597344
protein_co signal_reco	1705	1448	1318	1595	1221	1559	44.77401	44.81023	45.60913	36.23475	36.02187	40.68715
protein_co transmemb	2	2	3	435	363	328	0.021908	0.025817	0.043304	4.122186	4.467155	3.570745
protein_co angiotensir	79	78	86	0	4	4	1.733971	2.017514	2.487414	0	0.098633	0.087254
protein_co mediator_c	10	8	16	110	200	107	0.049275	0.046454	0.103892	0.468902	1.107147	0.523986
protein_co eukaryotic_	1898	1751	1356	2391	1319	1546	45.7152	49.70014	43.03868	49.82037	35.69096	37.00697
protein_co aldehyde_d	1	0	0	7	2	5	0.011499	0	0	0.069633	0.025837	0.057139

protein_co	oxysterol_b	227	191	271	487	480	461	2.867479	2.843249	4.511059	5.321896	6.811844	5.78742
protein_co	transient_r	208	176	186	249	212	180	2.546653	2.539371	3.000918	2.637356	2.916026	2.190224
protein_co	neutral_ch	65	51	67	183	132	111	0.734193	0.678851	0.997256	1.78818	1.67502	1.246034
protein_co	family_witl	0	4	0	4	8	8	0	0.196807	0	0.144476	0.375242	0.33195
protein_co	LIM_domai	2811	2441	2952	3244	3152	2758	8.141872	8.331789	11.26716	8.128441	10.25649	7.939028
protein_co	transmemb	336	299	269	268	225	264	7.143845	7.491539	7.536676	4.92936	5.37433	5.578357
protein_co	KIAA0226	331	294	241	546	482	474	2.51955	2.637238	2.417391	3.595428	4.121839	3.585774
protein_co	aminomet	88	80	56	121	108	170	1.423841	1.525372	1.193993	1.693664	1.963142	2.733615
protein_co	T-cell_leuk	400	354	326	501	330	339	9.867846	10.29136	10.59778	10.6921	9.145877	8.311353
protein_co	nicolin_1	144	108	103	215	166	190	2.914183	2.57564	2.746796	3.764054	3.774083	3.821357
protein_co	urocortin_	6	0	3	12	4	3	0.214481	0	0.141317	0.371092	0.160637	0.106578
protein_co	Vpr_(HIV-1	238	215	234	683	670	656	2.782062	2.961661	3.604462	6.906746	8.798601	7.620847
protein_co	mesenceph	1455	1346	973	2754	1938	2889	51.04649	55.6487	44.98322	83.58528	76.38458	100.7303
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.036377	0
protein_co	coiled-coil_	86	68	63	55	52	54	1.022899	0.953126	0.987438	0.565927	0.694843	0.638319
protein_co	syntaxin_bi	0	0	2	12	9	3	0	0	0.014693	0.057876	0.056369	0.016622
protein_co	ELL_associa	6	15	4	56	39	56	0.320208	0.943363	0.281304	2.585422	2.338267	2.970148
protein_co	immunoglo	0	0	0	60	48	44	0	0	0	1.033447	1.073653	0.870635
protein_co	transmemb	17	5	12	1	3	0	0.568898	0.19718	0.529178	0.02895	0.112786	0
protein_co	mucin_4_c	0	0	3	2	0	1	0	0	0.012232	0.005353	0	0.003075
protein_co	slit_homol	2014	1599	2012	1171	1461	1142	16.68594	15.61158	21.96615	8.392882	13.59848	9.403012
protein_co	eukaryotic_	565	477	383	1267	879	980	8.644989	8.600852	7.722352	16.77087	15.10963	14.90225
protein_co	alpha-2-HS	23	9	0	0	5	12	0.711656	0.328165	0	0	0.173805	0.369006
protein_co	endothelin	49	75	46	253	140	180	0.753007	1.358223	0.931527	3.363461	2.417018	2.749065
protein_co	von_Willeb	8	11	7	9	11	9	0.102798	0.166569	0.11853	0.100046	0.158795	0.114934
protein_co	diacylglyce	389	322	269	289	256	423	4.442202	4.333229	4.047956	2.855022	3.284261	4.800635
protein_co	FIP1_like_1	502	412	484	939	800	751	8.357352	8.082939	10.61806	13.52364	14.96249	12.42552
protein_co	solute_carr	31	32	25	5	3	8	0.448407	0.545466	0.476525	0.062567	0.048751	0.115003
protein_co	Ly1_antibo	296	290	210	1143	896	1221	9.987594	11.53119	9.337342	33.36402	33.96458	40.94439
protein_co	centromere	173	122	159	275	226	268	2.357475	1.959151	2.855177	3.241879	3.45986	3.629489
protein_co	EPH_recept	606	576	738	2	0	0	3.881229	4.347367	6.228563	0.011081	0	0
protein_co	corin_serin	96	83	121	8	1	11	0.945023	0.962845	1.569609	0.068128	0.011059	0.107615
protein_co	ATPase_cla	704	547	714	332	354	372	5.60037	5.127887	7.484746	2.284784	3.163708	2.941011
protein_co	OCIA_doma	546	408	388	628	407	763	15.3265	13.49639	14.35215	15.25011	12.83494	21.28554
protein_co	solute_carr	25	38	24	19	13	20	0.739399	1.324432	0.935374	0.486134	0.431948	0.587866
protein_co	stearoyl-Co	793	732	627	275	275	276	13.53828	14.7268	14.10564	4.061496	5.274388	4.682837
protein_co	placenta-sp	4	4	4	187	85	117	0.093992	0.110764	0.123858	3.801329	2.243876	2.732288
protein_co	enolase-ph	540	454	425	1739	1200	1562	14.1176	13.98717	14.64168	39.33052	35.24499	40.58427
protein_co	group-spec	0	0	0	0	1	0	0	0	0	0	0.03016	0
protein_co	tRNA_meth	85	66	69	274	189	247	1.218187	1.11467	1.303104	3.397103	3.043029	3.518048
protein_co	kelch-like_f	218	201	223	360	272	265	2.053218	2.230908	2.767695	2.933216	2.878038	2.48047
protein_co	synuclein_a	95	72	79	113	85	103	1.58506	1.415669	1.736936	1.631036	1.593272	1.707925
protein_co	TBC1_doma	441	361	364	424	288	271	4.337169	4.183907	4.717413	3.607419	3.182067	2.648785
protein_co	calcium/ca	2069	1803	1890	2010	1755	1647	18.41852	18.91459	22.17128	15.47937	17.55175	14.57127

protein_co	CDGSH_iro	255	245	227	841	479	513	5.801441	6.56854	6.805443	16.55216	12.24279	11.59906
protein_co	DNA-damag	226	266	246	72	32	39	4.594725	6.37294	6.59054	1.266329	0.730887	0.787998
protein_co	ankyrin_2_	272	172	228	70	113	100	1.014367	0.755895	1.120458	0.225833	0.473428	0.370626
protein_co	TRAF-intera	68	71	69	172	105	98	1.171871	1.441904	1.566949	2.564262	2.032868	1.678443
protein_co	spermatoge	63	47	56	200	157	189	0.998289	0.877648	1.169334	2.741629	2.794887	2.976371
protein_co	cyclin_A2	313	292	236	2684	2309	2114	5.924394	6.513127	5.886355	43.94861	49.099	39.76621
protein_co	methyltran	368	308	259	479	521	434	5.012165	4.943509	4.648492	5.643858	7.971946	5.874581
protein_co	ubiquitin_s	129	107	110	2174	2059	1790	1.124735	1.099389	1.263828	16.3977	20.16813	15.5104
protein_co	SET_domai	908	958	1098	1077	955	732	6.526873	8.115064	10.40055	6.697274	7.712084	5.229258
protein_co	nuclear_ass	174	126	180	478	358	379	3.955231	3.375206	5.391752	9.399689	9.142284	8.561926
protein_co	membrane-	64	60	80	72	43	44	0.576523	0.636934	0.949645	0.561089	0.435165	0.393912
protein_co	secreted_fr	111	80	50	428	345	340	2.891954	2.45621	1.716616	9.64662	10.09803	8.803532
protein_co	ribosomal_	8657	8055	6034	8283	5911	7208	300.3343	329.314	275.853	248.5926	230.3815	248.5204
protein_co	ring_finger_	62	64	57	22	10	14	1.024771	1.246586	1.241495	0.314573	0.185688	0.229971
protein_co	platelet_de	422	391	397	925	717	687	5.364009	5.856807	6.649705	10.17143	10.23871	8.678476
protein_co	carbonyl_r	277	260	224	476	417	398	4.259267	4.711243	4.538767	6.331768	7.203444	6.082019
protein_co	glycine_rec	0	1	0	0	1	1	0	0.007114	0	0	0.006782	0.005999
protein_co	cytochrom	92	66	69	95	72	103	0.563332	0.476242	0.556751	0.503226	0.495289	0.626792
protein_co	rhophilin_a	32	35	31	16	9	11	1.312248	1.691379	1.675183	0.567608	0.414627	0.448299
protein_co	NADH_dehy	860	720	593	1305	1150	1777	42.07879	41.51494	38.23441	55.23805	63.21378	86.40958
protein_co	membrane-	2120	1768	1793	1334	1231	1189	23.70826	23.29985	26.42281	12.90573	15.46575	13.21464
protein_co	naked_cuti	7	9	3	10	5	8	0.171966	0.260552	0.097118	0.212524	0.137995	0.195319
protein_co	cadherin_1	47	46	35	6	4	11	0.702492	0.81023	0.68936	0.077581	0.067166	0.163398
protein_co	ADAM_met	127	100	91	12	20	4	1.350373	1.253017	1.275047	0.110381	0.238907	0.042269
protein_co	steroid-5-al	609	474	417	427	341	369	13.96927	12.81273	12.60454	8.473194	8.787386	8.411865
protein_co	myosin_X	791	678	869	1942	2318	1939	5.209794	5.262364	7.542211	11.06512	17.15168	12.69204
protein_co	family_with	6	7	13	98	125	101	0.088309	0.121411	0.252133	1.247788	2.066858	1.477348
protein_co	ribosomal_	14414	12717	9203	8719	8601	12777	99.28331	103.2247	83.53259	51.95429	66.55638	87.46418
protein_co	S-phase_kir	607	495	501	5716	4120	4604	8.548865	8.215463	9.298059	69.6426	65.18776	64.44136
protein_co	oncostatin_	3941	3438	3668	191	119	113	37.66753	38.72342	46.19818	1.579273	1.277782	1.073368
protein_co	UDP_glycos	0	0	0	14	2	12	0	0	0	0.125182	0.023224	0.123266
protein_co	polo-like_k	1413	1162	1189	3969	2581	2896	25.27217	24.4914	28.02316	61.41076	51.86059	51.47645
protein_co	family_with	0	0	0	8	11	14	0	0	0	0.432575	0.772415	0.869654
protein_co	granzyme_A	0	1	1	4	3	0	0	0.069785	0.078035	0.204917	0.199584	0
protein_co	phosphoin	3519	3035	3739	1421	1701	1229	26.57244	27.0071	37.20509	9.282591	14.42997	9.223031
protein_co	hyaluronan	441	332	427	9355	7364	7137	4.163898	3.694083	5.312809	76.41319	78.11319	66.97101
protein_co	lipoma_HM	623	461	572	697	846	730	6.540202	5.703102	7.912869	6.32993	9.977519	7.616152
protein_co	single-stran	686	593	518	659	557	607	4.136392	4.213659	4.115875	3.437526	3.773131	3.637441
protein_co	betaine--hc	0	0	0	30	9	29	0	0	0	0.550247	0.214371	0.611056
protein_co	ankyrin_rep	5	1	2	23	15	22	0.043854	0.010336	0.023116	0.174515	0.147803	0.191768
protein_co	IQ_motif_c	8	9	5	388	457	313	0.072472	0.09608	0.059688	3.040721	4.651009	2.817967
protein_co	corticotrop	19	18	7	14	4	7	0.50802	0.567161	0.246638	0.323831	0.120153	0.186009
protein_co	RAS_p21_p	774	698	725	919	931	834	8.229831	8.74606	10.15834	8.453343	11.12112	8.813038
protein_co	Lix1_homo	5	3	3	27	35	40	0.065798	0.046523	0.052023	0.307375	0.517439	0.523132

protein_co	gypsy_retro	55	53	51	132	82	89	0.875716	0.994451	1.070053	1.818182	1.466775	1.408316
protein_co	diphosphoi	622	588	792	683	727	603	5.660873	6.306341	9.498456	5.377454	7.433212	5.454061
protein_co	peptidylgly	8029	6668	6478	2425	2094	2029	78.2517	76.58346	83.19708	20.44594	22.92757	19.65278
protein_co	B_double_	650	491	741	711	775	669	3.107708	2.766403	4.668526	2.940759	4.162723	3.178795
protein_co	general_tra	41	73	59	259	136	190	1.045056	2.192732	1.981721	5.711082	3.894427	4.813033
protein_co	solute_carr	682	624	634	876	646	676	8.281137	8.928886	10.14448	9.201798	8.812257	8.157591
protein_co	basic_trans	8662	7689	6030	10620	6707	9079	370.7154	387.7924	340.0749	393.1967	322.4778	386.1625
protein_co	F-box_and_	197	186	213	265	241	211	2.010288	2.236723	2.864221	2.339381	2.762856	2.139854
protein_co	spermatoge	6	7	7	30	8	27	0.146448	0.201344	0.225147	0.633457	0.219367	0.654947
protein_co	thymic_str	0	0	0	6	7	10	0	0	0	0.104843	0.158844	0.20074
protein_co	tumor_nec	364	297	275	402	376	356	5.366339	5.159887	5.342496	5.127029	6.227498	5.215985
protein_co	fem-1_hom	1199	1035	1117	469	470	410	10.91971	11.10809	13.4054	3.695112	4.808822	3.710951
protein_co	COMM_dor	223	204	209	366	270	273	8.036652	8.663783	9.925477	11.41076	10.93158	9.777832
protein_co	autophagy_	955	928	841	1240	773	987	11.66828	13.3616	13.54048	13.10654	10.6104	11.98478
protein_co	multiple_E	56	52	56	41	51	33	0.3904	0.427201	0.514451	0.247268	0.39943	0.228636
protein_co	ADAM_met	15	21	16	621	740	615	0.151722	0.250314	0.213262	5.433917	8.408899	6.182201
protein_co	Yip1_doma	1674	1323	1409	1206	863	890	28.16118	26.22783	31.23497	17.55115	16.31005	14.87973
protein_co	Rho_GTPas	31	11	29	58	60	50	0.178388	0.074594	0.219906	0.288732	0.387886	0.285946
protein_co	chemokine_	64	70	47	7726	6396	7185	1.719038	2.215698	1.663559	179.5243	193.0025	191.797
protein_co	leukocyte_(	0	0	0	85	122	96	0	0	0	3.614584	6.737291	4.689832
protein_co	solute_carr	0	0	0	76	87	77	0	0	0	1.688029	2.509411	1.964734
protein_co	DEAD_(Asp-	1072	831	885	2184	1963	1801	9.975874	9.113061	10.85261	17.58214	20.52228	16.65634
protein_co	interleukin	0	0	0	1	0	2	0	0	0	0.077494	0	0.178051
protein_co	ring_finger_	751	637	668	1116	822	1091	11.00434	10.99944	12.89839	14.14658	13.53147	15.88761
protein_co	C1q_and_t	12	4	8	3	1	3	0.26317	0.103377	0.231196	0.056917	0.024638	0.065386
protein_co	gamma-am	3	0	5	6	8	12	0.021506	0	0.047233	0.03721	0.064429	0.085493
protein_co	F-box_prot	466	380	437	645	472	505	5.576515	5.358801	6.891174	6.677282	6.345532	6.005899
protein_co	prenylcyste	161	131	117	150	126	122	1.744117	1.672354	1.670207	1.405737	1.533449	1.313467
protein_co	glycine_rec	0	2	2	0	2	4	0	0.069204	0.077386	0	0.065974	0.116726
protein_co	TNFAIP3_in	1616	1183	908	1882	1221	1410	26.1789	22.58405	19.38343	26.37501	22.22157	22.70068
protein_co	GTPase_act	2517	2239	2357	6964	5438	5260	13.01294	13.64122	16.05782	31.14683	31.58496	27.02636
protein_co	zinc_finger_	190	110	166	169	127	131	2.420888	1.651661	2.787173	1.862819	1.817916	1.65883
protein_co	NEDD4_bin	9	6	3	289	235	280	0.078367	0.061567	0.034423	2.176955	2.298822	2.423015
protein_co	NHP2_ribo	1305	1115	949	1237	1387	1847	79.87052	80.41887	76.53798	65.49508	95.36774	112.3447
protein_co	required_fo	253	207	164	748	596	666	3.151546	3.038649	2.692042	8.060607	8.340623	8.244931
protein_co	biorientati	1214	1130	875	1453	1214	1244	41.1462	45.13325	39.07994	42.60295	46.2252	41.90261
protein_co	complexin_	131	100	145	0	7	3	1.380703	1.242041	2.013871	0	0.082885	0.031424
protein_co	teneurin_tr	1367	1168	1603	696	877	767	7.676921	7.729805	11.86279	3.381355	5.533084	4.280787
protein_co	potassium_	0	1	0	33	25	29	0	0.036	0	0.872108	0.857991	0.880443
protein_co	family_with	2	0	0	81	67	82	0.054804	0	0	1.92014	2.062571	2.233102
protein_co	myosin_ligh	21	29	32	32	24	21	0.191749	0.312046	0.385034	0.252771	0.246192	0.190565
protein_co	-	3	1	1	12	8	8	0.108486	0.042615	0.047653	0.375401	0.325005	0.287508
protein_co	family_with	1	5	1	3	5	7	0.023374	0.137721	0.030801	0.060661	0.131293	0.162604
protein_co	TBC1_doma	161	137	121	485	290	359	5.520402	5.535699	5.4672	14.38631	11.17099	12.23345

protein_co	phenylalan	245	256	202	402	251	292	7.665806	9.439278	8.328713	10.8813	8.822964	9.079966
protein_co	glucose-fru	79	78	79	197	165	138	0.477927	0.556078	0.629791	1.031012	1.121418	0.829704
protein_co	CDK5_regu	188	165	185	527	390	346	3.041842	3.14608	3.94444	7.376535	7.089122	5.563711
pseudogen	protocadhe	13	3	9	3	1	0	0.21752	0.059154	0.198442	0.043425	0.018798	0
protein_co	pleckstrin_	7	1	4	1	0	3	0.082115	0.013824	0.061833	0.010148	0	0.034975
protein_co	leucine_ric	1	2	0	4	0	7	0.02389	0.056307	0	0.08267	0	0.1662
protein_co	zinc_finger_	1004	827	770	1585	1164	1512	32.52923	31.57567	32.87499	44.4255	42.3684	48.68571
protein_co	GDNF_fami	0	4	0	5	2	7	0	0.122389	0	0.112307	0.058338	0.180627
protein_co	kelch-like_f	17	24	13	94	61	62	0.128921	0.214483	0.129913	0.616688	0.519701	0.467278
protein_co	doublecort	0	0	0	53	43	52	0	0	0	0.515688	0.543332	0.581247
protein_co	tripartite_r	42	47	43	16	2	0	0.510333	0.672991	0.688506	0.168185	0.027301	0
protein_co	tripartite_r	532	510	448	867	705	1044	4.014912	4.535672	4.455303	5.660392	5.977266	7.830231
protein_co	HIG1_hypo	336	364	246	489	343	437	26.629	33.99571	25.69127	33.52644	30.53928	34.41967
protein_co	family_with	836	775	625	1000	749	987	9.613091	10.50184	9.470472	9.947634	9.675817	11.27934
protein_co	phospholip	0	3	1	42	35	36	0	0.099449	0.037069	1.02208	1.106088	1.006432
protein_co	tumor_nec	2456	2022	1952	9493	7683	7612	36.16776	35.08984	37.87981	120.9371	127.1081	111.4042
protein_co	ring_finger_	504	435	352	1399	1274	1554	6.421723	6.531567	5.91015	15.42062	18.23642	19.67803
protein_co	methylmal	423	394	381	371	368	401	5.973337	6.556619	7.08984	4.532247	5.838127	5.627696
protein_co	RasGEF_do	0	0	0	5	2	1	0	0	0	0.095614	0.049667	0.021968
protein_co	docking_pr	49	41	38	234	178	265	1.13181	1.116011	1.156634	4.675804	4.618985	6.083213
protein_co	activator_c	535	442	334	1445	1036	1176	12.56028	12.22855	10.33301	29.34786	27.32463	27.43864
protein_co	protein_ph	3855	3091	2910	3542	2854	3304	44.3765	41.93096	44.14246	35.27283	36.90895	37.79883
protein_co	dishevelled	530	459	494	294	404	400	4.510324	4.603113	5.539794	2.164423	3.862445	3.382996
processed_	primase_DI	217	168	193	572	507	449	5.016679	4.576916	5.879613	11.43973	13.16781	10.31603
protein_co	muscular_L	117	87	71	0	2	0	1.078547	0.945104	0.862475	0	0.020712	0
protein_co	3-hydroxyn	0	0	0	2	5	6	0	0	0	0.036176	0.117448	0.124678
protein_co	lengsin_len	0	0	0	0	0	1	0	0	0	0	0	0.010093
protein_co	signal_pept	404	284	404	572	555	495	2.90758	2.408662	3.83148	3.561307	4.487375	3.540505
protein_co	anoctamin_	63	110	50	44	40	43	0.807966	1.662464	0.845001	0.488167	0.576317	0.548063
protein_co	cysteine-ric	0	1	0	0	0	5	0	0.064852	0	0	0	0.273462
protein_co	t-complex-	1	0	10	4	2	0	0.017261	0	0.227464	0.059731	0.038784	0
protein_co	ribosomal_	3339	2890	2510	5614	3902	4575	39.49285	40.28162	39.12105	57.44304	51.84876	53.77777
protein_co	nuclear_fac	148	120	102	405	282	240	3.065441	2.929001	2.783981	7.256869	6.561897	4.940286
protein_co	cytochrom	24	12	10	15	25	12	0.583908	0.34405	0.320603	0.315709	0.683317	0.290151
protein_co	trophoblas	1628	1291	1173	1856	1281	1291	13.2924	12.42174	12.62066	13.10962	11.75025	10.47575
protein_co	interleukin	20	26	19	84	66	60	0.915143	1.401971	1.145637	3.325072	3.392749	2.728473
protein_co	pleckstrin_	144	128	305	183	406	245	1.318717	1.381358	3.680644	1.449784	4.176997	2.229795
protein_co	protease_se	87	69	54	91	102	122	1.768766	1.653131	1.446704	1.600499	2.329702	2.465021
protein_co	MMS22-like	138	99	158	926	709	672	0.845292	0.714611	1.275321	4.906836	4.878911	4.090783
protein_co	failed_axon	35	34	34	394	262	301	0.918659	1.051652	1.17598	8.94634	7.725677	7.851675
protein_co	gamma-am	1	0	0	0	1	0	0.017023	0	0	0	0.019124	0
protein_co	proline-rich	1555	1311	1016	492	369	372	39.86598	39.6079	34.32421	10.91189	10.6279	9.478173
protein_co	peptidase_I	158	162	148	1074	832	773	1.776694	2.146732	2.193068	10.44775	10.51061	8.638628
protein_co	arginyl-tRN	815	682	578	870	735	830	23.73317	23.40398	22.17997	21.91697	24.04554	24.02072

protein_co	sex_comb_	0	0	0	8	7	3	0	0	0	0.085267	0.096889	0.036733
protein_co	chromoson	85	101	106	66	59	73	0.845385	1.183761	1.389237	0.567862	0.65923	0.721553
protein_co	clavesin_2	0	0	0	0	0	1	0	0	0	0	0	0.017393
protein_co	ring_finger_	359	394	398	959	796	780	1.678218	2.170487	2.451725	3.878247	4.180382	3.623749
protein_co	R-spondin_	29	42	25	8	9	3	0.569258	0.971555	0.646675	0.135851	0.198474	0.058525
protein_co	Rho_GTPas	402	313	391	531	418	405	4.769673	4.376369	6.113277	5.450296	5.571702	4.775592
protein_co	ABRA_C-ter	330	260	245	2763	2031	2748	20.67518	19.19622	20.22722	149.7543	142.9534	171.1046
protein_co	solute_carr	189	184	151	622	523	549	4.225443	4.847695	4.448588	12.02995	13.13594	12.19811
protein_co	mitochond	22	31	21	324	169	211	0.649583	1.07865	0.817082	8.275987	5.605929	6.191614
protein_co	solute_carr	122	125	167	734	653	520	1.445569	1.745404	2.607535	7.523813	8.692429	6.12339
protein_co	SNF2_histo	255	192	228	362	345	350	1.1578	1.027311	1.364153	1.421887	1.759793	1.579324
protein_co	androgen-i	460	380	327	918	741	762	7.177382	6.987131	6.723429	12.39122	12.98899	11.81606
protein_co	dynein_ligh	1085	887	786	1531	930	1339	19.8689	19.14144	18.96712	24.25393	19.13269	24.3688
protein_co	T-cell_lymp	245	186	175	318	307	277	1.857978	1.662243	1.748829	2.086241	2.615543	2.08768
protein_co	transmemb	1102	868	1162	1149	990	997	10.82393	10.04686	15.03988	9.763069	10.92415	9.732135
protein_co	poly(A)-spe	2	1	1	3	23	12	0.055118	0.032477	0.036316	0.071524	0.712101	0.328667
protein_co	Wilms_tum	850	738	707	1961	1351	1488	12.30849	12.59358	13.49088	24.56555	21.97811	21.41403
protein_co	zinc_finger_	1094	1037	1099	1654	1458	1312	8.281019	9.250225	10.96223	10.83091	12.39861	9.869836
protein_co	vasoactive_	2	0	0	0	1	0	0.066845	0	0	0	0.037548	0
protein_co	chromoson	331	291	340	1556	1223	1376	6.802589	7.047682	9.207887	27.66425	28.23721	28.1044
protein_co	solute_carr	5	7	4	1	3	6	0.047042	0.07761	0.049592	0.008139	0.031709	0.056102
protein_co	von_Willeb	2	0	0	61	64	37	0.017837	0	0	0.470642	0.64125	0.327951
protein_co	guanine_nu	1839	1484	1556	2427	2102	2309	22.23812	21.14742	24.79481	25.38921	28.55605	27.74916
protein_co	chromoson	811	717	576	2042	1844	2374	16.38121	17.06677	15.33142	35.68156	41.84418	47.65576
protein_co	sidekick_ce	70	64	71	748	820	780	0.356436	0.384035	0.476406	3.294949	4.6908	3.947192
pseudogen	WAS_prote	215	205	120	343	269	328	4.065112	4.567673	2.989855	5.610366	5.713936	6.16336
protein_co	CCZ1_vacu	171	181	158	479	246	269	3.137924	3.9141	3.820658	7.604047	5.07143	4.905781
protein_co	chromoson	455	359	305	977	677	710	11.03948	10.26453	9.751513	20.50666	18.45334	17.12006
protein_co	RB-associat	346	313	301	339	325	331	2.796151	2.980821	3.205426	2.369994	2.950645	2.658411
protein_co	cAMP_resp	329	277	263	221	184	192	2.041442	2.025481	2.150462	1.186305	1.28265	1.184001
protein_co	epidermal_	978	898	924	919	879	679	5.271998	5.704529	6.563616	4.285632	5.323219	3.637607
protein_co	cell_divisio	427	308	289	2184	1842	2168	8.738231	7.427685	7.793424	38.6644	42.34814	44.09249
protein_co	insulin-like	121	71	82	28358	21881	23671	2.831945	1.958236	2.528996	574.1668	575.3283	550.5867
protein_co	purine-rich	1216	954	1165	1415	1377	1349	7.101627	6.565681	8.965717	7.148974	9.034566	7.829714
pseudogen	-	5	8	3	23	1	8	0.530471	1.000204	0.419419	2.110972	0.11919	0.843512
protein_co	insulin-like	4	7	2	3	1	1	0.128109	0.264195	0.084408	0.08312	0.035981	0.031829
protein_co	scavenger_	14	16	12	44	34	20	0.26461	0.356374	0.298879	0.71944	0.72195	0.37568
protein_co	malate_deh	3985	3289	2722	8007	4623	5434	95.50469	92.88965	85.96453	166.0081	124.4713	129.4272
protein_co	POM121_a	227	200	167	409	224	324	7.57253	7.862348	7.34119	11.80325	8.394836	10.74162
pseudogen	-	3	2	0	5	0	5	0.162064	0.127322	0	0.233668	0	0.268439
protein_co	glioblastom	726	672	520	894	636	647	9.03294	9.853009	8.525712	9.622614	8.889937	8.000303
protein_co	chaperonin	3828	3159	3323	9707	7124	8001	74.53407	72.48357	85.26053	163.505	155.8317	154.8235
protein_co	phosphose	584	508	380	1576	1202	1279	14.19538	14.55141	12.17174	33.14007	32.82372	30.89686
protein_co	tripartite_r	4	0	2	0	2	2	0.103451	0	0.068161	0	0.05811	0.051406

protein_co	zinc_finger_	148	173	143	363	302	261	2.440893	3.362329	3.107835	5.179129	5.595554	4.277965
protein_co	ataxin_7-lil	182	151	132	106	92	114	1.778708	1.739071	1.699973	0.896194	1.010113	1.107255
protein_co	transmemb	376	326	337	473	386	403	4.751925	4.855192	5.612372	5.171373	5.480474	5.0617
protein_co	chromoson	226	187	178	297	251	312	4.747883	4.629566	4.927724	5.397728	5.92399	6.51412
protein_co	solute_carr	1432	1184	914	1457	1288	1853	16.99048	16.5547	14.29037	14.95495	17.16831	21.84981
protein_co	GRB10_int	1087	839	584	930	972	1333	8.812689	8.01582	6.239166	6.522662	8.853077	10.74036
protein_co	tripartite_r	430	329	334	239	191	222	6.729124	6.067267	6.887655	3.235571	3.357937	3.452651
protein_co	methylpho	1095	974	807	1656	1505	1686	19.18279	20.10776	18.62971	25.09695	29.61987	29.35383
polymorph	zonadhesin	2	0	1	0	0	0	0.011986	0	0.007897	0	0	0
protein_co	transmemb	307	209	213	550	428	442	4.584735	3.678148	4.191701	7.105613	7.180731	6.560059
protein_co	ATP/GTP_b	32	22	7	54	44	45	0.449724	0.364356	0.129637	0.656528	0.694701	0.628519
protein_co	stimulated_	0	0	0	0	2	0	0	0	0	0	0.11979	0
protein_co	zinc_finger_	271	179	254	186	230	258	8.184261	6.370453	10.10831	4.859439	7.803457	7.74354
protein_co	transmemb	151	100	142	120	167	120	4.758387	3.713555	5.896658	3.27135	5.912189	3.758146
protein_co	tousled-like	660	536	571	1096	836	861	9.684328	9.268244	11.0407	13.91231	13.78101	12.55563
protein_co	EPH_recept	30	20	19	1063	891	1054	0.472266	0.371024	0.394143	14.47643	15.75767	16.4898
protein_co	nucleolar_p	453	425	365	1214	892	983	3.9464	4.363137	4.190159	9.14923	8.730051	8.510714
protein_co	canopy_1_l	0	0	0	11	8	8	0	0	0	0.211854	0.200087	0.177003
protein_co	non-SMC_c	388	290	341	1820	1661	1622	3.910357	3.444211	4.528703	15.86789	18.8063	16.24595
protein_co	neuroligin_	3	10	1	361	406	348	0.027057	0.106282	0.011885	2.816594	4.113667	3.119198
protein_co	shroom_fa	523	448	482	395	401	342	3.718026	3.753149	4.515362	2.429242	3.202611	2.416276
protein_co	RAB19_me	0	0	0	0	7	3	0	0	0	0	0.380907	0.144412
protein_co	C7orf55-LU	579	444	534	775	647	850	10.80467	9.763889	13.13133	12.51116	13.56395	15.76381
protein_co	DENN/MAD	639	541	522	268	196	191	9.057375	9.036616	9.750049	3.28624	3.121092	2.690571
protein_co	transmemb	1	3	3	27	17	20	0.033549	0.118608	0.13263	0.783631	0.640742	0.666845
protein_co	SH3-domai	1392	1002	1043	1816	1294	1364	15.5768	13.21338	15.38007	17.57996	16.26756	15.16922
protein_co	transmemb	304	244	275	654	552	544	3.969922	3.75496	4.732339	7.388378	8.098349	7.060198
protein_co	LanC_lantil	122	144	117	14	8	8	0.62719	0.872386	0.792611	0.062263	0.046204	0.040873
protein_co	synaptotag	116	111	163	242	283	246	1.271987	1.434349	2.355306	2.295637	3.486264	2.680832
protein_co	calcium/ca	922	672	865	967	1019	919	5.882333	5.052369	7.272263	5.337134	7.303683	5.826984
protein_co	lysine_(K)-s	150	157	181	1081	964	904	1.460307	1.80119	2.322022	9.104196	10.54336	8.746433
protein_co	spindlin_fa	22	25	10	3	15	13	0.471921	0.631966	0.282671	0.055671	0.361482	0.27714
protein_co	moesin	19042	14968	14082	8981	9027	10121	255.7337	236.8898	249.2153	104.343	136.1971	135.0854
protein_co	A_kinase_(I	0	0	0	5	3	2	0	0	0	0.079347	0.061825	0.036462
protein_co	cyclin_B3	11	0	0	17	10	3	0.124089	0	0	0.165903	0.126733	0.033634
protein_co	histone_de	307	235	222	372	278	345	6.951619	6.270794	6.62423	7.28708	7.071987	7.763835
protein_co	solute_carr	2859	2469	2319	323	291	243	34.69134	35.30491	37.08023	3.390568	3.966879	2.930372
protein_co	zinc_finger_	3	0	5	10	6	10	0.068517	0	0.150482	0.197579	0.15395	0.22698
protein_co	zinc_finger_	88	97	63	168	139	149	1.299165	1.687565	1.225624	2.145626	2.305397	2.186139
protein_co	carbohydra	369	266	262	323	247	295	8.534394	7.24995	7.985138	6.462668	6.417891	6.780754
protein_co	KRAB_box_	252	209	184	368	224	243	4.809348	4.700445	4.627413	6.075702	4.80267	4.608945
protein_co	NADH_deh	1606	1340	1100	1934	1153	1561	61.25593	60.23023	55.2879	63.8149	49.40615	59.17185
protein_co	zinc_finger_	148	115	133	142	171	142	1.729258	1.583445	2.047786	1.435322	2.244622	1.648906
protein_co	RAB41_me	12	14	14	15	11	3	0.591519	0.813248	0.909391	0.63965	0.609157	0.146967

protein_co	zinc_finger_	1351	1049	1036	1680	1439	1469	11.7889	10.787	11.91277	12.68208	14.10678	12.73942
protein_co	TAF1_RNA_	653	562	601	559	675	568	4.485012	4.548768	5.439509	3.321431	5.208387	3.877112
protein_co	non-POU_d	8754	7293	6838	9470	8073	8510	144.151	141.5221	148.3799	134.9038	149.3465	139.2677
protein_co	coiled-coil_	310	219	210	791	711	807	4.13081	3.438941	3.687463	9.118282	10.64369	10.68702
protein_co	lysophosph	13	19	18	30	25	20	0.26359	0.45399	0.480942	0.526223	0.569475	0.403018
protein_co	emopamil_	702	547	522	1705	1017	1439	20.93779	19.22597	20.5163	43.99275	34.07719	42.65443
protein_co	O-linked_N	2362	2195	2402	1610	1582	1319	17.26448	18.90668	23.13563	10.18034	12.9906	9.58138
protein_co	sorting_nex	1673	1410	1404	1954	1928	2151	37.27706	37.02302	41.22376	37.66459	48.2616	47.63166
protein_co	integrin_be	9	11	4	23	13	39	0.331111	0.476904	0.193922	0.732019	0.537308	1.425954
protein_co	interleukin	0	0	0	0	4	2	0	0	0	0	0.116906	0.051709
protein_co	acidic_repe	24	38	47	36	24	28	0.395451	0.737857	1.020502	0.513153	0.444265	0.45851
protein_co	zinc_finger_	339	272	337	960	966	859	3.704995	3.503192	4.853474	9.076579	11.8608	9.330196
protein_co	diaphanous	295	281	280	383	262	327	1.673373	1.878383	2.092973	1.879458	1.669634	1.843437
protein_co	nuclear_RN	0	0	0	1	3	4	0	0	0	0.020123	0.078395	0.092468
protein_co	ripply1_ho	0	0	3	0	0	0	0	0	0.178575	0	0	0
protein_co	phosphorib	498	432	420	963	728	842	12.7181	13.00121	14.13438	21.27561	20.88686	21.37049
protein_co	chromoson	14	21	16	133	93	102	0.191964	0.339327	0.289099	1.577636	1.432598	1.389959
protein_co	FERM_and_	6	7	7	1	4	2	0.044395	0.061036	0.068252	0.006401	0.03325	0.014707
protein_co	dedicator_(	250	209	234	137	124	118	1.986082	1.956638	2.449671	0.941544	1.106695	0.931641
protein_co	immunoglo	139	109	114	74	42	42	1.420617	1.312792	1.535331	0.65427	0.482237	0.4266
protein_co	Rho_GTPas	2	0	0	0	0	0	0.034344	0	0	0	0	0
protein_co	glypican_3	36	37	17	1244	745	787	0.742163	0.898889	0.461829	22.18607	17.2545	16.12432
protein_co	G_protein-(	0	0	0	2	0	0	0	0	0	0.076779	0	0
protein_co	RNA_bindir	3629	3281	2854	7320	5552	6083	39.31305	41.88544	40.74164	68.59996	67.56912	65.49033
protein_co	microcepha	232	221	236	432	335	378	3.889269	4.365956	5.213469	6.265081	6.309193	6.297692
protein_co	malignant_	557	355	446	915	766	713	4.597464	3.453016	4.851017	6.53352	7.102986	5.84874
protein_co	F-box_prot	86	85	65	213	145	198	1.929206	2.247016	1.921446	4.133545	3.654241	4.41423
protein_co	family_with	241	241	165	769	441	645	9.791849	11.5391	8.834184	27.02944	20.12961	26.04456
protein_co	NAD(P)_dep	764	702	582	1163	740	1121	20.96782	22.70409	21.04833	27.6123	22.81606	30.57561
protein_co	zinc_finger_	100	78	76	369	320	314	1.197489	1.100711	1.199278	3.822618	4.304975	3.736895
protein_co	centrin_EF-	1223	1054	929	1290	804	942	44.53015	45.22467	44.57365	40.63314	32.88765	34.08696
protein_co	gamma-am	3	0	0	6	23	15	0.025724	0	0	0.044508	0.221566	0.127828
protein_co	ribosomal_	41014	34861	25053	30461	19587	27875	936.7221	938.2652	754.0032	601.8466	502.5689	632.7078
protein_co	chondroitir	17	15	19	270	229	195	0.212665	0.221129	0.313209	2.921953	3.218333	2.424324
protein_co	ATPase_H+_	1313	1028	1194	2532	2076	2233	10.06392	9.285447	12.05985	16.78917	17.87636	17.00987
protein_co	coiled-coil_	640	545	540	836	622	602	9.36232	9.395223	10.40955	10.57969	10.22217	8.752047
protein_co	homeobox_	326	246	215	300	235	282	4.228017	3.75977	3.67445	3.365917	3.424018	3.634778
protein_co	gonadotrop	20	23	20	39	29	34	0.601602	0.815294	0.792765	1.014862	0.980001	1.016408
protein_co	bridging_in	351	297	269	366	317	380	5.177567	5.162763	5.228844	4.670493	5.253236	5.570727
protein_co	docking_pr	0	3	0	2	0	3	0	0.096675	0	0.047313	0	0.08153
protein_co	solute_carr	679	506	536	746	764	825	7.453231	6.545343	7.753083	7.083969	9.421439	8.999915
protein_co	charged_m	710	743	658	1118	917	1021	11.04558	13.62153	13.48934	15.04648	16.02686	15.78576
protein_co	dedicator_(	296	276	323	962	874	947	1.555388	1.709083	2.23658	4.373057	5.159499	4.94546
protein_co	steroidoger	108	69	83	2	3	5	1.658245	1.248478	1.679337	0.026565	0.051748	0.076296

protein_co	proline_syr	282	230	181	1133	848	922	5.840908	5.613919	4.940201	20.30131	19.73223	18.97893
protein_co	ER_lipid_ra	784	654	735	985	877	862	6.83447	6.718521	8.443276	7.428276	8.588898	7.468024
protein_co	syntrophin_	4	8	4	0	0	3	0.060435	0.142438	0.079638	0	0	0.045046
protein_co	peroxidasir	7	4	0	7	10	2	0.077125	0.051936	0	0.066721	0.123779	0.0219
protein_co	regulator_c	23	31	12	344	179	306	0.578728	0.919211	0.397889	7.488034	5.059976	7.652043
protein_co	transformir	934	685	927	1538	1349	1056	6.30861	5.45236	8.250901	8.986823	10.23641	7.088599
protein_co	golgin_A7	775	584	549	1221	872	1024	20.24138	17.97456	18.89494	27.5878	25.58609	26.57957
protein_co	phosphatid	507	465	388	334	245	252	12.28425	13.27702	12.38817	7.00084	6.668924	6.068074
protein_co	GINS_comp	119	143	80	1219	1036	1103	1.62664	2.303497	1.441018	14.41489	15.90939	14.98407
protein_co	Wolf-Hirsch	521	422	581	671	753	604	5.07867	4.847656	7.463168	5.658454	8.246247	5.851388
protein_co	DnaJ_(Hsp4	2	2	0	5	1	3	0.042694	0.050313	0	0.092337	0.023982	0.063646
protein_co	corticotrop	15	2	2	886	573	692	0.515659	0.081023	0.090602	26.34924	22.12968	23.64216
protein_co	tripartite_r	11	6	1	2838	1853	2217	0.199983	0.128546	0.023957	44.63506	37.84645	40.05678
protein_co	alcohol_de	7	13	19	275	179	158	0.166257	0.363858	0.594662	5.650381	4.776218	3.729484
protein_co	mitochond	55	45	46	169	109	143	3.425594	3.30288	3.775425	9.1059	7.626912	8.85154
protein_co	lactamase_	64	80	37	192	72	119	2.246833	3.309694	1.711699	5.83116	2.839699	4.151904
protein_co	telomeric_	434	385	340	2229	1529	1751	6.385879	6.67573	6.592417	28.37292	25.27479	25.60511
protein_co	ribosomal_	34250	30560	22234	33035	23140	29331	1188.223	1249.39	1016.459	991.4593	901.8825	1011.286
protein_co	solute_carr	8	3	6	1	4	2	0.080473	0.035562	0.079533	0.008702	0.045203	0.019994
protein_co	ATPase_H+_	0	0	0	1	0	0	0	0	0	0.018724	0	0
protein_co	syntabulin_	2	0	2	544	475	486	0.030824	0	0.040619	7.25316	8.224472	7.444084
protein_co	dihydropyr	2	4	0	10	1	6	0.04978	0.117325	0	0.215322	0.027962	0.148418
protein_co	metadherir	2476	2033	2076	2402	1779	1732	21.22097	20.53331	23.44643	17.80945	17.1293	14.75272
protein_co	low_densit	503	384	417	276	289	280	5.317356	4.783724	5.808963	2.524061	3.432216	2.94168
protein_co	estrogen_re	101	94	80	424	260	279	2.2476	2.465089	2.34597	8.162562	6.5001	6.170374
protein_co	R-spondin_	17	7	17	5	9	4	0.289295	0.140377	0.38122	0.073608	0.172061	0.067649
protein_co	polymerase	445	347	334	1105	676	986	23.07418	21.20327	22.82168	49.56689	39.37877	50.81043
processed_	mal_T-cell_	0	0	0	689	692	622	0	0	0	11.19384	14.59998	11.60906
protein_co	eukaryotic_	4792	4147	3335	6777	4058	4382	64.08013	65.35032	58.7675	78.39838	60.96319	58.23561
protein_co	UTP23_sma	296	256	198	478	320	395	4.243307	4.324738	3.740355	5.927938	5.153613	5.627552
protein_co	NADH_dehy	620	535	460	1206	766	1046	24.88508	25.30511	24.32988	41.87527	34.54022	41.72426
protein_co	TatD_DNas	308	336	211	387	261	335	8.088207	10.39795	7.301613	8.791754	7.700007	8.74291
protein_co	gasdermin_	30	11	29	0	0	0	0.585199	0.252861	0.745444	0	0	0
protein_co	family_with	0	0	0	17	4	5	0	0	0	0.111833	0.034172	0.037787
protein_co	zinc_finger_	368	295	269	413	323	378	3.453694	3.262609	3.326772	3.35312	3.405552	3.525636
protein_co	Rho_GTPas	258	252	225	582	540	596	2.907979	3.347181	3.341865	5.674891	6.837768	6.676171
protein_co	solute_carr	2	2	2	7	9	14	0.038114	0.044916	0.050226	0.115404	0.192687	0.265154
protein_co	nicotinate_	104	79	63	171	100	175	2.801966	2.508209	2.236685	3.985554	3.026764	4.68573
protein_co	very_low_d	505	372	390	1248	862	834	7.447131	6.46469	7.578741	15.92118	14.28085	12.22287
protein_co	adenylate_k	584	519	509	1192	685	784	11.30027	11.83451	12.97862	19.95332	14.89072	15.07654
protein_co	ubiquitin-li	859	771	830	1074	860	754	12.21496	12.91994	15.55292	13.21193	13.73873	10.65565
protein_co	nuclear_fac	124	117	112	27	32	44	0.800766	0.890384	0.953097	0.150838	0.232158	0.282388
protein_co	cerberus_1	0	0	0	1	0	0	0	0	0	0.037695	0	0
protein_co	perilipin_2	3979	3104	3091	2659	1586	1971	106.8216	98.20056	109.3501	61.7542	47.83408	52.58737

protein_co	HAUS_augn	357	291	334	1191	966	900	2.891667	2.777667	3.565015	8.345547	8.790351	7.244897
protein_co	cyclin-depe	430	399	385	244	242	246	5.820667	6.364793	6.867518	2.857308	3.680177	3.309398
protein_co	cyclin-depe	819	573	422	697	469	729	33.79476	27.86295	22.9463	24.88062	21.74139	29.89528
protein_co	chromoson	70	60	63	182	131	125	0.770772	0.778549	0.91412	1.733652	1.620496	1.367878
protein_co	interferon_	1	0	0	0	1	0	0.046439	0	0	0	0.052172	0
protein_co	zinc_finger_	440	367	310	381	244	227	8.340149	8.197743	7.74315	6.247541	5.195891	4.276187
protein_co	F-box_prot	181	182	216	437	340	379	2.094496	2.481873	3.293742	4.374671	4.420068	4.358628
protein_co	sigma_non-	2709	2306	1754	1352	932	1235	82.28179	82.53936	70.20356	35.52503	31.80238	37.27961
protein_co	COBW_don	76	93	89	169	137	201	1.209716	1.744455	1.866787	2.327124	2.44985	3.179622
protein_co	centrosom	312	332	315	1483	1368	1273	1.475048	1.849681	1.962443	6.065349	7.265856	5.981219
protein_co	neurotroph	80	44	69	64	107	95	0.514865	0.333705	0.585177	0.356325	0.773635	0.607626
protein_co	idnK_gluco	12	4	22	52	39	51	0.391431	0.153759	0.945651	1.467371	1.429181	1.653307
protein_co	SHC_(Src_h	56	58	32	60	48	28	1.238386	1.511482	0.932508	1.147842	1.1925	0.615369
protein_co	AU_RNA_bi	169	131	140	216	197	253	5.673448	5.182494	6.193316	6.273027	7.429775	8.440935
protein_co	hippocamp	840	606	729	2007	1729	1480	13.00305	11.05467	14.87059	26.87673	30.06838	22.76865
protein_co	chromoson	203	178	115	650	487	629	3.654207	3.775932	2.727908	10.12217	9.848613	11.25272
protein_co	Lipid_phos	0	0	0	9	5	12	0	0	0	0.165206	0.11919	0.253054
protein_co	zinc_finger_	1046	829	904	1457	2342	1990	5.317484	4.966336	6.055887	6.407625	13.37551	10.05396
protein_co	INTS3_and_	550	477	380	1121	664	948	6.878702	7.030226	6.262709	12.12865	9.329556	11.78316
protein_co	UDP-glucos	900	736	812	2361	1818	1860	11.89091	11.45929	14.13721	26.98558	26.98458	24.42279
protein_co	actin-like_7	0	0	0	4	0	0	0	0	0	0.07733	0	0
protein_co	sorting_nex	258	291	319	488	455	425	1.79202	2.381898	2.91977	2.932284	3.550452	2.933741
protein_co	stomatin	1234	1088	920	2361	1743	1791	21.70405	22.55078	21.323	35.92399	34.44071	31.30623
protein_co	gelsolin	10023	8026	6906	6215	5242	5955	82.21686	77.5835	74.64909	44.10291	48.3069	48.54612
protein_co	mitochond	444	399	304	969	549	595	12.07283	12.78516	10.89267	22.7936	16.77056	16.07877
protein_co	nuclear_rec	70	41	35	1149	973	982	0.527076	0.363803	0.347278	7.484418	8.230702	7.348456
protein_co	crumbs_ho	15	6	6	2	6	0	0.143084	0.067446	0.07542	0.016504	0.064298	0
protein_co	olfactory_r	0	1	0	0	0	0	0	0.057342	0	0	0	0
protein_co	aminolevul	718	578	574	457	403	529	11.70669	11.10567	12.33265	6.445981	7.381828	8.571861
protein_co	astrotactin	463	435	395	415	316	307	5.163615	5.717013	5.805034	4.003907	3.959214	3.402678
protein_co	WD_repeat	55	56	37	79	57	71	0.596916	0.716218	0.52916	0.741721	0.694983	0.765805
protein_co	polymerase	611	537	532	1520	995	1083	13.5004	13.98256	15.49001	29.0544	24.69889	23.78173
protein_co	surfeit_4	8439	6898	6464	6977	5708	6293	149.7215	144.2194	151.1226	107.0841	113.7696	110.9585
protein_co	globoside_	6	5	1	94	55	61	0.10775	0.105814	0.023665	1.460345	1.109625	1.08869
protein_co	surfeit_1	385	290	243	413	327	525	18.64802	16.55301	15.51004	17.30553	17.7938	25.27207
protein_co	surfeit_2	94	87	67	520	272	326	5.910277	6.446238	5.551235	28.28436	19.21312	20.37076
protein_co	surfeit_6	754	716	556	1286	1030	1260	15.93513	17.83218	15.48439	23.51193	24.45517	26.46455
protein_co	mediator_c	918	780	603	1674	1431	1829	11.09585	11.11014	9.604397	17.50397	19.43152	21.97057
protein_co	REX4_RNA_	1004	755	664	1344	1059	1332	22.52236	19.95879	19.62831	26.08209	26.68856	29.69573
protein_co	ribosomal_	46728	39713	27732	36143	23974	32070	2125.281	2128.526	1662.092	1422.087	1224.979	1449.598
protein_co	general_tra	1226	960	842	2310	1734	2098	26.99903	24.91357	24.43456	44.0081	42.89985	45.91692
protein_co	ankyrin_rep	447	337	299	577	440	461	10.15649	9.023461	8.952456	11.34162	11.2315	10.4099
protein_co	prostaglanc	850	684	556	1489	1076	1356	19.30495	18.30682	16.64023	29.2555	27.45435	30.60689
protein_co	N-terminal_	1660	1415	1021	1919	1198	1866	59.10024	59.36694	47.90068	59.1043	47.91671	66.02409

protein_co	CDKN1A_in	4089	3355	2663	3030	2403	2784	68.6353	66.36361	58.90286	43.99831	45.31409	46.44182
protein_co	solute_carr	700	535	476	294	282	288	9.978109	8.986924	8.941121	3.625438	4.515942	4.079926
protein_co	SH3-domai	583	526	377	2212	1652	2259	6.392833	6.797006	5.447547	20.98326	20.35091	24.61788
protein_co	family_witl	385	358	323	600	426	607	4.690974	5.140347	5.186085	6.32436	5.831241	7.350225
protein_co	prostaglanc	43	26	17	20	22	35	1.218663	0.868352	0.634891	0.490352	0.700466	0.985809
protein_co	leucine_ric	470	438	314	664	446	626	7.37034	8.094143	6.488646	9.007842	7.857304	9.756041
protein_co	hemicentin	29	13	20	1	3	0	0.319719	0.168896	0.290559	0.009537	0.037157	0
protein_co	G_protein-(	1856	1750	1761	1453	1776	1777	13.36305	14.84816	16.70789	9.050158	14.36546	12.71524
protein_co	chromoson	235	223	132	609	385	621	12.98657	14.5224	9.612477	29.11434	23.90212	34.10577
protein_co	isopenteny	0	1	2	0	0	5	0	0.045907	0.102669	0	0	0.193576
protein_co	inositol_pc	337	277	192	539	435	487	5.256663	5.09175	3.946538	7.273309	7.622871	7.549512
protein_co	lipocalin_9	0	0	0	0	2	3	0	0	0	0	0.149062	0.197797
protein_co	SEC16_hon	2937	2359	2499	2693	3040	2583	17.65702	16.71277	19.79769	14.00596	20.53223	15.4329
protein_co	WD_repeat	317	245	206	932	619	756	9.086245	8.275579	7.780853	23.11022	19.93264	21.53558
protein_co	notch_1	1662	1465	1255	1927	2383	2017	9.389386	9.753284	9.342964	9.417831	15.12444	11.32457
protein_co	calcium_ch	12	14	3	17	15	18	0.064852	0.089162	0.021365	0.07948	0.091072	0.096678
protein_co	NACC_fami	1191	865	1131	1063	1213	1253	9.269733	7.933753	11.59986	7.157341	10.60633	9.692062
protein_co	proline_an	19	24	20	469	376	400	0.301794	0.449237	0.418622	6.44455	6.709554	6.314317
protein_co	USP6_N-ter	237	183	197	634	584	513	2.607985	2.373094	2.856655	6.035441	7.219691	5.61027
protein_co	COMM_dor	41	57	41	24	26	48	0.947852	1.552882	1.249037	0.479989	0.675272	1.102827
protein_co	methionine	248	217	169	308	241	360	7.281956	7.508673	6.539099	7.823662	7.949915	10.5053
protein_co	prenyl_(dec	116	79	78	479	287	338	3.776848	3.031138	3.346578	13.49181	10.4979	10.93699
protein_co	family_witl	843	663	686	1441	941	1070	11.29283	10.46636	12.10972	16.69945	14.16165	14.2452
protein_co	family_witl	377	288	323	691	482	564	8.139786	7.327759	9.189861	12.90662	11.69143	12.10209
protein_co	solute_carr	9	5	9	0	0	0	0.169683	0.111089	0.2236	0	0	0
protein_co	transmemb	0	0	0	4	6	2	0	0	0	0.033528	0.06531	0.019258
protein_co	Ras_suppre	2068	1652	1618	3042	2090	2330	27.9362	26.29868	28.8025	35.54995	31.71847	31.28113
protein_co	ST8_alpha-I	3	2	1	0	0	4	0.069782	0.054822	0.030652	0	0	0.092468
protein_co	par-3_parti	971	752	870	907	735	675	8.560484	7.812751	10.10725	6.917503	7.279733	5.914152
protein_co	zinc_finger_	1999	1569	1809	120	138	125	16.88672	15.61933	20.13751	0.876954	1.309666	1.049427
protein_co	family_witl	24	27	38	5	7	8	0.367646	0.487404	0.767073	0.06626	0.120466	0.121792
protein_co	nuclear_rec	534	458	408	479	359	432	15.28135	15.44518	15.38563	11.8582	11.54154	12.28609
protein_co	APOBEC1_c	2	0	0	0	0	0	0.047481	0	0	0	0	0
protein_co	cadherin-re	0	4	0	10	22	5	0	0.045975	0	0.084375	0.241059	0.048465
protein_co	leucine-rich	0	0	0	0	0	2	0	0	0	0	0	0.04723
protein_co	polymerase	900	704	778	1238	1058	1139	7.175737	6.614603	8.174071	8.539013	9.476735	9.025211
protein_co	HECT_and_	921	813	805	1000	867	838	7.629269	7.936352	8.78727	7.166156	8.068474	6.898854
protein_co	chromoson	15	30	21	5	1	3	0.202425	0.477092	0.373446	0.058372	0.015161	0.040235
protein_co	calcium/ca	429	365	360	532	515	581	5.811588	5.826899	6.426505	6.234651	7.837794	7.822099
protein_co	adipogenes	1	4	4	8	1	1	0.057733	0.272138	0.304311	0.399554	0.064859	0.057376
protein_co	glutamate_	1824	1512	1470	2376	1582	1762	31.77505	31.0399	33.74532	35.80724	30.96114	30.50542
protein_co	ankyrin_rep	36	48	49	14622	10536	12105	0.96305	1.513194	1.727337	338.3889	316.6439	321.8257
protein_co	5-hydroxyt	115	125	157	21	16	8	1.820638	2.332077	3.275369	0.287613	0.284574	0.125871
protein_co	ribonuclea	343	284	230	1293	715	963	4.250646	4.147499	3.755982	13.86189	9.95442	11.86033

protein_co fragile_site_	407	456	305	485	377	366	4.507737	5.951633	4.451423	4.64696	4.690883	4.028607
protein_co adducin_3_	1966	1762	1942	986	993	874	23.99862	25.34636	31.23825	10.4122	13.61761	10.60288
protein_co hyaluronan	0	0	1	0	0	0	0	0	0.023185	0	0	0
protein_co ventral_ant	0	1	1	66	40	41	0	0.013882	0.015524	0.672614	0.529381	0.480012
protein_co DnaJ_(Hsp4	826	650	613	1097	867	952	10.02965	9.300923	9.808461	11.52326	11.82698	11.48821
protein_co eukaryotic_	2310	1804	1970	5184	4653	4494	16.85183	15.50881	18.93808	32.71621	38.13441	32.582
protein_co transcriptic	445	420	406	705	769	666	5.784125	6.433304	6.954062	7.927382	11.22931	8.60323
protein_co antigen_ide	1212	917	1095	3542	3959	3187	5.061089	4.512506	6.025461	12.79537	18.57274	13.22614
protein_co cytochrom	2	2	0	0	0	0	0.047481	0.055953	0	0	0	0
protein_co internexin_	311	233	292	2567	1653	1687	5.095837	4.499022	6.304822	36.38681	30.42825	27.47134
protein_co fucose_mut	131	96	52	83	105	161	7.999158	6.907984	4.184188	4.38444	7.202966	9.770314
protein_co leucine_ric	350	283	197	125	121	107	2.274377	2.167145	1.686924	0.702696	0.883342	0.691016
protein_co mitochond	104	74	28	76	114	128	2.0168	1.691096	0.715521	1.274988	2.48361	2.466886
protein_co NK6_home	4	0	2	0	0	0	0.199589	0	0.131505	0	0	0
protein_co polyamine_	41	36	26	32	14	25	1.168235	1.208804	0.976235	0.788786	0.44815	0.707939
protein_co glutathione	1204	880	825	1404	999	1310	60.59026	52.18745	54.7098	61.12325	56.47951	65.5175
protein_co TAF5_RNA_	91	38	79	219	229	217	1.474183	0.725439	1.686444	3.069143	4.167682	3.49365
protein_co peroxisome	967	841	899	2171	2317	1733	9.604867	9.843918	11.76683	18.65468	25.85473	17.10697
protein_co inositol_14	901	715	773	484	353	303	10.93531	10.22632	12.36291	5.081768	4.813159	3.654759
protein_co cyclin_M2	61	84	73	83	100	77	0.796793	1.29301	1.256531	0.9379	1.467454	0.999576
protein_co programme	1637	1301	1168	2958	2660	2874	13.4301	12.57809	12.62723	20.99383	24.51665	23.43294
protein_co ADAM_met	7283	6410	6795	74	60	70	48.5726	50.3786	59.718	0.426949	0.449553	0.463969
protein_co regulator_c	664	629	425	472	341	326	41.25918	46.05855	34.79976	25.37216	23.80433	20.13167
protein_co BTB_(POZ)_	339	272	327	919	622	641	7.167331	6.776942	9.110461	16.80878	14.77397	13.46869
protein_co adrenomed	3384	2732	2383	3449	2550	2878	94.83977	90.22937	88.00736	83.62119	80.28777	80.16053
protein_co growth_arr	55	58	67	13	17	12	1.273733	1.582891	2.044681	0.260449	0.442297	0.276189
protein_co solute_carr	2	4	2	29	8	17	0.016941	0.039928	0.022324	0.212507	0.076129	0.14311
protein_co lin-7_homo	551	523	467	1266	840	981	6.222374	6.960065	6.949542	12.36805	10.65695	11.00989
protein_co leucine_ric	307	262	317	16	12	5	4.009098	4.031965	5.455096	0.180755	0.176051	0.064892
protein_co IMP1_inner	93	96	80	267	195	236	4.614351	5.613142	5.230612	11.46046	10.86954	11.63722
protein_co post-GPI_at	373	299	257	882	596	752	9.57662	9.046523	8.695036	19.59003	17.19091	19.18805
protein_co terminal_u	187	179	102	301	204	297	2.94379	3.320667	2.115925	4.099159	3.607817	4.646558
protein_co secretoglob	0	0	1	0	0	0	0	0	0.149707	0	0	0
protein_co synaptotag	1	0	0	1	1	1	0.01498	0	0	0.01296	0.01683	0.014888
protein_co zinc_finger_	32	26	29	19	37	15	0.631895	0.605028	0.75462	0.324573	0.820816	0.294372
protein_co zinc_finger_	59	49	49	184	84	89	0.905893	0.886601	0.991416	2.444025	1.448949	1.358077
protein_co hydroxyste	1464	1430	1369	2487	1677	1786	18.05816	20.78622	22.25208	26.53818	23.23884	21.89392
protein_co APAF1_inte	250	261	188	302	208	285	2.887901	3.552956	2.861771	3.017951	2.699322	3.271875
protein_co peptidase_(	1793	1501	1390	603	423	424	30.20146	29.79446	30.85299	8.786745	8.004554	7.097791
protein_co diacylglyce	1292	920	890	3043	2079	2736	11.92257	10.00466	10.82261	24.2925	21.55315	25.09187
protein_co eukaryotic_	2830	2277	1753	4595	2835	3134	29.66205	28.1245	24.21204	41.66422	33.38235	32.6455
protein_co tankyrase_1	4463	4052	3219	2655	4272	5377	39.69685	42.47229	37.72984	20.42945	42.68836	47.53121
protein_co glycine-N-a	0	4	0	8	8	7	0	0.143833	0	0.211177	0.274241	0.212276
protein_co serpin_pep	12	7	8	585	366	360	0.284757	0.195748	0.25016	12.00913	9.757143	8.489941

protein_co	structure_s	2647	2150	1746	6442	4726	5122	22.25775	21.30458	19.34668	46.86095	44.64472	42.80323
protein_co	solute_carr	169	151	171	42	21	35	3.443814	3.626077	4.59181	0.740398	0.480752	0.708811
protein_co	protein_tyr	56	41	38	119	233	149	0.578816	0.499394	0.517572	1.064051	2.705562	1.530553
protein_co	chromoson	651	503	468	745	441	537	16.09743	14.65718	15.24952	15.93656	12.25076	13.19652
protein_co	ADP-ribosy	1153	905	750	1648	1321	1640	20.51108	18.97207	17.58147	25.36176	26.40043	28.9943
protein_co	CUGBP_Ela	2353	1821	1884	3224	4100	4021	16.24969	14.81973	17.14506	19.26111	31.80945	27.59733
protein_co	chromoson	461	431	311	880	577	975	14.4072	15.87315	12.80778	23.79164	20.25833	30.28258
protein_co	coiled-coil_	16	3	1	57	49	58	0.321341	0.071003	0.026466	0.990341	1.105584	1.157669
protein_co	sestrin_3	1993	1708	2059	2837	2990	2372	11.07034	11.18017	15.07109	13.63251	18.65838	13.09417
protein_co	endonuclea	2046	1730	2258	2162	1954	1883	23.11015	23.02769	33.60902	21.12593	24.79538	21.13767
protein_co	coiled-coil_	421	379	460	755	591	592	5.951444	6.313738	8.569055	9.233157	9.385919	8.317094
protein_co	kelch-like_f	60	43	39	10	17	1	1.27211	1.074358	1.089615	0.183416	0.404922	0.021071
protein_co	teneurin_tr	2939	2315	2753	456	633	583	11.11383	10.31626	13.71845	1.491736	2.689161	2.190999
protein_co	serpin_pep	33210	28184	22469	21451	15361	19118	518.4814	518.5302	462.2563	289.7176	269.4219	296.6309
protein_co	calpain_5	783	515	552	277	221	221	9.427518	7.307182	8.758092	2.885216	2.989351	2.644463
protein_co	integrator_	373	405	295	606	445	460	5.708873	7.304721	5.949745	8.023746	7.651571	6.996954
protein_co	p21_protei	1059	867	1004	1247	836	881	15.00255	14.47422	18.74293	15.28264	13.30529	12.40379
protein_co	ribosomal_	39793	33495	23906	33802	25192	38726	1004.617	996.5079	795.3081	738.2425	714.5052	971.6413
protein_co	zinc_finger_	504	403	496	435	430	422	2.796296	2.634904	3.626345	2.087877	2.680218	2.326884
protein_co	tetratricop	81	47	57	317	169	284	1.43659	0.982319	1.332163	4.863736	3.367313	5.005826
protein_co	neural_cell	133	125	127	101	95	83	1.206296	1.33604	1.517892	0.792477	0.967999	0.748153
protein_co	dopamine_	45	34	30	96	50	109	0.854193	0.760553	0.750412	1.576441	1.066259	2.056268
protein_co	nuclear_pr	129	129	154	310	276	169	1.11646	1.31568	1.756342	2.321017	2.683563	1.453617
protein_co	ataxia_telar	1403	1167	1336	941	926	831	5.64967	5.537878	7.089355	3.278069	4.189146	3.325647
protein_co	aminoadipa	434	521	419	1069	696	730	4.465771	6.317591	5.681402	9.515846	8.045722	7.465162
protein_co	galactosida	12	9	5	214	127	155	0.113021	0.099891	0.062056	1.743634	1.34379	1.450841
protein_co	SLX4_interа	11	5	25	18	24	24	0.413895	0.221705	1.239575	0.585914	1.014515	0.897468
protein_co	late_endos	1564	1277	1014	2347	1588	1977	61.51539	59.18955	52.5557	79.85886	70.16921	77.27933
protein_co	prolyl_4-hy	232	145	139	18	3	11	4.675413	3.443556	3.691319	0.313811	0.067921	0.22031
protein_co	glutamate_	11	5	15	3	7	12	0.100371	0.053764	0.18036	0.023681	0.071757	0.108819
protein_co	suppressior	0	3	0	2727	2154	2593	0	0.052886	0	35.29065	36.19981	38.54994
protein_co	hypoxia_up	2748	2291	2160	4643	5568	5617	32.1152	31.55194	33.26461	46.94135	73.10417	65.2391
protein_co	ADAM_met	548	513	336	13	10	12	7.890037	8.704081	6.374888	0.161922	0.161751	0.171708
protein_co	CSRP2_bin	222	176	161	440	343	352	2.992845	2.796089	2.86017	5.13153	5.194866	4.716105
protein_co	dihydroxya	476	389	286	432	289	404	5.366251	5.167978	4.248786	4.213187	3.660251	4.526422
protein_co	metastasis_	1992	1741	1475	3874	3636	4223	34.48609	35.51898	33.64972	58.01993	70.7176	72.65832
protein_co	transmemb	272	222	175	733	385	493	5.072191	4.878505	4.300308	11.8248	8.065596	9.136572
protein_co	fatty_acid_	3654	2896	2989	1863	1599	1616	42.76949	39.9458	46.10269	18.86433	21.02631	18.79821
protein_co	transmemb	2	1	1	1	1	0	0.033412	0.019687	0.022014	0.014452	0.018768	0
protein_co	retinal_out	35	73	26	22	14	19	0.986653	2.425082	0.965839	0.536515	0.443377	0.532304
protein_co	echinoderm	641	582	447	456	410	565	9.259257	9.907137	8.508646	5.698309	6.653513	8.111034
protein_co	inner_centr	725	468	487	1421	1924	1913	9.682699	7.365655	8.570817	16.41782	28.86773	25.39119
protein_co	zona_pellu	46	37	34	1	3	5	1.246308	1.181344	1.213895	0.023439	0.091314	0.134632
protein_co	phospholip	8	33	20	1	7	11	0.060625	0.294703	0.199723	0.006556	0.059595	0.082845

protein_co	FSHD_regic	157	155	144	183	113	105	8.077489	9.397569	9.762792	8.144995	6.531369	5.368781
protein_co	cleavage_ar	1256	1075	967	2518	2212	2341	18.03469	18.19008	18.29701	31.27791	35.68232	33.40643
protein_co	beta-13-glu	1896	1517	1177	1279	897	1258	48.82107	46.03219	39.93744	28.49066	25.94839	32.19284
protein_co	etoposide_	2790	2083	2123	5664	4004	4448	60.36182	53.10733	60.52613	106.0094	97.31981	95.63845
protein_co	coiled-coil_	11	18	35	46	87	57	0.148407	0.286182	0.622251	0.536888	1.318656	0.764271
protein_co	checkpoint	612	475	390	1337	1023	1026	9.251824	8.462071	7.769183	17.48519	17.37403	15.41462
protein_co	fasciculatic	189	173	154	165	103	69	5.195144	5.603882	5.578165	3.923582	3.180695	1.884927
protein_co	endothelial	4	2	3	10	4	9	0.090652	0.053414	0.089593	0.196057	0.101842	0.202708
protein_co	kin_of_IRR	9	16	13	9	11	2	0.125123	0.262133	0.238162	0.108243	0.171805	0.027633
protein_co	myelin_prc	0	0	0	87	66	67	0	0	0	1.520803	1.498248	1.345474
protein_co	SID1_transı	849	728	735	606	529	605	10.20129	10.30828	11.63777	6.299169	7.14089	7.22458
protein_co	transmemb	410	292	272	415	325	346	6.697256	5.620863	5.854864	5.864408	5.964108	5.616927
protein_co	transgelin	3481	2952	2660	15116	11582	16567	55.87859	55.8425	56.26753	209.914	208.869	264.2987
protein_co	junctophili	7	4	3	600	814	850	0.077415	0.052131	0.04372	5.74041	10.11352	9.342374
protein_co	dual_specif	15	10	5	1	1	4	0.458496	0.360206	0.201395	0.026443	0.034339	0.121511
protein_co	COMM_dor	766	574	461	993	633	694	21.26523	18.77848	16.86464	23.84809	19.74214	19.14743
protein_co	KIAA1755	5	4	1	9	6	7	0.041174	0.038816	0.010851	0.064114	0.055507	0.057287
protein_co	spermatoge	10	9	17	5	1	4	0.699353	0.74173	1.566679	0.302503	0.078568	0.278013
protein_co	DSN1_MIN	197	160	157	684	449	617	4.262107	4.079296	4.476026	12.80198	10.91324	13.2664
protein_co	suppressor_	2231	1780	1976	1649	2226	1862	8.218729	7.727379	9.592391	5.255194	9.212539	6.817018
protein_co	cyclic_nucl	2	7	0	0	7	2	0.041834	0.172546	0	0	0.164493	0.041576
protein_co	LSM14B_SC	1436	1189	1116	1401	1272	1611	29.30735	28.59638	30.01381	24.73565	29.16475	32.67588
protein_co	YTH_domai	1063	869	842	2193	1788	1918	17.04825	16.42379	17.79481	30.42623	32.21537	30.57066
protein_co	Cdk5_and_	156	189	155	364	335	309	2.18198	3.115266	2.856885	4.404439	5.264051	4.295308
protein_co	oral_cancer	325	331	223	767	444	634	4.556627	5.46884	4.120024	9.302903	6.993461	8.834033
protein_co	tRNA_phos	185	148	107	328	164	213	5.414087	5.104137	4.126408	8.304058	5.391957	6.195021
protein_co	nudix_(nuc	311	255	149	261	239	296	8.011995	7.741543	5.058262	5.816795	6.91715	7.578471
protein_co	fermitin_fa	9	20	9	31	32	49	0.19143	0.501308	0.252258	0.570416	0.764656	1.035793
protein_co	phospholip	1345	1066	987	2533	2425	2801	15.93324	14.88148	15.40755	25.95852	32.27324	32.97649
protein_co	mitochond	874	699	681	1572	1157	1297	18.31767	17.26406	18.80792	28.50193	27.24214	27.01521
protein_co	CDC42_effe	575	543	412	401	214	306	14.30501	15.91943	13.5068	8.630339	5.981131	7.565742
protein_co	Finkel-Biski	1422	1393	1046	2121	1244	2015	50.72917	58.56207	49.17277	65.45787	49.85717	71.44024
protein_co	transmemb	90	84	43	734	654	735	2.275401	2.50266	1.432579	16.05368	18.57557	18.46768
protein_co	vacuolar_p	2053	1705	1182	1496	1116	1365	40.04711	39.19347	30.38327	25.24509	24.45657	26.46211
protein_co	T-box_6	12	3	7	11	17	18	0.293845	0.086569	0.225876	0.233019	0.467664	0.438045
protein_co	protein_ph	1924	1569	1221	3807	2866	3942	68.36139	65.69554	57.16843	117.0177	114.4013	139.1977
protein_co	aldolase_A_	32213	27686	19199	35135	21979	25204	673.0025	681.6364	528.5656	635.0215	515.8726	523.3167
protein_co	family_with	2	0	2	1	5	1	0.045777	0	0.060323	0.019801	0.128569	0.022747
protein_co	double_C2-	3	0	1	8	5	8	0.042364	0	0.018609	0.09773	0.079322	0.112273
protein_co	HIRA_interı	148	133	115	231	220	334	2.314702	2.451276	2.370097	3.12542	3.865495	5.19146
protein_co	TAO_kinase	2079	1786	1590	1679	2048	2665	21.29316	21.55629	21.4594	14.87645	23.56484	27.12642
protein_co	transmemb	1042	926	686	942	553	668	42.69699	44.71443	37.04149	33.39208	25.4568	27.20293
protein_co	high_mobil	4211	3704	4134	15434	13378	13064	27.54318	28.55006	35.63151	87.33139	98.30354	84.92092
protein_co	matrix_met	5	1	0	1	0	1	0.131302	0.030946	0	0.022718	0	0.026098

protein_co connector_	3	0	5	607	465	402	0.028021	0	0.061541	4.904717	4.879376	3.731625
protein_co contactin_	0	1	0	5	11	7	0	0.009969	0	0.036592	0.104544	0.058852
protein_co killer_cell_	0	0	0	0	3	0	0	0	0	0	0.143431	0
protein_co C-type_lect	103	115	72	97	62	65	2.030884	2.6721	1.870747	1.65456	1.373373	1.273711
protein_co mohawk_h	285	294	307	7	6	9	3.922065	4.767869	5.56728	0.083336	0.092762	0.12309
protein_co membrane_	19	18	24	287	303	245	0.198008	0.221059	0.32959	2.587458	3.547481	2.537489
protein_co chromoson	10	3	5	1	1	2	0.193994	0.068583	0.127818	0.016782	0.021794	0.038559
protein_co glutamate_	4	1	2	3	5	0	0.033947	0.010001	0.022367	0.022026	0.047672	0
protein_co integrin_be	17175	14772	15966	20828	18170	15260	240.2911	243.5496	294.3553	252.0876	285.5913	212.1803
protein_co annexin_A8	0	0	0	0	0	2	0	0	0	0	0	0.053853
protein_co tripartite_r	0	0	0	3	1	2	0	0	0	0.095084	0.04116	0.072822
protein_co protocadhe	0	2	1	11	7	10	0	0.013478	0.007535	0.054417	0.04497	0.056831
protein_co cardiotropl	102	74	37	109	98	119	3.245181	2.774454	1.551227	3.000048	3.502788	3.762663
processed_ CWC15_spl	514	528	414	1389	741	960	17.27725	20.91474	18.33778	40.39027	27.982	32.06952
protein_co Fc_fragmen	2	3	0	1	2	0	0.04857	0.085855	0	0.021009	0.054565	0
protein_co AT_rich_int	945	781	888	620	492	393	6.340038	6.174733	7.85069	3.598444	3.708294	2.620368
protein_co kelch-like_f	0	0	0	0	1	0	0	0	0	0	0.014453	0
protein_co cadherin_8	15	9	7	270	239	241	0.081691	0.05776	0.050236	1.272061	1.462272	1.304391
protein_co DCN1_defe	213	229	195	381	273	341	3.56398	4.51542	4.29957	5.514976	5.131772	5.670478
protein_co transmemb	1657	1322	1245	1408	1254	1231	28.76171	27.0415	28.47714	21.14258	24.45338	21.23538
protein_co transmemb	222	223	188	225	163	194	2.584759	3.059702	2.884429	2.266275	2.132081	2.244804
protein_co toll-interle	87	65	60	130	120	127	2.051611	1.806326	1.864498	2.652052	3.179114	2.976385
protein_co N-6_adenin	77	99	53	153	82	123	3.912146	5.927433	3.54842	6.724791	4.680446	6.21068
protein_co large_tumc	492	320	499	796	814	656	4.72636	3.622586	6.316799	6.61512	8.784866	6.262895
protein_co Sin3A-assoc	2188	1951	1542	2420	2064	2617	50.40683	52.96713	46.81244	48.23035	53.41962	59.91774
protein_co latrophilin_	99	58	113	173	159	156	0.774517	0.534726	1.164955	1.17086	1.397469	1.212914
protein_co KIAA1328	92	121	85	68	67	46	0.828188	1.283611	1.008311	0.529557	0.677587	0.411537
protein_co family_witl	63	88	67	28	21	39	0.700542	1.153144	0.981756	0.269349	0.262339	0.430991
protein_co CTAGE_fam	1	6	0	10	10	4	0.013715	0.096976	0	0.11865	0.154083	0.054522
protein_co histamine_	28	20	6	403	288	341	0.450425	0.379141	0.127189	5.608313	5.20482	5.451653
protein_co LY6/PLAUR	394	325	262	480	529	560	11.03054	10.72238	9.665775	11.62532	16.63816	15.5811
protein_co LY6/PLAUR	6	8	3	1976	1352	1740	0.184785	0.290344	0.121751	52.64609	46.77803	53.2568
protein_co programme	426	415	340	202	211	285	6.172103	7.085634	6.491384	2.53185	3.434433	4.103723
protein_co adrenocept	58	40	37	56	47	47	0.793636	0.645001	0.66716	0.662894	0.722504	0.639147
protein_co glycoprotei	1	3	5	16	12	2	0.01855	0.065579	0.12222	0.256756	0.250074	0.03687
protein_co WD_repeat	43	14	25	41	39	42	0.307755	0.118079	0.235782	0.253854	0.313581	0.298741
protein_co spermatoge	0	0	4	6	0	2	0	0	0.13194	0.129926	0	0.049753
protein_co vascular_er	94	72	61	58	22	35	2.407573	2.173157	2.05881	1.285117	0.633029	0.890901
protein_co coiled-coil_	137	76	103	37	17	22	2.675366	1.748974	2.650542	0.625068	0.372959	0.426968
protein_co CD226_mo	0	2	0	2	1	3	0	0.047299	0	0.034722	0.022546	0.059834
protein_co carnosine_(	0	0	1	7	0	0	0	0	0.01697	0.077984	0	0
protein_co fibrous_she	9	11	12	9	15	10	0.169864	0.244658	0.298453	0.146948	0.318053	0.187572
protein_co discs_large_	52	39	44	16	22	24	0.348914	0.30838	0.389047	0.092875	0.165839	0.160043
protein_co coiled-coil_	2	0	0	0	0	0	0.044903	0	0	0	0	0

protein_co regulator_c	0	0	0	6	1	0	0	0	0	0.127811	0.027663	0
protein_co protease_se	2811	2204	2023	23642	19133	20871	27.95738	25.83178	26.51345	203.4149	213.7803	206.2949
protein_co myotubula	535	538	525	719	743	649	5.460465	6.470908	7.061061	6.348451	8.519492	6.583096
protein_co protein_ph	9	6	6	389	283	348	0.158611	0.124609	0.139341	5.930684	5.603091	6.095103
protein_co chaperonin	5176	4376	4030	14952	10336	11762	74.56397	74.28808	76.50232	186.3361	167.277	168.3936
protein_co family_with	147	132	151	194	164	146	4.036476	4.271359	5.463826	4.608396	5.059155	3.984259
protein_co dedicator_c	1198	1063	1136	989	994	792	9.331074	9.756975	11.65972	6.663987	8.697817	6.130694
protein_co DIX_domai	273	215	296	157	149	120	2.451305	2.274994	3.502363	1.219543	1.503038	1.070842
protein_co dihydrolipo	596	529	518	1774	1607	1557	7.0778	7.40312	8.106187	18.22505	21.43961	18.37597
protein_co PIH1_doma	10	18	12	24	24	17	0.288036	0.610979	0.455473	0.598027	0.776617	0.486637
protein_co chromoson	767	644	615	731	688	677	10.86005	10.74557	11.47484	8.953998	10.94395	9.526534
protein_co translocase	967	754	503	1491	1415	1850	44.32376	40.72757	30.38176	59.12222	72.86444	84.27359
protein_co interleukin	1	1	7	31	17	26	0.031197	0.036764	0.287768	0.836633	0.595811	0.806108
protein_co testis_expr	0	0	0	1	3	3	0	0	0	0.039929	0.15556	0.137613
protein_co 6-pyruvoyl	252	205	158	1069	770	975	12.48001	11.96397	10.31113	45.79891	42.84046	47.98756
protein_co phosphatid	1064	872	863	893	780	733	14.81568	14.30881	15.83527	10.75708	12.20179	10.14363
protein_co chromoson	0	0	0	1	4	0	0	0	0	0.017064	0.088638	0
protein_co FRAS1_rela	0	1	0	5910	6297	4640	0	0.004194	0	18.19518	25.17611	16.41094
protein_co forkhead_b	106	66	95	223	253	199	0.978508	0.717976	1.155625	1.780847	2.623785	1.825666
protein_co cysteine_ri	1237	1048	1349	3313	2996	2840	11.07713	11.05926	15.91858	25.66505	30.14037	25.27468
protein_co SEC24_fam	3197	2632	2900	1224	1089	981	41.6365	40.39471	49.76962	13.79037	15.9334	12.69727
protein_co ATP-bindin	169	168	117	250	196	221	1.478603	1.732133	1.348918	1.892204	1.926505	1.921617
protein_co Rab_intera	170	174	146	82	98	94	6.271755	7.564784	7.097867	2.61708	4.06177	3.446495
protein_co DEAH_(Asp	1097	885	746	2187	1980	2187	12.76402	12.13476	11.43811	22.01367	25.88183	25.28943
protein_co ubiquitin_(	5964	5127	5139	8677	5606	6311	84.30977	85.41038	95.73124	106.114	89.03124	88.66416
protein_co inositol_14	103	123	130	29	44	23	0.534758	0.752544	0.889401	0.130251	0.256638	0.118674
protein_co protease_se	61	74	33	21	22	42	0.58834	0.841081	0.419419	0.175219	0.23838	0.402585
protein_co solute_carr	442	343	532	1141	895	777	2.426119	2.218662	3.848011	5.417994	5.51902	4.238581
protein_co CCR4_carb	133	104	79	576	447	409	3.984806	3.671943	3.119015	14.92935	15.04569	12.17835
protein_co enkurin_TR	0	8	6	22	17	9	0	0.147576	0.123767	0.297923	0.298962	0.140014
protein_co G_protein-c	0	1	0	7	12	5	0	0.008965	0	0.046069	0.102559	0.037803
protein_co calcium_ch	1	6	0	7	5	5	0.008919	0.06306	0	0.054008	0.050098	0.044318
protein_co DCP1_deca	360	331	239	430	276	284	9.136509	9.899491	7.993013	9.44081	7.869297	7.163178
protein_co calcium_ch	146	114	130	152	235	218	0.917434	0.844178	1.076466	0.826283	1.658972	1.361408
protein_co potassium_	10	6	15	37	54	32	0.088575	0.062628	0.175079	0.283513	0.537343	0.281688
protein_co thyroid_ho	8	8	3	605	606	592	0.056781	0.066913	0.028059	3.714752	4.832069	4.17583
protein_co N-glycanase	281	261	244	788	524	644	4.654699	5.094868	5.326108	11.2921	9.751371	10.60183
protein_co 3-oxoacyl-A	113	101	60	191	109	140	3.938336	4.14823	2.755627	5.758783	4.267857	4.849221
protein_co UEV_and_la	353	322	378	409	396	402	4.496672	4.833698	6.345169	4.507159	5.667099	5.089232
protein_co transmemb	17	24	20	7	13	7	0.250347	0.416497	0.388113	0.089177	0.215073	0.102447
protein_co chromoson	198	186	139	505	400	526	9.268185	10.26005	8.573914	20.44956	21.03481	24.46949
protein_co chromoson	2747	2487	2294	772	761	688	43.25667	46.15059	47.60172	10.51658	13.46257	10.76694
protein_co BTB_(POZ)_	590	496	496	108	110	89	5.416193	5.365756	6.000102	0.857687	1.134446	0.811973
protein_co ubiquitin_p	1192	911	945	1081	917	803	11.0286	9.932755	11.52155	8.652327	9.53153	7.383622

protein_co ankyrin_3_	1229	1107	1295	447	573	459	4.40488	4.675595	6.116272	1.385966	2.307203	1.63495
protein_co inositol_pc	184	140	205	496	544	474	1.588316	1.424145	2.331889	3.703939	5.275542	4.066372
protein_co RAD9_hom	6	15	10	13	27	15	0.111729	0.329165	0.245386	0.209422	0.564843	0.277598
protein_co phospholip	3124	2616	2162	969	1209	1174	64.27814	63.43035	58.61959	17.24801	27.94652	24.00657
protein_co discs_large_	903	781	858	684	1375	1100	6.447164	6.571115	8.072407	4.224741	11.02891	7.805186
protein_co methionine	3	2	0	0	1	0	0.046576	0.036591	0	0	0.017442	0
protein_co solute_carr	86	90	81	147	160	122	0.650139	0.801784	0.806915	0.961365	1.358867	0.916595
protein_co glucoside_x	313	249	287	950	869	810	2.210288	2.072101	2.670677	5.803516	6.894034	5.684591
protein_co twinfilin_a	1275	1125	1213	2150	1568	1700	20.33126	21.14042	25.48881	29.65893	28.08983	26.94093
protein_co DIP2_disco	1374	1244	1155	377	484	373	9.214711	9.83156	10.20732	2.187255	3.646611	2.486071
protein_co eukaryotic_	823	698	683	2335	1727	1729	3.781171	3.779106	4.135062	9.280608	8.913903	7.894619
protein_co membrane_	162	143	189	459	634	497	1.156634	1.203162	1.778187	2.835023	5.085331	3.526525
protein_co testis_expr	81	64	76	475	302	330	2.538911	2.364011	3.139141	12.88009	10.63453	10.27983
protein_co casein_kina	569	509	545	713	635	542	6.751104	7.116843	8.521064	7.318382	8.464188	6.391039
processed_ ankyrin_rep	3	2	1	1	1	1	0.03483	0.027363	0.015299	0.010044	0.013043	0.011538
protein_co serum_resp	110	118	138	376	320	361	2.039758	2.578547	3.372096	6.03166	6.666302	6.652775
protein_co A_kinase_(P	17	11	18	20	23	18	0.103615	0.079008	0.14457	0.105455	0.157489	0.109032
protein_co neuronal_P	49	25	32	4	8	5	0.443665	0.266751	0.381807	0.031332	0.081376	0.044992
protein_co family_with	727	598	637	915	692	772	11.3367	10.98906	13.08961	12.34345	12.12293	11.96408
protein_co MAP3K12_	204	205	193	351	250	231	6.577322	7.788967	8.199947	9.790144	9.055408	7.401855
protein_co mirror-ima	118	78	104	140	106	92	0.840333	0.654593	0.975973	0.862503	0.848056	0.651129
protein_co exostosin_g	1625	1368	1438	1468	1112	1192	24.9071	24.70944	29.04447	19.4652	19.14801	18.15748
protein_co transmemb	402	368	295	365	253	396	7.705387	8.31234	7.451183	6.052354	5.448011	7.543506
protein_co potassium_	6	4	4	32	11	5	0.187845	0.147576	0.165023	0.866685	0.386892	0.155571
protein_co thyroid_ho	1	2	4	0	0	1	0.045095	0.106282	0.237694	0	0	0.044816
protein_co NADH_dehy	128	89	114	374	215	365	2.691202	2.205126	3.158465	6.802538	5.078365	7.626739
protein_co malic_enzy	39	27	20	266	230	246	0.893422	0.728892	0.60375	5.271531	5.919282	5.60063
protein_co mesogenin_	0	0	0	5	0	0	0	0	0	0.377879	0	0
protein_co ADAM_met	4419	3736	4791	343	383	327	26.66358	26.56491	38.0939	1.790406	2.596225	1.960884
protein_co nucleotide_	169	167	144	320	234	233	1.778026	2.070499	1.996406	2.91249	2.765772	2.436223
protein_co NIMA-relate	525	486	598	569	454	417	6.698969	7.30789	10.05506	6.28093	6.50809	5.288035
protein_co ATPase_H+_	1	0	1	3	2	2	0.078084	0	0.102896	0.20265	0.175445	0.155204
protein_co fer_(fps/fes_	324	323	404	673	562	469	1.415371	1.66278	2.325635	2.543334	2.758104	2.036141
protein_co VPS33B_int	612	477	540	535	302	304	11.04291	10.14279	12.83987	8.351198	6.121925	5.45149
protein_co ankyrin_rep	820	647	835	810	990	715	4.936504	4.590046	6.624101	4.218457	6.695606	4.277808
protein_co UPF2_regul	561	478	480	675	583	576	5.333076	5.354881	6.012996	5.551133	6.226335	5.441855
protein_co cell_divisio	763	657	561	2147	1368	1650	26.19584	26.58154	25.3808	63.768	52.76463	56.29908
protein_co sodium_ch	149	116	97	409	250	305	2.14762	1.970318	1.842374	5.099851	4.048184	4.368986
protein_co coiled-coil_	18	27	20	248	206	196	0.299666	0.529707	0.438763	3.571739	3.852842	3.242879
protein_co chromoson	67	60	44	164	78	131	1.239359	1.307919	1.072531	2.624396	1.620937	2.40826
protein_co FERM_dom	333	285	283	735	713	621	2.586845	2.609025	2.896993	4.939427	6.222499	4.794325
protein_co solute_carr	0	0	0	0	0	1	0	0	0	0	0	0.028673
protein_co protein_tyr	8	0	13	11	7	2	0.079896	0	0.171085	0.095036	0.078538	0.019851
protein_co epidermal_	3540	2879	3403	779	737	590	46.14901	44.22907	58.4596	8.78536	10.79383	7.644001

protein_co	acyl-CoA_d	280	201	185	280	297	282	4.471638	3.782785	3.893275	3.868384	5.328612	4.475765
protein_co	thymocyte_	173	163	138	406	240	321	7.050648	7.828483	7.411342	14.31436	10.98862	13.00162
protein_co	vacuolar_p	1103	881	876	928	713	853	15.82062	14.89125	16.5572	11.51487	11.48912	12.15925
protein_co	non-SMC_c	276	241	252	1342	1115	1157	2.641785	2.718395	3.178511	11.1123	11.98981	11.00605
protein_co	vesicle_trar	412	310	306	571	488	474	5.280002	4.681723	5.167651	6.330471	7.025962	6.037052
protein_co	quinoid_di	565	394	410	998	726	869	18.15028	14.91551	17.35616	27.73502	26.20116	27.7437
protein_co	family_witl	374	358	483	202	217	167	3.410253	3.846849	5.803594	1.593417	2.22292	1.513356
protein_co	anoctamin_	35	40	41	345	325	284	0.474018	0.638401	0.73172	4.042114	4.944915	3.822561
protein_co	testis_expr	60	45	49	83	73	80	0.715419	0.632308	0.76991	0.856151	0.97787	0.948001
protein_co	queuine_tR	359	299	338	917	733	817	4.72429	4.636821	5.861295	10.43937	10.83665	10.68498
protein_co	methylmal	136	65	101	62	40	62	1.018672	0.573741	0.9969	0.401745	0.336593	0.461527
protein_co	zinc_finger_	870	680	688	575	652	591	6.171602	5.684531	6.431346	3.528657	5.196074	4.166542
protein_co	endothelin_	1583	1273	1320	1166	1228	1193	20.26737	19.20667	22.27026	12.91452	17.66298	15.17982
protein_co	nuclear_rec	11	1	6	6	17	10	0.098553	0.010558	0.070838	0.046504	0.17111	0.089041
pseudogen	aldo-keto_r	1	3	1	5	1	0	0.053857	0.1904	0.07097	0.232955	0.060504	0
protein_co	aldo-keto_r	73	46	35	20	25	15	1.143062	0.848813	0.722187	0.270919	0.439781	0.233425
protein_co	dihydropyr	982	967	684	483	332	412	19.05022	22.10661	17.48556	8.105852	7.235619	7.943198
protein_co	VENT_hom	0	0	0	0	0	4	0	0	0	0	0	0.072297
protein_co	ADAM_met	44	28	21	38	38	38	0.710401	0.532741	0.446791	0.530759	0.68926	0.609739
protein_co	inter-alpha	19	14	13	8	23	17	0.315026	0.273545	0.284035	0.114748	0.42842	0.280125
protein_co	KIN_antige	228	153	184	373	328	325	5.800359	4.586892	6.168402	8.20903	9.374388	8.216995
protein_co	phosphatid	110	44	91	129	50	71	1.686019	0.794748	1.838002	1.710498	0.860972	1.081528
protein_co	ankyrin_an	63	52	51	29	30	32	0.7563	0.735638	0.806786	0.301172	0.404598	0.38178
protein_co	inositol_pc	285	222	225	322	283	287	6.978808	6.406141	7.260286	6.821114	7.785238	6.984381
protein_co	major_facil	23	75	37	116	104	112	0.253834	0.975418	0.538095	1.107499	1.289451	1.228429
protein_co	ring_finger_	2948	2766	2518	539	459	435	27.1757	30.04779	30.58749	4.298382	4.753517	3.985219
protein_co	ArfGAP_wit	257	223	271	241	356	212	2.381974	2.435655	3.309848	1.932342	3.706832	1.952762
protein_co	ADAM_met	354	305	341	537	466	414	4.309292	4.375318	5.470057	5.655096	6.372908	5.008558
protein_co	Friend_leuk	297	252	318	269	204	199	2.928021	2.927692	4.131233	2.29421	2.25942	1.949757
protein_co	transmemb	12	5	6	12	5	25	0.284374	0.139632	0.187368	0.24601	0.133115	0.588787
protein_co	WW_and_C	307	256	356	1114	1321	1078	1.841478	1.809569	2.813928	5.780646	8.901845	6.426235
protein_co	MLF1_inter	125	78	88	1408	747	827	3.312124	2.435557	3.072657	32.2747	22.23649	21.77769
protein_co	acyl-CoA_sy	1857	1580	1499	404	328	276	24.90158	24.96773	26.48814	4.686615	4.941262	3.678186
protein_co	solute_carr	192	165	156	2889	2158	2758	6.101243	6.178857	6.532456	79.41959	77.04023	87.10057
protein_co	antagonist_	25	22	27	27	18	39	0.627263	0.650488	0.892706	0.586052	0.507377	0.972487
protein_co	bicaudal_D	144	149	203	327	273	305	0.865226	1.055019	1.607303	1.699721	1.842802	1.821279
protein_co	salvador_h	634	631	471	891	720	683	10.95808	12.85232	10.72756	13.3225	13.98063	11.73209
protein_co	coiled-coil_	29	20	22	104	92	98	0.442829	0.359895	0.442686	1.373835	1.578248	1.487216
protein_co	stress-assoc	47	21	23	24	28	42	2.586514	1.361894	1.667937	1.142592	1.731108	2.297079
protein_co	neuroblast	1329	1043	1124	719	641	596	9.663313	8.937014	10.76966	4.52265	5.236103	4.306822
protein_co	zinc_finger_	22	24	17	40	13	16	0.258938	0.332883	0.263667	0.407282	0.171896	0.187155
protein_co	tryptophan	45	35	38	977	829	939	0.75895	0.695626	0.844538	14.25471	15.7074	15.73896
protein_co	GUF1_GTPa	394	381	351	1228	835	778	4.688413	5.342712	5.503914	12.64128	11.1626	9.200659
protein_co	solute_carr	18	20	16	0	0	2	0.35294	0.462131	0.413412	0	0	0.038973

protein_co	gamma-am	2	1	3	78	62	55	0.018218	0.010734	0.03601	0.614645	0.634464	0.497896
protein_co	spastic_ata	3015	2549	3239	1075	939	730	10.20635	10.16857	14.4487	3.148144	3.571065	2.455928
protein_co	poly(A)_bin	1	6	1	5	4	5	0.017133	0.121141	0.022577	0.074108	0.076991	0.085136
protein_co	centromere	196	145	202	659	550	541	2.387034	2.081026	3.241818	6.943059	7.525133	6.54801
protein_co	F-box_prot	50	37	39	89	34	51	1.529203	1.333533	1.57179	2.354768	1.168216	1.550154
protein_co	chromoson	162	127	137	220	180	204	2.907268	2.685845	3.239854	3.415512	3.629039	3.638395
protein_co	chemokine	113	79	52	53	41	30	1.913734	1.576657	1.16049	0.776501	0.780074	0.504933
protein_co	poly_(ADP-	382	368	400	643	437	438	2.817815	3.198925	3.888158	4.103204	3.621426	3.210945
protein_co	GDNF_fami	432	343	321	228	192	168	2.481609	2.321939	2.429906	1.133046	1.239082	0.95911
protein_co	CDK2-assoc	755	609	662	1287	1100	1067	5.936499	5.642972	6.859244	8.754373	9.716844	8.337916
protein_co	dystonin	4452	3964	4943	2288	2130	1903	9.711702	10.19016	14.20907	4.317767	5.21998	4.125614
protein_co	BEN_domai	265	212	225	116	76	80	4.011828	3.782156	4.48863	1.519209	1.292585	1.203639
protein_co	TIA1_cytot	1375	1228	1107	2180	1853	1974	31.36315	33.00824	33.27357	43.01664	47.48336	44.74801
protein_co	BCL2-assoc	1997	1613	1460	2322	1680	1680	41.12142	39.14096	39.61664	41.36331	38.86408	34.38024
protein_co	glycosyltra	0	0	0	9	5	5	0	0	0	0.13694	0.098797	0.087399
protein_co	transmemb	1	1	0	0	4	1	0.009166	0.010801	0	0	0.041188	0.009109
protein_co	RNA_bindir	0	0	0	0	4	0	0	0	0	0	0.06561	0
protein_co	schwannon	12	11	7	41	24	30	0.10679	0.115358	0.082088	0.315642	0.239943	0.265326
protein_co	Lix1_homo	1855	1597	1248	303	229	229	24.68096	25.03976	21.88102	3.487577	3.422967	3.028052
protein_co	neuroblast	16	15	17	8	12	7	0.150134	0.165866	0.210205	0.06494	0.1265	0.065278
protein_co	potassium_	1590	1212	1197	7	0	8	25.57769	22.97597	25.37425	0.097415	0	0.127898
protein_co	adaptor-rel	114	126	109	500	396	462	2.399711	3.125588	3.023538	9.10515	9.364797	9.665086
protein_co	RAB_GTPas	299	278	354	311	276	172	2.32068	2.542705	3.620613	2.088178	2.40659	1.326729
protein_co	coiled-coil_	125	100	76	63	54	79	1.954985	1.843064	1.566325	0.852387	0.948803	1.22792
protein_co	transmemb	1	3	3	140	90	115	0.00776	0.027435	0.030679	0.939878	0.784643	0.886927
protein_co	mitotic_spi	72	97	99	118	66	123	4.085479	6.486184	7.402535	5.792359	4.2073	6.936257
protein_co	tubulin_alp	0	1	1	0	1	2	0	0.040512	0.045301	0	0.038621	0.06833
protein_co	astrotactin	7	7	12	2	5	9	0.052034	0.061319	0.117546	0.012861	0.041755	0.066488
protein_co	family_with	3341	2751	3042	3807	3981	3683	33.46752	32.47467	40.15514	32.99081	44.80106	36.66557
protein_co	protein_tyr	230	182	224	353	728	533	2.193161	2.045131	2.814657	2.911926	7.798715	5.051025
pseudogen	-	397	293	266	626	473	552	5.55286	4.829486	4.902783	7.574667	7.432525	7.673172
protein_co	mannosyl_	1238	1022	1385	1067	1210	982	7.942432	7.726643	11.70894	5.921889	8.72102	6.261148
protein_co	transmemb	0	4	1	2	5	4	0	0.049144	0.013738	0.018038	0.058562	0.041445
protein_co	G_patch_d	281	268	278	328	227	208	3.808607	4.280571	4.965231	3.845889	3.456486	2.801772
protein_co	heat_shock	18	18	35	557	393	386	0.443227	0.522316	1.135681	11.86511	10.87164	9.446057
protein_co	gem_(nucle	178	168	150	441	279	453	7.788014	8.662098	8.648341	16.692	13.71387	19.69766
protein_co	transmemb	7	5	1	466	206	227	0.222977	0.187689	0.041976	12.84133	7.371865	7.186155
protein_co	POU_class_	0	0	1	24	22	23	0	0	0.018383	0.289637	0.344788	0.318873
protein_co	ring_finger_	155	98	112	492	396	453	2.325263	1.732501	2.21408	6.385112	6.673977	6.753801
protein_co	cysteinyl_le	1	0	0	4	12	13	0.020777	0	0	0.071898	0.280106	0.268439
protein_co	glutamate_	2	3	1	4	8	4	0.019828	0.035049	0.013064	0.034306	0.089102	0.039411
protein_co	ADP-ribosy	0	0	0	1	5	1	0	0	0	0.012181	0.07909	0.013993
protein_co	SET_bindin	484	374	459	189	269	159	2.588488	2.357108	3.234806	0.874431	1.616226	0.845099
protein_co	ADP-ribosy	411	334	358	512	386	351	6.367793	6.098186	7.309118	6.862464	6.718673	5.404604

protein_co	ectopic_P-g	479	366	532	423	351	346	2.007341	1.807481	2.937866	1.533518	1.652501	1.441024
protein_co	proline-seri	204	155	133	2532	1616	1748	3.599988	3.223366	3.092839	38.65428	32.03769	30.65645
protein_co	ATP_syntha	7571	6388	5494	11305	7838	8618	88.14961	87.64742	84.29282	113.8677	102.523	99.72023
protein_co	HAUS_augn	283	282	208	923	591	768	13.3176	15.63852	12.89846	37.57546	31.24468	35.91786
protein_co	chromoson	282	303	368	1075	901	811	2.737323	3.465985	4.707167	9.027104	9.825413	7.823615
protein_co	SPC25_NDC	62	63	49	545	340	475	2.424181	2.902826	2.524668	18.43457	14.93487	18.45766
protein_co	pyruvate_d	637	564	455	131	119	124	11.29006	11.77994	10.62681	2.008589	2.369479	2.184179
processed_	spondin_1_	14	13	16	164	185	132	0.13797	0.150976	0.207783	1.39818	2.048221	1.292825
protein_co	phosphodi	52	43	62	604	592	544	0.498629	0.485903	0.783431	5.010422	6.377421	5.184214
protein_co	transcriptic	832	658	556	1479	1022	1089	14.8406	13.83124	13.06886	22.8223	20.47991	19.30482
protein_co	trans-golgi_	3300	2777	2861	2463	2615	2341	26.9233	26.69914	30.75863	17.38368	23.96818	18.98127
protein_co	SH2_domai	8	12	10	2	4	5	0.214445	0.379065	0.353232	0.046379	0.120458	0.1332
protein_co	potassium_	0	0	1	2	3	0	0	0	0.027662	0.03632	0.070749	0
protein_co	U2AF_hom	1124	989	1324	1247	1247	1039	7.018834	7.277833	10.89486	6.736404	8.748109	6.447983
protein_co	autophagy_	127	77	60	247	186	233	2.216784	1.583863	1.380085	3.729749	3.647386	4.041897
protein_co	POC5_cent	128	83	81	355	226	219	3.040129	2.323096	2.535139	7.294128	6.030308	5.169348
protein_co	sparc/ostec	141	143	150	329	331	266	1.54038	1.840992	2.159408	3.109336	4.062429	2.888018
protein_co	family_witl	27	30	28	46	43	39	0.654191	0.856582	0.893992	0.964187	1.170464	0.939107
protein_co	transcriptic	95	117	106	350	220	219	1.980856	2.874897	2.912528	6.313358	5.153486	4.538195
protein_co	guanylate_(	203	196	263	59	45	45	1.854534	2.110094	3.166133	0.466287	0.461849	0.408565
protein_co	CWF19-like	106	89	112	359	253	245	1.711942	1.693871	2.383614	5.015804	4.590423	3.932411
protein_co	junction_m	129	104	143	112	117	117	0.755296	0.717576	1.103312	0.567295	0.769595	0.680806
protein_co	homer_hor	240	194	193	759	839	693	2.160489	2.058021	2.28946	5.910792	8.485002	6.199887
protein_co	X-ray_repai	61	49	68	274	152	188	1.904128	1.802476	2.797113	7.399116	5.330389	5.832218
protein_co	zinc_finger_	54	40	54	65	64	58	1.043744	0.911102	1.375399	1.086867	1.389726	1.114135
protein_co	zinc_finger_	165	112	107	123	69	99	1.497816	1.198118	1.27995	0.965923	0.703676	0.89314
protein_co	zinc_finger_	270	289	247	362	362	320	2.701071	3.40704	3.256147	3.132881	4.068458	3.1815
protein_co	zinc_finger_	67	71	43	111	72	92	1.633079	2.039378	1.381133	2.340552	1.971577	2.228588
protein_co	suppressor_	149	129	145	668	507	599	2.555299	2.607067	3.276863	9.910486	9.768154	10.20921
protein_co	DNA_cross-	195	196	176	356	249	281	2.809879	3.328251	3.341954	4.437782	4.030894	4.024101
protein_co	oleoyl-ACP_	3	6	5	13	6	4	0.089883	0.211843	0.197406	0.336947	0.201956	0.119104
protein_co	ribonuclea	78	57	52	234	170	172	2.834178	2.4407	2.489836	7.355487	6.939537	6.21113
protein_co	N-myristoy	326	325	268	651	406	486	5.936967	6.974892	6.431565	10.25631	8.306578	8.796157
protein_co	zinc_finger_	0	2	0	4	0	0	0	0.060748	0	0.08919	0	0
protein_co	zinc_finger_	82	58	53	113	78	144	2.130109	1.775509	1.814256	2.53939	2.276311	3.717578
protein_co	ubiquitin_s	684	516	572	1787	1699	1646	8.052399	7.158565	8.873604	18.19939	22.47044	19.25789
processed_	ARL5B_anti	6	3	11	18	8	5	0.461025	0.271645	1.113782	1.196488	0.690577	0.381815
protein_co	coiled-coil_	758	633	652	2302	1451	1565	4.760858	4.685186	5.396329	12.5079	10.23841	9.768773
protein_co	calcium/ca	174	139	174	160	126	116	0.752593	0.708488	0.991733	0.598679	0.612252	0.49863
protein_co	tripartite_r	14	23	16	116	74	75	0.175717	0.340189	0.264631	1.259524	1.043437	0.935527
protein_co	ZFP36_ring	1762	1546	1360	1910	1802	1630	25.23864	26.09617	25.67047	23.66772	28.99773	23.20371
protein_co	PAN3_poly	635	544	511	590	527	515	6.805168	6.870228	7.216404	5.46991	6.3449	5.485068
protein_co	pleckstrin_	596	559	583	13	3	0	4.519816	4.995665	5.826098	0.085287	0.025559	0
protein_co	phosphofru	2491	2153	1982	1502	1239	1507	36.84717	37.53025	38.63393	19.22044	20.58973	22.15406

protein_co transmemb	1736	1543	1583	6860	5896	5745	25.67912	26.89697	30.85646	87.78443	97.97988	84.45591
protein_co glutamate_	184	126	152	0	2	1	1.732991	1.39848	1.8865	0	0.021162	0.00936
protein_co immunoglc	193	151	267	21	28	32	0.92325	0.851229	1.683094	0.086905	0.150477	0.152132
protein_co sperm_flag	113	92	97	62	49	50	0.957786	0.918935	1.08342	0.454616	0.46659	0.421182
protein_co SPARC-like_	34	23	14	23	17	21	0.6012	0.479264	0.326214	0.351829	0.337706	0.369036
protein_co dentin_sial	0	0	0	5	0	0	0	0	0	0.052873	0	0
protein_co dentin_mat	0	0	0	1	2	0	0	0	0	0.017076	0.044352	0
protein_co matrix_extı	0	0	0	0	3	0	0	0	0	0	0.080156	0
protein_co muscleblin	1084	965	1104	1018	920	757	8.936163	9.374674	11.99294	7.259932	8.520374	6.201936
protein_co calcyphosir	3	1	2	0	0	0	0.15819	0.062139	0.138971	0	0	0
protein_co NAD_kinase	647	500	553	390	358	321	9.477815	8.631396	10.6749	4.942328	5.891638	4.673246
protein_co glycerol-3-p	182	164	147	126	121	88	2.373217	2.520095	2.525912	1.421345	1.772558	1.140403
protein_co gap_junctic	13310	12482	11668	5012	4745	4475	232.02	256.4121	268.027	75.58252	92.925	77.52647
protein_co cyclin_O	0	0	0	43	24	15	0	0	0	1.140992	0.827012	0.457248
protein_co solute_carr	603	518	514	1246	896	907	6.273024	6.350333	7.046242	11.21349	10.47169	9.377273
protein_co pelota_hon	516	449	396	972	693	739	6.281341	6.441042	6.352325	10.23604	9.477308	8.940396
protein_co RAS_guanyl	56	54	33	9	5	10	0.616746	0.70084	0.478924	0.085748	0.061864	0.109453
protein_co SAR1_hom	586	508	437	934	586	729	4.642835	4.743036	4.562489	6.401703	5.215936	5.740144
protein_co cation_cha	3	3	4	3	1	5	0.11661	0.137418	0.204885	0.100879	0.043668	0.19315
protein_co family_witl	12	27	13	3	18	4	0.150152	0.398125	0.214352	0.032474	0.253029	0.049741
protein_co G_protein-r	344	314	305	379	333	321	2.064351	2.220556	2.411902	1.967557	2.24501	1.914431
protein_co Tctex1_dor	0	0	2	30	9	27	0	0	0.069728	0.68664	0.267508	0.709935
protein_co WD_repeat	51	36	45	77	50	91	0.641938	0.533989	0.746397	0.838449	0.707037	1.138345
protein_co ankyrin_rep	0	1	1	16	24	24	0	0.03909	0.043711	0.459137	0.894375	0.791189
protein_co FERM_RhoC	4235	3547	3129	4447	3160	3191	27.31211	26.95691	26.59146	24.8103	22.89486	20.45212
protein_co interferon-i	410	396	379	124	100	103	5.406179	6.15331	6.585376	1.414462	1.481343	1.34975
protein_co solute_carr	45	32	35	122	149	153	0.515436	0.431936	0.528281	1.208885	1.917333	1.741659
protein_co pantothena	234	191	206	422	338	339	3.679297	3.539072	4.268261	5.740166	5.970555	5.297346
protein_co PR_domain	159	132	126	51	26	27	2.055584	2.011033	2.146563	0.570389	0.377625	0.346906
protein_co bone_morp	1	3	4	2	0	3	0.009233	0.032641	0.048666	0.015975	0	0.027527
protein_co heterogene	3785	3331	3024	7630	6173	7354	52.997	54.96258	55.79586	92.42149	97.10258	102.3337
protein_co hematopoi	23	22	14	0	4	2	0.348895	0.393275	0.279853	0	0.068167	0.030151
protein_co utrophin	866	693	1068	1427	1679	1364	3.715609	3.503906	6.038349	5.296624	8.093044	5.816157
protein_co glutamate_	2	0	0	2	3	0	0.015259	0	0	0.0132	0.025714	0
protein_co protein_tyr	834	655	759	870	801	698	7.135228	6.603743	8.556938	6.439083	7.698806	5.93481
protein_co geranylgera	567	487	378	922	708	866	10.36875	10.49493	9.108988	14.58604	14.54541	15.73878
protein_co contactin_a	0	0	0	10	13	14	0	0	0	0.09412	0.158896	0.151376
protein_co zinc_finger_	78	86	107	84	51	58	1.436812	1.866856	2.597311	1.33859	1.055418	1.061801
processed_ prostate_ar	68	60	60	7	4	5	1.554399	1.616262	1.807339	0.138425	0.102722	0.113588
protein_co RAB3C_mer	0	0	0	10	3	13	0	0	0	0.051529	0.020075	0.076956
protein_co intermedia	12	8	28	4	2	1	0.367433	0.288665	1.12977	0.105955	0.068798	0.03043
protein_co MARVEL_do	2	0	0	537	419	467	0.024196	0	0	5.620204	5.694792	5.614891
protein_co RAD17_hor	388	290	309	690	492	418	6.353574	5.596177	6.667756	9.774589	9.051083	6.802559
protein_co mediator_c	317	217	234	498	369	354	9.573471	7.722839	9.312383	13.01076	12.51946	10.62486

protein_co procollagen	2826	2706	2317	1059	922	872	39.01206	44.02117	42.14903	12.64695	14.29903	11.96335
protein_co serine/thre	709	548	619	171	138	102	10.47883	9.544521	12.05569	2.18638	2.291367	1.498223
protein_co neurensin_	0	0	0	5	0	0	0	0	0	0.097279	0	0
protein_co janus_kinas	4	1	1	0	0	0	0.071181	0.020971	0.02345	0	0	0
protein_co Zic_family_	4514	3790	3228	1141	1097	1201	45.59734	45.11534	42.96811	9.970721	12.44898	12.05676
protein_co G_protein-r	584	525	491	1195	926	830	6.784626	7.187526	7.516737	12.01003	12.08574	9.582985
protein_co carboxypep	1	0	4	0	0	0	0.014813	0	0.078079	0	0	0
protein_co SREK1-inter	326	344	324	752	428	594	3.827626	4.759676	5.01293	7.63823	5.64553	6.931192
protein_co leucine-rich	85	80	79	40	26	43	0.70006	0.77645	0.857389	0.284996	0.240568	0.351961
protein_co CWC27_spl	403	347	293	661	562	555	10.14514	10.29412	9.719754	14.39519	15.89418	13.88531
protein_co major_hist	43	21	25	3	6	5	0.295491	0.17006	0.226387	0.017834	0.046321	0.034147
protein_co signal_reco	59	65	51	152	106	107	1.099443	1.427386	1.25235	2.450346	2.219094	1.981592
protein_co centromere	175	158	110	1008	636	782	6.670032	7.09666	5.52481	33.23635	27.23303	29.62145
protein_co chromodor	287	284	242	763	766	624	4.444009	5.182251	4.93791	10.2207	13.32511	9.602564
protein_co calcium_re	1171	1017	720	1635	1530	1712	20.48708	20.96772	16.59933	24.74594	30.07209	29.7671
protein_co tektin_5	0	1	0	5	4	0	0	0.038702	0	0.142056	0.147583	0
protein_co B-cell_scaff	5	4	6	56	49	41	0.074691	0.070415	0.118109	0.723685	0.822325	0.608684
protein_co thioredoxir	376	282	210	598	360	427	6.263629	5.535979	4.609909	8.617919	6.73736	7.069289
protein_co Dab_mitog	3286	2768	2916	1048	860	818	38.36879	38.08761	44.86761	10.58607	11.28127	9.492345
protein_co aminocarb	10	7	5	1	2	3	0.273456	0.225575	0.180174	0.023656	0.061442	0.08153
protein_co acyl-CoA_o	1	0	0	117	52	58	0.019507	0	0	1.974382	1.139553	1.124398
protein_co BCL2-like_1	1012	909	867	339	321	358	10.53407	11.1503	11.8924	3.05266	3.753789	3.703466
protein_co anaphase_p	489	374	416	1285	1147	988	3.134538	2.825162	3.513927	7.125753	8.259944	6.294065
protein_co calpastatin	1548	1348	1253	5075	3799	3869	17.70418	18.16778	18.88386	50.21159	48.81162	43.97575
protein_co short_coile	563	488	476	1168	848	909	13.59133	13.88291	15.14242	24.39267	22.99844	21.80856
protein_co calmegin	13	16	7	20	23	33	0.226169	0.328033	0.160481	0.301012	0.449539	0.570576
protein_co centrin_EF-	161	104	108	581	353	556	3.504729	2.667896	3.09804	10.94127	8.632812	12.02854
protein_co SWI/SNF_re	1757	1607	1539	4220	3416	3432	11.74016	12.65393	13.55114	24.39371	25.64303	22.79079
protein_co synaptoner	11	12	7	52	27	19	0.186055	0.239186	0.15602	0.760876	0.513051	0.319382
protein_co bone_morp	51	31	32	871	739	722	0.97122	0.695691	0.803031	14.34923	15.81032	13.66451
protein_co RANBP2-lik	6	4	4	8	5	12	0.056783	0.04461	0.049884	0.065497	0.05316	0.112865
protein_co Ras_associa	394	338	316	1324	1244	1142	5.973297	6.038675	6.313058	17.36476	21.18787	17.20654
protein_co heterogene	7599	6038	5959	11951	13591	12643	67.72704	63.41702	69.98643	92.14524	136.0837	111.9864
protein_co RAN_bindir	1305	1107	1515	2567	2222	1948	5.899411	5.897295	9.024966	10.03892	11.28473	8.751786
protein_co AT_hook_c	683	554	746	1676	1333	1192	4.131951	3.949583	5.947138	8.771451	9.059696	7.166718
protein_co c-mer_prot	33	29	26	239	226	167	0.441844	0.457573	0.458737	2.76832	3.399483	2.222192
protein_co transmemb	408	377	402	741	582	582	4.144268	4.512696	5.380821	6.511318	6.641401	5.875168
protein_co protein_tyr	0	0	1	47	43	44	0	0	0.019769	0.60996	0.724699	0.655998
protein_co nuclear_rec	49	40	56	4	9	15	0.747151	0.718753	1.125214	0.052764	0.154171	0.227307
protein_co coiled-coil_	18	1	10	25	10	9	0.305233	0.019983	0.223457	0.366743	0.190506	0.151674
protein_co phospholip	413	357	349	8	24	27	2.564465	2.612294	2.855663	0.042973	0.16742	0.166617
protein_co RNA_bindir	1517	1232	1452	3831	3569	3225	18.79511	17.98776	23.70613	41.06146	49.67694	39.70988
protein_co sodium_ch	1	4	4	0	3	1	0.005803	0.027354	0.030588	0	0.019558	0.005767
protein_co FEZ_family_	4	4	0	5	5	2	0.102104	0.120323	0	0.110412	0.143385	0.050737

protein_co	CD96_mole	0	0	0	0	0	5	0	0	0	0	0	0.06084
protein_co	solute_carr	32	24	19	21	15	12	0.571756	0.505334	0.447351	0.324596	0.301093	0.213084
protein_co	G_protein-r	2	0	3	2	3	0	0.011597	0	0.022923	0.010033	0.019543	0
protein_co	G_protein-r	0	0	0	5	18	14	0	0	0	0.072421	0.338573	0.232953
protein_co	family_with	493	444	396	1862	1353	1528	5.733724	6.085271	6.069038	18.73409	17.67814	17.66131
protein_co	ArfGAP_wit	1769	1524	1906	2509	1971	1897	15.50027	15.73633	22.00742	19.01845	19.40202	16.51917
protein_co	trafficking_	402	304	366	838	550	569	3.418291	3.046237	4.101086	6.164388	5.254056	4.808448
protein_co	family_with	0	0	1	0	0	0	0	0	0.04472	0	0	0
processed_	long_interg	43	19	32	112	64	74	3.201776	1.667183	3.139838	7.214455	5.353669	5.476005
protein_co	INO80_com	121	86	100	333	199	264	1.974071	1.653419	2.14987	4.699857	3.647367	4.280465
protein_co	lysophosph	2450	1920	2025	4387	4248	4694	23.1204	21.35195	25.18193	35.81458	45.03631	44.02324
protein_co	pleckstrin_	797	732	590	1359	1218	1329	3.664898	3.966631	3.575118	5.406125	6.292163	6.073488
protein_co	NmrA-like_	660	570	441	1840	1241	1782	20.32639	20.68703	17.89739	49.02268	42.93753	54.54231
protein_co	UBA-like_d	187	130	118	906	620	728	3.748567	3.07096	3.117027	15.7114	13.96254	14.50323
protein_co	chromosom	7	3	0	2	0	1	0.197963	0.09998	0	0.04893	0	0.028106
protein_co	transmemb	32	21	28	87	91	87	1.300163	1.005481	1.499134	3.057947	4.153729	3.512987
protein_co	inhibitor_c	458	367	287	638	445	604	8.448423	7.977804	6.976328	10.18108	9.221876	11.07278
protein_co	testis_expr	38	24	12	5	2	10	2.409291	1.79318	1.002586	0.274245	0.142457	0.630108
protein_co	ADP-ribosy	6	11	12	54	30	37	0.169683	0.366595	0.447201	1.321122	0.95314	1.039914
protein_co	CKLF-like_M	459	415	293	1021	494	583	11.76182	12.5319	9.893825	22.63344	14.22125	14.84704
protein_co	F-box_and_	314	244	272	303	246	204	4.321152	3.957007	4.932574	3.607244	3.803243	2.790035
protein_co	upstream_b	1230	971	1052	2153	1851	1821	8.806792	8.192925	9.925747	13.33582	14.88909	12.95783
protein_co	required_fo	451	365	427	871	729	780	3.789301	3.613954	4.72765	6.330876	6.881121	6.513087
protein_co	CD8a_mole	3	0	0	1	6	9	0.052107	0	0	0.015026	0.117079	0.155356
protein_co	ribose_5-ph	362	313	261	912	634	891	10.37048	10.56675	9.852931	22.60206	20.40462	25.36749
protein_co	tubulin_gar	314	215	222	561	440	493	4.318907	3.484895	4.023759	6.675289	6.799014	6.739082
protein_co	golgin_A8_	0	3	1	0	0	0	0	0.035555	0.013253	0	0	0
protein_co	golgin_A8_	0	0	0	0	2	0	0	0	0	0	0.022524	0
protein_co	protein_tyr	897	817	916	636	529	438	4.791451	5.142849	6.447701	2.938967	3.174529	2.32519
protein_co	leucine_ric	267	280	219	184	96	124	8.06346	9.964954	8.715436	4.807187	3.257095	3.721701
protein_co	CNKSR_fam	285	289	260	193	192	151	4.616947	5.517152	5.550322	2.70477	3.494301	2.431065
protein_co	general_tra	209	159	123	571	470	473	3.673528	3.293376	2.848899	8.682329	9.280771	8.262432
protein_co	craniofacia	879	723	551	662	529	637	36.49814	35.37751	30.14868	23.77951	24.67667	26.28639
protein_co	zinc_finger_	1496	1359	1196	1810	1706	1865	23.0098	24.63246	24.24082	24.08368	29.47877	28.50819
protein_co	family_with	8	4	5	0	0	1	0.223262	0.13155	0.183878	0	0	0.027735
protein_co	chromosom	65	49	46	85	75	81	1.025071	0.910634	0.955946	1.159639	1.328774	1.269508
protein_co	transmemb	3	4	1	0	0	0	0.05638	0.088587	0.024765	0	0	0
protein_co	JAZF_zinc_f	294	231	251	45	25	33	4.980689	4.611701	5.603387	0.659504	0.475807	0.555604
protein_co	c-Maf_indu	646	604	495	2682	1793	2083	7.849411	8.648655	7.925826	28.19203	24.47563	25.15379
protein_co	SPHK1_inte	1	2	1	0	0	0	0.007654	0.018039	0.010086	0	0	0
protein_co	potassium_	1	0	0	10	12	7	0.013189	0	0	0.114098	0.177805	0.091753
protein_co	phosphotyr	53	29	48	37	16	10	1.022176	0.659105	1.219904	0.617326	0.346672	0.191672
protein_co	thyroid_ho	2727	2163	2651	3434	3115	2677	14.62124	13.66667	18.73025	15.92804	18.76316	14.26451
protein_co	F-box_prot	41	39	43	47	28	41	0.695699	0.779847	0.961481	0.689919	0.533758	0.691403

protein_co	CCAAT/enh	342	339	264	928	796	768	4.407454	5.148354	4.483327	10.346	11.52454	9.836317
protein_co	potassium_	764	554	580	1324	1134	1347	8.227608	7.030676	8.230818	12.33477	13.71963	14.41642
protein_co	zinc_finger_	119	141	83	126	72	103	1.854571	2.589541	1.704549	1.698752	1.260602	1.595304
protein_co	mucolipin_	5	5	13	65	63	94	0.092264	0.108727	0.316111	1.037619	1.306024	1.723848
protein_co	leucine-rich	1	2	0	4	0	4	0.018312	0.04316	0	0.063368	0	0.072797
protein_co	dimethylar	666	494	622	5137	3139	3244	8.994567	7.862127	11.06958	60.0176	47.62625	43.54081
protein_co	splicing_re	1078	1035	1047	1198	1180	1047	6.101827	6.903806	7.80949	5.866256	7.503644	5.889758
protein_co	chromodor	515	401	499	1199	1105	900	4.607065	4.227354	5.882372	9.27896	11.10525	8.001461
pseudogen	chloride_ch	0	0	0	2	3	0	0	0	0	0.026846	0.052294	0
protein_co	ankyrin-rep	0	0	0	1	0	0	0	0	0	0.011927	0	0
protein_co	diacylglyce	90	67	85	218	178	231	0.613374	0.538102	0.763373	1.285294	1.362862	1.564604
protein_co	heparan_su	1363	1157	1188	916	709	731	10.71238	10.71594	12.30386	6.227998	6.260158	5.709749
protein_co	musashi_RI	1565	1354	1565	2406	2565	2378	10.88448	11.09734	14.34308	14.47611	20.04148	16.43671
protein_co	calcium_ch	423	383	520	201	149	154	2.961	3.159394	4.796629	1.217186	1.171746	1.071343
protein_co	zinc_finger_	162	151	160	280	228	251	3.907262	4.291821	5.085251	5.842229	6.177908	6.016459
protein_co	heparan_su	303	230	229	110	115	118	6.347891	5.678345	6.322039	1.993621	2.70666	2.456849
protein_co	glyceropho	14	5	8	26	9	26	0.407015	0.171301	0.306483	0.653911	0.29395	0.751217
protein_co	nuclear_un	1177	1037	1104	1814	1630	1505	13.32582	13.83577	16.47106	17.76715	20.73262	16.93416
protein_co	sema_dom	7	5	16	602	682	593	0.059152	0.049791	0.178166	4.400789	6.474473	4.980069
protein_co	protein_ph	720	668	646	1656	1357	1279	5.72421	6.258448	6.767845	11.38955	12.12026	10.10563
protein_co	solute_carr	0	2	0	1	1	3	0	0.028128	0	0.010324	0.013408	0.035582
protein_co	adenylate_k	676	568	556	175	131	133	9.108708	9.019147	9.87233	2.039911	1.983035	1.78103
protein_co	chromoson	226	185	191	225	201	203	2.429374	2.343498	2.70554	2.092336	2.427342	2.16866
protein_co	calcium_bi	79	66	66	115	86	96	1.858817	1.83004	2.04639	2.340833	2.273302	2.244866
protein_co	impact_RW	408	402	404	627	544	583	5.696183	6.613889	7.432586	7.572762	8.53241	8.089133
protein_co	ankyrin_rep	28	17	18	1	7	5	0.412107	0.294854	0.349107	0.012733	0.115744	0.073136
protein_co	chromoson	139	122	109	265	203	247	6.152841	6.363966	6.358025	10.14775	10.09499	10.86595
protein_co	Thy-1_cell_	3258	2759	2006	858	639	626	48.53173	48.43212	39.3768	11.05669	10.69362	9.267416
protein_co	dynein_axo	12	13	5	7	16	29	0.134939	0.172269	0.07409	0.068095	0.202127	0.324088
protein_co	chromoson	17	20	16	102	45	113	0.727564	1.008694	0.902354	3.776466	2.163635	4.806296
protein_co	tubulin_fol	316	308	327	552	457	419	3.253472	3.736955	4.436521	4.916569	5.285977	4.287298
protein_co	junctophili	21	3	12	166	203	263	0.276351	0.046523	0.208093	1.889788	3.001146	3.439596
protein_co	ankylosis_p	1032	686	802	402	332	319	6.660381	5.217357	6.820694	2.244442	2.407169	2.046066
protein_co	family_with	388	303	341	609	533	551	2.633475	2.423523	3.049908	3.575838	4.064188	3.71671
protein_co	ubiquitin_a	1043	926	1056	1630	1548	1514	7.988637	8.358078	10.65828	10.80038	13.32013	11.52455
protein_co	roundabou	23	14	11	7	4	7	0.258523	0.185441	0.162929	0.068066	0.05051	0.078195
protein_co	roundabou	158	136	88	203	96	208	1.830746	1.857021	1.343657	2.034839	1.249658	2.395212
protein_co	transformir	335	287	301	485	364	431	3.975618	4.013736	4.707184	4.979258	4.853	5.083312
protein_co	neurograni	13	9	15	64	53	37	0.34918	0.284875	0.530923	1.487128	1.599302	0.987681
protein_co	family_with	36	55	26	75	54	43	0.583193	1.049977	0.555032	1.051076	0.982772	0.69229
protein_co	translocase	1765	1586	1406	2126	1736	1529	21.19321	22.44204	22.24703	22.08403	23.41805	18.24606
protein_co	ABI_family_	398	313	447	9	10	13	3.106371	2.878868	4.597403	0.060768	0.087684	0.100838
protein_co	angiopoieti	202	179	243	487	610	432	2.456715	2.56545	3.894435	5.123838	8.334553	5.221518
protein_co	phosphatid	393	239	240	318	206	238	3.365547	2.411949	2.708377	2.35588	1.981889	2.025581

protein_co	coiled-coil_	512	494	448	1047	771	883	4.807696	5.466396	5.543446	8.505047	8.133369	8.240193
protein_co	protein_kir	1253	1112	1234	500	466	453	7.580284	7.927683	9.837492	2.616781	3.167155	2.723593
protein_co	leucine-rich	203	146	124	100	75	91	1.395536	1.182783	1.123315	0.594714	0.579236	0.621722
protein_co	centrosom	205	171	186	42	50	46	3.085841	3.033353	3.6895	0.54693	0.845549	0.688156
protein_co	galactose-3	1	0	3	4	5	0	0.038643	0	0.152766	0.133719	0.217065	0
protein_co	ATP-bindin	18	29	12	7	13	3	0.146291	0.277747	0.128517	0.049216	0.118696	0.024231
protein_co	ATP-bindin	20	35	26	0	0	0	0.129345	0.266745	0.221579	0	0	0
protein_co	ATP-bindin	17	6	14	10	4	2	0.141464	0.058838	0.153519	0.071988	0.037394	0.01654
protein_co	ATP-bindin	122	87	97	141	85	116	0.785742	0.660308	0.823241	0.785602	0.615019	0.742485
protein_co	ectonucleo	0	0	0	2	0	8	0	0	0	0.026838	0	0.123326
protein_co	chromoson	0	2	6	29	24	34	0	0.06402	0.214766	0.681461	0.732387	0.917844
protein_co	ubiquitin_	5980	4742	4038	9793	6443	7908	200.6256	187.4795	178.5197	284.226	242.8412	263.6704
protein_co	melanoma_	1137	912	1129	810	700	602	7.393013	6.988161	9.673636	4.556265	5.11338	3.890157
protein_co	dispatched	175	140	179	104	87	82	1.945543	1.834163	2.622349	1.000228	1.086603	0.905996
protein_co	TRAF2_and	42	44	31	360	427	403	0.319013	0.393839	0.310281	2.36551	3.643647	3.042104
pseudogen	L-threonine	0	1	0	23	32	24	0	0.043265	0	0.730496	1.319854	0.875685
protein_co	family_with	10	5	7	173	89	72	0.129314	0.076194	0.119283	1.935323	1.292955	0.925308
protein_co	nei_endonu	317	271	213	308	191	291	6.283151	6.329867	5.563302	5.281192	4.253051	5.732193
protein_co	phosphoglu	0	2	0	10	17	16	0	0.030946	0	0.113589	0.250767	0.208786
protein_co	wingless-ty	0	0	0	2	0	0	0	0	0	0.031241	0	0
protein_co	obscurin_c	814	873	634	508	983	1052	1.6004	2.022672	1.642586	0.864034	2.171234	2.055557
protein_co	LON_peptic	326	268	193	378	342	273	4.802105	4.652173	3.746331	4.816913	5.659645	3.99656
protein_co	tripartite_r	408	309	270	1129	832	965	3.740895	3.338727	3.262225	8.955138	8.570136	8.793308
protein_co	enabled_ho	4880	4022	4559	2246	2614	2155	36.04745	35.01095	44.37712	14.3525	21.69249	15.82019
protein_co	centriole_c	133	84	93	406	390	352	1.365358	1.016205	1.258093	3.605654	4.497888	3.591263
protein_co	ankyrin_rep	0	0	0	2	0	0	0	0	0	0.031585	0	0
protein_co	SH3_domai	291	229	263	536	674	410	2.922198	2.709937	3.480224	4.656338	7.603712	4.09176
protein_co	guanylate_l	1	2	0	2	3	9	0.011266	0.026554	0	0.019493	0.037971	0.100772
protein_co	BUB3_mitc	1416	1108	1128	3303	2099	2512	27.44945	25.31146	28.81471	55.39135	45.71218	48.39491
protein_co	G_protein-r	0	0	0	7	4	0	0	0	0	0.042666	0.031661	0
protein_co	coiled-coil_	13	2	5	10	7	6	0.315558	0.05721	0.159934	0.20999	0.19089	0.144743
protein_co	matrix_met	1	0	0	0	5	6	0.027588	0	0	0	0.154966	0.164505
protein_co	chromoson	36	42	24	0	0	0	0.619596	0.851848	0.544317	0	0	0
protein_co	family_with	100	90	88	170	102	102	2.05676	2.181389	2.385069	3.024792	2.356855	2.084939
protein_co	ATP_syntha	2793	2485	2064	4903	3631	4884	26.96284	28.27015	26.25664	40.94676	39.37948	46.85759
protein_co	contactin_	0	4	4	12	5	9	0	0.031434	0.03515	0.069226	0.037458	0.059646
protein_co	family_with	2	0	1	3	0	5	0.171886	0	0.113252	0.223047	0	0.427062
protein_co	melanoma_	50	45	34	23	17	15	0.87796	0.93116	0.786717	0.349378	0.335353	0.261761
protein_co	serine/argi	53	46	25	214	144	195	0.779626	0.797398	0.484602	2.723247	2.379698	2.85072
protein_co	PDZ_and_L	32	40	16	163	71	102	0.329786	0.485791	0.217289	1.453226	0.822034	1.044702
protein_co	sorbin_and	50	67	58	944	755	622	0.437529	0.690905	0.668805	7.146143	7.422201	5.409246
protein_co	transcriptic	800	743	622	1969	1254	1815	15.23482	16.67413	15.60891	32.43815	26.82835	34.35054
protein_co	lymphocyt	44	27	35	1	0	2	3.837568	2.775072	4.022595	0.075451	0	0.173358
pseudogen	centrosom	3	7	20	3	6	8	0.034625	0.095207	0.304178	0.029954	0.077797	0.091762

protein_co	proteasom	0	0	0	0	0	1	0	0	0	0	0	0.028046
protein_co	thymosin_b	0	0	0	130	102	87	0	0	0	3.56732	3.634837	2.742614
protein_co	coxsackie_v	99	59	75	1314	1306	1130	0.838049	0.588563	0.836624	9.622603	12.42014	9.506536
protein_co	BTG_family	545	569	462	1655	1062	1150	19.42952	23.90479	21.70413	51.04188	42.53429	40.74489
protein_co	chromoson	203	200	213	243	257	200	1.978101	2.296622	2.73506	2.048433	2.81342	1.936832
protein_co	chondrolec	1	0	0	20	18	26	0.020777	0	0	0.359489	0.42016	0.536878
protein_co	neural_cell	60	36	51	117	125	116	0.390468	0.276086	0.43736	0.658694	0.913889	0.750243
protein_co	l(3)mbt-like	0	0	1	16	7	10	0	0	0.015387	0.161619	0.091824	0.116043
protein_co	phosphodi	16	24	31	429	311	247	0.095691	0.169149	0.244313	2.219581	2.089585	1.468106
protein_co	RAB_guanir	8	6	8	16	11	4	0.113455	0.100275	0.149506	0.196299	0.175257	0.056377
protein_co	mitochond	256	196	189	953	535	803	11.3035	10.19849	10.99688	36.4023	26.53846	35.23693
protein_co	junctional_	182	222	129	11	8	11	2.221642	3.193469	2.075043	0.11616	0.109709	0.133446
protein_co	ATP_synthe	331	336	227	880	550	714	14.86299	17.77971	13.43195	34.18409	27.74534	31.86296
protein_co	GA_binding	382	340	424	545	403	355	3.949894	4.142935	5.777272	4.875079	4.681405	3.648044
protein_co	ADAM_met	5473	4781	4418	1353	1181	1196	61.4129	63.2208	65.3273	13.13394	14.88789	13.33752
protein_co	ADAM_met	123	128	120	21	14	11	0.719053	0.881805	0.924425	0.106203	0.091946	0.063908
protein_co	tRNA_splici	213	149	156	329	290	279	2.878109	2.372581	2.777711	3.845799	4.40225	3.746636
protein_co	schlafen_fa	1	6	6	357	241	310	0.006251	0.0442	0.049425	1.930595	1.69249	1.925889
protein_co	wingless-ty	0	0	0	1	0	3	0	0	0	0.011334	0	0.03906
protein_co	xeroderma_	687	598	595	1126	997	996	9.491248	9.735872	10.83224	13.45761	15.47429	13.67526
protein_co	coiled-coil_	489	361	293	379	320	349	8.799506	7.655326	6.947873	5.899995	6.469168	6.241436
protein_co	FYVE_RhoG	2	0	0	214	193	202	0.018511	0	0	1.713456	2.006792	1.858049
protein_co	folliculin	594	551	454	577	436	547	8.644022	9.449049	8.706028	7.263873	7.127955	7.910909
protein_co	DPH3_KTI1	578	435	460	1414	790	1011	9.773202	8.66773	10.24948	20.68338	15.0067	16.98908
protein_co	oxidoreduc	121	91	101	280	187	216	1.630405	1.444969	1.793355	3.263857	2.830745	2.892501
protein_co	phospholip	99	96	67	113	103	109	1.262017	1.442144	1.125485	1.246154	1.475083	1.380913
protein_co	CXXC_finge	738	675	540	1642	1001	1405	13.30738	14.34323	12.83112	25.61369	20.27772	25.17805
protein_co	spindle_an	136	113	89	854	571	724	2.478477	2.426786	2.137326	13.46377	11.69045	13.11276
protein_co	protein_ph	999	840	918	2143	1613	1774	13.47466	13.35177	16.31661	25.00562	24.44195	23.78021
protein_co	adenomatc	3618	2925	2360	302	236	223	74.76211	71.22721	64.26282	5.398622	5.478656	4.579599
protein_co	piezo-type_	75	72	87	115	171	143	0.424388	0.480111	0.648718	0.562941	1.087044	0.804169
pseudogen	coiled-coil_	1	0	0	0	0	0	0.006098	0	0	0	0	0
protein_co	metallopho	157	137	105	128	145	109	1.962166	2.017733	1.72926	1.383914	2.035885	1.353855
pseudogen	coiled-coil_	7	0	5	12	27	16	0.070899	0	0.066734	0.105144	0.307222	0.161053
protein_co	ubiquitin_s	34	40	32	142	87	122	0.496687	0.688606	0.616011	1.794549	1.427816	1.771224
protein_co	RAB6B_mer	110	107	106	162	191	202	1.053838	1.208014	1.338203	1.342639	2.055718	1.923279
protein_co	essential_m	55	34	17	236	186	191	1.236939	0.901097	0.503813	4.591564	4.699457	4.269024
protein_co	EPH_recept	42	31	31	277	214	169	0.475925	0.41396	0.462898	2.715389	2.724282	1.903205
protein_co	acyl-CoA_sy	183	95	128	26	23	25	1.986508	1.215262	1.830982	0.244161	0.280489	0.269705
protein_co	ankyrin_rep	540	480	485	1067	901	947	6.832729	7.157292	8.086805	11.6796	12.80779	11.90858
protein_co	zinc_finger_	102	109	96	77	57	91	1.951565	2.45763	2.42041	1.274491	1.2252	1.73035
protein_co	carbonic_a	0	0	0	2	0	0	0	0	0	0.028723	0	0
protein_co	vesicular_o	1620	1293	1338	1586	1116	1163	28.9549	27.23408	31.5136	24.52298	22.40889	20.65839
protein_co	apolipopro	82	51	83	103	82	74	3.394184	2.487705	4.52725	3.688262	3.813155	3.044128

protein_co dickkopf_2	1150	1128	1196	655	460	386	16.73506	19.34397	22.93482	8.245817	7.520319	5.582469
protein_co cytochrom	78	70	52	90	72	51	0.835234	0.883321	0.733756	0.833718	0.866154	0.542742
protein_co radial_spok	0	4	0	4	1	5	0	0.077452	0	0.056858	0.018459	0.081648
protein_co F-box_and_	199	196	215	547	632	518	3.011795	3.49571	4.287909	7.161807	10.74579	7.791332
protein_co contactin_	0	0	0	0	5	0	0	0	0	0	0.056279	0
protein_co prominin_2	16	9	18	292	341	392	0.179157	0.118758	0.265596	2.828528	4.289612	4.362248
protein_co adenylate_l	48	64	23	47	43	33	0.401702	0.631175	0.253645	0.34027	0.404278	0.274465
protein_co outer_dens	0	3	0	0	0	0	0	0.184761	0	0	0	0
protein_co Kruppel-lik	833	747	758	860	538	499	12.05243	12.73671	14.45219	10.76443	8.745024	7.175297
protein_co protein_tyr	2	3	4	8	8	9	0.022418	0.039628	0.059084	0.077576	0.100743	0.10026
protein_co antizyme_i	2413	1966	2014	5315	4854	4627	27.05923	25.98057	29.76133	51.56136	61.15147	51.56645
protein_co ATPase_H+_	617	534	489	1435	1054	975	5.820491	5.936395	6.078803	11.71087	11.17028	9.140894
protein_co transmemb	199	179	184	278	184	225	3.547225	3.760069	4.322035	4.286901	3.684703	3.985913
protein_co OTU_doma	114	123	115	591	365	392	1.82998	2.326771	2.432619	8.207142	6.582386	6.253702
protein_co cyclin-depe	901	796	854	390	368	336	7.636861	7.95079	9.53856	2.859682	3.504185	2.830343
protein_co general_tra	1132	869	833	1841	1288	1973	62.95085	56.94846	61.04287	88.567	80.46742	109.0415
protein_co myristoylat	11293	9481	8739	4633	4381	4484	139.9164	138.4269	142.6776	49.65746	60.97917	55.21212
protein_co tetratricop	91	79	88	20	19	14	1.477801	1.51185	1.883181	0.280975	0.346639	0.22595
protein_co 1-acylglyce	569	437	526	1634	1070	1241	8.181267	7.404519	9.966183	20.32466	17.28388	17.73331
protein_co MMS19_nu	1929	1683	1460	2936	2097	2139	26.89575	27.65303	26.82496	35.41364	32.84725	29.63957
protein_co phosphatid	615	439	361	750	563	730	7.77243	6.538127	6.012066	8.199852	7.993541	9.168837
protein_co MARVEL_d	2797	2129	2045	1945	1487	1438	46.00061	41.26234	44.31995	27.67284	27.47458	23.50388
protein_co zinc_finger_	523	448	369	566	549	667	9.087017	9.172859	8.448523	8.507444	10.71621	11.51742
protein_co golgin_A7_	6	2	0	12	6	4	0.10976	0.043115	0	0.189906	0.123309	0.072722
protein_co G_protein-	0	2	0	4	5	9	0	0.025238	0	0.037054	0.06015	0.095778
protein_co tRNA_meth	146	151	154	248	181	237	1.859366	2.266189	2.584447	2.73229	2.589642	2.999646
protein_co Protein_LO	0	0	0	0	2	0	0	0	0	0	0.116963	0
protein_co solute_carr	288	268	233	435	236	318	10.5297	11.5469	11.22572	13.75865	9.693589	11.55474
protein_co heat_shock	816	712	833	916	852	722	10.8379	11.14402	14.57923	10.52479	12.71287	9.530192
protein_co SAM_doma	0	0	0	4	0	0	0	0	0	0.083842	0	0
protein_co ubiquitin_s	568	526	468	1084	775	742	5.765047	6.291401	6.259436	9.518024	8.837008	7.484591
protein_co GRAM_dom	179	123	121	265	159	204	2.984705	2.41691	2.658695	3.822586	2.978479	3.380556
protein_co zinc_finger_	159	152	138	383	290	383	3.864838	4.353965	4.420263	8.05371	7.919199	9.252149
protein_co chromoson	179	143	145	511	345	395	1.427174	1.343591	1.523445	3.524584	3.09024	3.129902
protein_co Mov10_Mo	1063	869	821	994	925	1053	12.00177	11.56215	12.2149	9.708704	11.73283	11.81544
protein_co ras_homolo	2545	2028	1602	4060	2571	3224	61.27095	57.5363	50.82346	84.55823	69.53733	77.13856
protein_co protein_ph	98	74	54	172	105	153	2.097097	1.866084	1.522723	3.184079	2.524241	3.25382
protein_co diazepam_b	2476	2221	1713	3163	2765	3920	155.6792	164.5643	141.9293	172.0451	195.3099	244.949
protein_co solute_carr	1764	1525	1681	8349	7525	6925	21.35069	21.75155	26.81117	87.42	102.322	83.29957
protein_co HEAT_repea	330	220	261	834	572	681	4.907452	3.855421	5.114668	10.72929	9.556243	10.06465
protein_co tripartite_r	16	14	3	7	0	2	0.627449	0.646984	0.15503	0.237476	0	0.077947
protein_co MKI67_(FH	497	474	355	1387	753	829	15.17398	17.05409	14.28256	36.63384	25.82778	25.15401
protein_co oxidase_(cy	2473	2119	1774	2864	1824	2118	74.81319	75.54263	70.72004	74.95318	61.9909	63.67803
protein_co solute_carr	63	44	43	439	343	383	1.105496	0.909864	0.994306	6.664143	6.761763	6.679212

protein_co	La_ribonuc	4686	4025	4045	6074	7295	6676	37.6166	38.07591	42.78885	42.18083	65.78875	53.26026
protein_co	CCR4-NOT_	1357	1250	1080	950	652	806	26.52915	28.79788	27.82287	16.06682	14.3199	15.65987
protein_co	glutamate_	168	246	126	222	136	180	1.558179	2.688749	1.539974	1.781247	1.417086	1.659168
protein_co	leucine-rich	1	7	3	20	17	9	0.016738	0.13807	0.066168	0.289592	0.319662	0.149708
protein_co	SET_domai	55	62	51	249	161	191	1.79849	2.389153	2.197608	7.043809	5.914529	6.207093
protein_co	mesoderm_	339	296	342	594	526	431	3.424999	3.524192	4.553252	5.191708	5.970292	4.327606
protein_co	nucleopori	752	588	730	2952	2387	2092	6.353595	5.85445	8.127545	21.5765	22.65704	17.56601
protein_co	zinc_finger_	145	172	152	307	248	214	1.020397	1.426384	1.409547	1.86897	1.960658	1.496664
protein_co	chromoson	197	212	145	353	251	258	3.140432	3.982595	3.045973	4.868116	4.495169	4.087451
protein_co	phosphoin	0	3	0	9	7	9	0	0.038968	0	0.085819	0.086682	0.09859
protein_co	RNA_bindi	150	149	125	296	206	211	3.986521	4.666552	4.377716	6.80546	6.150622	5.573075
protein_co	chromoson	74	49	104	95	151	68	0.862535	0.673051	1.597398	0.957925	1.977293	0.787705
protein_co	titin	124	140	189	115	174	114	0.060103	0.079967	0.120718	0.048221	0.094748	0.054915
protein_co	protein_dis	7750	6682	5682	9443	7432	7961	141.334	143.6014	136.5467	148.9766	152.2649	144.2854
protein_co	lysine_(K)-s	101	83	84	105	95	123	2.175362	2.106665	2.384099	1.956422	2.298703	2.632843
protein_co	PDZ_domai	0	2	2	2	1	0	0	0.093746	0.104828	0.068819	0.044685	0
protein_co	otoancorin	0	0	0	2	8	0	0	0	0	0.019762	0.102655	0
protein_co	potassium_	184	200	164	90	149	134	3.313314	4.244063	3.891557	1.402007	3.014256	2.398055
protein_co	family_with	77	56	91	114	127	100	0.853172	0.731208	1.328685	1.092732	1.580879	1.101173
protein_co	amyotroph	10	10	8	4	6	2	0.255137	0.300664	0.268967	0.088287	0.171979	0.050712
protein_co	amyotroph	6	0	4	0	7	2	0.057628	0	0.050626	0	0.075532	0.019091
protein_co	transmemb	361	275	299	1265	756	879	3.417686	3.068066	3.73019	10.36045	8.040736	8.270342
protein_co	frizzled_fan	712	563	548	351	302	269	9.788104	9.120824	9.927364	4.174348	4.664172	3.675196
protein_co	sperm_assc	15	19	11	31	10	18	0.11469	0.171197	0.110831	0.20505	0.085898	0.136778
protein_co	DEP_domai	7	9	5	3	1	0	0.144253	0.218563	0.135779	0.053483	0.023151	0
protein_co	formin_2	277	262	286	36	30	42	2.279244	2.540501	3.101072	0.256257	0.27732	0.343455
protein_co	ring_finger_	730	614	606	668	724	583	9.818833	9.732232	10.74099	7.772782	10.94018	7.793189
protein_co	peroxisome	32	30	48	47	72	45	0.160306	0.177104	0.316866	0.203686	0.405211	0.224038
protein_co	engulfment	103	64	64	1635	1333	1207	1.355774	0.992744	1.110107	18.6179	19.71193	15.78945
protein_co	solute_carr	273	195	314	251	313	229	1.788724	1.505644	2.711098	1.422714	2.303956	1.491166
protein_co	LSM11_U7_	173	109	153	322	256	264	1.391068	1.032847	1.62117	2.239861	2.312551	2.109676
protein_co	mediator_c	117	129	97	272	175	248	2.578725	3.350548	2.817252	5.186221	4.333175	5.432258
protein_co	family_with	1	1	0	0	0	0	0.025222	0.029723	0	0	0	0
protein_co	Ras-related	2671	1997	1803	1725	1242	1369	85.80424	75.59969	76.32476	47.93878	44.82348	43.7067
protein_co	acid_phosp	279	209	258	179	170	143	3.552318	3.135891	4.328746	1.971622	2.431675	1.809478
protein_co	adenylate_c	3	1	1	4	6	5	0.026747	0.010507	0.011749	0.030851	0.060097	0.044303
protein_co	RAS_p21_p	184	148	154	410	342	294	1.735152	1.644707	1.913706	3.344772	3.623221	2.755349
protein_co	required_fo	438	459	378	745	476	454	12.5071	15.44551	14.22358	18.40355	15.26998	12.88392
protein_co	Src-like-ada	3	3	6	1	2	5	0.046076	0.054297	0.121433	0.013287	0.034509	0.076319
protein_co	transmemb	112	129	68	177	117	144	2.008601	2.726293	1.607013	2.746073	2.357277	2.566539
protein_co	von_Hippel	690	539	476	1849	1202	1351	21.66624	19.94483	19.69592	50.22668	42.40217	42.15989
protein_co	RAB39B_m	15	6	10	19	24	20	0.226566	0.106798	0.199039	0.248268	0.407253	0.300223
protein_co	chloride_in	62	75	50	13	15	7	1.236287	1.762365	1.313809	0.224251	0.336022	0.138719
protein_co	AF4/FMR2_	759	665	779	241	202	206	2.923193	3.018175	3.953557	0.802963	0.87401	0.788484

protein_co mitochond	175	171	196	175	147	112	2.32081	2.67242	3.425251	2.007718	2.19012	1.476146
protein_co glutamate_	37	20	18	255	269	167	0.37554	0.239217	0.240748	2.239019	3.067297	1.684537
protein_co vacuolar_p	679	681	741	919	658	620	7.327137	8.660017	10.53701	8.579126	7.976998	6.649146
protein_co kinesin_fan	30	31	27	3	2	9	0.272704	0.332078	0.323422	0.023591	0.020424	0.081306
protein_co transmemb	119	95	123	90	95	131	1.718957	1.617144	2.341305	1.124666	1.541668	1.880611
protein_co N-acetyltra	0	0	0	4	3	0	0	0	0	0.138575	0.134968	0
protein_co melanoma_	2	3	2	0	0	0	0.050134	0.088619	0.066064	0	0	0
protein_co pleckstrin_	1043	928	1141	204	163	149	4.722266	4.951322	6.807484	0.799023	0.829092	0.670443
protein_co chromoson	343	285	242	407	386	367	4.396794	4.305207	4.087824	4.513355	5.558766	4.675389
protein_co mitochond	310	311	281	685	487	535	5.09048	6.018171	6.080485	9.730847	8.98411	8.73093
protein_co ELM2_and_	1130	1001	828	1026	1248	1206	7.393811	7.718467	7.13929	5.807648	9.17389	7.842361
protein_co tetratricop	13	3	4	34	11	11	0.102936	0.027993	0.041737	0.232899	0.097851	0.086562
protein_co guanine_nu	30	9	24	119	105	105	0.639899	0.226225	0.674585	2.195838	2.516104	2.225816
protein_co family_witl	118	86	100	65	42	57	1.531888	1.31568	1.710723	0.729997	0.612552	0.73541
protein_co guanine_nu	875	774	1031	1452	1252	1180	7.084167	7.384631	10.99953	10.16975	11.38765	9.494507
protein_co WNT_inhib	3	0	1	19	32	24	0.070966	0	0.031172	0.38882	0.850415	0.564226
protein_co G_protein-(	0	0	4	9	9	0	0	0	0.056707	0.083761	0.108775	0
protein_co matrix_met	519	452	668	312	284	281	2.37726	2.439804	4.032001	1.236309	1.461426	1.279161
protein_co adenosine_	320	279	248	1917	1183	1370	8.133038	8.356302	8.30595	42.14906	33.77821	34.60454
protein_co potassium_	3221	2467	2888	3804	3158	3387	14.96209	13.50448	17.67802	15.28639	16.48021	15.63603
protein_co deoxycytid	187	135	186	735	443	416	3.645054	3.10101	4.777603	12.39403	9.700969	8.058706
protein_co ADAM_met	104	101	107	80	82	51	0.9457	1.082302	1.282149	0.629322	0.837689	0.460893
protein_co dpy-19-like	454	430	499	541	480	442	3.878524	4.328986	5.617537	3.998258	4.606816	3.752688
protein_co NADH_dehy	109	64	62	395	286	330	2.263856	1.566424	1.696871	7.097123	6.673249	6.811548
protein_co DNA-damag	378	351	262	841	475	544	8.909927	9.749819	8.138014	17.1491	12.57839	12.74356
protein_co chromoson	43	34	42	79	51	65	0.682802	0.636228	0.878842	1.085217	0.9098	1.025769
protein_co protein_ph	1	0	1	1	0	0	0.012726	0	0.01677	0.011009	0	0
protein_co chromoson	0	0	0	1	2	3	0	0	0	0.02808	0.072932	0.096776
protein_co ADAMTS-lik	0	0	0	224	235	197	0	0	0	1.39844	1.90524	1.412891
protein_co ADP-ribosy	1	2	0	0	0	0	0.033571	0.079122	0	0	0	0
protein_co WAS_prote	198	156	152	295	213	184	2.721266	2.526606	2.752861	3.507445	3.288777	2.513236
protein_co chemokine_	3	1	1	2	5	2	0.132022	0.05186	0.057991	0.076141	0.247198	0.087471
protein_co N-6_adenin	169	109	116	180	112	116	1.83906	1.397793	1.66342	1.694512	1.36923	1.254518
protein_co RWD_doma	364	225	250	204	173	214	6.228352	4.536923	5.636981	3.019708	3.325576	3.63911
protein_co ubiquitin_s	553	559	480	1058	763	751	7.633995	9.093805	8.73178	12.635	11.83315	10.3033
protein_co chaperonin	3626	2962	2781	9747	7087	7865	95.74267	92.16581	96.76393	222.6444	210.2273	206.3888
protein_co MAP3K7_C	17	8	15	45	15	18	0.430003	0.238462	0.499976	0.984687	0.426249	0.452486
protein_co N(alpha)-ac	0	3	1	0	0	0	0	0.092931	0.034639	0	0	0
protein_co BTB_and_C	542	469	546	584	521	465	4.973829	5.071909	6.602661	4.636256	5.371287	4.240862
protein_co tetraspanin	2	4	5	10	6	6	0.055465	0.130723	0.182722	0.23991	0.186933	0.165366
protein_co T-cell_lymp	197	200	209	490	641	512	1.448524	1.732992	2.025073	3.11687	5.295009	3.741444
protein_co SR-related_	678	548	514	1590	1439	1432	8.560456	8.153703	8.55195	17.3671	20.4116	17.96883
protein_co retinitis_pi	91	77	65	105	108	143	1.010621	1.007731	0.951251	1.008786	1.347472	1.578311
protein_co cyclin-depe	226	198	171	167	111	124	2.174208	2.244734	2.167821	1.389863	1.199678	1.185561

protein_co	polycomb_	102	88	83	344	249	266	2.421516	2.461937	2.596571	7.064943	6.641033	6.275936
protein_co	ankyrin_rep	311	225	160	417	269	260	10.00891	8.533276	6.785486	11.60981	9.725849	8.315899
protein_co	SWI5-depe	108	78	45	215	202	172	3.611893	3.074064	1.983163	6.220319	7.589473	5.716751
protein_co	sortilin-rela	3	1	1	120	129	158	0.027588	0.010837	0.012118	0.954641	1.332707	1.443985
protein_co	sideroflexin	176	169	114	705	582	684	3.628355	4.105735	3.096968	12.5733	13.47936	14.01402
protein_co	chromoson	1138	1012	767	1661	1062	1331	36.31516	38.05689	32.25343	45.85412	38.07319	42.21175
protein_co	fucosyltran	3	0	0	0	0	1	0.050629	0	0	0	0	0.016772
protein_co	fibroblast_g	12	8	10	19	9	16	0.319885	0.25131	0.351275	0.438157	0.269528	0.42388
protein_co	protocadhe	3	9	5	674	536	564	0.03506	0.123949	0.077001	6.81423	7.037327	6.550623
protein_co	SH3_domai	205	184	189	621	431	486	1.935599	2.047323	2.351571	5.072431	4.571807	4.560447
protein_co	growth_dif	52	66	49	2310	2829	2752	0.744639	1.113765	0.924642	28.61657	45.51187	39.16523
protein_co	ubiquinol-c	1973	1785	1385	1523	1085	1696	18.73589	19.97526	17.33133	12.51152	11.57513	16.006
protein_co	MTERF_dor	155	159	101	548	217	373	5.366811	6.487671	4.608301	16.41452	8.44099	12.83521
protein_co	phosphatid	2009	1684	1550	2894	1943	2279	20.54442	20.29379	20.88721	25.60209	22.32214	23.16156
protein_co	protein_ph	293	219	206	151	86	112	4.461234	3.929512	4.133229	1.988966	1.471075	1.694787
protein_co	ribosomal_	1028	978	852	1102	797	983	48.20491	54.04358	52.64687	44.70363	41.9861	45.81011
protein_co	potassium_	10	7	11	3	3	3	0.101439	0.083678	0.147039	0.026326	0.034188	0.030244
protein_co	family_with	33	27	27	60	27	26	0.703606	0.678401	0.758602	1.106699	0.646738	0.550932
protein_co	suppressor_	327	302	239	859	578	675	6.969285	7.584982	6.712329	15.83787	13.8394	14.2973
protein_co	family_with	429	381	340	769	714	724	5.348961	5.598145	5.58632	8.294715	10.00137	8.971402
protein_co	eukaryotic_	355981	312037	248745	261130	192699	206876	4243.636	4383.535	3907.514	2692.967	2580.714	2450.931
protein_co	F-box_prot	16	14	13	25	11	19	0.27484	0.283397	0.294264	0.371503	0.212276	0.324357
protein_co	hexokinase	0	4	0	22	17	15	0	0.067647	0	0.27313	0.274083	0.213936
protein_co	hexokinase_	3494	3041	2523	4339	4322	4766	46.33663	47.52532	44.09137	49.77992	64.39251	62.81527
protein_co	trypsin_do	172	127	97	350	307	401	2.498861	2.174325	1.857036	4.398907	5.010732	5.789856
protein_co	PHD_finger	779	571	684	946	1005	933	8.665903	7.485479	10.02691	9.103964	12.56005	10.31496
protein_co	CD109_mo	4125	3761	4462	355	371	307	23.22961	24.95907	33.11177	1.729456	2.347151	1.71817
protein_co	leucine_ric	29	26	24	0	0	0	0.469507	0.496049	0.512024	0	0	0
protein_co	nodal_grov	1	1	0	5	5	8	0.031796	0.03747	0	0.137534	0.178606	0.2528
protein_co	ubiquitin-c	292	264	224	161	107	90	9.827572	10.47067	9.934504	4.687618	4.045724	3.01034
protein_co	zinc_finger_	1575	1418	1278	2614	2232	2393	17.87014	18.95967	19.1079	25.6576	28.45055	26.98359
protein_co	mediator_c	428	352	279	550	373	531	14.95627	14.49537	12.8475	16.62667	14.64325	18.44096
protein_co	zinc_finger_	2523	2140	1963	2239	1779	2363	39.68215	39.66421	40.68488	30.46457	31.43424	36.93613
protein_co	neuroplasti	2097	1886	1808	2984	2232	2443	39.40975	41.76899	44.7753	48.514	47.12469	45.62873
protein_co	K(lysine)_ac	649	602	621	190	210	190	4.146097	4.532088	5.227826	1.050053	1.507173	1.206307
protein_co	sterile_alph	655	561	629	576	426	415	5.112998	5.160648	6.470231	3.889733	3.73588	3.219527
protein_co	RAB11_fam	120	141	118	1057	1062	1051	0.81333	1.12619	1.053907	6.197599	8.086471	7.079422
protein_co	unc-5_hom	13	5	16	21	63	47	0.079454	0.036012	0.128863	0.111034	0.432577	0.285484
protein_co	glycine-N-a	27	18	14	5	8	7	0.873721	0.686418	0.596996	0.139972	0.290836	0.225121
protein_co	UTP14_U3_	559	482	382	899	745	819	11.8947	12.08637	10.71124	16.54872	17.80931	17.3195
protein_co	apoptosis-i	623	594	497	1002	818	979	14.59391	16.39748	15.34175	20.30553	21.52712	22.79166
protein_co	mitogen-ac	28	8	10	304	229	285	0.722392	0.243227	0.339977	6.785023	6.63742	7.307507
protein_co	BCL2-assoc	405	356	383	592	391	440	4.814979	4.987656	6.0003	6.088693	5.222341	5.198783
pseudogen	aquaporin_	0	0	2	0	0	0	0	0	0.059348	0	0	0

IG_V_pseuc	immunoglc	3	2	20	9	5	5	0.45378	0.356501	3.986473	1.177686	0.849656	0.751629
protein_co	WD_repeat	96	73	63	265	198	212	1.451267	1.300487	1.255022	3.465651	3.362716	3.185088
protein_co	WDYHV_m	148	106	108	311	207	267	5.255042	4.435345	5.053276	9.552957	8.25722	9.421832
protein_co	ATPase_fam	144	115	170	1565	1066	1087	1.369902	1.289234	2.131134	12.87966	11.39287	10.27699
protein_co	F-box_prot	19	16	26	6	14	11	0.149152	0.148014	0.268957	0.040746	0.123467	0.085818
protein_co	non-SMC_e	355	248	246	539	319	364	15.72724	12.94741	14.36131	20.65741	15.87683	16.02637
protein_co	zinc_finger_	199	165	168	296	271	287	2.970188	2.902164	3.304266	3.821955	4.544114	4.257184
protein_co	proline_ric	543	498	392	596	524	681	12.41233	13.41498	11.80795	11.7859	13.45655	15.47071
protein_co	fibrosin	2317	1802	1570	1825	1925	2643	23.58929	21.61975	21.06314	16.07365	22.01753	26.7421
protein_co	ferric-chela	153	99	88	73	109	96	2.993338	2.282478	2.268725	1.235521	2.395741	1.866574
protein_co	phosphoryl	295	220	181	783	408	573	2.823137	2.481074	2.282566	6.482383	4.38651	5.44972
protein_co	hippocamp	779	504	653	1151	847	790	14.85093	11.3228	16.40455	18.98255	18.14048	14.96763
protein_co	spindle_ass	43	39	38	378	239	280	0.573128	0.612568	0.667423	4.358506	3.578737	3.708946
protein_co	integrin_al	6	0	0	0	0	0	0.081198	0	0	0	0	0
protein_co	G_protein-	0	0	2	0	0	0	0	0	0.01405	0	0	0
protein_co	Zic_family_	22	7	18	274	212	220	0.335746	0.12589	0.361989	3.61744	3.634735	3.336723
protein_co	mitochond	284	242	228	639	537	626	4.939304	4.959865	5.225371	9.614159	10.4923	10.8201
protein_co	vacuolar_p	567	502	540	729	574	465	5.947601	6.205397	7.46427	6.615297	6.764251	4.84754
protein_co	galactokina	133	187	135	206	155	137	2.185336	3.620889	2.923043	2.928173	2.861194	2.237159
protein_co	UDP-GlcNA	0	9	4	16	17	17	0	0.151508	0.075298	0.197729	0.272825	0.241349
protein_co	MPV17_mi	0	0	0	21	17	11	0	0	0	0.446715	0.469619	0.268813
protein_co	BUB1_mitc	233	211	232	1169	1058	927	3.311477	3.533909	4.344988	14.37286	16.89276	13.09348
protein_co	phosphodi	200	128	137	273	155	218	9.011233	6.79628	8.134102	10.64094	7.845759	9.761585
protein_co	eukaryotic_	5656	5029	4779	6442	4750	5036	56.21067	58.89767	62.58658	55.38512	53.03372	49.73988
protein_co	bromodom	451	362	416	744	696	706	5.041467	4.768657	6.127856	7.19476	8.740549	7.843226
protein_co	RNA_pseud	418	437	305	1119	754	1016	8.883716	10.94478	8.541871	20.57366	18.00275	21.4596
protein_co	somatostat	0	0	0	1	3	2	0	0	0	0.074108	0.288718	0.170272
protein_co	TatD_DNas	1005	895	850	997	851	964	9.959884	10.45246	11.10048	8.547643	9.47473	9.494561
protein_co	ghrelin/obe	10	9	7	10	9	11	0.371516	0.394028	0.342697	0.321396	0.375637	0.406144
protein_co	SEC13_hon	4166	3430	2816	4063	2708	3475	92.90319	90.13897	82.75206	78.38288	67.84363	77.01509
pseudogen	family_with	3	0	0	3	0	4	0.178453	0	0	0.154378	0	0.236468
protein_co	endo/exon	301	249	247	278	195	200	5.707464	5.563949	6.171752	4.560206	4.153941	3.768915
protein_co	N-terminal_	964	827	696	933	629	706	21.28237	21.5157	20.24823	17.81917	15.60065	15.49021
protein_co	nicotinami	7	8	7	1252	1450	1374	0.06544	0.088134	0.086234	10.12542	15.22869	12.76562
protein_co	zinc_finger_	288	241	236	217	160	178	3.102769	3.059716	3.350455	2.022459	1.936538	1.905841
protein_co	ATPase_Ca+	2	0	4	0	0	0	0.011634	0	0.030662	0	0	0
protein_co	lysozyme-li	0	0	0	0	2	0	0	0	0	0	0.131584	0
protein_co	smg-1_hom	1656	1364	1925	1724	1886	1569	5.440291	5.2806	8.333498	4.899616	6.960694	5.122646
protein_co	FCH_domai	328	362	343	271	274	225	3.486177	4.534101	4.804016	2.491769	3.271713	2.376664
protein_co	RNA_bindi	572	464	437	3954	2336	2471	9.737057	9.308008	9.802751	58.22793	44.67387	41.80364
protein_co	transmemb	36	6	25	12	9	3	1.241613	0.243861	1.13621	0.358037	0.348719	0.102829
protein_co	TIMP_meta	158	95	103	2	5	2	5.069501	3.592021	4.35492	0.055514	0.18023	0.063775
polymorph	synapsin_II	22	16	15	56	37	49	0.298871	0.256147	0.268527	0.658132	0.564693	0.661557
protein_co	neuregulin_	65	38	63	305	144	203	1.100468	0.75815	1.405528	4.467114	2.738897	3.415623

protein_co	chromoson	301	254	224	664	405	488	4.168255	4.145039	4.087621	7.95461	6.300745	6.716102
protein_co	carnitine_p	122	99	89	291	204	198	2.087525	1.996246	2.006765	4.307525	3.921489	3.367027
protein_co	NECAP_end	1524	1166	1157	1331	1069	1330	17.46743	15.74888	17.4748	13.1973	13.76483	15.14975
protein_co	low_densit	111	125	156	356	276	269	1.315525	1.745795	2.436327	3.649969	3.674805	3.168386
protein_co	CUB_doma	1	0	0	0	0	0	0.019442	0	0	0	0	0
protein_co	PAX_intera	204	199	186	521	603	523	1.958289	2.251162	2.35285	4.326606	6.502988	4.98951
protein_co	STEAP_fami	82	105	97	41	14	20	0.631625	0.953108	0.984583	0.273207	0.12115	0.153104
protein_co	single_stra	855	676	668	903	848	932	15.53881	14.47789	15.9979	14.19719	17.31396	16.83361
protein_co	claudin_12	403	291	380	681	489	530	5.947929	5.061285	7.39059	8.695025	8.108091	7.77403
protein_co	matrix_met	37529	30799	26968	14649	13934	20137	532.3747	514.8659	504.1201	179.7717	222.0625	283.8931
protein_co	frizzled_fan	1283	1020	959	302	320	305	15.64692	14.65918	15.41188	3.186194	4.384311	3.696679
protein_co	GATA_zinc_	648	490	439	514	452	420	10.20701	9.095504	9.112193	7.004058	7.998546	6.574799
protein_co	sushi_dom	0	0	0	5	0	6	0	0	0	0.191627	0	0.264171
processed_	-	14	6	6	4	13	9	0.293651	0.148307	0.16584	0.072581	0.306334	0.18761
protein_co	transmemb	11	10	3	35	18	18	0.620843	0.665114	0.223124	1.708914	1.141329	1.009651
protein_co	C-type_lect	2	3	1	4	2	5	0.03315	0.058598	0.021842	0.057356	0.037242	0.082364
protein_co	dehydroger	206	168	141	212	201	255	7.557758	7.263436	6.816786	6.728599	8.284587	9.297701
protein_co	chromoson	0	0	0	0	1	0	0	0	0	0	0.015801	0
protein_co	C-type_lect	0	0	0	0	2	3	0	0	0	0	0.032501	0.043126
protein_co	armadillo_	11	18	8	9	6	4	0.464395	0.895518	0.445061	0.3287	0.284574	0.167828
protein_co	DEAD_(Asp	156	150	102	382	189	252	2.439101	2.76378	2.101552	5.166917	3.319831	3.915753
protein_co	ST3_beta-g	799	625	549	487	503	486	7.913911	7.295104	7.165583	4.172884	5.597079	4.78399
protein_co	fucokinase	175	134	122	291	251	280	2.087108	1.883297	1.917351	3.002361	3.363022	3.318751
protein_co	interleukin	45	43	35	0	0	0	1.339148	1.507966	1.372521	0	0	0
protein_co	dehydroger	380	293	264	473	352	454	7.562999	6.872032	6.923875	8.143941	7.870497	8.979992
protein_co	calcium_ch	33	47	38	8	6	4	0.226273	0.379772	0.34335	0.047454	0.046219	0.027258
protein_co	arylsulfatas	236	156	187	50	52	58	5.789655	4.509956	6.045289	1.061142	1.433155	1.414094
protein_co	v-kit_Hardy	16	10	9	279	198	230	0.163335	0.1203	0.12107	2.463921	2.270774	2.333442
protein_co	HYDIN_axo	1	0	0	82	47	47	0.003368	0	0	0.238915	0.177834	0.157317
protein_co	aminoadip	150	155	170	183	113	172	2.212019	2.693621	3.303554	2.334596	1.872083	2.520785
protein_co	zinc_finger_	26	21	15	47	35	38	0.428405	0.407763	0.325692	0.66995	0.647886	0.622264
protein_co	calcium_ch	152	106	96	80	75	37	2.189668	1.799483	1.822388	0.996983	1.213794	0.52972
protein_co	ring_finger_	659	583	646	704	598	543	5.900239	6.1512	7.621695	5.452804	6.014984	4.83163
protein_co	cyclin_B2	449	313	359	2112	1512	1629	15.27667	12.54972	16.09577	62.16407	57.79408	55.08245
protein_co	family_with	3	0	5	28	24	15	0.045836	0	0.100669	0.370092	0.411954	0.227766
protein_co	myosin_IE	2565	2073	1994	880	870	913	21.92696	20.88322	22.46213	6.507837	8.355248	7.756601
protein_co	adaptor_pr	512	512	522	1050	777	768	4.474379	5.272783	6.011296	7.938074	7.62839	6.670121
protein_co	melanoma_	902	721	900	393	329	380	11.08467	10.4414	14.5745	4.178034	4.542149	4.640979
protein_co	actin_filam	76	73	50	242	211	193	0.963255	1.090329	0.835088	2.65342	3.00441	2.431054
protein_co	TSC22_dom	1377	1200	1035	278	177	199	32.17112	33.03852	31.86452	5.618754	4.645736	4.620563
protein_co	Down_sync	826	628	647	1300	900	990	7.742433	6.936879	7.991651	10.54153	9.477395	9.222364
protein_co	dual-specifi	846	651	758	926	868	834	7.015677	6.361907	8.283297	6.643137	8.086638	6.873452
protein_co	potassium_	10	14	18	25	21	17	0.208923	0.344684	0.495556	0.451844	0.492894	0.352975
protein_co	potassium_	37	21	17	20	9	24	0.672209	0.449603	0.406992	0.314337	0.183694	0.433335

protein_co	v-ets_eryth	5	0	5	1	1	3	0.052583	0	0.069292	0.009098	0.011815	0.031355
protein_co	v-ets_eryth	1485	1329	1132	782	541	574	19.97393	21.06537	20.06403	9.099274	8.174916	7.672882
protein_co	tetraspanin	19	7	8	189	155	144	0.237853	0.103267	0.131971	2.046818	2.179893	1.79154
protein_co	Leber_cong	21	18	17	11	11	12	0.433604	0.437979	0.462549	0.196485	0.255162	0.246244
protein_co	solute_carr	1697	1507	1309	2211	1644	2228	43.97497	46.01973	44.69904	49.56504	47.86021	57.37842
protein_co	transmemb	655	562	515	582	717	642	6.228912	6.298168	6.453761	4.78803	7.660182	6.06758
protein_co	myxovirus_	19	6	14	14	15	9	0.289879	0.107875	0.281466	0.184779	0.257101	0.136463
protein_co	cAMP_resp	4297	3508	2634	989	555	716	84.66224	81.45	68.38723	16.85713	12.28475	14.01997
protein_co	C2_calcium	304	290	302	83	71	88	2.536495	2.851449	3.32049	0.599103	0.66553	0.729714
protein_co	TGF-beta_a	357	236	272	714	597	559	2.366337	1.843434	2.375812	4.094205	4.445614	3.682391
protein_co	solute_carr	3104	2565	2119	2989	2774	3288	38.21601	37.21501	34.3787	31.83556	38.36888	40.23139
protein_co	chromoson	11	11	12	16	8	20	0.273404	0.32219	0.393033	0.344029	0.223384	0.494029
protein_co	PALM2-AKA	0	3	0	0	0	0	0	0.024932	0	0	0	0
protein_co	zinc_finger_	1061	883	1007	375	500	389	6.166472	6.047685	7.712331	1.885453	3.264679	2.246884
protein_co	diacylglyce	158	137	127	6	1	7	1.62484	1.66028	1.721044	0.053379	0.011553	0.071542
protein_co	chromoson	185	190	133	155	123	97	2.13938	2.589268	2.026762	1.55064	1.597977	1.114802
protein_co	SVOP-like	0	0	0	45	14	33	0	0	0	0.357742	0.144534	0.301382
protein_co	sorting_nex	40	47	29	47	38	45	0.570331	0.789718	0.544879	0.579733	0.608695	0.63766
protein_co	ubinuclein_	365	305	363	388	400	362	1.337912	1.317473	1.75338	1.230352	1.64719	1.318721
protein_co	v-raf_murin	156	126	193	110	126	129	3.330159	3.169699	5.429159	2.031403	3.02176	2.736779
protein_co	solute_carr	1	0	0	31	18	18	0.012844	0	0	0.344436	0.25972	0.229756
protein_co	aggrecan	5	15	9	64	49	53	0.029944	0.105862	0.071026	0.331576	0.329674	0.315446
protein_co	proteasom	255	173	137	425	328	430	9.705215	7.759222	6.871006	13.9932	14.02452	16.26459
protein_co	calcium_bi	15	8	3	2	4	0	0.260536	0.163747	0.068665	0.030052	0.078052	0
protein_co	WD_repeat	571	492	431	354	292	230	6.6879	6.790877	6.652207	3.586905	3.84225	2.677264
protein_co	solute_carr	770	596	632	949	734	694	11.68709	10.66029	12.64059	12.46077	12.51586	10.46851
protein_co	adaptor-rel	196	192	148	223	130	143	1.761405	2.033346	1.752668	1.733688	1.312488	1.27717
protein_co	formin-like	2546	2323	2605	1161	1010	930	24.17718	25.99582	32.59791	9.537673	10.77501	8.776873
protein_co	GRB2_asso	144	129	93	168	120	197	1.483749	1.566372	1.262745	1.497512	1.389083	2.017316
protein_co	signal_pept	619	501	439	1214	900	998	7.900307	7.535259	7.383337	13.40402	12.90461	12.65883
protein_co	dihydropyr	10	1	3	199	219	229	0.101634	0.011977	0.040179	1.749661	2.500523	2.313038
protein_co	dynein_reg	0	3	6	0	1	1	0	0.075136	0.168037	0	0.023876	0.021122
protein_co	RAB28_mer	143	183	159	379	245	266	4.182631	6.30771	6.128377	9.589937	8.050608	7.732231
protein_co	family_with	324	238	262	385	332	428	6.203574	5.370083	6.610481	6.377063	7.141412	8.144236
protein_co	tumor_nec	1	1	0	0	0	0	0.012442	0.014662	0	0	0	0
protein_co	pantothena	369	309	265	762	526	683	7.374567	7.277391	6.978962	13.17432	11.80987	13.56565
protein_co	multiple_E	12	33	16	19	38	26	0.103082	0.334057	0.181115	0.141194	0.366718	0.221964
protein_co	chromoson	284	216	216	532	390	389	5.935745	5.320075	5.94902	9.619036	9.157366	8.080089
protein_co	peroxisoma	957	865	712	1289	870	1159	24.85993	26.47958	24.37265	28.96702	25.38962	29.92134
protein_co	RER1_reten	2601	2255	1801	2842	2284	2447	55.77138	56.98029	50.88849	52.7179	55.01944	52.14523
protein_co	Ras_associa	25	30	12	71	37	96	0.233467	0.330152	0.147673	0.573597	0.388183	0.890977
protein_co	v-ski_sarco	2458	2033	1828	2604	2162	2249	23.1835	22.59652	22.71999	21.24717	22.90877	21.08124
protein_co	WD_repeat	1158	1036	874	1670	1184	1342	13.69653	14.44006	13.62223	17.08762	15.73268	15.77481
protein_co	low_densit	291	219	224	364	308	254	3.298893	2.925677	3.346247	3.569765	3.922609	2.861664

protein_co	ArfGAP_wit	926	747	688	786	954	885	7.986862	7.592642	7.819671	5.864767	9.244058	7.586092
protein_co	keratinocyt	21	8	10	10	13	16	1.16293	0.522073	0.729741	0.479068	0.808773	0.88057
protein_co	ankyrin_rep	9	23	16	26	47	30	0.379052	1.141542	0.887997	0.947312	2.223841	1.255705
protein_co	platelet-act	175	185	164	430	388	351	2.587175	3.223047	3.194967	5.49945	6.444193	5.157088
protein_co	exostosin-li	17	20	26	8	14	11	0.224159	0.310773	0.451767	0.091256	0.207388	0.144148
protein_co	solute_carr	0	0	0	2	3	9	0	0	0	0.029576	0.057613	0.152898
protein_co	brain_and_	842	772	605	631	341	380	24.06929	26.00612	22.78984	15.60427	10.95102	10.79554
protein_co	tripartite_r	3	2	0	3	3	0	0.08973	0.070495	0	0.077625	0.100807	0
protein_co	WD_repeat	62	53	56	22	37	19	0.702105	0.707283	0.835667	0.215524	0.470718	0.213833
protein_co	mitochond	1182	983	736	1397	1024	1242	31.78073	31.14634	26.07708	32.4942	30.9311	33.18774
protein_co	dual_specif	6	8	6	11	7	11	0.188179	0.295676	0.247974	0.298453	0.246642	0.342864
protein_co	grainyhead	5	0	10	841	833	868	0.092264	0	0.243162	13.42519	17.26854	15.91809
protein_co	UBX_doma	313	264	193	424	261	451	6.262483	6.224626	5.088554	7.338902	5.866672	8.967852
protein_co	NLR_family	4	0	0	0	1	0	0.058369	0	0	0	0.016394	0
protein_co	protein_tyr	92	75	102	131	104	83	1.078276	1.035882	1.57535	1.328239	1.369381	0.966785
protein_co	UDP-N-acet	6	5	0	113	49	87	0.116226	0.114138	0	1.893625	1.066345	1.674871
protein_co	NCK_adapt	243	214	210	339	243	249	5.353584	5.555961	6.096666	6.461019	6.014419	5.451893
protein_co	4-hydroxyp	5	2	1	19	23	7	0.154889	0.073011	0.040821	0.509174	0.800437	0.215505
protein_co	rhophilin_F	9	6	12	256	228	274	0.12937	0.101636	0.227304	3.183416	3.681919	3.914268
protein_co	tumor_pro	736	573	597	666	510	548	16.14108	14.80869	17.25297	12.63549	12.56533	11.94387
protein_co	leucine_ric	6	5	2	11	3	0	0.15663	0.153816	0.0688	0.248416	0.087982	0
protein_co	AhpC/TSA_a	189	210	154	361	195	278	3.494882	4.576117	3.752548	5.774853	4.050927	5.108874
protein_co	xanthine_d	7	3	3	47	26	26	0.065152	0.032905	0.036795	0.378437	0.271866	0.2405
protein_co	XK_Kell_blo	208	209	151	312	215	285	4.090537	4.843624	3.913171	5.308045	4.75012	5.57021
protein_co	cyclin_M4	158	163	100	270	254	264	1.742641	2.118583	1.453402	2.576188	3.147267	2.893773
protein_co	eyes_absen	417	378	332	701	589	536	3.628002	3.875524	3.806312	5.276094	5.756995	4.634533
protein_co	DAZ_intera	130	118	134	123	180	140	1.97032	2.107573	2.67629	1.61273	3.064891	2.10878
protein_co	thymosin_b	295	263	204	214	156	211	22.79941	23.95325	20.77622	14.30798	13.54488	16.20666
protein_co	Fanconi_an	226	180	191	463	376	439	2.609523	2.449246	2.906169	4.62484	4.877414	5.037638
protein_co	muscle_RAS	531	522	513	428	319	286	6.194726	7.176376	7.886418	4.319509	4.180877	3.315914
protein_co	WAS_prote	3796	2913	2867	3923	4114	3869	35.46841	32.07474	35.30027	31.71004	43.1846	35.92724
protein_co	abhydrolas	93	86	92	506	381	457	2.367073	2.579493	3.085684	11.14146	10.89439	11.55991
protein_co	extended_s	9	7	4	32	21	22	0.103132	0.094527	0.060401	0.317222	0.270345	0.250543
protein_co	Fas_apoptc	119	97	82	413	247	298	1.993033	1.914461	1.80974	5.983849	4.647438	4.960135
protein_co	family_witl	236	166	148	1378	1005	1335	5.276214	4.373464	4.360205	26.65156	25.2421	29.66206
protein_co	calsyntenin	21	12	32	267	259	307	0.227727	0.15335	0.457277	2.504774	3.155318	3.308585
protein_co	collectin_s	10876	9226	8716	2034	1732	1644	122.0145	121.9727	128.8529	19.74041	21.82926	18.32962
protein_co	ring_finger_	120	97	66	37	23	40	1.618991	1.542204	1.173389	0.431845	0.34861	0.536331
protein_co	cullin_4B	1387	1219	1331	1319	1076	1065	14.97943	15.51421	18.94225	12.32329	13.0551	11.43084
protein_co	G_protein-r	614	561	441	131	99	154	7.963197	8.57411	7.536895	1.469784	1.442459	1.984949
protein_co	solute_carr	48	29	21	25	39	20	0.632603	0.450397	0.364707	0.285032	0.577436	0.261957
protein_co	G_protein-r	224	231	205	150	137	101	2.507672	3.047487	3.024207	1.452704	1.723028	1.123709
protein_co	rhomboid_	25	11	8	6	4	22	0.621665	0.322341	0.262145	0.129072	0.111744	0.543687
protein_co	autism_sus	722	708	671	759	902	806	6.192029	7.155437	7.583211	5.631195	8.690633	6.869743

protein_co	shroom_fa	67	55	54	138	213	169	0.371185	0.359075	0.394225	0.661391	1.325698	0.930491
protein_co	histone_clu	688	596	472	190	110	149	46.16401	47.12685	41.73418	11.02889	8.291953	9.935987
protein_co	cell_divisio	86	54	59	310	210	264	2.139533	1.583147	1.934226	6.671833	5.869334	6.527307
protein_co	histone_clu	226	215	184	76	99	145	11.57124	12.9723	12.41436	3.366264	5.694503	7.378179
protein_co	MIT_microt	308	291	217	740	508	576	4.986491	5.551936	4.629551	10.36428	9.239684	9.267796
protein_co	eukaryotic_	2588	2124	1929	7317	3982	5034	29.05244	28.09829	28.53549	71.05823	50.21906	56.16182
protein_co	RIB43A_do	2	11	9	25	21	40	0.054326	0.352111	0.32215	0.587467	0.640839	1.079816
protein_co	thymosin_b	270	201	208	218	147	226	6.272079	5.502384	6.367162	4.38094	3.836314	5.217541
protein_co	chromoson	1	0	0	3	2	1	0.022216	0	0	0.057657	0.049917	0.022079
protein_co	CCR4-NOT_	557	491	440	2348	1609	1802	11.34595	11.78622	11.81064	41.37585	36.8206	36.47961
protein_co	potassium_	11	4	9	0	2	0	0.079578	0.034101	0.085798	0	0.016255	0
protein_co	tetraspanin	1	0	0	17	13	15	0.028115	0	0	0.413479	0.410614	0.419124
protein_co	neuregulin_	1	0	0	0	1	0	0.01422	0	0	0	0.015975	0
protein_co	adenosylho	268	265	288	348	384	299	2.806208	3.269926	3.973858	3.152298	4.517158	3.111472
protein_co	UDP-Gal:be	2823	2226	2077	2460	2540	2578	31.65024	29.41023	30.6858	23.85966	31.99255	28.72491
protein_co	CD1d_mole	0	0	0	5	0	7	0	0	0	0.10164	0	0.16347
protein_co	spermatoge	238	192	157	471	361	382	3.044939	2.894742	2.646891	5.212974	5.188692	4.857073
pseudogen	sorting_nex	3	8	6	2	6	0	0.131367	0.412822	0.34622	0.075763	0.295166	0
protein_co	family_with	41	63	27	127	76	75	1.028711	1.862762	0.892706	2.756617	2.142261	1.870168
protein_co	dynein_axo	1	0	0	8	7	5	0.004272	0	0	0.029562	0.033591	0.021226
protein_co	carboxypep	1	2	1	2	2	4	0.038756	0.091344	0.051071	0.067055	0.08708	0.154067
protein_co	neutrophil_	1	0	1	3	4	1	0.02249	0	0.029636	0.058367	0.101064	0.022351
protein_co	carboxypep	4	6	3	0	1	1	0.082302	0.145482	0.081341	0	0.023115	0.020449
protein_co	TSR2_20S_r	429	417	337	818	803	1119	14.80553	16.95938	15.32609	24.4221	31.13374	38.38013
protein_co	protein_ph	9	11	8	200	196	164	0.046626	0.067156	0.054615	0.896348	1.140746	0.844379
protein_co	zinc_finger_	1265	934	901	2613	2459	3178	14.38985	12.52044	13.50596	25.71391	31.42486	35.92769
protein_co	zinc_finger_	378	264	218	446	242	313	9.901878	8.149609	7.525183	10.10703	7.121807	8.148539
protein_co	POM121_tr	0	0	0	0	0	1	0	0	0	0	0	0.016929
protein_co	glycerophо	105	87	85	333	259	275	1.339471	1.307887	1.428886	3.674948	3.71187	3.486473
protein_co	dynein_cyt	3	7	6	103	61	74	0.053838	0.148039	0.141891	1.59908	1.229841	1.31981
protein_co	6-phosphot	0	0	1	9	4	2	0	0	0.036166	0.213681	0.12333	0.054551
protein_co	aminolevul	1	0	0	2	0	2	0.026118	0	0	0.045189	0	0.051913
protein_co	transmemb	1230	1061	839	2187	1689	1968	28.04368	28.50705	25.20732	43.13618	43.2622	44.59279
protein_co	protein_ph	735	655	676	925	897	895	7.444353	7.817862	9.02238	8.104838	10.2066	9.00891
protein_co	coatomer_b	180	132	155	275	231	256	10.64735	9.201319	12.08191	14.07229	15.35077	15.04938
protein_co	chromoson	268	281	268	430	421	424	2.071873	2.560011	2.730222	2.875807	3.656449	3.257646
protein_co	1-acylglyce	1023	967	921	1286	981	1105	8.599339	9.579062	10.20197	9.351761	9.264191	9.231268
protein_co	polycystic_	0	1	0	5	5	6	0	0.006862	0	0.025186	0.032708	0.034721
protein_co	zinc_finger_	127	130	135	228	249	229	1.223568	1.475961	1.71393	1.9003	2.695087	2.192651
protein_co	transgelin_	6076	4650	3761	19197	13026	17549	200.5421	180.8622	163.5784	548.1307	483.0008	575.6384
protein_co	ELK4_ETS-d	715	572	661	457	457	403	3.696925	3.48528	4.503714	2.044155	2.654604	2.070853
protein_co	SLAM_fami	1	0	0	2	0	0	0.017671	0	0	0.030573	0	0
protein_co	solute_carr	74	76	51	159	143	162	1.172593	1.419176	1.064929	2.179595	2.545662	2.551175
protein_co	dual_specif	276	254	231	406	211	383	19.32766	20.96096	21.31656	24.59571	16.59976	26.655

protein_co	ring_finger_	174	126	108	361	317	336	3.808075	3.24963	3.11469	6.83481	7.794074	7.308111
protein_co	neuroblast	1251	1010	886	174	98	95	30.49226	29.01087	28.45777	3.668973	2.683536	2.301259
protein_co	5-hydroxyt	13	2	0	0	0	2	0.346892	0.062891	0	0	0	0.053038
protein_co	intelectin_	0	0	0	19	8	23	0	0	0	0.75602	0.413386	1.051367
protein_co	F11_recept	6	1	0	3341	2080	2671	0.065697	0.012903	0	31.64719	25.58633	29.06559
protein_co	upstream_t	535	505	407	1082	861	1116	15.67428	17.43542	15.71315	27.42358	28.33911	32.49434
protein_co	phospholip	0	0	0	0	0	2	0	0	0	0	0	0.025485
protein_co	spermatoge	156	157	105	456	327	468	3.536957	4.194807	3.137107	8.944026	8.329176	10.54534
protein_co	nitrilase_1	320	223	209	671	387	603	8.140854	6.68547	7.0065	14.76745	11.06063	15.24569
protein_co	death_effec	259	265	240	365	225	297	5.592054	6.742556	6.82838	6.817537	5.457619	6.372909
protein_co	zinc_finger_	150	180	129	229	263	304	1.730475	2.447111	1.961095	2.285454	3.408622	3.485437
protein_co	nucleophos	0	1	4	26	21	26	0	0.033291	0.148908	0.635417	0.666486	0.729971
protein_co	ectodyspla	2	0	0	67	31	34	0.020061	0	0	0.581381	0.349328	0.338931
protein_co	fibroblast_	5	3	1	4	4	5	0.102678	0.0726	0.027061	0.071061	0.092282	0.102044
protein_co	cytidine_de	18	9	7	0	2	0	0.989551	0.583063	0.507106	0	0.123522	0
protein_co	PTEN_indu	266	205	199	109	70	81	3.685502	3.347156	3.633314	1.306485	1.089588	1.115346
protein_co	UDP-Gal:be	815	632	524	1016	753	822	13.57675	12.40687	11.50282	14.64181	14.09231	13.60879
protein_co	erythrocyte	25	9	6	102	143	144	0.477462	0.202558	0.151003	1.685241	3.068202	2.733197
protein_co	ADAM_met	180	142	132	5	3	2	2.199257	2.044555	2.12526	0.052849	0.041179	0.024285
protein_co	family_with	616	572	375	327	273	365	7.682368	8.406544	6.162834	3.527972	3.824953	4.523941
protein_co	NADH_dehy	1730	1454	1255	1759	1158	1520	44.37399	43.9495	42.41905	39.03114	33.36876	38.74678
protein_co	solute_carr	0	0	0	3	0	1	0	0	0	0.050053	0	0.019167
protein_co	Fc_fragmen	4	3	6	21	9	4	0.358315	0.316689	0.708257	1.627372	0.905725	0.356102
protein_co	apolipopro	0	3	0	0	1	1	0	0.201902	0	0	0.06416	0.056757
protein_co	translocase	130	119	108	216	155	190	2.541481	2.741558	2.782287	3.653088	3.404271	3.691532
protein_co	myelin_pro	6	6	6	9	10	37	0.162479	0.191471	0.214107	0.210839	0.304225	0.995765
protein_co	WAP_four-d	0	0	0	2	0	0	0	0	0	0.072238	0	0
protein_co	KIAA1967	1120	952	900	2874	2348	2882	12.21799	12.23843	12.93776	27.12262	28.7759	31.24535
protein_co	cache_dom	125	160	130	297	323	239	1.19301	1.799538	1.634979	2.452186	3.463263	2.266948
protein_co	CDC42_sma	424	386	403	851	718	753	5.157854	5.53347	6.460157	8.955622	9.812433	9.103488
protein_co	Rap_guanir	73	99	82	253	116	209	0.46245	0.739067	0.684527	1.386517	0.82556	1.315823
protein_co	erythrocyte	148	101	108	489	567	481	1.321293	1.06259	1.270562	3.776672	5.68682	4.267683
protein_co	MIS18_kine	138	139	120	716	556	709	4.638639	5.505965	5.315298	20.82033	20.99594	23.68467
protein_co	ALG8_alpha	675	628	506	1607	944	1126	21.30899	23.36285	21.04962	43.8872	33.47959	35.32702
protein_co	F-box_and_	2619	2024	1425	2738	2145	2802	57.96508	52.78962	41.56048	52.42366	53.33438	61.63234
protein_co	chromosom	44	40	24	140	109	146	0.930645	0.997007	0.668925	2.561665	2.590042	3.068978
protein_co	synaptojan	202	128	214	309	312	266	1.507482	1.125688	2.104503	1.994906	2.6158	1.972841
protein_co	PAX3_and_	407	377	431	885	747	712	5.393488	5.887403	7.526402	10.14569	11.12103	9.377022
protein_co	interferon_	109	80	97	77	49	65	1.347005	1.165037	1.579607	0.823183	0.68028	0.798299
protein_co	mitochond	1020	859	692	1449	929	951	26.82554	26.62248	23.98221	32.96702	27.44815	24.85641
protein_co	interferon_	989	870	657	450	371	384	23.57436	24.43824	20.63686	9.279382	9.934969	9.096711
protein_co	phosphorib	909	818	844	3367	2690	2869	13.47616	14.291	16.48844	43.18256	44.80264	42.27099
protein_co	SON_DNA_b	2766	2171	2817	3906	3848	3485	16.61577	15.36863	22.29924	20.29848	25.96883	20.80562
protein_co	downstrean	111	108	98	687	456	508	2.519919	2.889312	2.931733	13.49222	11.62994	11.46138

protein_co	synaptic_ve	665	520	479	292	274	337	7.972319	7.346381	7.567168	3.02837	3.690308	4.015157
protein_co	ladinin_1	1	0	0	863	708	805	0.018218	0	0	13.60098	14.49035	14.57478
protein_co	stanniocalc	212	259	261	471	555	458	2.890417	4.161324	4.689214	5.555314	8.500936	6.205829
protein_co	troponin_I_	0	1	1	16	2	7	0	0.011526	0.012888	0.135375	0.021975	0.06804
protein_co	cysteine_ar	16	8	8	4387	3388	4239	0.099948	0.058891	0.065853	23.70735	23.77633	26.31634
protein_co	prostate_ca	74	54	38	0	1	0	10.22881	8.796181	6.921683	0	0.15529	0
protein_co	homeobox_	298	221	197	20	4	9	4.550452	3.976835	3.964052	0.264199	0.068619	0.136581
protein_co	potassium_	0	0	0	0	1	0	0	0	0	0	0.074067	0
protein_co	ATP_syntha	968	735	607	1736	1064	1560	23.14674	20.71137	19.12661	35.91098	28.58283	37.07223
protein_co	regulator_c	2897	2274	2610	878	462	587	54.4638	50.37986	64.65986	14.27963	9.757768	10.96749
protein_co	ubiquitin-c	2632	2235	2094	3169	2586	2748	32.78605	32.80861	34.37278	34.14982	36.18935	34.01963
protein_co	chromoson	123	123	84	10	9	13	3.611615	4.256068	3.250203	0.254015	0.296885	0.379358
protein_co	SNF8_ESCR	379	417	279	527	450	678	8.65228	11.21849	8.393254	10.40794	11.54125	15.38263
protein_co	chloride_in	0	4	1	9	7	8	0	0.06465	0.018073	0.106785	0.107858	0.109045
protein_co	coiled-coil_	41	14	17	139	87	134	0.817853	0.329099	0.446864	2.398662	1.949663	2.656474
protein_co	runt-relate	690	561	554	861	773	739	5.021898	4.811591	5.313288	5.421069	6.32044	5.34531
protein_co	insulin-like	1009	919	984	8191	9755	9459	6.456063	6.929457	8.296721	45.33948	70.12178	60.14942
protein_co	gastric_inh	9	6	3	6	10	4	0.665459	0.522802	0.292304	0.38379	0.830669	0.293933
protein_co	carbonyl_r	249	193	180	264	160	228	6.851511	6.258229	6.52671	6.284257	4.946022	6.234929
protein_co	carbonyl_r	106	74	50	111	57	97	4.800467	3.949266	2.983887	4.348741	2.900023	4.365751
protein_co	chromoson	69	60	49	78	37	27	1.517627	1.555157	1.420191	1.484136	0.914254	0.590187
pseudogen	tubulin_be	0	0	0	6	13	5	0	0	0	0.158382	0.445641	0.151626
protein_co	gap_junctic	0	0	0	114	141	158	0	0	0	1.807226	2.902771	2.877473
protein_co	actin_alpha	0	2	0	16840	10679	11938	0	0.030389	0	187.8357	154.6866	152.9729
protein_co	MORC_fam	399	339	330	452	379	342	4.974907	4.981027	5.422017	4.875437	5.308849	4.237872
protein_co	chromatin_	69	87	57	796	560	594	1.593773	2.368121	1.734951	15.90573	14.53164	13.63558
protein_co	single-minc	13	18	10	19	4	13	0.154938	0.252809	0.157054	0.195898	0.053558	0.153981
protein_co	holocarbox	284	255	296	260	243	207	2.325277	2.460388	3.193618	1.841589	2.235176	1.684366
protein_co	signal_pept	2	0	0	0	1	0	0.027374	0	0	0	0.015376	0
protein_co	Rho_GTPas	29	12	22	442	422	504	0.322947	0.157478	0.322842	4.258123	5.27952	5.57793
protein_co	ADP-depen	1230	1022	762	1608	1077	1311	14.23021	13.93362	11.61705	16.09367	13.99816	15.07365
protein_co	parathymo	14868	12096	8759	6351	4218	5790	691.0682	662.5478	536.4852	255.3721	220.2541	267.4586
protein_co	peptidyl_ar	0	0	0	6	0	2	0	0	0	0.121215	0	0.046417
protein_co	adiponectii	965	828	784	2153	1541	1582	23.46718	23.72854	25.12375	45.294	42.10032	38.234
protein_co	cytochrom	738	640	580	471	422	469	12.88178	13.16457	13.34082	7.112194	8.275251	8.135836
protein_co	proteasom	2445	1928	1518	3921	2958	3642	95.88202	89.09892	78.44493	133.0204	130.3183	141.941
protein_co	ATPase_typ	447	397	304	3708	2834	2881	5.944392	6.221534	5.327314	42.65821	42.3398	38.07613
protein_co	meiosis_1_	18	8	2	17	13	9	0.37473	0.196265	0.054867	0.306166	0.304045	0.186208
protein_co	proteasom	3876	3297	2390	5296	3725	4316	99.27397	99.5125	80.66485	117.3445	107.1833	109.8608
protein_co	iroquois_h	0	0	0	96	93	103	0	0	0	1.405593	1.768306	1.732496
protein_co	BTG_family	764	635	676	1069	1096	1108	14.91406	14.60775	17.38937	18.05274	24.03599	21.49571
protein_co	hexokinase	1137	1050	1073	1181	1191	1004	10.42861	11.34912	12.96882	9.370843	12.27232	9.151855
protein_co	complemer	325	339	213	6	3	7	8.146697	10.01394	7.035786	0.130111	0.084483	0.174384
protein_co	CUGBP_Ela	2	2	3	5	0	0	0.032619	0.03844	0.064476	0.070547	0	0

protein_co	aldehyde_d	127	105	76	608	410	533	1.999258	1.947877	1.576571	8.280028	7.251004	8.338772
protein_co	StAR-relate	723	754	710	118	126	141	2.458813	3.021799	3.181855	0.347162	0.481401	0.476558
protein_co	thioesteras	118	138	105	215	158	201	2.596441	3.578349	3.044532	4.092587	3.905734	4.395438
protein_co	trichohyali	0	0	0	83	113	122	0	0	0	0.550914	0.974026	0.930277
protein_co	ubiquitin_p	488	476	557	647	580	443	3.32885	3.826383	5.006848	3.818051	4.444792	3.003224
protein_co	autocrine_r	1043	933	799	998	794	927	15.33818	16.16882	15.48357	12.69647	13.11774	13.54812
protein_co	mediator_c	554	423	361	757	470	704	15.24392	13.71622	13.08968	18.01963	14.52894	19.25171
protein_co	ral_guanine	44	31	26	2	16	34	0.616407	0.511781	0.47998	0.024239	0.251817	0.473373
protein_co	ISL_LIM_ho	19	14	26	4	4	8	0.534758	0.464342	0.964298	0.097393	0.126477	0.223771
protein_co	ring_finger_	873	700	676	1153	896	838	12.88831	12.17831	13.15114	14.72564	14.86069	12.2952
protein_co	coiled-coil_	18	14	6	35	21	15	0.318922	0.292312	0.140087	0.536466	0.418003	0.264127
protein_co	GC-rich_pr	811	740	784	1627	1221	1265	11.49228	12.35731	14.63983	19.94508	19.43793	17.81498
protein_co	NEDD8_act	404	423	358	2334	1409	1674	11.20386	13.824	13.0829	55.9951	43.89815	46.1372
protein_co	transmemb	301	333	275	1570	884	1005	6.533513	8.517882	7.865889	29.48105	21.55667	21.67984
protein_co	G_protein-r	0	0	0	44	55	51	0	0	0	0.422641	0.686069	0.562776
protein_co	coiled-coil_	1	0	0	1	0	0	0.017409	0	0	0.01506	0	0
protein_co	angiotensir	11	13	12	16	12	31	0.119875	0.166949	0.172326	0.15084	0.146915	0.335742
protein_co	testis_prost	5	2	4	1	6	10	0.112163	0.052871	0.118243	0.019406	0.15121	0.222941
protein_co	urocanate_	0	0	0	0	0	2	0	0	0	0	0	0.033416
protein_co	EF-hand_ca	1003	793	987	1111	997	916	9.207529	8.578718	11.93972	8.823059	10.28221	8.356939
protein_co	spondin_2_	369	312	220	4	3	9	10.45223	10.41465	8.211836	0.098018	0.095467	0.253358
protein_co	coiled-coil-	201	149	122	239	179	231	9.181311	8.020511	7.343503	9.444295	9.185668	10.48649
protein_co	C-terminal_	2623	2046	1780	4094	3225	3908	32.67394	30.03419	29.2185	44.11782	45.13173	48.38017
pseudogen	ankyrin_rep	1	2	5	20	29	35	0.017765	0.041871	0.117052	0.307375	0.578792	0.61795
protein_co	tubulin_po	11	10	14	0	4	3	0.335456	0.359376	0.562607	0	0.137041	0.090923
protein_co	zinc_finger_	315	269	220	70	36	32	8.146758	8.198485	7.497764	1.566157	1.045986	0.822496
protein_co	ATPase_H+_	2158	1509	1594	2738	1752	2102	33.70108	27.77082	32.80315	36.99038	30.738	32.62382
protein_co	agouti_rela	1	0	0	0	0	0	0.069294	0	0	0	0	0
protein_co	zinc_finger_	241	215	138	9	21	24	3.088545	3.247001	2.330509	0.09978	0.302347	0.305673
protein_co	RGD_motif	94	84	51	184	112	175	1.061757	1.118107	0.759105	1.797951	1.42123	1.964467
protein_co	chromoson	14	3	4	9	13	13	0.431166	0.108879	0.162335	0.239785	0.449789	0.397896
protein_co	family_with	252	259	197	39	28	52	2.278199	2.759293	2.346886	0.305013	0.284379	0.467201
protein_co	regulator_c	826	623	542	740	740	714	7.007894	6.228775	6.059567	5.43128	7.053234	6.020262
protein_co	protein_ser	1120	932	764	886	759	903	17.03359	16.70364	15.31145	11.65695	12.96818	13.64852
protein_co	zyxin	8423	6294	5724	11578	8022	9472	178.8696	157.5084	160.1785	212.6994	191.3822	199.9038
protein_co	active_BCR	1691	1276	1357	931	892	952	16.00058	14.22819	16.92025	7.620872	9.48213	8.952382
pseudogen	family_with	9	20	7	3	0	3	0.183257	0.479906	0.187824	0.052845	0	0.060709
protein_co	LY6/PLAUR	2	0	0	19	9	10	0.04237	0	0	0.348211	0.214199	0.21054
protein_co	coiled-coil_	438	333	350	939	659	663	5.81886	5.213328	6.127264	10.79176	9.835541	8.753605
protein_co	zinc_finger_	62	87	58	61	66	62	0.797653	1.319012	0.983298	0.678915	0.953927	0.792727
protein_co	coiled-coil_	46	33	31	10	31	54	1.83934	1.554981	1.63343	0.345913	1.392563	2.14589
protein_co	zinc_finger_	40	38	24	42	32	44	1.325181	1.483563	1.047759	1.203726	1.191007	1.448697
protein_co	natriuretic_	371	278	337	149	137	145	5.32857	4.705314	6.378249	1.851339	2.210581	2.069733
pseudogen	zinc_finger_	0	2	0	0	5	5	0	0.09229	0	0	0.219955	0.194579

protein_co	zinc_finger_	149	105	86	35	44	36	3.111719	2.584107	2.366723	0.632332	1.032324	0.747182
protein_co	zinc_finger_	31	26	22	26	32	28	0.558601	0.552104	0.522394	0.4053	0.647798	0.501427
protein_co	zinc_finger_	62	60	49	78	88	85	0.77799	0.88724	0.81024	0.846721	1.24055	1.060013
protein_co	glucosamin	628	504	521	324	256	246	6.275376	5.93496	6.860451	2.800839	2.873884	2.443008
protein_co	tumor_nec	0	3	0	9	2	14	0	0.20212	0	0.44513	0.128458	0.795461
protein_co	Rho_GTPas	4130	3176	3267	2466	3550	3825	24.5974	22.29086	25.6403	12.7056	23.7529	22.6402
protein_co	prostaglanc	23	2	3	5	0	0	0.577904	0.059219	0.099331	0.108683	0	0
protein_co	calmodulin	8667	7348	5849	14608	10683	12416	180.9304	180.767	160.9012	263.8133	250.5446	257.5931
protein_co	DNA_fragm	1173	1081	884	3022	2030	2512	10.29506	11.18056	10.22393	22.94501	20.01593	21.91089
protein_co	coiled-coil_	170	135	131	50	55	70	6.360402	5.952186	6.45865	1.618336	2.311785	2.602815
protein_co	IQ_motif_c	36	40	36	74	58	104	0.831171	1.088316	1.09528	1.478028	1.504406	2.386333
protein_co	transmemb	115	132	101	146	118	170	2.225225	3.009934	2.575326	2.443947	2.565116	3.269148
protein_co	BSD_domai	746	556	586	1352	1133	1281	8.587515	7.542417	8.889168	13.46382	14.65236	14.65506
protein_co	zinc_finger_	10	6	4	12	11	5	0.27247	0.192654	0.14362	0.282855	0.336714	0.135394
protein_co	ATPase_fam	1046	870	640	4153	3110	4201	12.83641	12.58167	10.34968	44.08967	42.8767	51.23589
protein_co	SSU72_RNA	2033	1502	1263	4157	2602	3190	40.17508	34.97811	32.88952	71.06609	57.76646	62.6498
protein_co	ubiquitin-c	1023	833	730	1956	1563	2035	22.06054	21.16863	20.74428	36.48988	37.86593	43.61287
protein_co	zinc_finger_	265	185	182	246	371	314	4.516859	3.715947	4.087868	3.627344	7.104174	5.318999
protein_co	fibronectin	26	26	28	15	16	20	0.503831	0.593734	0.714997	0.251458	0.348322	0.385169
protein_co	C3_and_PZ	46	53	31	27	36	17	0.406423	0.551827	0.360925	0.20637	0.357332	0.149272
protein_co	nuclear_rec	463	400	257	2799	1873	2217	10.19621	10.38065	7.458055	53.3241	46.33877	48.52136
protein_co	ankyrin_rep	18	20	12	94	36	58	0.296127	0.387742	0.260149	1.337818	0.665361	0.948295
protein_co	coiled-coil_	236	242	207	661	540	739	16.24717	19.63307	18.77893	39.36681	41.76462	50.56149
protein_co	VMA21_vac	721	638	604	1756	1338	1258	8.092104	8.438281	8.933013	17.04958	16.87063	14.0319
protein_co	kalirin_Rho	379	403	311	810	838	841	1.856805	2.326694	2.007809	3.433011	4.612328	4.094801
protein_co	cartilage_ir	47	27	36	33	16	30	0.587678	0.397843	0.593169	0.356959	0.224755	0.372797
pseudogen	family_witl	57	41	36	107	76	107	1.208989	1.024798	1.006201	1.963334	1.810965	2.25549
protein_co	ATP-bindin	0	0	0	0	1	1	0	0	0	0	0.017115	0.015141
protein_co	radial_spok	13	8	4	4	0	5	0.23897	0.173299	0.096893	0.06361	0	0.091344
protein_co	solute_carr	122	86	114	194	193	243	1.762773	1.464341	2.170582	2.424942	3.132874	3.489414
protein_co	phosphodi	25	7	21	40	24	33	0.387903	0.127994	0.429375	0.536916	0.418353	0.50887
protein_co	WD_repeat	219	160	210	698	579	635	5.258085	4.527001	6.644122	14.49779	15.61749	15.15189
protein_co	NADH_deh	486	363	310	811	523	710	12.68079	11.16153	10.65876	18.30602	15.33066	18.41103
protein_co	PBX/knotte	470	403	392	554	489	497	4.538075	4.585492	4.987636	4.627502	5.304345	4.769138
protein_co	cystathioni	1574	1294	881	5741	4467	5992	31.37392	30.39523	23.14061	98.9953	100.0297	118.6986
protein_co	U2_small_r	1930	1584	1310	4113	3606	4660	21.76739	21.05287	19.46951	40.13014	45.69028	52.23295
protein_co	heat_shock	12	11	4	15	22	21	0.33454	0.361382	0.146947	0.361761	0.689031	0.58183
protein_co	ribosomal_	791	619	774	2212	1715	1628	8.23041	7.590017	10.61257	19.911	20.04741	16.83484
protein_co	pyridoxal_(	2427	2014	1674	2491	1967	2273	17.44336	17.05795	15.85443	15.48806	15.88231	16.23564
protein_co	glucose-6-p	3035	2295	2031	3014	2071	2234	61.07028	54.42031	53.85375	52.46594	46.81666	44.67495
protein_co	cystatin_B_	1614	1221	1038	3043	2112	2970	39.50382	35.21748	33.47863	64.43184	58.07357	72.24398
protein_co	ribosomal_	746	610	538	1795	1370	1666	13.06882	12.59316	12.4198	27.20352	26.96294	29.00563
protein_co	1-acylglyce	204	176	213	620	637	546	1.872718	1.903978	2.576657	4.92376	6.569474	4.98132
protein_co	trafficking_	573	447	543	1200	1058	972	4.348508	3.997608	5.430255	7.878252	9.020287	7.330971

protein_co	GRB2-assoc	43	46	37	14	12	9	0.482506	0.608274	0.547105	0.135902	0.151274	0.100366
protein_co	chromoson	1283	1222	845	1261	1039	1345	40.57545	45.5423	35.21504	34.49965	36.91486	42.27353
protein_co	inducible_T	103	58	66	481	513	557	0.770187	0.511086	0.650336	3.111479	4.309484	4.139269
protein_co	autoimmur	0	1	0	0	0	0	0	0.014489	0	0	0	0
protein_co	chromoson	85	75	43	89	73	105	0.992936	1.032454	0.66192	0.899405	0.958019	1.218993
protein_co	zinc_finger_	23	11	18	98	120	99	0.69779	0.393275	0.719621	2.572088	4.090034	2.98498
protein_co	leucine_ric	147	129	120	63	76	94	3.077235	3.182292	3.310239	1.140898	1.787335	1.955603
protein_co	integrin_be	11	2	14	3	7	5	0.121805	0.026098	0.204285	0.028738	0.08708	0.055024
protein_co	family_witl	624	529	382	844	850	1271	35.63666	35.60206	28.74819	41.69825	54.53563	72.13857
protein_co	ral_guanine	650	581	544	848	613	611	5.915703	6.231265	6.524192	6.676547	6.267619	5.52642
protein_co	formiminot	59	35	24	12	8	11	1.597708	1.116916	0.856429	0.281119	0.24338	0.296038
protein_co	spermatoge	756	648	440	524	312	313	17.37881	17.55417	13.32863	10.42059	8.057528	7.150759
protein_co	lanosterol_	5643	4540	4379	4409	4206	4740	60.52391	57.38255	61.89089	40.90911	50.67984	50.52484
protein_co	vav_2_guar	618	550	543	1081	1367	1344	6.413945	6.726769	7.426282	9.705669	15.93875	13.86263
protein_co	minichrom	996	911	1025	828	1177	1001	8.326106	8.974455	11.29123	5.987919	11.05371	8.316227
protein_co	chromoson	176	153	104	771	549	812	3.131971	3.208512	2.438784	11.86923	10.97556	14.36054
protein_co	pericentrin	954	786	793	1403	1664	1618	4.782738	4.643632	5.238853	6.084836	9.371963	8.061509
protein_co	DIP2_disco	884	813	681	924	971	904	6.41709	6.954782	6.514301	5.802576	7.918705	6.521747
protein_co	S100_calci	1	0	0	0	1	0	0.054522	0	0	0	0.061252	0
protein_co	protein_arg	2597	2232	2080	2735	1916	2476	34.10761	34.54463	35.99792	31.07418	28.26987	32.31764
protein_co	claudin_do	5	7	4	17	12	30	0.271771	0.448372	0.286502	0.799365	0.732763	1.620556
protein_co	ADAM_met	77	73	56	25	26	39	0.826197	0.923045	0.791801	0.232058	0.313412	0.415879
protein_co	calcium_ch	511	386	356	445	360	449	9.68248	8.619064	8.888951	7.294385	7.663325	8.455157
protein_co	solute_carr	247	178	175	345	191	246	3.826873	3.249931	3.572893	4.624121	3.324524	3.787842
processed_	zinc_finger_	270	244	215	503	500	543	3.398495	3.61926	3.566121	5.47714	7.070366	6.792541
protein_co	chromoson	104	73	89	96	63	104	4.308187	3.563618	4.858319	3.440293	2.931911	4.281582
protein_co	lipocalin_1	0	0	0	0	1	0	0	0	0	0	0.076644	0
protein_co	zinc_finger_	111	83	118	814	743	714	0.863042	0.760491	1.208998	5.475152	6.490029	5.517173
protein_co	G-protein_s	4723	4007	2945	780	749	971	68.82475	68.81025	56.55185	9.832961	12.26189	14.06227
protein_co	chromoson	266	252	204	1218	941	1252	3.881561	4.333437	3.922742	15.37571	15.42636	18.15678
protein_co	homeodom	12	25	8	3	6	0	0.259091	0.63609	0.227613	0.056035	0.145537	0
protein_co	chromoson	38	53	44	50	32	62	0.742894	1.22103	1.133525	0.845622	0.702817	1.204605
protein_co	torsin_fami	174	151	107	516	300	376	2.634935	2.694665	2.135203	6.759793	5.103769	5.658719
protein_co	ST6_(alpha-	1657	1481	1165	90	98	145	35.65985	37.55944	33.0383	1.67557	2.369366	3.101235
protein_co	SH3KBP1_b	1154	899	788	868	651	589	25.85438	23.73532	23.26427	16.8233	16.38545	13.11455
protein_co	retinol_deh	180	125	119	436	300	411	3.153335	2.580565	2.747131	6.607651	5.904294	7.15565
protein_co	zyg-11_rela	656	624	494	868	624	716	8.15433	9.14063	8.09182	9.333987	8.714011	8.845189
protein_co	zinc_finger_	195	169	117	1158	710	888	4.070778	4.157542	3.218574	20.91291	16.65138	18.42322
protein_co	protein_kir	67	23	29	743	666	816	1.050977	0.425161	0.599447	10.08254	11.73658	12.72091
protein_co	spectrin_be	25	3	11	0	1	2	0.15255	0.021573	0.08845	0	0.006855	0.012129
protein_co	BR_serine/t	271	252	139	222	223	232	4.659633	5.106108	3.14943	3.302162	4.307609	3.964423
protein_co	cytochrom	10	4	1	1	1	4	0.254157	0.119804	0.033492	0.021987	0.028553	0.101035
protein_co	transmemb	3	0	0	1	0	1	0.26783	0	0	0.077233	0	0.088725
protein_co	phosphatid	7	6	3	5	5	1	0.176891	0.178676	0.0999	0.109305	0.141947	0.025114

protein_co	TAO_kinase	1310	1195	1694	1503	1580	1321	5.589804	6.008974	9.525187	5.548139	7.574107	5.601931
protein_co	mediator_c	134	107	99	626	310	345	4.957438	4.664911	4.826391	20.03502	12.88437	12.68473
protein_co	death_effec	286	312	226	460	341	453	7.994258	10.27718	8.324447	11.12328	10.70818	12.58404
protein_co	SIK_family_	1016	854	890	617	633	517	8.49598	8.415593	9.80719	4.463422	5.946652	4.296551
protein_co	myelin_prc	6	6	4	90	91	84	0.080133	0.094431	0.070397	1.039834	1.365365	1.114929
protein_co	NIMA-relat	77	81	59	136	90	137	1.138357	1.411172	1.149409	1.739361	1.494787	2.01288
protein_co	TLC_domai	41	17	47	209	128	159	2.134298	1.042863	3.224065	9.411968	7.485661	8.225795
protein_co	proprotein	1334	1146	1120	1957	1780	2160	7.555717	7.649121	8.359353	9.589008	11.32632	12.15859
protein_co	scaffold_at	1923	1476	1219	4111	3418	4204	29.33032	26.52961	24.50056	54.24353	58.56776	63.725
protein_co	S100_calci	8	15	3	8	21	29	0.161714	0.357318	0.079912	0.139897	0.476897	0.582592
protein_co	chromatin_	785	585	626	1205	1060	1499	16.27837	14.29566	17.10608	21.6168	24.69427	30.89246
protein_co	zinc_finger	847	727	554	1062	931	1323	12.47663	12.61989	10.75372	13.53323	15.40681	19.36794
protein_co	flavin_aden	444	387	310	1268	902	1232	8.850076	9.090381	8.142552	21.86484	20.19852	24.40531
protein_co	SHC_(Src_h	7321	6158	6375	3182	2900	3091	111.3419	110.3659	127.7624	41.86501	49.54903	46.71934
processed_	vacuolar_p	777	580	529	744	530	622	12.14501	10.68346	10.89601	10.06034	9.306831	9.66222
protein_co	NLR_family	64	56	67	307	260	237	0.828012	0.853791	1.142263	3.436037	3.779017	3.047295
protein_co	adenosine_	2976	2468	2832	4073	3839	3772	23.79946	23.25875	29.84435	28.17809	34.49064	29.97888
protein_co	interleukin	110	98	82	82	72	42	0.984699	1.033818	0.967296	0.63502	0.72409	0.373654
protein_co	ubiquitin-c	1070	974	850	1705	1052	1288	17.647	18.93011	18.47314	24.32621	19.4918	21.11118
protein_co	cholinergic	6	2	1	10	18	19	0.054141	0.021267	0.011891	0.078062	0.182473	0.170388
protein_co	CREB_regul	609	580	419	1159	874	1150	12.19405	13.68566	11.05553	20.076	19.66034	22.88433
protein_co	anoctamin_	981	753	776	1016	618	641	16.16909	14.62577	16.85439	14.48683	11.44337	10.49988
protein_co	farnesyl_di	130	158	124	166	157	231	3.412161	4.88709	4.288868	3.76927	4.629509	6.025704
protein_co	RUN_and_S	706	642	534	1094	687	898	10.98335	11.76989	10.94728	14.72348	12.00704	13.88405
pseudogen	glucosidase	210	213	142	198	186	217	3.81001	4.554005	3.394923	3.107671	3.791131	3.912697
protein_co	family_with	1756	1356	1197	1615	1087	1305	30.16366	27.44898	27.09495	23.9991	20.97674	22.27818
protein_co	progestin_a	44	35	21	40	49	40	1.100332	1.031446	0.692031	0.865355	1.376627	0.994125
protein_co	polyamine-	163	146	98	413	246	280	8.079946	8.52866	6.4015	17.71063	13.69951	13.79395
protein_co	solute_carr	397	411	395	732	569	473	3.023241	3.688342	3.963823	4.822324	4.867922	3.579753
protein_co	lamin_A/C	24739	19554	16154	13713	12111	13990	410.5665	382.4231	353.2778	196.8779	225.8034	230.7431
protein_co	chemokine_	0	0	0	9	7	16	0	0	0	0.113332	0.114471	0.231461
protein_co	neurobeach	113	75	58	1137	1096	1276	0.677731	0.530087	0.458397	5.899327	7.384797	7.605702
protein_co	coiled-coil_	447	391	259	599	542	795	9.811204	10.11343	7.491165	11.37377	13.36482	17.3417
protein_co	parathyroid	672	681	440	731	599	756	16.75758	20.01227	14.45871	15.76967	16.78101	18.73586
protein_co	ubiquilin_4	994	724	679	1557	1575	1691	14.7157	12.63107	13.24644	19.94097	26.19535	24.87985
protein_co	myosin_ligh	28	40	23	32	34	43	1.464771	2.465918	1.585529	1.448187	1.998203	2.235577
protein_co	protein_ph	57	46	30	190	148	154	2.926903	2.783546	2.029969	8.440147	8.537765	7.858937
protein_co	G_patch_d	491	482	405	1196	1122	1432	10.54952	12.20409	11.46677	22.23031	27.08278	30.57765
pseudogen	-	180	151	81	437	252	437	7.111477	7.030259	4.217034	14.93591	11.18502	17.15846
protein_co	leucine_ric	7	8	5	4	3	3	0.189171	0.254774	0.178058	0.093515	0.091081	0.080573
protein_co	fibroblast_	23	15	21	199	114	126	0.39002	0.299749	0.46926	2.919277	2.171766	2.123437
protein_co	cytochrom	0	0	0	1	0	0	0	0	0	0.019758	0	0
protein_co	cytochrom	2	2	4	7	7	2	0.045757	0.053922	0.120593	0.138545	0.179919	0.045475
protein_co	nucleus_ac	2758	2330	2043	4445	4513	5650	32.84843	32.70268	32.06443	45.79891	60.38579	66.87725

protein_co	hexokinase	2	0	0	2	0	3	0.034534	0	0	0.029875	0	0.051481
protein_co	lymphocyt	45	62	46	121	134	178	0.874576	1.419985	1.178088	2.034386	2.925761	3.438069
protein_co	immediate_	308	329	263	597	521	704	5.557541	6.995761	6.253491	9.319	10.56133	12.6245
protein_co	zinc_finger_	233	259	155	318	283	350	5.660969	7.415522	4.96251	6.683824	7.7245	8.451087
protein_co	cleavage_ar	543	470	419	1186	851	1198	16.54025	16.87125	16.81865	31.25288	29.12198	36.26676
protein_co	lymphocyt	3437	2842	1891	5349	3624	5059	128.2299	124.9513	92.96855	172.6415	151.8962	187.5789
protein_co	vacuolar_p	1518	1142	793	1251	652	839	34.38786	30.48643	23.67235	24.51623	16.5932	18.88883
protein_co	tonsoku-lik	346	309	226	1638	1450	1808	2.775392	2.92088	2.388864	11.36646	13.06668	14.41306
protein_co	prostaglanc	21	8	11	0	2	2	0.782379	0.351233	0.540039	0	0.08371	0.074052
protein_co	melanoma_	956	737	716	858	862	1063	12.13707	11.02632	11.97854	9.423372	12.29454	13.41217
processed_	RecQ_prote	323	257	174	1163	883	1315	4.387976	4.114356	3.114912	13.66798	13.47632	17.75404
protein_co	leucine_ric	352	302	309	542	443	572	3.500889	3.539563	4.049757	4.663349	4.949809	5.653811
protein_co	zinc_finger_	259	232	258	147	154	160	2.934871	3.098021	3.85251	1.441019	1.960465	1.801851
polymorph	collagen_ty	69	53	51	1857	1700	2306	1.204792	1.090551	1.173459	28.05032	33.34732	40.01583
protein_co	protein_ph	215	187	102	378	237	285	2.640295	2.706218	1.650627	4.01577	3.269727	3.478312
protein_co	forkhead_b	0	0	0	1	0	4	0	0	0	0.018298	0	0.084082
protein_co	ORAI_calciu	1389	1065	1002	1077	934	1091	6.8284	6.169833	6.491114	4.580316	5.158372	5.330293
protein_co	alkB_alkyla	233	200	163	259	219	231	5.859977	5.927575	5.402097	5.635115	6.187756	5.773798
protein_co	SH2B_adap	77	79	33	152	80	102	1.977902	2.391378	1.117025	3.377697	2.308624	2.603898
protein_co	chromoson	402	364	306	500	412	520	5.134446	5.478681	5.150196	5.524597	5.91172	6.600556
protein_co	sequestoso	2524	1980	1807	1595	1308	1420	44.74986	41.36896	42.21777	24.46392	26.05308	25.02075
protein_co	mannosyl_(	2559	2061	1693	4247	2853	3168	44.75587	42.47807	39.01858	64.25766	56.05708	55.06485
protein_co	ribosomal_	37201	31023	21743	33439	25937	37408	1891.89	1859.226	1457.121	1471.152	1481.87	1890.669
protein_co	mastermin	1061	831	819	1337	1196	1109	8.563866	7.904285	8.711104	9.335743	10.84513	8.896018
protein_co	leucine-rich	608	470	376	1331	937	1183	5.861979	5.340053	4.777089	11.1015	10.14914	11.33535
protein_co	F-box_and_	13	25	11	35	10	32	0.22699	0.514411	0.253099	0.528681	0.196161	0.555293
protein_co	N-acyl_pho	223	252	244	196	147	138	2.366849	3.151906	3.412638	1.799636	1.752799	1.455641
protein_co	secretoglob	3	2	0	0	1	2	0.222441	0.174756	0	0	0.0833	0.147378
protein_co	proteasom	1267	1013	929	3034	1809	2061	21.96341	20.69377	21.22138	45.49898	35.22984	35.50673
protein_co	CUGBP_Ela	2	0	3	8	0	4	0.024808	0	0.049037	0.085846	0	0.04931
protein_co	major_facil	1230	928	734	1801	1174	1345	30.65792	27.25792	24.1084	38.83419	32.87417	33.31728
processed_	-	0	2	0	0	1	0	0	0.021077	0	0	0.010047	0
pseudogen	-	3	7	6	7	5	11	0.128083	0.352189	0.337564	0.258542	0.239822	0.466738
protein_co	ubiquitin_s	3	0	2	0	0	1	0.111299	0	0.097776	0	0	0.03687
pseudogen	tubulin_alp	28	21	9	28	15	11	0.750936	0.663699	0.31807	0.64963	0.451945	0.293189
protein_co	YdjC_homo	399	349	217	1167	671	940	13.09576	13.49865	9.385389	33.13535	24.74169	30.66163
protein_co	coiled-coil_	1	1	2	5	2	10	0.023425	0.027605	0.061737	0.101325	0.052634	0.232806
protein_co	dishevelled	2560	2140	1968	3166	2734	2812	25.79538	25.41107	26.13135	27.59789	30.94921	28.15963
protein_co	adaptor-rel	15536	12525	10648	16971	10602	12741	393.3483	373.6998	355.2556	371.7136	301.5608	320.5909
protein_co	ATP-bindin	1091	973	825	1085	785	927	20.30894	21.34433	20.23724	17.47251	16.41652	17.14952
protein_co	phosphate_	1450	1185	1186	1505	1196	1309	13.71528	13.20877	14.78279	12.31505	12.70917	12.30513
protein_co	F-box_prot	50	37	25	101	61	101	1.136073	0.990706	0.748533	1.985274	1.557095	2.280695
protein_co	dermokine	0	0	0	2126	1654	2286	0	0	0	34.63838	34.99579	42.78752
protein_co	U2_small_r	8	14	3	54	15	23	0.164031	0.338276	0.081057	0.957839	0.345522	0.468677

protein_co	3-hydroxyb	90	66	79	323	238	316	1.34368	1.161193	1.55423	4.171756	3.991897	4.688675
protein_co	nephrosis_	0	1	0	0	0	0	0	0.01459	0	0	0	0
protein_co	THAP_dom	136	86	55	151	84	125	3.945192	2.939915	2.102455	3.789389	2.737522	3.603702
protein_co	cytochrom	12	8	12	7	5	43	0.833716	0.654989	1.098634	0.420725	0.390262	2.969034
protein_co	zinc_finger_	57	53	69	81	56	68	0.78076	0.855511	1.245451	0.959822	0.861747	0.925681
protein_co	dual_specif	433	322	248	2008	1313	1546	10.3867	9.102333	7.839281	41.66933	35.38372	36.85606
protein_co	leucine_ric	30	36	19	19	13	21	0.573575	0.811108	0.478694	0.314258	0.27923	0.399023
protein_co	plexin_dom	222	177	170	8	4	6	1.879863	1.766255	1.896954	0.058604	0.038052	0.050493
protein_co	post-GPI_at	202	207	184	242	170	291	3.531731	4.264947	4.239248	3.660282	3.339137	5.05637
protein_co	IKAROS_fan	0	0	0	0	0	2	0	0	0	0	0	0.043179
protein_co	glutamate_	13	5	12	18	11	12	0.105622	0.047873	0.128477	0.126516	0.100404	0.096895
protein_co	ferredoxin_	1180	999	692	1668	1095	1754	25.16937	25.11094	19.45052	30.77864	26.23938	37.18173
protein_co	SAP30_bin	2124	1719	1488	2258	1644	1951	40.36133	38.49408	37.2605	37.11914	35.09634	36.84494
protein_co	acyl-CoA_o	581	468	444	839	690	774	3.968355	3.766928	3.996245	4.957461	5.294592	5.253938
protein_co	phosphorib	528	449	420	941	694	778	7.637389	7.653577	8.005623	11.77507	11.27767	11.18408
protein_co	cytoglobin	698	604	482	137	101	133	17.12364	17.46163	15.58197	2.90753	2.783627	3.242664
protein_co	serine/argi	872	945	742	4966	2531	3098	16.00158	20.4355	17.94258	78.83444	52.17801	56.49855
protein_co	zinc_finger_	101	98	68	120	93	104	1.698552	1.942185	1.506958	1.745829	1.757071	1.738202
protein_co	transmemb	108	117	76	141	106	116	2.233448	2.851314	2.071097	2.522518	2.462675	2.384074
protein_co	chemokine	3	0	6	3	2	2	0.116354	0	0.306652	0.100657	0.087144	0.07709
protein_co	TBC1_dom	0	0	0	0	0	1	0	0	0	0	0	0.015525
protein_co	kelch-like_f	4	1	0	0	1	1	0.102948	0.030329	0	0	0.028914	0.025578
protein_co	hypocretin	1	0	0	0	0	0	0.091752	0	0	0	0	0
protein_co	aldehyde_d	296	221	198	763	547	798	3.922537	3.451236	3.457604	8.747075	8.143511	10.50964
protein_co	integrin_al	6388	5533	4943	2421	1937	2278	67.69157	69.09354	69.0232	22.19358	23.05942	23.99015
protein_co	zinc_finger_	351	236	274	1685	1504	1832	7.450797	5.90357	7.66445	30.94272	35.86679	38.64833
pseudogen	sialic_acid_	1	5	1	17	4	6	0.021092	0.124278	0.027794	0.310192	0.094782	0.125771
protein_co	membrane_	132	133	85	31	21	39	2.332514	2.769549	1.979265	0.473887	0.416887	0.684896
protein_co	N-acetylglu	71	34	33	39	16	33	1.722645	0.972128	1.055082	0.818587	0.43612	0.795721
protein_co	LSM12_hor	560	470	405	1106	836	888	11.93517	11.80444	11.37445	20.39194	20.01685	18.80889
protein_co	ankyrin_rep	38	24	19	64	60	100	0.940513	0.700003	0.619683	1.370327	1.668329	2.45975
protein_co	ER_membr	1716	1496	1218	2666	1717	2303	41.71109	42.85218	39.01363	56.06055	46.88712	55.63368
protein_co	Josephin_d	663	563	451	425	329	515	35.24084	35.26535	31.5896	19.54271	19.64616	27.20506
protein_co	SH3_and_n	0	1	0	0	0	0	0	0.009391	0	0	0	0
protein_co	family_with	961	824	590	440	390	418	16.10009	16.26819	13.02542	6.377063	7.340382	6.959707
protein_co	DBF4_hom	173	140	168	1030	844	1079	3.054967	2.91337	3.90935	15.73478	16.74372	18.93614
protein_co	phospholip	1540	1312	1009	1253	812	1064	13.3523	13.40529	11.52819	9.398301	7.909342	9.168252
protein_co	formin-like_	753	516	553	374	400	436	3.561881	2.876346	3.447024	1.530449	2.125658	2.049654
protein_co	aquaporin_	4	0	0	0	0	0	0.146044	0	0	0	0	0
protein_co	Rac_GTPase	557	438	483	1955	1586	1692	8.916883	8.263026	10.18919	27.07495	28.52398	26.91956
protein_co	La_ribonuc	563	470	692	1383	1306	1216	4.637588	4.562351	7.511466	9.85528	12.08582	9.954673
protein_co	GRP1_(gen	418	387	256	61	49	88	11.44818	12.49046	9.239214	1.445284	1.507667	2.395259
protein_co	ribonucleo	806	687	595	1065	990	1132	9.092359	9.13283	8.844908	10.39332	12.54659	12.69105
protein_co	synaptoner	16	10	8	11	15	16	0.688104	0.506805	0.453376	0.409251	0.724727	0.683854

protein_co	SPC24_NDC	310	217	170	1164	964	1328	7.089291	5.848007	5.123006	23.02805	24.76665	30.18206
protein_co	inositol_he	6	5	1	21	10	9	0.112561	0.110538	0.024721	0.340814	0.210758	0.167798
protein_co	LEM_doma	1085	919	777	1192	1155	1408	11.79486	11.77296	11.13061	11.20992	14.10568	15.21162
protein_co	arachidona	2	0	0	4	8	6	0.038032	0	0	0.065803	0.170908	0.113392
protein_co	triggering_	0	3	0	1	4	0	0	0.156753	0	0.038358	0.199249	0
pseudogen	adenylate_	138	138	116	165	138	94	1.599706	1.885156	1.77196	1.654657	1.79717	1.082925
protein_co	zinc_finger_	96	53	45	109	89	107	2.2689	1.476138	1.401495	2.228607	2.363106	2.51326
protein_co	mediator_c	55	42	29	72	79	75	3.495504	3.1456	2.428734	3.958609	5.640573	4.737159
protein_co	chemokine_	20	30	11	75	54	83	0.476517	0.842319	0.345363	1.545868	1.445409	1.965331
protein_co	SLP_adaptc	8	6	0	0	0	1	0.177729	0.157082	0	0	0	0.022079
protein_co	RNASEK-C1	3	8	3	6	14	12	0.085573	0.268913	0.112764	0.148057	0.448633	0.340177
protein_co	B-cell_CLL/	3	0	0	0	0	1	0.044676	0	0	0	0	0.0148
protein_co	asialoglyco	1	0	0	0	1	4	0.036411	0	0	0	0.040905	0.144743
protein_co	tumor_nec	12	18	17	33	46	39	0.312029	0.551561	0.582503	0.74232	1.343758	1.007833
protein_co	SUMO1/ser	288	220	202	403	311	626	5.837292	5.254709	5.39517	7.066217	7.081551	12.60965
protein_co	fibroblast_	110	120	55	35	40	50	1.048714	1.348195	0.690974	0.288666	0.428424	0.473744
protein_co	eukaryotic_	106	113	99	74	130	197	3.195755	4.0147	3.933124	1.930022	4.403115	5.902601
protein_co	ribosomal_	161	122	108	235	196	272	8.506487	7.596111	7.519396	10.74126	11.63401	14.28246
protein_co	polymerase	82	81	75	586	298	473	3.118651	3.63032	3.758798	19.28029	12.73263	17.87819
protein_co	small_nucl	504	478	276	975	720	1085	14.00644	15.65424	10.10744	23.44038	22.47909	29.96653
protein_co	chromoson	0	0	0	2	1	0	0	0	0	0.041335	0.026839	0
protein_co	WD_repeat	384	303	194	406	417	651	3.637384	3.382266	2.421556	3.326956	4.437548	6.128421
protein_co	jumonji_dc	471	381	302	390	392	403	11.30848	10.77992	9.55488	8.100487	10.5735	9.616083
protein_co	coiled-coil_	53	50	18	10	29	35	0.811415	0.902078	0.36314	0.132443	0.498786	0.532531
protein_co	splA/ryanoc	4	15	4	12	0	11	0.091435	0.404066	0.120489	0.2373	0	0.249894
protein_co	meiosis_sp	2	4	1	3	5	7	0.056201	0.132458	0.037029	0.072928	0.157845	0.195487
protein_co	heparan_su	0	6	3	0	0	0	0	0.294051	0.164407	0	0	0
protein_co	chromoson	126	100	93	701	430	590	3.093954	2.893679	3.00927	14.89102	11.86208	14.39809
protein_co	cyclin_F	298	257	228	1965	1472	1519	3.683497	3.743555	3.713759	21.01211	20.44094	18.65999
protein_co	TBC1_dom	263	208	175	304	262	291	2.116674	1.972735	1.855971	2.116581	2.36891	2.32756
protein_co	amidohydr	127	146	80	225	186	198	2.054233	2.782954	1.705183	3.148412	3.379933	3.182885
protein_co	netrin_3	18	21	14	5	8	13	0.479828	0.659689	0.491785	0.115304	0.239581	0.344402
protein_co	coiled-coil_	0	0	0	127	89	144	0	0	0	1.652873	1.504222	2.153005
protein_co	progestin_a	42	32	39	235	219	216	0.796105	0.71479	0.974138	3.85347	4.663525	4.068971
protein_co	FLYWCH_fa	446	331	291	247	184	228	22.7912	19.93276	19.59567	10.91924	10.56329	11.57915
protein_co	zymogen_g	0	0	0	0	1	1	0	0	0	0	0.070054	0.061972
protein_co	zinc_finger_	263	218	210	494	270	355	3.490469	3.409507	3.672672	5.671762	4.025695	4.682373
protein_co	adenylate_c	764	593	673	159	218	228	5.235847	4.789116	6.077759	0.942657	1.678414	1.552881
protein_co	SH3_and_m	10	8	11	157	191	164	0.058908	0.055536	0.08539	0.800092	1.264037	0.960132
protein_co	ClpB_caseir	267	167	189	552	397	439	4.36273	3.215664	4.069525	7.802776	7.287636	7.128879
protein_co	sialidase_3_	111	122	70	81	183	121	1.669921	2.162916	1.387732	1.054195	3.092951	1.809122
protein_co	cytochrom	595	487	456	611	320	417	7.69416	7.421305	7.77041	6.835157	4.648826	5.359076
protein_co	protein_ph	25	14	10	33	12	27	0.862231	0.569009	0.454484	0.984602	0.464958	0.925459
protein_co	asparaginas	2	0	0	69	55	72	0.046685	0	0	1.393353	1.442317	1.670287

protein_co	guanine_nu	2	2	1	1	9	8	0.120048	0.141469	0.079097	0.051926	0.606897	0.477225
protein_co	UBX_doma	1811	1405	1216	1708	1386	1663	46.24995	42.28401	40.92241	37.73494	39.76537	42.20799
protein_co	chromoson	88	66	58	313	152	201	1.598219	1.412552	1.388086	4.917687	3.101317	3.627933
protein_co	tetratricop	600	529	477	759	495	605	17.32929	18.00497	18.15444	18.96419	16.06142	17.36579
protein_co	TAF6-like_R	286	235	167	360	283	371	7.155541	6.928694	5.505892	7.791874	7.954482	9.224864
protein_co	nuclear_RN	1513	1304	1184	2469	1484	1683	19.404	19.70775	20.00962	27.3928	21.38136	21.45093
protein_co	syntaxin_5	808	658	544	965	640	743	23.8441	22.88246	21.15453	24.63542	21.21772	21.79055
protein_co	solute_carr	42	42	30	30	5	20	0.31238	0.368121	0.294029	0.193027	0.041779	0.147834
protein_co	ribosomal_	30779	25906	16529	25791	16942	21865	1851.671	1836.61	1310.361	1342.272	1145.047	1307.28
protein_co	inter-alpha	20	6	0	0	4	1	0.352118	0.124485	0	0	0.079117	0.017497
processed_	DCP1_deca	503	513	429	601	577	573	4.4397	5.33593	4.989738	4.589053	5.721508	5.026317
protein_co	synovial_ap	1054	878	718	952	774	825	12.27179	12.04672	11.01606	9.588863	10.12412	9.546204
protein_co	zinc_finger_	43	57	29	35	22	47	1.662865	2.59759	1.47782	1.1709	0.955785	1.806326
protein_co	ribosomal_	995	802	682	2784	2339	3515	16.87802	16.03171	15.24465	40.85362	44.57359	59.25613
protein_co	low_densit	1078	1068	898	1352	1150	1285	11.0623	12.91531	12.14333	12.00235	13.25786	13.10507
protein_co	two_pore_s	689	665	501	378	297	372	8.335545	9.480768	7.987067	3.956121	4.036642	4.472675
protein_co	fibroblast_	0	0	0	7	2	0	0	0	0	0.131014	0.048611	0
protein_co	cytidine_m	1473	1251	1427	2822	2230	2453	26.61505	26.63722	33.97686	44.11075	45.26665	44.04855
protein_co	BEN_domai	12	20	7	53	59	32	0.370217	0.72713	0.284582	1.414535	2.044918	0.981148
protein_co	ELAV_(emb	0	0	0	2	1	0	0	0	0	0.023096	0.014996	0
protein_co	Sel1_repeat	183	165	159	366	357	314	5.980372	6.354306	6.847137	10.34716	13.10673	10.19803
protein_co	zyg-11_fam	671	652	669	805	719	704	4.389399	5.026171	5.766914	4.555557	5.283972	4.576831
protein_co	solute_carr	2	5	1	2	0	0	0.040152	0.118293	0.026456	0.034736	0	0
protein_co	chromoson	612	511	394	813	506	682	16.94555	16.67371	14.37591	19.47412	15.73997	18.76715
protein_co	mago-nashi	332	331	247	884	884	1458	23.24922	27.31526	22.79303	53.55322	69.54591	101.47
protein_co	acyl-CoA_th	0	0	6	54	35	58	0	0	0.065721	0.388309	0.326842	0.479136
protein_co	family_with	0	0	0	1	3	13	0	0	0	0.022842	0.088991	0.341138
protein_co	prolyl-tRNA	110	89	76	239	198	201	2.481257	2.365789	2.259058	4.6638	5.017568	4.505933
protein_co	chromoson	1	0	0	0	0	0	0.029792	0	0	0	0	0
protein_co	Bartter_syn	0	0	0	0	0	1	0	0	0	0	0	0.015154
protein_co	ubiquitin_s	730	567	794	1314	1133	1051	3.663563	3.353289	5.250929	5.704784	6.387924	5.241953
protein_co	phosphatid	3506	3135	3089	1066	900	917	56.38248	59.41237	65.46135	14.83039	16.26012	14.65586
protein_co	nucleolar_p	741	592	471	1920	1305	1666	5.900027	5.55475	4.941872	13.22513	11.67335	13.18319
protein_co	protein_kir	23	27	25	310	286	272	0.130271	0.180215	0.186593	1.518954	1.819847	1.531082
protein_co	kelch-like_f	690	627	557	1504	1290	1410	5.667849	6.069373	6.029193	10.6876	11.90441	11.5106
protein_co	zinc_finger_	8	10	11	25	16	11	0.072784	0.107214	0.131878	0.196765	0.163536	0.099459
protein_co	glucocortic	346	268	273	514	394	430	2.857657	2.608411	2.971198	3.672486	3.655774	3.529492
protein_co	solute_carr	79	33	39	7	6	5	1.502277	0.73951	0.977287	0.115155	0.128181	0.094494
protein_co	selenoprot	2700	2128	1994	1397	1319	1222	32.99646	30.6466	32.11172	14.76941	18.10913	14.84173
protein_co	adenylate_k	1866	1727	1613	1188	809	882	14.11659	15.39634	16.08005	7.77495	6.875681	6.631265
protein_co	Janus_kinas	2386	1917	2049	1099	1075	790	25.02818	23.69671	28.32276	9.972855	12.66824	8.235605
protein_co	ribonucleo	128	107	113	423	361	314	1.540802	1.517846	1.792463	4.404942	4.881948	3.756437
protein_co	chymotryp	0	7	1	2	0	0	0	0.138772	0.022168	0.029106	0	0
protein_co	leucine_zip	495	395	469	724	522	599	11.48873	10.80366	14.34414	14.53679	13.61089	13.81667

protein_co	retinol_bin	0	4	0	23	6	18	0	0.289838	0	1.223432	0.414466	1.099945
protein_co	filamin_bir	3701	3037	2558	4245	3224	4037	53.02696	51.27782	48.2962	52.61606	51.89455	57.48388
protein_co	transmemb	5	3	1	0	0	0	0.174148	0.123134	0.045897	0	0	0
protein_co	solute_carr	8	22	3	18	20	34	0.141838	0.459655	0.07009	0.276082	0.398365	0.599088
protein_co	aldo-keto_r	34	36	22	27	20	20	1.052628	1.313426	0.897539	0.723141	0.695625	0.615369
protein_co	dorsal_inhi	224	221	178	98	142	140	1.614318	1.876897	1.690425	0.610985	1.149684	1.002718
protein_co	podoplanir	23	16	14	475	423	423	0.392282	0.321586	0.314654	7.008531	8.105127	7.17002
protein_co	leucine_ric	0	0	0	0	1	0	0	0	0	0	0.026924	0
protein_co	dehydroger	649	627	428	470	301	420	19.94121	22.70291	17.32947	12.49303	10.39016	12.82525
protein_co	matrilin_1_	6	3	7	1	3	5	0.082893	0.048842	0.127438	0.011952	0.046563	0.068651
protein_co	lysosomal_	5	0	0	7	6	4	0.119076	0	0	0.144216	0.160529	0.094672
protein_co	syndecan_3	4376	3508	3185	2229	2599	2873	36.24371	34.23907	34.76159	15.97086	24.18303	23.64834
protein_co	penta-EF-ha	452	421	347	1662	895	1158	14.68958	16.12353	14.86056	46.72669	32.67707	37.40152
protein_co	syncoilin_i	664	642	617	211	184	215	10.29968	11.7354	12.61176	2.8314	3.206437	3.314392
protein_co	retinoblast	1062	960	1042	1961	1820	1638	23.57373	25.11204	30.47939	37.65688	45.38623	36.13493
protein_co	KIAA1522	510	472	421	1331	1687	1766	4.965044	5.415044	5.400946	11.2097	18.45088	17.0865
protein_co	testis-speci	3	1	5	1	1	5	0.116099	0.045605	0.254983	0.033479	0.043477	0.192303
protein_co	transmemb	73	39	37	105	64	92	1.299493	0.818131	0.867936	1.616975	1.279912	1.627603
protein_co	UBX_doma	0	0	0	7	4	6	0	0	0	0.057547	0.042704	0.056666
protein_co	calcium/ca	971	747	673	666	498	500	22.00587	19.95019	20.09875	13.05739	12.67937	11.26157
protein_co	alkaline_ph	552	406	316	481	306	401	11.28754	9.783476	8.514947	8.508796	7.029599	8.149183
protein_co	wingless-ty	0	2	4	66	70	48	0	0.105563	0.236086	2.557299	3.522262	2.136611
protein_co	sodium_ch	45	63	23	13	10	15	0.685567	1.131058	0.461743	0.171334	0.171154	0.227111
protein_co	matrix-rem	524	493	325	161	132	188	10.56803	11.71701	8.637359	2.809	2.990789	3.768168
protein_co	chromoson	1124	936	627	1300	797	1076	16.64029	16.32967	12.23198	16.64949	13.25568	15.8313
protein_co	multiple_E	46	71	61	71	95	128	0.446432	0.812013	0.780121	0.596099	1.035786	1.234573
protein_co	coiled-coil_	1	0	1	4	0	1	0.023508	0	0.030978	0.081348	0	0.023363
protein_co	DIRAS_fami	30	12	5	24	9	8	0.804982	0.379449	0.176795	0.557108	0.271304	0.213336
protein_co	chromoson	0	0	1	0	3	1	0	0	0.023162	0	0.059239	0.017468
protein_co	nuclear_fac	480	433	413	10	9	20	2.678579	2.847464	3.037023	0.048275	0.056423	0.110918
protein_co	OMA1_zinc	41	45	33	130	79	82	1.031155	1.333704	1.093676	2.828436	2.232113	2.049573
protein_co	Myb-like_S	759	715	736	808	826	644	5.156193	5.724012	6.588705	4.748558	6.304005	4.347934
protein_co	TM2_doma	238	244	203	298	202	285	10.07997	12.17808	11.32956	10.91846	9.611308	11.996
protein_co	ubiquitin_s	281	245	285	1766	1424	1463	3.722828	3.825073	4.975609	20.24046	21.19462	19.26285
protein_co	far_upstrea	1273	1238	1131	3642	3186	3337	26.70122	30.60064	31.26081	66.08543	75.07539	69.56144
protein_co	nexilin_(F_	158	111	113	295	194	217	2.618052	2.167461	2.467371	4.228694	3.61137	3.573474
protein_co	DnaJ_(Hsp4	1402	1334	1270	270	230	246	24.84045	27.85316	29.65173	4.138455	4.578133	4.331679
protein_co	EGF_latrop	21	6	11	175	117	87	0.315214	0.106132	0.217578	2.272415	1.972975	1.297823
protein_co	leucine-rich	5	10	9	12	17	16	0.058511	0.137904	0.138786	0.121483	0.223495	0.18608
protein_co	tRNA-yW_s	377	310	279	744	530	593	5.818879	5.638541	5.674623	9.934223	9.190156	9.096248
protein_co	LIM_homeo	3	5	9	56	33	21	0.066929	0.131453	0.264589	1.0808	0.827099	0.465611
protein_co	sorting_nex	378	303	296	749	468	521	11.48777	10.8516	11.85415	19.69195	15.9786	15.73589
protein_co	UDP-Gal:be	8	5	6	0	4	3	0.129361	0.095278	0.12785	0	0.072665	0.048211
protein_co	netrin_G1	169	110	94	173	91	131	1.902409	1.459207	1.394376	1.684714	1.15082	1.465541

protein_co family_with	225	181	235	504	519	507	1.429464	1.355116	1.967403	2.770029	3.704308	3.201167
protein_co HEN1_methy	85	41	65	161	98	122	2.401272	1.36494	2.419751	3.934698	3.110267	3.425248
protein_co AKNA_dom	3	10	7	0	2	2	0.052022	0.204349	0.159955	0	0.038962	0.034467
protein_co chromoson	305	333	264	774	511	626	4.76594	6.13197	5.4361	10.46291	8.970541	9.721486
protein_co WD_repeat	139	143	124	63	43	47	2.116422	2.565846	2.487963	0.829833	0.735538	0.711205
protein_co guanylate_l	138	135	76	87	47	64	1.981518	2.284335	1.438028	1.08069	0.758169	0.91329
protein_co ataxin_7-lik	154	156	84	211	104	183	1.863523	2.224568	1.339455	2.208816	1.413828	2.200771
protein_co guanylate_l	0	0	0	5	0	0	0	0	0	0.037375	0	0
protein_co zinc_finger_	499	358	391	822	828	1043	9.680306	8.184246	9.995399	13.79505	18.04546	20.10863
protein_co HFM1_ATP-d	0	4	2	21	11	10	0	0.050609	0.028296	0.195047	0.132678	0.106701
protein_co family_with	5	5	1	0	2	0	0.091625	0.107975	0.024148	0	0.041174	0
protein_co growth_fac	2	0	0	10	7	13	0.037087	0	0	0.160416	0.145825	0.239574
protein_co potassium_	99	95	97	25	14	8	0.890899	1.007451	1.15027	0.194624	0.141537	0.071547
protein_co amylo-alph	325	260	355	497	577	468	2.310747	2.17846	3.326076	3.056951	4.608864	3.306927
protein_co vascular_ce	392	268	278	35	41	34	5.369436	4.32598	5.017902	0.414738	0.630922	0.46284
protein_co exostosin-li	869	735	796	581	360	385	11.54472	11.5069	13.93515	6.677331	5.372981	5.083164
protein_co solute_carr	651	587	610	792	638	577	4.363711	4.636819	5.388149	4.592648	4.804461	3.843797
protein_co zinc_finger_	298	212	357	301	369	280	5.03717	4.222924	7.951945	4.401491	7.00722	4.703683
protein_co actin_relate	2088	1922	1799	4323	3559	4041	37.03209	40.17059	42.04494	66.32786	70.91283	71.22726
protein_co cell_adhesi	0	1	1	142	123	156	0	0.016659	0.018628	1.736567	1.953415	2.191667
protein_co NLR_family	0	1	2	26	25	9	0	0.014448	0.032313	0.275769	0.344349	0.109663
protein_co zinc_finger_	963	874	813	1765	1484	1623	5.515761	5.899262	6.136271	8.745545	9.549092	9.238624
protein_co tripartite_m	0	1	4	211	265	254	0	0.019345	0.086528	2.996456	4.887168	4.143866
protein_co SLAM_fami	0	0	0	0	2	0	0	0	0	0	0.1029	0
protein_co potassium_	0	1	0	0	2	5	0	0.014961	0	0	0.028526	0.063086
protein_co immunoglo	553	554	389	895	643	783	12.37378	14.60812	11.46996	17.32461	16.16357	17.412
protein_co discoidin_d	455	369	701	26	61	38	7.511117	7.178382	15.24916	0.371304	1.131285	0.623428
protein_co phosphopr	4801	3923	3791	8257	6964	8313	94.34659	90.84895	98.17097	140.3718	153.7455	162.3536
protein_co peroxisoma	400	345	323	742	576	597	5.784321	5.879204	6.155023	9.282379	9.357588	8.579784
protein_co nicastrin	2076	1725	1589	3253	2063	2154	36.26048	35.50605	36.57336	49.15336	40.4813	37.39052
protein_co VANGL_pla	919	568	617	1125	1332	1313	9.111006	6.635998	8.060664	9.648646	14.83557	12.93675
protein_co olfactomed	2048	1578	1536	262	311	301	34.31113	31.15438	33.91025	3.797251	5.853484	5.011655
protein_co Fc_recepto	10	18	5	34	37	31	0.266169	0.564595	0.175373	0.782887	1.10639	0.820028
protein_co solute_carr	2	0	2	0	0	2	0.023912	0	0.03151	0	0	0.023764
protein_co kelch_dom	14	4	9	74	48	45	0.556019	0.18721	0.47102	2.542475	2.141668	1.776168
protein_co chromoson	45	24	23	111	79	86	1.51164	0.950067	1.018119	3.225684	2.981344	2.871071
protein_co LIM_homeo	0	0	0	2	19	6	0	0	0	0.025839	0.318771	0.089051
protein_co feline_leuk	156	111	107	455	292	400	1.390604	1.166028	1.25689	3.508756	2.924224	3.54363
protein_co activating_	175	139	98	994	764	915	4.376322	4.096313	3.229476	21.50407	21.46415	22.7406
protein_co RNA_bindi	163	150	172	337	396	374	2.033313	2.205033	2.827353	3.636718	5.549591	4.636582
protein_co DENN/MAD	9	0	3	16	6	6	0.148572	0	0.06526	0.228495	0.111274	0.098436
protein_co axonemal_d	1	1	0	0	0	0	0.014536	0.01713	0	0	0	0
protein_co tudor_dom	1	0	0	19	13	17	0.014394	0	0	0.23659	0.210219	0.243186
protein_co immediate_	1898	1574	1317	1145	968	1011	42.94103	41.96508	39.26421	22.41015	24.60371	22.73197

protein_co	sushi_nido	4489	3706	3427	20	34	21	29.07415	28.2859	29.24869	0.11206	0.247392	0.135172
protein_co	3'(2')_5'-bis	529	535	440	1214	697	761	10.23229	12.1949	11.21514	20.31417	15.14604	14.6289
protein_co	spermatoge	19	13	1	9	19	16	0.172891	0.139402	0.011991	0.070847	0.194232	0.144693
protein_co	chromoson	6	5	2	89	73	87	0.093069	0.091397	0.040881	1.194287	1.272119	1.341173
protein_co	BRO1_dom	559	529	425	933	740	723	7.176046	8.002694	7.189475	10.36139	10.67221	9.224044
protein_co	neuroblast	3	4	2	1	2	3	0.013585	0.021346	0.011935	0.003917	0.010175	0.013501
protein_co	acid_phosp	55	65	67	202	110	157	1.628498	2.26801	2.614172	5.174149	3.659033	4.619914
protein_co	WD_repeat	0	0	0	0	1	0	0	0	0	0	0.013607	0
protein_co	kinesin_fam	6081	5187	5462	516	559	562	26.57758	26.71552	31.45769	1.950981	2.74474	2.441104
protein_co	transcriptic	164	119	129	418	351	362	4.698227	4.017392	4.869839	10.35928	11.29656	10.30643
protein_co	consortin_	370	274	334	236	200	159	3.821336	3.33481	4.545637	2.108572	2.320559	1.632
protein_co	protein_ph	259	270	262	469	358	434	4.274226	5.250838	5.697625	6.695663	6.637275	7.117986
protein_co	kelch_dom	0	0	1	1	4	1	0	0	0.021959	0.014416	0.074883	0.016561
protein_co	peptidase_	9	2	2	2	5	8	0.221408	0.057981	0.064836	0.042564	0.138188	0.195591
protein_co	protein_kir	467	440	288	306	225	284	9.881472	10.97146	8.030306	5.601305	5.348554	5.972178
protein_co	oxoeicosan	11	4	4	59	21	43	0.330881	0.14179	0.158553	1.535304	0.709656	1.285457
protein_co	3-hydroxya	10	21	15	65	67	67	0.347838	0.860803	0.687549	1.955932	2.618191	2.316124
protein_co	beta-13-N-a	367	328	336	239	287	222	6.403871	6.744619	7.725927	3.607758	5.6261	3.849809
protein_co	chromoson	10	8	6	0	4	2	0.252581	0.238121	0.199704	0	0.113504	0.050204
protein_co	mitogen-ac	2903	2234	2126	2980	2206	2521	51.90399	47.06997	50.09008	46.09279	44.31066	44.79568
protein_co	interleukin	7	0	1	26	10	5	0.203731	0	0.038353	0.65463	0.32697	0.144624
protein_co	Fas_apoptc	2	3	2	42	17	23	0.054298	0.095981	0.071552	0.986438	0.518508	0.620576
protein_co	Fc_recepto	1	0	0	0	0	0	0.018602	0	0	0	0	0
protein_co	calpain_2_	8194	6870	6973	13121	10142	10706	105.036	103.7781	117.7868	145.503	146.0544	136.3889
protein_co	mitochond	384	305	229	807	475	654	14.28626	13.37193	11.22684	25.9731	19.85317	24.18102
protein_co	chromoson	29	24	15	9	8	10	0.530691	0.517562	0.361718	0.142478	0.164468	0.181867
protein_co	WD_repeat	1959	1643	1858	1494	1328	1373	15.09188	14.91604	18.86207	9.956863	11.4936	10.51209
protein_co	v-rel_reticu	33	29	40	34	33	20	0.553741	0.573453	0.884479	0.493554	0.622094	0.333528
protein_co	pseudourid	84	74	104	74	62	107	0.698562	0.725211	1.139708	0.532378	0.57925	0.884339
protein_co	peroxisoma	285	271	249	423	329	398	8.676356	9.722297	9.989107	11.14027	11.2522	12.04163
protein_co	KIAA1841	239	218	193	806	708	716	2.801793	3.011631	2.981469	8.17403	9.324391	8.34182
protein_co	tripartite_r	51	69	48	165	162	218	1.018096	1.62321	1.262684	2.849479	3.633144	4.324986
protein_co	raftlin_fam	331	267	254	34	41	39	5.390178	5.123815	5.450592	0.47898	0.750081	0.631174
protein_co	disrupted_i	66	76	65	143	96	94	0.494986	0.671691	0.642387	0.927786	0.808852	0.700626
lincRNA	-	1	0	1	0	0	2	0.028898	0	0.03808	0	0	0.057439
protein_co	calpain_13	0	0	0	0	3	0	0	0	0	0	0.066503	0
protein_co	leucine_ric	6	25	19	16	16	17	0.078957	0.387694	0.329481	0.182148	0.236544	0.222331
protein_co	mediator_c	64	63	36	57	76	62	1.929512	2.238284	1.430227	1.486639	2.574129	1.857671
protein_co	dpy-30_hor	454	407	337	956	695	933	15.82305	16.71613	15.47744	28.82406	27.21248	32.3166
protein_co	tRNA-yW_s	127	124	132	351	219	214	1.030422	1.185606	1.411303	2.463665	1.996203	1.72558
protein_co	chromoson	101	113	89	379	194	270	3.576616	4.715594	4.153132	11.61056	7.717945	9.502203
protein_co	potassium_	0	0	0	5	2	2	0	0	0	0.100085	0.051989	0.045991
protein_co	PQ_loop_re	276	290	216	146	93	108	7.984543	9.88658	8.234355	3.653902	3.022547	3.105091
protein_co	ADP-ribosy	729	700	736	1460	963	1238	7.246336	8.199664	9.640589	12.55471	10.75391	12.22985

protein_co	family_witl	735	600	604	1020	922	881	6.122995	5.890266	6.630531	7.350886	8.628921	7.293938
protein_co	potassium_	12	10	12	2	0	0	0.126527	0.124254	0.166732	0.018243	0	0
protein_co	neuronal_d	0	0	0	0	0	5	0	0	0	0	0	0.092241
protein_co	clathrin_he	136	83	104	124	81	155	3.202836	2.303462	3.227483	2.526274	2.143038	3.627748
pseudogen	prolyl-tRNA	24	6	10	14	10	16	0.589872	0.173782	0.323878	0.297672	0.276118	0.390819
protein_co	frizzled-rela	46	28	31	78	89	90	0.770173	0.552453	0.683954	1.129764	1.674053	1.497554
protein_co	dual_specif	43	51	28	90	78	66	0.439811	0.614717	0.37739	0.796349	0.896275	0.67089
protein_co	coiled-coil_	860	726	533	478	305	348	22.23108	22.11596	18.15617	10.68939	8.857497	8.940278
protein_co	nucleopori	128	104	122	448	288	381	2.396198	2.294315	3.00959	7.255272	6.056953	7.088385
protein_co	coiled-coil_	78	89	57	461	291	323	1.732857	2.330049	1.668698	8.859964	7.262901	7.131489
protein_co	chromoson	0	5	0	12	34	12	0	0.164438	0	0.289714	1.065989	0.332825
protein_co	zinc_finger_	0	1	0	0	0	5	0	0.029836	0	0	0	0.125811
protein_co	F-box_prot	347	285	238	114	137	145	2.504161	2.423733	2.263313	0.711706	1.110714	1.039945
pseudogen	Alstrom_sy	0	1	0	0	1	0	0	0.038968	0	0	0.037149	0
protein_co	actin_gamr	1566	1299	1036	1102	742	721	40.16744	39.26437	35.01684	24.45271	21.38136	18.37923
protein_co	chromoson	233	206	204	421	350	345	3.231661	3.367009	3.728507	5.051438	5.453647	4.755527
protein_co	structural_	485	383	461	1212	918	943	4.906628	4.566119	6.145781	10.60735	10.43357	9.481187
protein_co	visinin-like_	417	386	344	19	22	16	8.101429	8.837308	8.806814	0.319332	0.480173	0.308927
protein_co	coiled-coil_	194	126	95	88	86	99	3.656302	2.798453	2.359385	1.434782	1.820907	1.854322
protein_co	H3_histone	2862	2386	2028	5706	3807	4410	81.32964	79.90184	75.94199	140.273	121.5377	124.5453
protein_co	aarF_doma	158	140	90	213	171	216	1.514517	1.581438	1.136827	1.76628	1.84146	2.057692
protein_co	solute_carr	3	0	7	8	9	4	0.036178	0	0.11124	0.08346	0.121932	0.04794
protein_co	engrailed_h	304	233	223	214	156	160	6.55029	5.916297	6.331792	3.988997	3.776249	3.42623
protein_co	zinc_finger_	103	127	80	123	73	82	1.402501	2.037871	1.435458	1.448885	1.116703	1.109658
protein_co	sarcoglycar	1937	1794	1716	1168	1043	989	23.14302	25.25922	27.01733	12.07247	13.99986	11.74347
protein_co	spermatoge	493	444	421	544	599	531	5.937195	6.301217	6.681151	5.667562	8.104203	6.355337
protein_co	nitric_oxid	21	13	4	67	37	36	0.438219	0.319685	0.109993	1.20951	0.867406	0.746593
protein_co	Homo_sapi	0	0	0	2	2	6	0	0	0	0.027807	0.036112	0.095836
protein_co	coiled-coil_	0	0	0	56	42	55	0	0	0	1.509558	1.47027	1.703221
protein_co	sphingosin	11	9	8	71	48	85	0.174566	0.168312	0.167298	0.974737	0.855769	1.340586
protein_co	inhibin_be	1	0	0	0	1	2	0.016523	0	0	0	0.018563	0.032843
protein_co	xin_actin-b	0	0	0	2	2	3	0	0	0	0.007227	0.009385	0.012453
protein_co	Bardet-Biec	210	220	172	134	120	134	3.199312	3.949727	3.453032	1.766059	2.053845	2.028858
protein_co	SWI/SNF-re	673	534	670	1289	925	952	7.101712	6.640432	9.316603	11.76695	10.96576	9.98377
protein_co	hematopoi	0	0	4	0	0	0	0	0	0.17057	0	0	0
protein_co	PDZ_and_L	2332	1823	2216	4137	3511	3164	20.29564	18.69683	25.41434	31.14747	34.32845	27.36657
protein_co	OTU_doma	572	532	492	407	663	626	4.767357	5.225169	5.403579	2.934533	6.207892	5.185201
protein_co	sperm-tail_	2	0	1	0	3	2	0.025192	0	0.016598	0	0.042452	0.025036
protein_co	regulation_	784	701	733	893	972	904	5.457691	5.750664	6.724061	5.377833	7.601656	6.254188
protein_co	ankyrin_rep	7	4	5	10	9	9	0.142698	0.096092	0.134315	0.176353	0.206116	0.182336
protein_co	cathepsin_	18	24	12	5	1	0	0.232028	0.364574	0.203837	0.055757	0.014482	0
protein_co	msh_home	1236	987	904	12209	8241	9827	33.74681	31.75693	32.52502	288.3749	252.7803	266.652
protein_co	PARK2_co-l	180	211	175	390	242	339	4.596903	6.350126	5.889327	8.616292	6.943161	8.604034
protein_co	BCL2/aden	13	10	1	68	35	53	0.29462	0.267071	0.029864	1.333187	0.89112	1.193726

protein_co	C1q_and_t	9	6	0	0	0	2	0.105507	0.082889	0	0	0	0.023301
protein_co	tumor_nec	2	0	2	0	2	2	0.089883	0	0.118444	0	0.100978	0.089328
protein_co	LysM_putat	176	182	166	188	182	230	3.758618	4.580301	4.671523	3.473253	4.366526	4.881497
protein_co	sodium_ch	403	392	267	790	470	678	10.58295	12.13095	9.239482	17.94699	13.86591	17.69461
protein_co	vacuolar_p	762	681	493	1296	936	1225	9.454192	9.956889	8.0603	13.91033	13.04651	15.10481
protein_co	excision_re	663	597	476	1633	1096	1285	8.735659	9.269655	8.26464	18.61364	16.2234	16.82654
protein_co	ring_finger_	790	675	537	1325	967	1074	17.01521	17.13251	15.24121	24.68818	23.39838	22.98921
protein_co	IWS1_hom	624	480	519	1325	1207	1242	11.16808	10.12377	12.24041	20.51506	24.26891	22.0915
protein_co	bolA_homo	180	163	118	562	435	557	3.195633	3.410194	2.760586	8.63145	8.676064	9.827641
protein_co	CDC42_effe	1350	1159	1264	1488	996	933	12.53866	12.6855	15.47031	11.95592	10.39263	8.612089
protein_co	S100_calci	6757	5565	4636	20624	11092	16271	602.2261	584.4911	544.4825	1590.163	1110.618	1441.218
protein_co	involucrin	0	0	0	17	12	18	0	0	0	0.361626	0.331496	0.439876
protein_co	DEAH_(Asp-	450	375	355	673	560	543	4.317406	4.239833	4.488214	5.58584	6.035976	5.177497
protein_co	small_proli	0	0	0	35	13	19	0	0	0	2.003702	0.966484	1.249584
protein_co	Rho_GTPas	0	0	0	1	1	2	0	0	0	0.015374	0.019965	0.035323
protein_co	S100_calci	0	0	0	13	5	8	0	0	0	1.031864	0.515389	0.729484
protein_co	transformir	0	1	0	62	26	24	0	0.014475	0	0.658824	0.358787	0.292978
protein_co	cyclin_Y-lik	206	189	199	900	689	762	2.895101	3.130152	3.685398	10.94213	10.87839	10.64293
protein_co	frizzled_fan	14	6	6	103	83	78	0.110491	0.055803	0.0624	0.703233	0.735913	0.611791
protein_co	crystallin_g	0	0	0	0	0	1	0	0	0	0	0	0.083647
protein_co	DDB1_and_	797	677	659	1634	1225	1294	9.277478	9.286828	10.10862	16.45458	16.01979	14.96978
protein_co	chromoson	0	0	1	3	0	0	0	0	0.180267	0.35503	0	0
protein_co	natriuretic_	0	0	0	0	1	1	0	0	0	0	0.05659	0.050061
protein_co	glucosamin	396	371	406	404	244	332	3.895324	4.300603	5.262708	3.437896	2.696418	3.245608
protein_co	alkaline_ph	0	3	3	68	34	35	0	0.062997	0.070444	1.048242	0.68064	0.619822
protein_co	gamma-am	1	0	1	7	0	0	0.007803	0	0.010282	0.04725	0	0
protein_co	alkaline_ph	0	0	1	6	14	7	0	0	0.027984	0.110226	0.334	0.147733
protein_co	gamma-am	26	18	43	0	0	0	0.642308	0.524022	1.399823	0	0	0
protein_co	progestin_a	267	233	256	986	778	734	1.440755	1.481637	1.820345	4.602764	4.716366	3.936267
protein_co	NIPA-like_d	11	24	9	210	181	197	0.109919	0.282617	0.118511	1.815359	2.031925	1.956393
protein_co	anthrax_to	1274	1039	1089	815	652	626	8.152644	7.835229	9.183152	4.511798	4.687332	3.981191
protein_co	helicase_PO	121	160	107	289	212	251	1.789846	2.789057	2.085686	3.698207	3.523022	3.689893
protein_co	mitochond	168	161	96	366	318	355	3.583436	4.046908	2.698338	6.753586	7.620202	7.525378
protein_co	CGG_triple	1467	1377	1466	1459	1285	1142	14.6592	16.21516	19.30407	12.61242	14.42555	11.34112
protein_co	family_with	253	231	190	104	103	84	4.668551	5.023202	4.620085	1.66019	2.135246	1.54046
protein_co	G_protein-r	247	249	285	36	52	39	1.943005	2.308253	2.954314	0.244987	0.459546	0.304896
protein_co	phosphom	692	502	432	488	436	660	28.62122	24.46769	23.54511	17.46083	20.25898	27.12912
protein_co	pre-B-cell_l	1610	1296	1093	460	459	504	26.53643	25.17263	23.7395	6.558996	8.499205	8.255754
protein_co	claudin_1	31	18	16	138	82	65	0.471465	0.322602	0.320659	1.815642	1.401041	0.982451
protein_co	pygopus_h	478	467	476	1049	888	1109	8.0438	9.260988	10.55541	15.27115	16.78786	18.54704
protein_co	homeodom	676	573	677	957	1004	853	4.387411	4.382514	5.790087	5.373244	7.320562	5.501996
protein_co	lens_epithe	0	0	0	0	6	4	0	0	0	0	0.549854	0.324278
protein_co	DC-STAMP_	3	2	2	5	1	5	0.063682	0.05003	0.055945	0.091818	0.023848	0.105481
protein_co	DC-STAMP_	6	1	3	5	5	12	0.13938	0.027375	0.091834	0.10048	0.130487	0.277038

protein_co	collagen_ty	300621	248614	292580	177	256	291	1480.619	1442.968	1898.906	0.754154	1.416488	1.424383
protein_co	chromoson	61	31	40	508	509	478	0.751373	0.449981	0.649263	5.413179	7.043565	5.851446
lincRNA	-	28	21	17	2	1	0	1.053552	0.93116	0.842911	0.065102	0.042271	0
protein_co	YY1_associa	502	398	461	662	422	399	9.079733	8.483197	10.98766	10.35834	8.574936	7.172192
protein_co	kelch_repea	19	8	24	242	193	165	0.214748	0.106555	0.357455	2.366212	2.450652	1.853398
protein_co	family_with	0	4	0	2	8	2	0	0.108879	0	0.039964	0.207595	0.045911
protein_co	EGF_domai	421	353	360	506	434	337	4.711088	4.655013	5.308557	4.898382	5.456045	3.74782
protein_co	leiomodin_	1	0	1	3	4	8	0.012957	0	0.017074	0.033626	0.058224	0.103013
protein_co	apolipopro	875	703	491	1256	851	1048	41.17633	38.9854	30.4478	51.13193	44.99023	49.01291
protein_co	neuroblast	1565	1333	1185	542	415	433	7.74541	7.774408	7.728287	2.320558	2.307423	2.129745
protein_co	protein_O-p	419	305	349	447	407	349	6.165169	5.288565	6.766922	5.689858	6.727821	5.103475
protein_co	solute_carr	0	0	0	92	49	69	0	0	0	0.892691	0.617441	0.769146
protein_co	cholecystol	40	30	23	0	0	0	1.231186	1.088158	0.932881	0	0	0
protein_co	immunoglo	35	43	25	0	1	1	0.156895	0.227153	0.147678	0	0.005036	0.004455
protein_co	ATPase_Na-	3969	3184	3062	10341	8271	8411	55.83917	52.78834	56.76725	125.8588	130.7269	117.6021
protein_co	solute_carr	15	11	13	97	98	101	0.139981	0.12097	0.159867	0.783094	1.027435	0.936721
protein_co	eukaryotic_	81	73	60	90	65	42	0.691091	0.733973	0.674585	0.664287	0.623035	0.356131
protein_co	prokinetici	0	0	2	0	0	0	0	0	0.090075	0	0	0
protein_co	leucine_ric	819	755	842	1194	949	929	5.486356	5.960108	7.432707	6.919384	7.141927	6.184797
protein_co	follistatin-l	22681	19392	18316	18729	15649	14949	202.0452	203.5711	215.0066	144.3324	156.6109	132.3452
protein_co	leiomodin_	21	31	23	84	49	58	0.280041	0.487159	0.40417	0.969045	0.734086	0.768669
protein_co	E74-like_fa	0	6	0	102	78	66	0	0.074955	0	0.93542	0.928939	0.69534
protein_co	transmemb	1010	808	876	2240	1480	1560	17.7113	16.69735	20.24267	33.9813	29.15679	27.18712
protein_co	transmemb	1	11	9	68	77	50	0.015301	0.198342	0.181465	0.900094	1.323597	0.760319
protein_co	insulin-like	758	637	590	267	246	520	28.12142	27.84932	28.84396	8.569242	10.25303	19.1726
protein_co	tripartite_r	340	371	211	110	66	92	5.424936	6.975843	4.436423	1.518348	1.183065	1.458859
protein_co	keratinocyt	919	698	631	1075	715	823	14.90587	13.34149	13.48671	15.08389	13.02858	13.26635
protein_co	chemokine	0	0	0	1	0	0	0	0	0	0.018408	0	0
protein_co	actin_relat	6161	4854	4363	13771	7956	9218	146.5272	136.0422	136.7373	283.3319	212.5743	217.8779
protein_co	TSSK6_activ	3	6	5	25	9	27	0.211482	0.498437	0.464469	1.524597	0.712761	1.891584
protein_co	chaperonin	6964	5611	4920	13477	9416	10869	171.4796	162.8175	159.6443	287.0846	260.4769	265.9824
protein_co	transmemb	95	93	77	218	137	181	2.059539	2.375945	2.199743	4.088518	3.336692	3.899731
protein_co	signal_sequ	8240	7380	5164	6557	4149	4792	84.44324	89.12533	69.73627	58.13074	47.76724	48.80498
protein_co	ring_finger_	389	378	296	898	525	587	10.75969	12.32109	10.78889	21.48768	16.31393	16.13607
protein_co	serine/thre	674	686	547	701	495	557	7.233373	8.675853	7.735762	6.508217	5.968088	5.940812
protein_co	adenosine_	1	0	0	114	82	120	0.015539	0	0	1.532455	1.431472	1.853151
protein_co	SLIT-ROBO_	1226	1103	1098	2930	2928	2729	10.87744	11.53237	12.83729	22.48882	29.18476	24.06297
protein_co	NIMA-relat	140	122	123	14	18	30	1.743939	1.790895	2.019031	0.150867	0.251898	0.371393
protein_co	coiled-coil_	6	5	4	1	0	0	0.034803	0.034178	0.030574	0.005018	0	0
protein_co	FEV_(ETS_o	0	0	2	0	3	1	0	0	0.074256	0	0.094959	0.028001
protein_co	crystallin_b	41	24	31	14	5	9	2.430662	1.676714	2.421794	0.718012	0.333012	0.530265
protein_co	indian_hed	0	7	3	1	0	0	0	0.216302	0.10366	0.022684	0	0
protein_co	KIAA1524	190	132	158	956	845	823	2.468414	2.020903	2.704932	10.74448	12.33304	10.6261
protein_co	eomesoder	0	0	0	0	1	0	0	0	0	0	0.017565	0

protein_co	CWC22_spl	265	245	207	630	423	380	4.277245	4.660059	4.402744	8.796741	7.670217	6.09553
protein_co	5-azacytidi	378	323	306	374	260	334	4.252379	4.282031	4.536244	3.639777	3.285962	3.734189
protein_co	transformir	1764	1395	1612	1108	783	725	20.20946	18.83378	24.33638	10.98143	10.07783	8.254747
protein_co	ankyrin_rep	580	448	391	547	394	539	9.462489	8.61316	8.405992	7.720185	7.221421	8.739283
protein_co	histone_de	280	248	244	75	44	93	5.007932	5.22708	5.750757	1.160445	0.884101	1.653077
protein_co	fibulin_2	6367	5240	3908	89	60	68	78.06283	75.70906	63.13916	0.943979	0.826437	0.828568
protein_co	galactosida	146	124	120	155	89	111	2.815805	2.818244	3.049761	2.586095	1.928363	2.127563
protein_co	STT3B_subu	3568	2902	3339	7115	6519	5883	44.48739	42.63994	54.86095	76.74499	91.315	72.89884
protein_co	coiled-coil-	148	128	120	405	323	423	4.897042	4.991018	5.232246	11.59285	12.0067	13.90984
protein_co	developme	0	0	0	9	7	16	0	0	0	0.298041	0.301035	0.608695
protein_co	neurofascir	0	2	1	73	87	104	0	0.011712	0.006548	0.313809	0.485677	0.513597
protein_co	shugoshin-l	201	167	208	822	590	590	2.525187	2.472414	3.443465	8.933721	8.327193	7.366466
protein_co	serpin_pep	232	147	157	141	97	66	6.440645	4.809122	5.74349	3.386285	3.025256	1.820937
protein_co	cytoplasmi	350	298	411	1016	973	777	2.544541	2.553082	3.937477	6.38996	7.947002	5.613996
protein_co	succinate-C	968	891	641	1505	854	1108	29.03506	31.49432	25.33613	39.05232	28.77758	33.0291
protein_co	NUAK_fami	90	50	55	1370	899	1038	1.399321	0.916119	1.126867	18.42717	15.70304	16.03917
protein_co	protein_kir	615	526	578	1139	946	837	6.577517	6.629484	8.146096	10.53837	11.36651	8.896558
protein_co	pyrin_and_	0	0	0	1	0	2	0	0	0	0.021987	0	0.050518
protein_co	interferon_	1859	1510	1522	593	384	358	23.78379	22.76594	25.65967	6.563255	5.519273	4.551916
protein_co	absent_in_l	0	0	0	17	21	10	0	0	0	0.50921	0.81687	0.344108
protein_co	EF-hand_dc	38	34	32	2	0	14	0.712631	0.751393	0.790799	0.032447	0	0.260927
protein_co	eukaryotic_	176	182	163	134	123	94	1.665942	2.030139	2.033151	1.097274	1.307981	0.88427
protein_co	solute_carr	0	0	0	1	2	0	0	0	0	0.014268	0.037057	0
protein_co	ribosomal_	1159	1013	758	1878	938	1404	28.01763	28.85789	24.14638	39.27413	25.47416	33.73065
protein_co	fatty_acid_	7	5	0	0	1	3	0.177825	0.149683	0	0	0.028539	0.07574
protein_co	protein_ph	72	90	90	240	220	224	0.348615	0.513526	0.574236	1.005281	1.196699	1.077881
protein_co	islet_cell_a	50	16	34	58	34	40	0.511705	0.192964	0.458525	0.5135	0.390911	0.406836
processed_	small_nucl	2298	1824	1785	1567	1560	1593	33.72842	31.54844	34.52383	19.89656	25.72288	23.23654
protein_co	cytotoxic_T	0	2	0	0	0	0	0	0.063114	0	0	0	0
protein_co	RING1_and	1212	1175	1102	869	841	802	13.5254	15.45227	16.20555	8.389386	10.54369	8.894702
protein_co	protein_ph	970	811	864	1639	1241	1204	10.30352	10.15178	12.0938	15.06108	14.80931	12.71014
protein_co	CD200_rec	2	0	0	3	0	0	0.02878	0	0	0.037346	0	0
protein_co	GTP-bindin	217	235	196	443	425	440	6.428761	8.204318	7.651709	11.35362	14.14508	12.95477
protein_co	chromoson	835	603	601	876	587	703	8.855314	7.536018	8.398985	8.036827	6.993663	7.40939
protein_co	spindle_an	180	145	134	302	240	267	1.759162	1.669969	1.72573	2.553308	2.635078	2.593308
protein_co	KIAA1407	72	54	47	50	44	39	0.95869	0.847318	0.824667	0.575942	0.658184	0.516083
protein_co	Ca++-depen	476	386	370	57	58	40	4.606089	4.401693	4.718043	0.477159	0.630525	0.384676
protein_co	NK6_home	49	31	21	22	22	48	0.987104	0.735928	0.557469	0.3834	0.497896	0.960987
protein_co	CDP-diacyl	28	25	44	1171	888	856	0.33229	0.349629	0.688093	12.02208	11.83919	10.09586
protein_co	WD_repeat	981	816	1102	947	805	773	3.643291	3.571265	5.393135	3.042551	3.358689	2.85308
protein_co	cytochrom	301	227	254	442	393	510	5.094386	4.527498	5.664921	6.471584	7.472518	8.578378
protein_co	protein_tyr	1609	1295	1688	1368	1319	991	9.936085	9.424018	13.7362	7.308165	9.150675	6.081946
protein_co	synaptopor	0	0	0	56	34	36	0	0	0	0.946747	0.746468	0.69919
protein_co	albumin	91	71	0	5	11	34	2.128869	1.95737	0	0.101191	0.289101	0.790489

protein_co	chromoson	3	4	4	8	0	6	0.122928	0.193151	0.215985	0.283585	0	0.244338
protein_co	chromoson	32	60	26	84	66	64	0.734654	1.623271	0.786576	1.668304	1.70226	1.460234
protein_co	THO_comp	507	540	372	1660	1035	1181	27.11221	34.02967	26.21408	76.79412	62.17937	62.76484
protein_co	ataxin_7	264	296	288	403	381	376	1.918521	2.534903	2.757972	2.533556	3.110546	2.715564
protein_co	proteasom	1055	892	860	3228	2208	2436	12.18694	12.14267	13.09108	32.2581	28.65434	27.96592
protein_co	prickle_hor	816	746	648	709	432	490	5.201668	5.604003	5.4433	3.909864	3.09375	3.104261
protein_co	ADAM_met	585	556	558	839	889	680	4.149314	4.647317	5.215422	5.148082	7.083881	4.793349
protein_co	protein_ph	158	110	120	102	89	67	2.823996	2.316897	2.826331	1.57714	1.787089	1.190122
protein_co	family_witl	0	0	0	4	1	0	0	0	0	0.089277	0.028984	0
protein_co	clarin_1	0	0	0	0	3	0	0	0	0	0	0.075637	0
protein_co	guanine_m	1139	980	950	3017	2291	2161	11.18112	11.33691	12.2891	25.62123	25.26596	21.08269
protein_co	TCDD-indu	1078	1052	1019	1078	948	846	13.64994	15.69765	17.00282	11.80847	13.48557	10.64613
protein_co	cyclin_L1	816	791	802	1303	981	941	9.001844	10.28312	11.65871	12.43509	12.15792	10.3167
protein_co	pentraxin_	2165	1986	1583	54	56	66	59.08106	63.86703	56.9254	1.274815	1.716831	1.789963
protein_co	HESX_hom	5	12	13	15	5	12	0.302175	0.854626	1.0353	0.784228	0.339474	0.72074
protein_co	doublecort	0	0	0	0	0	3	0	0	0	0	0	0.029536
protein_co	sarcolemm	477	375	461	779	792	659	3.741718	3.466499	4.76528	5.286316	6.979542	5.137451
protein_co	ribosomal_	13465	11531	7972	11067	8975	10215	331.0964	334.1351	258.3153	235.4187	247.9314	249.6296
protein_co	small_integ	138	106	119	59	33	54	3.861447	3.495296	4.38786	1.42819	1.037371	1.50167
protein_co	ribonuclea	22	17	14	16	13	15	0.344688	0.313877	0.289046	0.216864	0.228821	0.233563
protein_co	abhydrolas	62	53	40	40	40	39	1.322458	1.332212	1.124308	0.738097	0.958516	0.826732
protein_co	chromoson	21	24	17	36	24	37	0.270633	0.364485	0.288699	0.401354	0.347474	0.473885
protein_co	RNA_bindi	38	7	16	464	349	350	0.406334	0.088207	0.225452	4.292202	4.192506	3.719434
protein_co	amyloid_be	893	790	846	2187	1950	1757	5.269316	5.493347	6.578214	11.16387	12.92667	10.30349
protein_co	interleukin	37	30	11	527	431	613	0.697584	0.666536	0.273289	8.59545	9.12896	11.4859
protein_co	interleukin	334	298	238	178	142	193	6.746391	7.093302	6.334857	3.110342	3.222274	3.874289
protein_co	cysteine-ric	417	325	262	405	304	424	8.188574	7.520776	6.779666	6.880028	6.706483	8.274613
protein_co	proline-rich	176	122	112	41	42	44	2.47743	2.023744	2.077503	0.49927	0.664182	0.615533
protein_co	FANCD2_or	2	1	0	2	3	1	0.100362	0.059135	0	0.086823	0.169126	0.049871
protein_co	procollage	1577	1371	1086	278	203	252	41.31022	42.3224	37.48784	6.299899	5.974078	6.560485
protein_co	U2_snRNP-	994	763	836	2316	1802	1655	7.092095	6.415342	7.860122	14.29518	14.44415	11.73534
protein_co	myotubula	455	352	374	937	722	839	9.658441	8.805325	10.4617	17.20673	17.21797	17.69975
protein_co	tetratricop	388	327	384	415	322	321	2.912806	2.892908	3.798795	2.695199	2.715718	2.394939
protein_co	chemokine	14	16	10	3	4	1	0.45166	0.60829	0.425127	0.083727	0.144975	0.032062
protein_co	chemokine	24	12	6	52	59	37	0.500624	0.294977	0.164925	0.938354	1.382616	0.767029
protein_co	methylenet	50	24	39	178	141	172	0.832144	0.470703	0.855318	2.562781	2.636311	2.844897
protein_co	chemokine	210	156	163	105	48	50	10.13456	8.87191	10.36592	4.383669	2.60241	2.398088
protein_co	ring_finger	189	166	190	443	312	337	2.135264	2.210065	2.828644	4.329687	3.959984	3.78381
protein_co	phospholip	0	0	0	0	4	3	0	0	0	0	0.165096	0.109537
protein_co	coiled-coil_	1	0	1	0	1	0	0.014453	0	0.019045	0	0.016237	0
protein_co	glycogenin	327	282	322	1147	802	824	8.436503	8.573752	10.94726	25.60007	23.24546	21.12767
protein_co	Hermansky	154	139	201	246	293	229	1.747677	1.858927	3.005878	2.415119	3.735572	2.582769
protein_co	transmemb	27	32	34	522	263	290	0.371082	0.518278	0.615771	6.206394	4.060791	3.961079
protein_co	topoisome	473	348	450	1521	1327	1143	4.656209	4.03699	5.837389	12.9528	14.67544	11.1822

protein_co	receptor-lik	1085	998	965	1866	1579	1598	10.89962	11.8146	12.77449	16.21646	17.8202	15.95394
protein_co	SNF_relatec	246	187	254	349	282	232	2.512731	2.250917	3.418845	3.083893	3.236004	2.355095
protein_co	urocortin	27	15	13	6	5	9	1.797996	1.177127	1.140783	0.345652	0.374062	0.595631
protein_co	zinc_finger_	408	323	275	410	331	493	10.09814	9.420868	8.969099	8.778659	9.203613	12.12657
protein_co	solute_carr	462	381	430	712	573	545	8.26588	8.033026	10.13796	11.02022	11.5173	9.690658
protein_co	phospholip	52	66	41	13	15	24	0.538208	0.805003	0.559197	0.1164	0.174416	0.246869
protein_co	speedy_hor	9	11	10	8	14	16	0.228962	0.329777	0.335239	0.176065	0.400126	0.404529
protein_co	KIAA1143	840	648	669	1434	998	1146	8.685632	7.895947	9.115554	12.82727	11.59316	11.7765
protein_co	kinesin_fan	149	119	119	379	355	347	1.629122	1.53328	1.714546	3.584838	4.360585	3.770565
protein_co	transglutan	4	2	9	2	0	6	0.062504	0.036829	0.185322	0.027036	0	0.093177
protein_co	WD_repeat	917	740	731	2185	1808	1780	13.74098	13.06734	14.43446	28.32454	30.43659	26.50807
protein_co	zinc_finger_	1661	1444	1371	1656	1246	1491	27.25821	27.92557	29.64831	23.50992	22.97179	24.31728
protein_co	CUB_doma	21	11	7	1888	1565	1301	0.185108	0.114263	0.081309	14.39699	15.4978	11.39708
protein_co	C-type_lect	132	103	126	0	0	0	7.466038	6.865316	9.391211	0	0	0
protein_co	solute_carr	2	0	0	364	414	356	0.019525	0	0	3.074092	4.540481	3.453919
protein_co	leucine_zip	264	291	263	492	242	287	3.431481	4.45736	4.504725	5.532301	3.533801	3.707398
protein_co	FYVE_and_(	522	475	481	360	512	457	3.249671	3.484733	3.945924	1.938806	3.580864	2.827448
protein_co	chemokine_	0	0	0	86	63	77	0	0	0	1.442221	1.372019	1.483443
protein_co	receptor_(c	0	0	0	2	2	4	0	0	0	0.06934	0.090047	0.159316
protein_co	leucine_ric	9	18	12	30	40	48	0.093425	0.220192	0.164149	0.269405	0.466478	0.495191
protein_co	elongator_a	513	432	313	866	643	805	19.38525	19.23733	15.58594	28.30967	27.29694	30.23148
protein_co	deltex_3-lik	284	288	203	156	137	129	2.562243	3.061974	2.41342	1.217558	1.388582	1.156648
protein_co	zinc_finger_	601	557	637	769	542	609	3.296812	3.60066	4.604622	3.649296	3.340167	3.320066
protein_co	nicotinami	2	0	0	5	0	0	0.043147	0	0	0.093315	0	0
protein_co	small_integ	505	380	301	1095	863	1052	7.74036	6.863734	6.079545	14.51934	14.86037	16.02489
protein_co	zinc_finger_	389	380	353	303	233	278	3.299799	3.798644	3.945912	2.223533	2.22046	2.343648
protein_co	transmemb	727	641	554	808	572	702	19.91107	20.68833	19.99424	19.14408	17.5997	19.10764
protein_co	YEATS_dom	1593	1326	1194	1440	1187	1213	12.96265	12.71536	12.80316	10.13686	10.8512	9.809536
protein_co	glutamate_	0	0	0	1	6	11	0	0	0	0.005032	0.039211	0.063592
protein_co	zinc_finger_	65	67	47	129	53	128	1.282103	1.557369	1.221637	2.201214	1.17445	2.509165
protein_co	MYST/Esa1-	593	534	538	988	745	718	14.62227	15.51702	17.48144	21.0756	20.63789	17.5952
protein_co	Smad_nucl	283	228	199	307	332	320	6.063254	5.756537	5.61833	5.690111	7.991099	6.813637
protein_co	dynein_axo	153	167	146	68	64	84	2.288774	2.943982	2.878056	0.880002	1.075575	1.248822
protein_co	polymerase	1087	852	597	1801	1303	1637	31.93499	29.49742	23.11247	45.77349	43.00617	47.79645
protein_co	Kruppel-lik	20	20	12	90	38	68	0.411352	0.484753	0.325237	1.60136	0.878044	1.389959
protein_co	coiled-coil_	3	5	0	1	5	1	0.076028	0.149324	0	0.021924	0.142355	0.025186
protein_co	calcium/ca	41	12	18	4	8	6	1.593672	0.549672	0.921982	0.134505	0.349345	0.23178
protein_co	lipase_mer	3	0	3	0	5	2	0.039449	0	0.051985	0	0.073865	0.026137
protein_co	transmemb	290	246	211	551	438	426	3.119872	3.118753	2.991273	5.128063	5.293731	4.554681
protein_co	ribophorin_	6894	5751	5227	6891	5513	6130	157.9979	155.3211	157.8583	136.6235	141.944	139.6208
protein_co	SUMO1/ser	642	509	471	990	836	854	5.945097	5.554549	5.747508	7.930893	8.697196	7.859437
protein_co	hairy/enhar	0	0	1	3	1	5	0	0	0.019056	0.03753	0.016246	0.071857
protein_co	intraflagell	672	638	479	611	499	502	7.850033	8.782739	7.37348	6.174566	6.54865	5.827946
protein_co	chromosor	14	16	15	4	18	22	0.385226	0.518817	0.543893	0.095216	0.556428	0.601616

protein_co replication	191	172	138	1352	853	984	6.983239	7.410697	6.648711	42.76251	35.03657	35.7543
protein_co ribosomal_	62	62	39	312	281	358	4.341722	5.116454	3.598899	18.90114	22.10679	24.91512
protein_co BRCA1_ass	1951	1568	1261	2514	1954	2566	26.23517	24.84734	22.34481	29.24522	29.51891	34.29201
protein_co transketola	11047	8775	7374	28812	19170	21652	80.26889	75.13757	70.60588	181.1087	156.4855	156.3546
protein_co protein_kir	356	358	293	468	425	488	6.707115	7.94833	7.27425	7.627718	8.995468	9.137244
protein_co RFT1_homc	461	411	297	1017	701	804	4.777956	5.019843	4.056322	9.118537	8.16222	8.28146
protein_co Scm-like_w	14	26	18	199	154	172	0.162967	0.356658	0.276108	2.003954	2.013916	1.989801
protein_co guanine_nu	1517	1404	1111	3904	2515	2918	37.91855	41.35617	36.59443	84.41876	70.62414	72.48716
protein_co polybromo	935	853	983	1660	1660	1500	6.579799	7.073871	9.115686	10.10583	13.12376	10.49064
protein_co UV-stimula	202	263	151	258	314	325	2.219149	3.40485	2.185984	2.451985	3.875376	3.548364
protein_co family_witl	952	902	943	1059	1060	1024	7.079622	7.904724	9.241013	6.812901	8.855805	7.568027
protein_co Rho_guanir	379	315	325	174	154	172	5.026212	4.922879	5.679626	1.996245	2.294412	2.266938
protein_co stem-loop_	592	546	518	2660	1601	1917	15.85284	17.23	18.2789	61.62119	48.16436	51.01727
protein_co low_densit	3363	2818	2134	3928	2736	3378	22.77025	22.4848	19.04014	23.00781	20.81163	22.73056
protein_co zinc_finger_	0	0	0	2	0	1	0	0	0	0.050523	0	0.02902
protein_co solute_carr	137	78	81	111	78	83	4.957564	3.326208	3.862492	3.474832	3.170965	2.984939
protein_co UBX_doma	1545	1271	1376	827	1400	1318	7.739765	7.503293	9.083486	3.583998	7.879096	6.56182
protein_co ring_finger_	350	306	295	545	489	552	3.465373	3.570347	3.848919	4.668114	5.43926	5.431636
protein_co phosphatid	253	206	196	576	397	466	4.381443	4.20408	4.472883	8.629431	7.723892	8.02033
protein_co antigen_p9	22	11	14	184	189	257	0.293894	0.173168	0.246451	2.126419	2.836474	3.412014
protein_co S100_calci	3	1	0	8	6	22	0.124177	0.048779	0	0.286467	0.279011	0.905011
protein_co actin_bindi	0	0	1	3	4	9	0	0	0.019449	0.038304	0.066324	0.132012
protein_co exonucleas	37	36	36	107	90	88	0.763076	0.874935	0.978371	1.909031	2.085248	1.803676
protein_co claudin_19	2	0	0	0	0	1	0.030106	0	0	0	0	0.01496
protein_co chromoson	175	144	121	235	161	240	5.946517	5.76626	5.418073	6.908051	6.146099	8.10486
protein_co erythroblas	144	131	110	93	56	57	1.93049	2.069585	1.943267	1.078576	0.843416	0.759433
protein_co zinc_finger_	114	106	86	192	163	171	3.119004	3.417622	3.10059	4.544388	5.010116	4.649614
protein_co aminoacyl_	641	543	461	1433	709	1024	13.12265	13.09998	12.43653	25.3789	16.30643	20.83402
protein_co sphingomy	179	150	187	143	86	143	1.541135	1.521899	2.121602	1.065091	0.831831	1.223583
protein_co methionyl_	938	748	801	2355	1716	1680	17.79242	16.72018	20.02164	38.64436	36.56778	31.67023
protein_co DnaJ_(Hsp4	509	537	684	764	728	602	4.169421	5.183693	7.383272	5.413951	6.699438	4.900767
protein_co H2A_histor	1812	1463	1057	9621	5307	6915	51.02611	48.5496	39.22329	234.3783	167.8929	193.5246
protein_co endomucin	17	5	13	5	5	0	0.222937	0.07727	0.224653	0.056724	0.073664	0
protein_co solute_carr	35	14	8	7	9	20	0.986128	0.464837	0.297023	0.170619	0.284877	0.560022
protein_co solute_carr	265	217	198	311	210	213	4.48796	4.330818	4.418788	4.556449	3.995503	3.585026
protein_co 3-hydroxyb	239	160	151	92	94	97	4.549765	3.58937	3.787938	1.515102	2.010333	1.835154
protein_co progesteroi	1717	1600	1428	2802	2042	2594	24.01577	26.37262	26.3202	33.9045	32.08714	36.05835
protein_co cell_divisio	114	85	100	1644	1705	2208	1.595367	1.401786	1.844126	19.90309	26.80583	30.70891
protein_co zinc_finger_	143	160	113	343	336	415	1.60973	2.122483	1.676217	3.340214	4.249183	4.642745
protein_co F-box_and_	5	0	0	11	5	1	0.12098	0	0	0.23025	0.135914	0.024047
protein_co plexin_B1	1514	1281	1116	1418	1473	1862	10.9678	10.93578	10.65351	8.886542	11.98796	13.4055
protein_co coiled-coil_	243	243	198	609	383	607	8.246578	9.718089	8.85457	17.87919	14.6021	20.47226
protein_co ATR_interac	187	152	116	476	321	362	3.638356	3.485092	2.974105	8.011863	7.016453	6.999738
protein_co shisa_homc	4674	3969	3309	6855	4745	5600	104.4518	104.5238	97.44479	132.5249	119.1276	124.3726

protein_co	sprouty_hc	470	444	357	1044	890	837	9.937008	11.06236	9.946283	19.09507	21.1396	17.58704
protein_co	bassoon_pr	150	136	128	35	72	42	0.497722	0.531791	0.55968	0.100468	0.268396	0.138501
protein_co	N-acylamin	1821	1460	1415	3814	2521	3059	29.93961	28.2876	30.65685	54.24752	46.56484	49.98335
protein_co	inturned_p	120	112	135	161	122	141	1.10678	1.217322	1.640774	1.284603	1.264122	1.292436
protein_co	ring_finger_	555	420	423	435	386	473	4.995282	4.454751	5.016979	3.387032	3.903044	4.23095
protein_co	heat_shock	148	101	142	543	533	428	1.898078	1.526444	2.399803	6.02442	7.679424	5.455139
protein_co	major_facil	167	130	158	409	304	280	1.960343	1.798316	2.444035	4.153382	4.00902	3.266504
protein_co	chromoson	164	111	108	429	270	345	1.593087	1.270649	1.382465	3.605088	2.946513	3.330614
protein_co	CaM_kinase	2	0	0	12	9	4	0.03195	0	0	0.165838	0.161522	0.063505
protein_co	MON1_hon	205	148	143	337	212	254	4.294778	3.653892	3.947823	6.107729	4.989669	5.288472
protein_co	macrophag	0	2	0	12	14	17	0	0.026644	0	0.117358	0.177805	0.190997
protein_co	RAD54-like	212	167	245	126	320	208	2.188242	2.031342	3.332424	1.125105	3.710722	2.133695
protein_co	testis_expr	729	627	505	557	430	638	9.802892	9.935765	8.948554	6.47955	6.495973	8.526229
protein_co	glutamate_	19	4	10	6	28	19	0.153569	0.038099	0.106509	0.041953	0.254248	0.152621
protein_co	dual_specif	450	333	351	653	541	606	7.132769	6.220094	7.331411	8.954097	9.633674	9.546142
protein_co	POC1_cent	134	93	96	1010	666	843	3.548821	2.902481	3.350313	23.14002	19.81539	22.18792
protein_co	protein_ph	383	325	264	93	69	91	8.347633	8.347473	7.582341	1.753519	1.689518	1.971132
protein_co	alanine-gly	0	0	0	1	0	6	0	0	0	0.021819	0	0.150397
protein_co	WD_repeat	2533	1963	1990	3186	3214	3250	30.94843	28.26382	32.03991	33.67535	44.11622	39.46357
protein_co	paired-like_	285	180	198	259	162	192	4.491868	3.343195	4.112274	3.531383	2.868443	3.007412
protein_co	chromoson	2824	2463	2017	1246	1214	1611	64.24812	66.03394	60.46951	24.52318	31.02869	36.42511
protein_co	protease_se	90	83	53	2115	2162	1960	0.990786	1.076769	0.768861	20.14238	26.73881	21.44386
protein_co	N-deacetyla	0	1	0	28	34	22	0	0.010466	0	0.215127	0.339235	0.19418
protein_co	high_mobil	1009	911	643	4686	3470	4865	28.27817	30.08747	23.74685	113.6123	109.2543	135.5042
protein_co	Sin3A-assoc	612	463	319	330	261	320	29.24178	26.06996	20.08528	13.64047	14.01012	15.19539
protein_co	stimulator_	348	296	229	2	1	3	11.22014	11.24651	9.729471	0.055784	0.036222	0.096128
protein_co	heart_and_	1758	1365	1342	162	105	163	33.47851	30.63282	33.6771	2.668857	2.246393	3.084925
protein_co	MAD2_mit	183	208	193	1996	1428	1735	5.857438	7.845615	8.140456	55.26881	51.34922	55.19068
protein_co	annexin_A5	8226	7012	6640	14431	9363	11393	247.1581	248.2763	262.8991	375.0988	316.046	340.1997
protein_co	transmemb	0	0	0	3	0	1	0	0	0	0.057512	0	0.022023
protein_co	microtubul	192	170	226	427	277	291	1.386154	1.446327	2.150075	2.666867	2.24667	2.087916
protein_co	guanylate_	1	0	0	2023	2055	1874	0.012032	0	0	21.05709	27.77796	22.4088
protein_co	F-box_prot	160	139	125	202	102	146	3.286984	3.365112	3.383939	3.58998	2.354111	2.98085
protein_co	centrosom	141	134	135	373	240	197	1.646379	1.843837	2.077204	3.767753	3.148262	2.286054
protein_co	hydroxypro	1	9	0	183	137	150	0.01749	0.185494	0	2.768814	2.69184	2.607237
protein_co	ankyrin_rep	0	0	2	0	0	0	0	0	0.046033	0	0	0
protein_co	transmemb	58	39	43	175	128	147	0.63025	0.499409	0.615727	1.645076	1.562586	1.587493
protein_co	family_with	935	901	804	1670	1142	1039	9.929755	11.2761	11.25169	15.34286	13.62518	10.9661
protein_co	neuropepti	0	1	0	7	4	5	0	0.020597	0	0.105841	0.078542	0.086851
protein_co	N(alpha)-ac	763	683	706	2716	2177	2039	6.492121	6.848412	7.915924	19.99194	20.80988	17.24205
protein_co	interleukin	11	12	8	1	4	3	0.09664	0.124237	0.092616	0.0076	0.03948	0.026194
protein_co	family_with	16	12	10	46	56	49	0.185108	0.163604	0.152455	0.460391	0.727852	0.563393
protein_co	ADP-ribosy	518	444	421	633	501	549	8.009181	8.089998	8.577787	8.466912	8.702522	8.436073
protein_co	KIAA0947	759	686	758	1195	1048	864	5.069032	5.399014	6.670943	6.904212	7.863096	5.734646

protein_co	hedgehog_i	359	304	326	64	44	55	1.886995	1.883029	2.258025	0.291018	0.259823	0.287309
protein_co	anaphase_p	62	52	62	226	151	222	3.202285	3.165036	4.219828	10.0981	8.761818	11.39543
protein_co	ATP-bindin	947	851	782	3647	2333	2457	12.78631	13.54041	13.91351	42.59847	35.38825	32.96932
protein_co	OTU_doma	580	594	636	813	751	665	4.343723	5.24237	6.276623	5.267295	6.318633	4.949546
protein_co	LSM6_hom	133	98	89	356	307	519	5.207953	4.522187	4.592405	12.05948	13.50526	20.19726
protein_co	transmemb	1102	1016	983	1300	1164	1111	13.96385	15.17136	16.41391	14.2505	16.57012	13.99095
protein_co	protein_arg	162	124	126	224	178	156	2.430964	2.192766	2.491546	2.907867	3.000769	2.326472
protein_co	integrin_al	348	286	340	1241	1001	1004	2.341272	2.267491	3.014299	7.222829	7.565814	6.712988
protein_co	molybdenu	522	456	406	1080	758	773	7.745291	7.97332	7.938311	13.8629	12.6353	11.39873
protein_co	solute_carr	2	0	3	2	1	0	0.038884	0	0.07686	0.033639	0.021842	0
protein_co	EGF-like_re	2032	1737	2246	1759	1466	1350	22.7578	22.92521	33.14752	17.04258	18.44546	15.02623
protein_co	transmemb	207	172	194	268	252	207	1.440429	1.410448	1.778927	1.613316	1.970022	1.431534
protein_co	ELOVL_fatt	6	18	4	363	295	288	0.076266	0.269623	0.067	3.991597	4.21258	3.638138
protein_co	NADH_deh	357	381	282	570	371	581	26.69482	33.57306	27.78707	36.872	31.16605	43.17622
protein_co	zinc_finger_	9	7	12	2	1	2	0.242601	0.22236	0.426252	0.046638	0.030283	0.053578
protein_co	LMBR1_do	147	151	175	242	167	165	0.950803	1.150953	1.491579	1.354103	1.213498	1.060638
protein_co	RAN_bindi	122	155	176	2	0	3	2.080799	3.115367	3.95565	0.02951	0	0.050851
protein_co	Nipped-B_h	738	541	703	944	912	840	3.744174	3.234476	4.699913	4.143188	5.198087	4.235343
protein_co	ring_finger_	0	6	1	42	33	20	0	0.0763	0.01422	0.392082	0.400062	0.214489
protein_co	G_protein-r	8	22	12	58	51	48	0.021901	0.070976	0.043291	0.137364	0.156856	0.130596
protein_co	solute_carr	677	614	616	1207	881	942	5.751132	6.146673	6.895729	8.870231	8.40794	7.952894
protein_co	StAR-relate	1283	1153	1245	1297	876	867	14.7467	15.61725	18.85699	12.89648	11.31153	9.903687
protein_co	protein_ge	200	162	139	371	408	377	3.882728	3.706202	3.555958	6.230801	8.898487	7.273743
protein_co	coagulatior	439	418	336	29	24	22	6.777806	7.605153	6.835947	0.387334	0.416279	0.337565
protein_co	coiled-coil_	264	209	182	182	141	155	5.446774	5.081464	4.948136	3.248402	3.268162	3.178167
protein_co	ankyrin_rep	136	94	140	44	103	96	4.52544	3.686013	6.138818	1.266594	3.850421	3.174701
protein_co	carboxyme	4493	3963	3490	1202	1006	1179	101.8689	105.8855	104.2715	23.57614	25.62431	26.56615
protein_co	chromoson	5	3	0	3	4	2	0.046603	0.032951	0	0.02419	0.041884	0.018526
protein_co	proline-rich	1754	1453	1550	1433	1066	1038	16.87109	16.46973	19.64627	11.92402	11.51914	9.92249
protein_co	coagulatior	392	402	318	1373	979	1017	7.121781	8.606681	7.613152	21.57924	19.98179	18.36256
protein_co	angiogenic_	556	531	475	682	730	633	6.528098	7.347058	7.349204	6.927224	9.629057	7.386271
protein_co	WD_repeat	1081	906	864	801	606	602	14.45912	14.28077	15.22877	9.268551	9.106217	8.00244
protein_co	NADH_deh	665	645	492	707	455	670	42.26382	48.30743	41.20472	38.87134	32.48685	42.31862
protein_co	secretoglob	1	0	0	138	145	141	0.078781	0	0	9.405132	12.83335	11.03956
protein_co	serine_pept	1	0	1	8	1	2	0.044563	0	0.058723	0.30841	0.050064	0.088576
protein_co	5-hydroxyt	0	0	0	9	20	9	0	0	0	0.133741	0.385957	0.153643
protein_co	GrpE-like_2	338	295	250	626	537	595	4.354844	4.479041	4.244541	6.977395	7.772832	7.61873
protein_co	cell_divisio	0	3	0	0	0	0	0	0.060965	0	0	0	0
protein_co	arylsulfatas	188	183	192	355	246	323	2.967474	3.403982	3.993605	4.847529	4.362277	5.066887
protein_co	Rho-related	2134	1818	2015	5143	3977	3892	20.40384	20.48418	25.38794	42.53996	42.71911	36.98282
protein_co	glutathione	3508	3004	2539	2871	1708	2123	54.27148	54.76702	51.76183	38.42451	29.68582	32.64162
protein_co	tigger_tran	89	49	54	93	75	57	1.176173	0.763105	0.940394	1.06323	1.113503	0.748627
protein_co	serine_incc	160	146	149	268	812	525	3.061279	3.291872	3.756678	4.43589	17.45372	9.982789
protein_co	ectonucleo	0	0	0	0	0	2	0	0	0	0	0	0.026735

protein_co	cancer_ant	5	0	0	1	8	4	0.080604	0	0	0.013946	0.144887	0.064085
protein_co	caspase_3_	796	608	626	2275	1318	1584	15.76544	14.1907	16.33813	38.97961	29.32632	31.1787
protein_co	coiled-coil_	106	83	71	229	185	150	2.451614	2.262203	2.163911	4.581891	4.806922	3.447841
protein_co	endoplasm	431	366	405	389	352	358	4.15772	4.160698	5.148347	3.246315	3.814782	3.432185
protein_co	endoplasm	19	12	7	4	5	2	0.176315	0.131227	0.085599	0.032111	0.052126	0.018445
protein_co	cardiomyo	6	10	6	21	14	13	0.024725	0.048562	0.032582	0.074864	0.064814	0.053241
protein_co	EGF-like_fil	174	139	126	34	50	24	2.088355	1.96597	1.992785	0.353018	0.674177	0.28627
protein_co	KIAA1430	635	570	648	603	561	509	6.928593	7.329144	9.317108	5.691826	6.87675	5.519487
protein_co	RPTOR_ind	325	260	300	245	262	191	1.802978	1.69976	2.193124	1.175808	1.632892	1.053053
protein_co	PAP_associ	453	433	491	1217	791	862	6.807343	7.667865	9.722899	15.82097	13.3538	12.87349
protein_co	early_B-cell	574	567	452	4	0	2	5.788215	6.737875	6.006286	0.034894	0	0.020043
protein_co	ankyrin_rep	120	129	123	192	150	133	3.079457	3.901123	4.15942	4.262428	4.324473	3.391987
protein_co	ubiquitin-li	340	319	388	919	602	691	7.537662	8.334039	11.33507	17.62529	14.99351	15.22458
protein_co	family_with	1	0	0	0	0	0	0.039626	0	0	0	0	0
protein_co	UTP15_U3_	160	123	199	667	558	501	2.297412	2.081283	3.765363	8.285292	9.001237	7.149346
protein_co	toll-like_re	26	28	18	22	13	17	0.451745	0.573304	0.412123	0.330678	0.253754	0.293547
protein_co	kallikrein_E	19	29	23	5	1	4	0.425679	0.765656	0.679033	0.096908	0.02517	0.089063
protein_co	NSA2_ribos	1229	1144	954	1699	932	1277	46.70817	51.23587	47.77758	55.85954	39.79293	48.23269
protein_co	G_elongati	277	230	253	339	315	281	4.51359	4.416491	5.432475	4.778648	5.766363	4.550492
protein_co	telomerase	0	0	0	51	47	67	0	0	0	0.58132	0.695711	0.877337
protein_co	coiled-coil_	390	342	326	585	346	461	14.18062	14.65426	15.62008	18.40135	14.1337	16.65871
protein_co	forkhead_b	12	8	10	13	11	12	0.274069	0.215316	0.300963	0.256853	0.282241	0.272376
protein_co	chromoson	0	0	0	0	0	4	0	0	0	0	0	0.086465
protein_co	G_protein-	0	0	0	4	0	3	0	0	0	0.035739	0	0.030792
protein_co	acyl-CoA_sy	0	6	0	0	0	0	0	0.057245	0	0	0	0
protein_co	septin_8	1106	913	858	1458	1485	1416	13.33775	12.97494	13.63483	15.21066	20.11885	16.97073
protein_co	shroom_fa	49	33	26	112	75	87	0.645461	0.512266	0.451318	1.276307	1.109901	1.138946
protein_co	growth_dif	3	0	1	10	1	1	0.06016	0	0.026425	0.173481	0.022529	0.01993
protein_co	ubiquinol-c	318	338	219	508	245	325	19.26228	24.12706	17.48073	26.61996	16.67231	19.56472
protein_co	liver_expre	22	6	14	39	25	25	0.527731	0.169609	0.44254	0.809315	0.673719	0.595991
protein_co	gap_junctic	1	1	0	11	19	19	0.02321	0.027351	0	0.220863	0.495415	0.438258
protein_co	solute_carr	75	85	67	112	50	81	2.145097	2.864915	2.525197	2.771193	1.606589	2.302398
protein_co	glutamate_	1	2	1	17	15	8	0.010758	0.025356	0.014177	0.158216	0.181292	0.085534
protein_co	Mab-21_dc	23	21	23	109	78	98	0.382666	0.411735	0.50426	1.56885	1.457926	1.62042
protein_co	fatty_acid_	0	0	0	15	6	10	0	0	0	0.329331	0.171072	0.252225
protein_co	T-cell_leuke	0	0	0	28	12	17	0	0	0	0.858921	0.478038	0.599088
protein_co	Cbp/p300-i	2461	2136	1822	3332	2405	2566	68.39254	69.95286	66.72373	80.10601	75.08639	70.87016
protein_co	family_with	0	0	0	2	2	0	0	0	0	0.0677	0.087917	0
protein_co	CREB3_regu	51	49	54	41	37	38	0.346686	0.392527	0.483721	0.241109	0.282564	0.25672
protein_co	discoidin_C	328	226	317	671	524	508	4.788926	3.88848	6.098996	8.475197	8.594975	7.371191
protein_co	sideroflexin	1329	1094	1045	2274	1546	1668	16.6293	16.13145	17.23059	24.61515	21.7324	20.7422
protein_co	sterile_alph	6	18	12	32	21	26	0.086083	0.30433	0.226872	0.397172	0.338481	0.370722
protein_co	transmemb	633	493	556	453	473	438	6.679619	6.130586	7.73139	4.135321	5.607357	4.593373
protein_co	dapper_ant	0	0	0	6	2	10	0	0	0	0.093404	0.040432	0.178838

protein_co	prenyl_(de	258	242	203	274	223	216	3.858411	4.264924	4.00055	3.544887	3.746647	3.210349
protein_co	syntaxin_bi	512	417	502	288	296	252	6.117307	5.871289	7.903671	2.976774	3.973115	2.992268
protein_co	interleukin	152	144	168	1	3	3	2.771971	3.094672	4.037283	0.015776	0.061463	0.054372
protein_co	ankyrin_rep	0	0	0	0	3	0	0	0	0	0	0.071371	0
protein_co	retinoic_ac	3	0	1	2	0	0	0.075666	0	0.033236	0.043639	0	0
protein_co	T-box_20	0	0	0	2	1	3	0	0	0	0.048957	0.031788	0.084362
protein_co	diacylglyce	366	276	255	511	364	473	6.688438	5.943739	6.14071	8.07844	7.472984	8.59042
protein_co	KIAA0895	12	14	18	150	120	134	0.149798	0.205949	0.296095	1.619862	1.682884	1.66241
protein_co	serine/thre	674	554	631	894	571	650	10.59449	10.26211	13.07026	12.15684	10.08336	10.15414
protein_co	transforme	1389	1166	1044	2432	2056	2338	39.85639	39.42769	39.47581	60.37016	66.27777	66.67298
protein_co	family_with	0	0	0	1	0	0	0	0	0	0.028714	0	0
protein_co	UDP-N-acet	1440	1068	1402	1111	1053	1017	12.78897	11.17767	16.40801	8.535914	10.50631	8.976428
protein_co	SAP30-like	184	152	155	335	330	343	6.555278	6.381517	7.276789	10.32479	13.20798	12.14443
protein_co	ribosomal_	24666	21301	13740	22956	16984	21281	418.6735	426.0728	307.3253	337.0823	323.8663	358.9867
protein_co	hyperpolar	16	4	6	11	21	17	0.156717	0.04617	0.077443	0.093208	0.231081	0.165484
protein_co	myozenin_	25	17	22	75	72	68	0.384187	0.307864	0.445513	0.997073	1.243038	1.038536
protein_co	componen	458	321	415	509	444	400	4.475263	3.696283	5.343625	4.302629	4.873995	3.884389
protein_co	chromoson	332	232	269	177	190	141	4.415074	3.635758	4.713972	2.036274	2.838589	1.863497
protein_co	G_protein-	81	75	54	51	37	47	0.869293	0.948526	0.763677	0.473494	0.4461	0.501289
protein_co	SLU7_splici	451	431	419	821	596	662	6.294856	7.089141	7.706516	9.913235	9.345544	9.182837
protein_co	retinitis_pi	327	258	195	623	352	408	15.44309	14.35864	12.13545	25.45292	18.67576	19.14945
protein_co	pituitary_t	286	244	238	1767	1184	1501	14.15058	14.22673	15.51744	75.6324	65.8126	73.80719
protein_co	calcium_m	1490	1326	1047	621	473	559	35.56451	37.29762	32.93154	12.82287	12.68355	13.26026
polymorph	F-box_and_	6	6	10	1199	1060	1057	0.182346	0.214883	0.400478	31.5229	36.19086	31.92483
protein_co	BMP_bindi	13	10	9	138	112	131	0.136798	0.124007	0.1248	1.256261	1.324051	1.369994
protein_co	RELT-like_2	43	60	49	90	44	54	0.903358	1.485422	1.356508	1.635675	1.038468	1.127444
antisense	SMAD5_ant	0	1	1	0	0	1	0	0.034354	0.038416	0	0	0.028972
protein_co	potassium_	7	8	5	43	42	77	0.098665	0.132881	0.092869	0.524322	0.665066	1.078616
protein_co	kinesin_fam	3	4	12	54	31	44	0.017488	0.027478	0.092178	0.272312	0.203012	0.254902
protein_co	zinc_finger_	358	345	337	451	383	300	3.752302	4.261288	4.654569	4.08935	4.509855	3.124968
protein_co	solute_carr	549	428	348	270	215	231	10.09188	9.27151	8.42973	4.293647	4.440042	4.220085
protein_co	six_transm	145	106	109	71	36	34	5.846492	5.036633	5.791468	2.476559	1.630718	1.362435
protein_co	cell_divisio	269	210	275	252	186	156	4.644856	4.273132	6.257307	3.764294	3.608128	2.677036
protein_co	Sp8_transc	0	0	0	23	40	26	0	0	0	0.614571	1.388003	0.798113
protein_co	missing_oo	269	261	240	837	695	609	4.124277	4.715667	4.848881	11.10156	11.97097	9.279455
protein_co	KIAA1324-l	341	283	263	376	290	256	2.638924	2.580869	2.682026	2.517233	2.521271	1.968893
protein_co	ubiquitin_s	144	149	127	132	152	141	0.843868	1.028976	0.980732	0.669189	1.000702	0.821185
pseudogen	integrator_	19	16	18	19	28	11	0.394462	0.391452	0.492447	0.341247	0.653069	0.226963
protein_co	synaptotag	62	49	45	20	13	29	1.432086	1.333769	1.369698	0.399641	0.337342	0.66571
protein_co	IQ_motif_a	3	4	7	11	9	8	0.046331	0.072798	0.142457	0.146963	0.15615	0.122787
protein_co	hairy/enha	29	13	29	577	534	515	0.66868	0.353241	0.881156	11.50957	13.83281	11.8015
protein_co	zinc_finger_	63	79	84	379	523	356	0.231842	0.342599	0.407349	1.206575	2.162234	1.302002
protein_co	fatty_acid_	629	555	477	1796	863	1353	33.7727	35.11683	33.74958	83.42275	52.05651	72.19758
protein_co	sonic_hedg	3	0	0	0	5	3	0.035659	0	0	0	0.066767	0.035438

protein_co	T-cell_activ	2	1	2	6	4	2	0.02724	0.01605	0.035896	0.070696	0.061205	0.027072
protein_co	collagen_ty	256498	215760	210372	44785	40426	39112	2265.853	2246.083	2448.897	342.25	401.197	343.3741
protein_co	fibronectin	134	84	115	39	25	27	1.082737	0.799843	1.224478	0.272613	0.226938	0.216816
protein_co	charged_m	0	3	0	400	264	365	0	0.100302	0	9.817557	8.414599	10.2916
protein_co	solute_carr	121	96	126	88	105	101	0.891436	0.833457	1.223236	0.560855	0.869047	0.739496
protein_co	brain_prot	2292	1924	1476	2936	2441	2705	148.1572	146.5616	125.7272	164.1826	177.2658	173.7741
protein_co	lemur_tyro	223	236	214	599	616	599	1.319678	1.64582	1.668829	3.066571	4.095368	3.522895
protein_co	cathepsin_l	28446	23960	19812	7246	5304	6309	388.6347	385.7574	356.6839	85.641	81.4091	85.66246
protein_co	SRY_(sex_d	0	0	0	3	1	2	0	0	0	0.058666	0.025395	0.044931
protein_co	deleted_in_	457	406	496	2032	1935	1680	3.24883	3.401292	4.646514	12.49676	15.45399	11.86942
protein_co	adenylate_(	39	32	31	133	127	113	0.165136	0.159674	0.172971	0.487183	0.60413	0.475517
protein_co	chromoson	53	51	42	38	36	60	1.94178	2.20192	2.027722	1.2044	1.481753	2.184666
protein_co	Sad1_and_l	0	0	0	1	0	4	0	0	0	0.031455	0	0.144544
protein_co	chromoson	0	0	0	2	5	1	0	0	0	0.043105	0.139943	0.02476
protein_co	hepatocyte	3	3	4	3	0	2	0.037734	0.044467	0.066299	0.032644	0	0.025001
protein_co	peroxisoma	465	379	339	282	265	310	5.612759	5.391005	5.3921	2.944663	3.593506	3.718731
protein_co	RAD21_hor	1401	1126	1255	4184	3297	3400	19.78403	18.73795	23.35367	51.113	52.30517	47.71613
protein_co	mediator_c	96	64	62	231	210	264	5.159731	4.053619	4.391191	10.74066	12.68014	14.10163
protein_co	tumor_nec	16	3	11	113	75	70	0.352646	0.07792	0.319482	2.15457	1.857075	1.533299
protein_co	somatomed	39	36	25	674	413	554	0.543199	0.590886	0.458848	8.121142	6.462392	7.668557
protein_co	phosphoryl	21	17	20	29	14	21	0.647502	0.6177	0.812618	0.77354	0.484952	0.643503
protein_co	engrailed_h	6	3	4	484	496	527	0.093563	0.055129	0.082195	6.529211	8.689265	8.167188
protein_co	potassium_	0	0	0	129	85	103	0	0	0	0.846548	0.724381	0.776508
protein_co	CUB_and_S	33	28	38	137	76	75	0.132232	0.132217	0.200651	0.474905	0.342126	0.298672
protein_co	KIAA0146	1156	901	859	710	565	505	15.34599	14.09512	15.02675	8.153767	8.426252	6.662511
protein_co	origin_recc	190	175	186	738	405	492	4.923538	5.34403	6.351429	16.5441	11.79038	12.67064
protein_co	HEAT_repea	739	614	512	1951	1329	1317	11.47314	11.23345	10.47472	26.20342	23.17991	20.32044
protein_co	oxidative_s	151	125	155	385	319	294	1.873908	1.828051	2.534765	4.133281	4.447449	3.626003
protein_co	Sad1_and_l	1112	1000	936	1824	1743	1679	13.04173	13.82094	14.46576	18.50625	22.96556	19.57
protein_co	oxidation_r	1468	1150	1570	696	655	588	17.08074	15.76833	24.07217	7.005723	8.561918	6.799354
protein_co	transmemb	0	0	1	16	7	16	0	0	0.040071	0.420897	0.239133	0.483529
pseudogen	family_with	32	28	18	60	53	45	1.748309	1.802741	1.295912	2.835846	3.253069	2.443377
protein_co	G_protein-r	10	2	4	7	9	6	0.269283	0.063467	0.14194	0.163068	0.27227	0.160572
protein_co	G_protein-r	715	483	419	124	111	116	12.74076	10.14247	9.838713	1.911499	2.222089	2.054268
protein_co	transmemb	21	14	22	12	12	11	0.391052	0.307221	0.53985	0.193312	0.251042	0.203572
protein_co	nitric_oxid	2	0	4	8	1	1	0.02413	0	0.063595	0.083498	0.013554	0.01199
protein_co	MICAL-like_	400	338	238	174	141	161	4.035137	4.018112	3.163807	1.518485	1.597962	1.614112
protein_co	carbonic_a	1	3	4	68	34	50	0.0302	0.106767	0.159186	1.776569	1.153555	1.500686
protein_co	integrator_	3177	2501	2159	4225	4473	4828	22.47075	20.84592	20.12277	25.85175	35.54252	33.93729
protein_co	cyclin-depe	327	229	204	560	353	426	9.847386	8.126729	8.095398	14.58896	11.94255	12.74948
protein_co	solute_carr	2244	1854	1556	2099	2004	2933	24.12174	23.48565	22.04095	19.51917	24.20096	31.3334
protein_co	Fas-activate	1194	927	635	1454	875	1186	20.99354	19.20738	14.71262	22.11611	17.28377	20.7241
protein_co	transmemb	881	725	527	1416	1004	1435	29.8407	28.93865	23.52223	41.49152	38.20462	48.30529
protein_co	chromoson	2	9	4	3	13	7	0.087506	0.464041	0.230622	0.113551	0.638997	0.304379

protein_co gastrulatio	0	0	0	0	1	1	0	0	0	0	0.054465	0.048181
protein_co phosphoryl	933	823	759	1638	1119	1427	11.51911	11.97414	12.34849	17.49501	15.52088	17.50939
protein_co aldehyde_d	1395	1154	1097	2683	2216	2453	14.87766	14.50351	15.41707	24.75392	26.55089	25.99965
protein_co forkhead_b	1286	1113	951	942	1402	1343	6.08909	6.210316	5.933716	3.858561	7.457762	6.319709
protein_co cytochrom	1383	1092	783	1447	1138	1517	88.42681	82.27947	65.9718	80.03746	81.74347	96.39555
protein_co odd-skippe	65	72	39	69	48	39	1.872233	2.443915	1.480287	1.719328	1.553234	1.116403
protein_co tyrosine_3-	8338	7371	7145	31978	24128	25052	84.11243	87.62575	94.98069	279.0696	273.4442	251.1599
protein_co brain_and_	2050	1665	1386	42	31	38	38.33594	36.69218	34.15468	0.679461	0.651273	0.706229
protein_co frizzled_fan	2015	1810	1947	1367	1130	981	28.16159	29.8104	35.85774	16.52775	17.74229	13.62576
protein_co collagen_tr	5058	4634	3561	828	622	692	210.681	227.4624	195.4579	29.83595	29.10623	28.64589
protein_co solute_carr	990	942	911	1221	695	782	18.12922	20.32834	21.98352	19.34295	14.29808	14.23182
protein_co DDB1_and_	1225	1165	1001	2014	1398	1573	12.23636	13.71353	13.17605	17.40358	15.68818	15.61545
protein_co dendrocyte	1	0	0	8	7	14	0.027108	0	0	0.187604	0.213175	0.377162
protein_co tumor_pro	1217	1013	1297	561	666	563	11.42767	11.20943	16.04877	4.557145	7.025711	5.253939
protein_co integrator_	491	458	476	908	664	692	5.610626	6.167403	7.167564	8.975913	8.524068	7.858606
protein_co KIAA1429	1167	925	1115	1394	1120	1083	9.464176	8.840173	11.91576	9.779975	10.2042	8.72871
protein_co FRAS1_rela	7	20	6	121	114	125	0.036732	0.123675	0.041489	0.549278	0.672044	0.651874
protein_co GTP_bindir	703	590	549	19	4	18	16.85576	16.67063	17.34603	0.394103	0.107746	0.428919
protein_co pyruvate_d	689	662	717	916	862	812	8.369974	9.47698	11.4778	9.626388	11.76417	9.80326
protein_co transmemb	268	280	209	188	153	154	3.050567	3.755873	3.134923	1.851257	1.956529	1.742112
protein_co KIAA0196	768	645	699	911	675	653	9.710696	9.61072	11.64665	9.964844	9.588308	8.20563
protein_co ribonuclea	261	227	132	262	149	206	12.65348	12.96888	8.432924	10.98838	8.115304	9.925361
protein_co family_witl	831	773	569	686	572	677	12.07299	13.23428	10.89333	8.621858	9.335956	9.774894
protein_co chromoson	0	2	2	2	0	0	0	0.108406	0.121222	0.079581	0	0
protein_co small_nucl	1170	1055	968	1236	1031	1044	10.9051	11.58786	11.88924	9.9661	10.79572	9.670611
protein_co KIAA1161	43	33	28	161	171	154	0.355808	0.321787	0.30531	1.152489	1.589619	1.266421
protein_co nudix_(nuc	322	292	204	472	354	431	15.88723	16.97784	13.26348	20.1464	19.62206	21.13388
protein_co transmemb	755	798	719	296	267	320	12.38242	15.42299	15.53897	4.199652	4.919476	5.215767
protein_co PC4_and_S	818	683	664	1944	1577	1617	12.77079	12.56586	13.66052	26.2557	27.65955	25.08904
protein_co coiled-coil_	55	45	43	44	23	29	0.447137	0.431119	0.46066	0.309452	0.210065	0.234307
protein_co ubiquitin_a	836	668	686	979	822	975	15.27214	14.38061	16.51401	15.47175	16.86998	17.70141
protein_co DIRAS_fami	210	175	181	202	157	197	2.535373	2.489818	2.879625	2.109779	2.129468	2.363733
protein_co spleen_tyrc	0	0	0	604	450	558	0	0	0	5.526981	5.347485	5.865862
protein_co nipsnap_hc	10	9	7	11	2	0	0.302175	0.320485	0.278735	0.28755	0.067895	0
protein_co ATP-bindin	89	125	97	76	63	61	0.448995	0.743136	0.644848	0.331686	0.35706	0.305837
protein_co nuclear_fac	672	703	504	551	300	340	17.063	21.03529	16.86364	12.10321	8.557686	8.579749
protein_co leucine_zip	64	69	48	120	75	76	1.234326	1.568216	1.219904	2.002138	1.625025	1.45671
protein_co methyltran	648	499	489	1454	1009	1420	5.973492	5.420769	5.940144	11.59527	10.44945	13.00922
protein_co frataxin	187	142	87	596	325	369	3.795999	3.396878	2.327226	10.46631	7.411684	7.444243
protein_co zinc_finger_	68	40	34	95	80	101	1.459849	1.011966	0.961862	1.764354	1.92947	2.154914
protein_co transmemb	1	0	0	15	7	9	0.026563	0	0	0.344698	0.208897	0.237595
protein_co MAM_dom	352	344	342	2000	1329	1138	5.153548	5.935116	6.598187	25.33125	21.85937	16.55829
protein_co protease_se	4	0	3	0	3	1	0.115466	0	0.114117	0	0.097289	0.028688
protein_co carboxypep	0	0	0	1	0	2	0	0	0	0.02461	0	0.056544

protein_co	chromoson	10	11	11	7	21	10	0.144964	0.187915	0.21013	0.087785	0.342003	0.144069
protein_co	transmemb	18	10	7	0	4	2	0.2977	0.194901	0.15256	0	0.074322	0.032874
protein_co	aldehyde_d	2	2	2	14	11	13	0.050252	0.059219	0.06622	0.304312	0.310506	0.324624
protein_co	lysine_(K)-s	304	239	234	415	380	277	3.518597	3.259875	3.569	4.155344	4.941156	3.18629
protein_co	heparan-alp	1495	1255	1280	838	612	744	15.07845	14.91648	17.01219	7.31177	6.934513	7.457583
protein_co	RAS_and_El	0	6	1	150	180	190	0	0.067132	0.012511	1.232037	1.919954	1.792803
protein_co	G_kinase_a	0	1	0	27	18	13	0	0.035089	0	0.695484	0.602118	0.384692
protein_co	kinesin_fam	23	24	31	63	42	52	0.26169	0.321794	0.464789	0.620101	0.536855	0.587993
protein_co	chromoson	16	18	15	552	461	501	0.346728	0.459672	0.428346	10.34834	11.22325	10.78986
protein_co	heterogene	8174	6848	6693	15900	14479	16559	147.0903	145.2179	158.7103	247.5196	292.7097	296.1373
protein_co	serine-rich_	0	3	0	0	0	1	0	0.161487	0	0	0	0.045396
pseudogen	-	9	5	3	47	27	14	0.287723	0.188369	0.126383	1.299848	0.969716	0.444805
protein_co	sushi_von_	797	670	921	611	644	563	3.419008	3.387066	5.206384	2.267493	3.103678	2.400268
protein_co	transient_r	0	0	0	18	12	33	0	0	0	0.079077	0.068461	0.166548
protein_co	chromoson	0	0	0	0	0	5	0	0	0	0	0	0.343434
protein_co	ankyrin_rep	395	369	315	515	476	406	2.918997	3.213438	3.067481	3.292356	3.951778	2.981757
protein_co	fructose-16	0	0	0	33	19	31	0	0	0	1.016385	0.759948	1.096863
protein_co	transmemb	149	135	101	154	125	112	1.55586	1.661212	1.389762	1.39113	1.466369	1.162283
protein_co	zinc_finger	345	280	404	432	404	374	3.575694	3.419844	5.517691	3.873361	4.704047	3.852321
protein_co	cytochrom	0	0	0	7	6	1	0	0	0	0.074143	0.082529	0.012168
protein_co	dynein_ligh	638	668	630	554	391	427	15.23516	18.79793	19.82448	11.44456	10.48944	10.1336
protein_co	Williams_B	31	30	10	41	18	42	1.744071	1.988982	0.741374	1.995489	1.13769	2.348342
protein_co	MID1_inter	991	748	623	1354	989	1340	20.6879	18.40143	17.13822	24.45257	23.19467	27.8008
pseudogen	neutrophil_	0	3	0	0	0	3	0	0.131159	0	0	0	0.110611
protein_co	chromoson	23	21	24	18	10	13	0.240641	0.258921	0.330893	0.162921	0.117541	0.135174
protein_co	chromoson	1	0	0	3	0	0	0.030217	0	0	0.078423	0	0
protein_co	KIAA1958	45	63	66	195	198	155	0.202322	0.333794	0.39103	0.758453	1.000105	0.692584
protein_co	patched_d	32	9	16	245	248	296	0.123532	0.040943	0.081392	0.818195	1.075545	1.13561
protein_co	ring_finger_	0	0	0	0	2	0	0	0	0	0	0.05145	0
protein_co	ankyrin_rep	4	13	0	0	0	0	0.073888	0.282987	0	0	0	0
protein_co	protocadhe	36	38	57	243	245	209	0.195354	0.243003	0.407596	1.140748	1.493604	1.127136
protein_co	phosphatid	155	153	103	275	278	294	2.285753	2.658864	2.001565	3.508273	4.605656	4.308783
protein_co	c-fos_induc	0	2	0	0	0	1	0	0.061255	0	0	0	0.025829
protein_co	olfactory_r	1	0	0	0	0	0	0.051599	0	0	0	0	0
protein_co	spermatid_	118	146	102	996	740	827	0.99317	1.448109	1.131296	7.2521	6.997167	6.917618
protein_co	claudin_3	1	1	0	285	251	259	0.041588	0.049008	0	10.25349	11.72699	10.70467
protein_co	GTPase_act	800	760	762	1043	948	817	4.746475	5.313759	5.957595	5.353385	6.318858	4.817402
protein_co	chromoson	649	568	471	334	260	333	12.77275	13.17332	12.21506	5.686556	5.748602	6.513189
protein_co	WNK_lysin	1	0	0	26	49	29	0.006794	0	0	0.15282	0.374014	0.195817
protein_co	ATPase_Cu-	373	290	459	126	123	70	2.327831	2.132788	3.774767	0.680262	0.862376	0.43416
protein_co	zinc_finger_	24	7	4	290	230	209	0.348487	0.119779	0.076537	3.642809	3.751909	3.016
protein_co	neuroligin_	447	422	445	819	698	677	3.576337	3.978785	4.691652	5.668627	6.273869	5.383061
protein_co	highly_dive	166	115	109	128	90	123	1.417452	1.157192	1.226484	0.945526	0.86336	1.043795
protein_co	NADH_deh	438	312	252	733	523	711	16.97522	14.24961	12.86995	24.57584	22.77153	27.3855

protein_co aquaporin_	1	5	0	0	2	2	0.031739	0.187014	0	0	0.071314	0.063086
protein_co nucleolar_p	822	751	677	2429	2078	2289	9.17897	9.882553	9.961979	23.46457	26.06854	25.40257
protein_co aquaporin_	16	12	3	21	29	21	0.290985	0.257181	0.071896	0.330394	0.592512	0.379559
protein_co tRNA_meth	191	174	141	276	219	238	4.433025	4.759082	4.312417	5.541647	5.710314	5.489761
protein_co valosin_cor	8304	7382	6437	13188	11317	12872	100.6	105.3882	102.7612	138.2142	154.0249	154.9767
protein_co phosphatid	516	424	380	929	734	719	4.104816	3.974816	3.983478	6.393266	6.559778	5.684373
protein_co stomatin_(I	2286	1901	1410	5606	3121	3945	94.69727	92.80053	76.96888	200.8988	145.246	162.4119
protein_co bromodom	611	503	614	668	1038	981	2.842189	2.757317	3.763699	2.688135	5.42448	4.535136
protein_co SLIT_and_N	402	330	309	56	52	47	4.788992	4.632752	4.850777	0.577124	0.695938	0.556449
protein_co maternal_e	350	253	303	2062	1505	1568	7.894907	6.725222	9.006508	40.23747	38.13858	35.15076
protein_co armadillo_I	2	0	2	1	7	5	0.037667	0	0.049636	0.016293	0.148108	0.093586
protein_co OTU_doma	42	42	31	35	16	18	0.714729	0.842264	0.695166	0.515256	0.305887	0.304421
protein_co Rho_GTPas	571	463	460	726	643	532	6.15167	5.878209	6.530547	6.766383	7.782461	5.696108
protein_co FAT_tumor	14	43	29	357	343	256	0.038752	0.140263	0.105779	0.854868	1.066623	0.704235
protein_co coiled-coil_	0	0	0	12	8	5	0	0	0	0.197409	0.170908	0.094494
protein_co HECT_dom	370	290	395	259	197	165	3.649063	3.370425	5.133475	2.209746	2.182704	1.617235
protein_co solute_carr	0	1	0	71	23	32	0	0.027901	0	1.454259	0.611783	0.752974
protein_co F-box_prot	203	125	213	259	188	179	2.789261	2.023998	3.856626	3.078618	2.902017	2.444307
protein_co DEAD/H_(A	251	238	191	254	235	219	1.956735	2.186464	1.962124	1.712991	2.058142	1.696728
protein_co claudin_2	8	2	4	0	0	1	0.134453	0.039611	0.088588	0	0	0.016703
protein_co leucine_ric	295	193	231	694	622	612	3.672136	2.831138	3.789165	7.473416	8.698335	7.571079
protein_co zinc_finger_	6	3	7	350	348	271	0.089201	0.052559	0.137136	4.501437	5.812305	4.004046
protein_co serine_paln	719	724	757	1398	1163	1468	13.70708	16.26529	19.01721	23.05613	24.90835	27.81326
protein_co annexin_A8	0	0	0	1	0	0	0	0	0	0.023236	0	0
protein_co Werner_syn	175	161	211	339	297	190	1.776543	1.926064	2.822637	2.977148	3.387219	1.916907
protein_co membrane-	492	421	406	278	224	249	5.187606	5.231076	5.641086	2.535769	2.653377	2.609221
protein_co thyroid_sti	97	82	80	3	2	0	1.124677	1.12041	1.222309	0.030091	0.026052	0
protein_co cofilin_2_(n	995	1008	936	1155	734	787	16.82411	20.08522	20.85546	16.89484	13.94293	13.22493
protein_co SGT1_supp	1001	896	867	1847	1138	1491	31.86647	33.61359	36.37088	50.86625	40.6997	47.17231
protein_co general_tra	1114	1069	1260	1076	1107	943	9.352405	10.57604	13.93938	7.81472	10.44082	7.867911
protein_co zinc_finger_	5327	4412	4707	716	888	728	57.16941	55.79863	66.56715	6.647479	10.70639	7.764652
protein_co phosphoglu	479	360	501	265	234	242	2.978125	2.637649	4.104686	1.425333	1.634453	1.495314
protein_co phytanoyl-C	3	9	3	53	44	37	0.044389	0.156928	0.058494	0.678407	0.731398	0.54408
protein_co solute_carr	30	52	31	452	298	337	0.380505	0.777231	0.518127	4.959536	4.246244	4.247948
protein_co inositol_pc	2827	2705	2053	1918	1825	2095	31.62142	35.65578	30.26073	18.55954	22.93335	23.28892
protein_co paired-like_	0	1	0	1	0	0	0	0.03672	0	0.026956	0	0
protein_co gap_junctic	156	180	111	27	20	27	3.576784	4.863487	3.353713	0.535544	0.515166	0.615236
protein_co crystallin_l	229	175	113	62	28	41	7.66824	6.905663	4.986243	1.796036	1.053337	1.364438
protein_co receptor_ac	931	743	665	1389	1092	1219	9.469369	8.905684	8.91308	12.22184	12.47794	12.3221
protein_co hepatic_an	6	1	0	6	3	3	0.088186	0.01732	0	0.076289	0.049536	0.043821
protein_co spindle_an	155	98	88	1133	786	960	2.811187	2.094552	2.103175	17.77669	16.0151	17.3037
protein_co mitochond	591	462	512	1146	866	1002	16.2959	15.01205	18.60354	27.33622	26.82612	27.45796
protein_co chromoson	79	27	45	603	350	413	1.183792	0.476781	0.888578	7.816796	5.892038	6.150468
protein_co PCF11_clea	622	592	621	723	636	706	4.289345	4.810933	5.64322	4.313222	4.927274	4.838546

protein_co	PBX/knotte	130	138	76	110	100	118	1.518943	1.900134	1.170163	1.111869	1.312644	1.370218
protein_co	leucine_ric	43	35	43	443	233	275	1.207032	1.157779	1.590573	10.75764	7.347767	7.67172
protein_co	ribosomal_	2788	2391	1724	2266	1995	3382	197.8545	199.9585	161.2224	139.1157	159.0542	238.5264
protein_co	dynein_axo	254	247	184	738	542	565	4.53831	5.200732	4.332246	11.40722	10.8795	10.03272
protein_co	chromoson	39	47	26	208	138	202	0.973915	1.383124	0.855587	4.493478	3.871546	5.013226
protein_co	chromoson	10	9	12	52	29	32	0.171998	0.18242	0.271982	0.773731	0.560364	0.546995
protein_co	zinc_finger_	147	114	100	576	288	338	3.050696	2.788005	2.734743	10.34111	6.714647	6.971207
protein_co	kelch_dom	493	400	397	539	393	485	11.24996	10.75651	11.93794	10.64035	10.07502	10.99906
protein_co	echinoderm	52	50	45	165	111	79	0.287663	0.325955	0.328041	0.789636	0.689846	0.434327
protein_co	nuclear_ex	582	606	555	1099	828	852	6.115851	7.50436	7.685316	9.99067	9.774922	8.897811
protein_co	RNA_pseud	660	579	483	883	635	742	13.93184	14.40291	13.43527	16.12457	15.0587	15.56604
protein_co	ADP-ribosy	1306	1060	1137	2629	2752	2952	43.67716	41.77574	50.10793	76.06148	103.3972	98.1154
protein_co	tetratricop	398	336	297	294	199	183	9.46564	9.417016	9.308039	6.048912	5.317029	4.325414
protein_co	transmemb	0	0	4	2	4	5	0	0	0.052316	0.017172	0.044601	0.04932
protein_co	neuroglobi	0	0	0	2	0	0	0	0	0	0.048619	0	0
protein_co	NADP-depe	13	10	10	36	9	12	0.340204	0.308392	0.344851	0.815008	0.264599	0.312095
protein_co	caudal_typ	0	0	0	1999	1622	1927	0	0	0	22.5887	23.80211	25.01537
protein_co	APC_memb	0	0	0	5	2	8	0	0	0	0.022774	0.01183	0.041861
protein_co	aldo-keto_r	38	31	35	88	86	61	1.215564	1.168592	1.475356	2.435229	3.090591	1.939249
protein_co	kelch_repe	222	203	229	435	356	367	2.269776	2.445869	3.085321	3.847533	4.089113	3.729115
protein_co	fatty_acid_	4	0	0	22	33	16	0.10679	0	0	0.508107	0.989766	0.424521
protein_co	dorsal_root	0	0	0	0	7	0	0	0	0	0	0.15267	0
protein_co	nudix_(nuc	611	525	472	1530	967	1282	9.422356	9.540798	9.591689	20.4114	16.75305	19.64789
protein_co	dapper_ant	202	123	130	525	592	573	2.863975	2.055086	2.428823	6.439321	9.429497	8.073875
protein_co	oxoglutarat	1	0	0	6	9	5	0.023169	0	0	0.12026	0.23426	0.115129
protein_co	upper_zone	0	0	0	0	4	0	0	0	0	0	0.288019	0
protein_co	BEN_domai	4	2	2	70	33	50	0.032459	0.019126	0.021387	0.491405	0.300844	0.403235
protein_co	ATP_syntha	1893	1736	1382	3832	2377	3130	86.17137	93.12562	82.90013	150.904	121.56	141.601
protein_co	PRP18_pre	57	75	53	73	58	86	1.757505	2.725148	2.153439	1.947187	2.009087	2.635299
protein_co	TAF3_RNA_	153	127	184	539	435	533	1.662556	1.626281	2.634738	5.066833	5.31035	5.756012
protein_co	V-set_and_t	4	4	5	4	0	0	0.096608	0.113846	0.159132	0.083575	0	0
protein_co	voltage-dep	3378	2899	2425	6335	3915	4881	113.1149	114.3972	107.0057	183.5143	147.2791	162.4346
protein_co	catechol-O-	119	84	66	326	212	297	5.758664	4.790283	4.208754	13.64757	11.5255	14.2837
protein_co	solute_carr	103	107	50	164	80	113	1.321921	1.6183	0.845616	1.820853	1.153472	1.441306
protein_co	PDZ_domai	339	280	319	429	440	430	2.76789	2.694103	3.432216	3.030187	4.035997	3.489211
protein_co	zinc_finger_	1515	1144	1004	525	452	626	23.96343	21.32404	20.9269	7.183874	8.032003	9.840572
protein_co	dachshund_	26	17	19	338	396	306	0.262734	0.202442	0.253007	2.954768	4.495603	3.073086
protein_co	family_with	310	233	273	612	447	486	5.485197	4.858403	6.365433	9.367958	8.885607	8.546266
protein_co	quiescin_Q	592	514	465	965	896	990	6.918558	7.078873	7.161132	9.756279	11.76389	11.49843
protein_co	family_with	640	505	485	1034	678	838	5.713699	5.312952	5.705766	7.985846	6.800113	7.435173
protein_co	nuclear_rec	1387	1202	1209	2217	2440	2274	5.695715	5.81679	6.542337	7.875905	11.25669	9.280511
protein_co	peroxiredo	1539	1454	1327	4073	2370	3265	35.78225	39.83828	40.65695	81.92312	61.9051	75.44351
protein_co	ecto-NOX_(	295	218	237	212	210	187	3.732694	3.250603	3.951696	2.320595	2.985168	2.351536
protein_co	growth_ho	2435	2075	1823	4748	3486	4032	60.57863	60.8339	59.76432	102.1867	97.43094	99.68978

protein_co	C-type_lect	1	0	0	6	10	4	0.017335	0	0	0.089978	0.194748	0.068912
protein_co	small_nucl	1059	802	626	1122	979	1114	11.19052	9.987018	8.716929	10.25676	11.62214	11.69901
protein_co	transmemb	0	0	0	3	8	4	0	0	0	0.05031	0.174225	0.077062
protein_co	peptidase_	1384	1108	964	2798	1835	2222	21.93066	20.69009	20.12924	38.35538	32.66636	34.99204
protein_co	serologicall	782	724	597	1797	1061	1314	17.89104	19.51976	17.99856	35.56639	27.2705	29.87678
protein_co	FERM_dom	0	0	0	1	10	6	0	0	0	0.014321	0.185978	0.098713
protein_co	adenylate_	9	2	3	11	7	11	0.193294	0.050619	0.084905	0.204376	0.168897	0.234789
protein_co	chromoson	148	120	105	105	45	48	3.089616	2.952101	2.888464	1.896248	1.055369	0.99585
protein_co	tuberous_s	909	848	798	689	673	649	5.593138	6.14886	6.470374	3.667532	4.652173	3.96868
protein_co	hypoxanthi	347	301	262	947	566	687	13.05652	13.34663	12.99075	30.82556	23.92564	25.69002
protein_co	loss_of_het	56	59	66	151	67	97	1.444783	1.793799	2.243848	3.370192	1.941952	2.487116
protein_co	family_witl	75	86	49	390	271	232	1.647541	2.226284	1.418424	7.411441	6.687956	5.064921
protein_co	zinc_finger_	548	430	321	1519	1222	1411	21.09939	19.51034	16.28656	50.5953	52.85787	53.99158
protein_co	storkhead_	3	1	0	24	15	13	0.047031	0.018474	0	0.325488	0.264181	0.202542
protein_co	ret_proto-c	56	44	29	2	13	9	0.52389	0.485079	0.357508	0.016186	0.13663	0.083677
protein_co	DEAD_(Asp	1540	1243	1505	6529	5246	5201	17.30612	16.46104	22.28693	63.47295	66.23024	58.08654
protein_co	BMS1_hom	1008	895	823	2086	1931	2033	12.63365	13.21899	13.59261	22.61755	27.18939	25.323
protein_co	serine/thre	355	299	196	224	168	213	9.009613	8.942441	6.554939	4.918003	4.790007	5.372384
protein_co	KIAA1462	503	508	608	434	536	489	2.874185	3.42072	4.578098	2.145356	3.440809	2.776932
protein_co	FUN14_dor	878	667	485	931	660	898	7.200959	6.446571	5.241703	6.605543	6.081194	7.319507
protein_co	transmemb	480	337	364	694	498	657	7.359304	6.088811	7.354137	9.204877	8.57776	10.01084
protein_co	methyltran	234	181	173	580	418	538	4.291026	3.911389	4.180481	9.201027	8.611338	9.804766
protein_co	solute_carr	0	2	1	3	2	1	0	0.090483	0.05059	0.099635	0.086259	0.038154
protein_co	NDRG_fami	85	46	41	111	63	96	1.562495	0.996471	0.993158	1.765166	1.301036	1.753802
protein_co	Rho_guanir	3297	2722	2499	1021	1226	1188	29.48918	28.69056	29.45404	7.900098	12.31922	10.56014
protein_co	NMDA_rece	3238	2716	2103	1473	1106	1260	47.01671	46.47424	40.23922	18.50296	18.04179	18.18258
protein_co	zinc_finger_	316	220	190	1160	829	945	5.447527	4.469326	4.316191	17.29949	16.05521	16.19026
protein_co	caspase_7_	433	381	344	395	331	350	8.509076	8.823209	8.908155	6.715133	7.307546	6.83553
protein_co	protein_ph	13	16	6	14	12	13	0.408205	0.592054	0.248268	0.380299	0.423316	0.405684
protein_co	butyrophili	1	0	0	3	1	0	0.015126	0	0	0.039256	0.016993	0
protein_co	chromoson	226	174	220	220	254	268	1.651437	1.498339	2.118416	1.390719	2.085146	1.946248
protein_co	von_Willeb	1	0	0	42	32	53	0.01797	0	0	0.652938	0.646038	0.946553
protein_co	methyltran	652	533	512	1284	1012	998	13.68114	13.17981	14.15727	23.30789	23.85637	20.81206
protein_co	sal-like_2_(	475	374	385	408	514	502	5.105984	4.737667	5.453576	3.794102	6.207233	5.362894
protein_co	TruB_pseuc	366	359	327	603	512	471	5.693918	6.581603	6.703671	8.11541	8.948478	7.282168
protein_co	family_witl	5	6	4	3	3	5	0.109337	0.154616	0.115264	0.056752	0.0737	0.108662
protein_co	zinc_finger_	727	686	588	336	314	307	8.581517	9.542471	9.146223	3.431089	4.163977	3.601452
polymorph	pancreatic_	0	0	0	1	0	0	0	0	0	0.030924	0	0
protein_co	chromoson	1	1	2	130	94	143	0.029559	0.034834	0.077904	3.32432	3.121572	4.200898
protein_co	heat_shock	104	100	99	35	27	30	0.962227	1.090313	1.207019	0.28014	0.280645	0.275851
pseudogen	family_witl	0	1	0	2	0	0	0	0.018696	0	0.027449	0	0
protein_co	frequently_	22	19	19	22	9	8	0.439344	0.44714	0.500001	0.380074	0.201917	0.158775
protein_co	ubiquitin_(	1078	869	692	1085	620	848	33.45275	31.77898	28.29788	29.12767	21.61493	26.15282
protein_co	ankyrin_rep	1	1	0	8	9	23	0.035675	0.04204	0	0.246894	0.360703	0.815447

protein_co	E2F_transcr	266	181	274	781	738	719	2.453363	1.967279	3.330164	6.231524	7.646904	6.590506
protein_co	Rho_GTPas	228	138	232	437	469	312	2.123227	1.514425	2.84698	3.520514	4.906632	2.887526
protein_co	iron-sulfur_	99	154	68	297	187	219	1.995871	3.658686	1.806513	5.179846	4.235338	4.387843
protein_co	otogelin-lik	32	10	24	6	7	6	0.209589	0.077184	0.207141	0.033996	0.051507	0.039055
protein_co	glycosyltra	1	5	4	211	159	154	0.020942	0.123393	0.110385	3.822614	3.740772	3.205128
protein_co	protein_kir	548	532	383	1396	994	1422	14.44085	16.52079	13.29982	31.82443	29.42711	37.24101
protein_co	tetratricop	370	297	244	638	435	408	5.622321	5.318357	4.885833	8.386826	7.425954	6.161462
protein_co	solute_carr	1972	1565	1183	660	431	614	29.38352	27.4801	23.22825	8.507537	7.214782	9.092324
protein_co	proteasom	2351	1862	1528	5504	3593	4763	80.61158	75.23702	69.04035	163.2624	138.4048	162.3062
protein_co	receptor-as	6	11	1	21	3	23	0.190093	0.410691	0.041749	0.57557	0.106779	0.724191
protein_co	ATP/GTP_b	10	3	0	20	27	27	0.148004	0.052324	0	0.256074	0.448938	0.397143
protein_co	tandem_C2	12	3	9	151	116	145	0.123454	0.036371	0.122011	1.343885	1.340693	1.482518
protein_co	cleavage_ar	719	513	692	1600	1413	1244	7.18064	6.037522	9.106997	13.82348	15.85351	12.34708
protein_co	single-pass_	58	51	33	4	0	12	2.413976	2.501395	1.809896	0.144022	0	0.496359
protein_co	modulator_	134	126	112	401	259	306	2.805098	3.108285	3.089556	7.261906	6.091049	6.366113
protein_co	interferon_	288	310	219	195	145	246	18.41426	23.35772	18.45188	10.78597	10.41547	15.63171
protein_co	interferon_	19	21	8	32	11	23	0.413942	0.539153	0.229673	0.603113	0.269233	0.497993
protein_co	calmin_(cal	34	21	27	80	81	64	0.286213	0.208323	0.299508	0.582591	0.766028	0.535427
protein_co	PDZ_domai	0	2	0	1	6	0	0	0.03658	0	0.013427	0.104619	0
protein_co	solute_carr	0	0	0	2	0	3	0	0	0	0.01293	0	0.022282
protein_co	coiled-coil_	0	0	6	3	4	1	0	0	0.161054	0.052865	0.091537	0.020244
protein_co	NEL-like_1_	1	0	0	6	16	4	0.015903	0	0	0.082545	0.285856	0.063219
protein_co	phosphotri	42	34	27	370	344	356	0.5887	0.561605	0.498705	4.486522	5.416922	4.959121
protein_co	complemer	0	0	4	80	87	109	0	0	0.111935	1.46968	2.075574	2.300414
protein_co	calcium_ch	149	117	132	18	15	25	1.767072	1.635162	2.062893	0.184673	0.199852	0.294658
protein_co	protein_tyr	169	179	121	885	653	623	6.829792	8.524736	6.443784	30.94048	29.64716	25.0218
protein_co	ADP-ribosy	581	494	668	1240	1104	867	4.274419	4.282871	6.47608	7.891974	9.12471	6.33913
protein_co	single-pass_	48	50	28	213	141	152	2.301782	2.825531	1.769359	8.836202	7.596109	7.243963
protein_co	KIAA1731	186	129	177	244	234	203	1.222474	0.999133	1.532973	1.387329	1.727792	1.325966
protein_co	TATA_box_l	1455	1424	1182	2196	1867	1886	17.67534	20.38553	18.92157	23.07811	25.47993	22.76964
protein_co	ankyrin_rep	181	207	147	164	129	135	1.954778	2.634488	2.092045	1.532236	1.565156	1.448979
protein_co	R3H_doma	249	195	183	428	392	313	3.856731	3.559277	3.735132	5.734913	6.821112	4.81808
protein_co	angiomotin	2634	2312	2632	3801	4327	4385	15.54588	16.08032	20.47012	19.40709	28.69033	25.72047
protein_co	HtrA_serine	27646	23066	19684	44	44	43	690.3805	678.7903	647.7455	0.950543	1.234406	1.067172
protein_co	centrosoma	647	596	576	1243	843	831	10.77811	11.70015	12.64432	17.91317	15.77665	13.7578
protein_co	t-complex_	20	24	24	14	23	0	0.331088	0.468201	0.523552	0.200496	0.42775	0
protein_co	sprouty-rel	1347	1329	1428	1111	1080	959	9.166005	10.65724	12.80488	6.540178	8.256297	6.485459
protein_co	transmemb	0	0	2	0	0	0	0	0	0.048212	0	0	0
protein_co	G_protein-r	614	485	436	108	61	90	8.456236	7.871501	7.912797	1.286754	0.943817	1.231859
protein_co	junctional_	1744	1432	1469	888	714	664	23.60151	22.83723	26.1969	10.39607	10.85527	8.930401
protein_co	galactosida	0	1	0	24	19	18	0	0.016154	0	0.284613	0.292605	0.245223
protein_co	ADAM_met	1422	1099	1054	542	614	618	13.27961	12.09457	12.97063	4.378728	6.441738	5.735665
protein_co	SV2_relate	0	0	1	0	2	0	0	0	0.022475	0	0.038322	0
protein_co	glutamic_p	1148	1009	783	1258	930	1156	14.37471	14.88865	12.91974	13.62702	13.08245	14.38549

protein_co amnion_as	13	15	2	6	18	3	0.24828	0.337596	0.050334	0.099132	0.386207	0.056942
protein_co RAB8B_mei	577	471	541	500	454	506	6.179841	5.944694	7.635431	4.632703	5.462688	5.385942
protein_co IKBKB_inte	1731	1641	1430	2753	1761	2103	28.73655	32.10356	31.283	39.53728	32.84324	34.69657
protein_co RNA_pseud	162	144	83	424	356	440	4.574102	4.791378	3.088188	10.35666	11.29249	12.34676
protein_co hypoxia_in	749	709	682	606	728	815	13.13442	14.65151	15.75971	9.193156	14.34199	14.20353
protein_co NADH_deh	12	10	12	8	7	23	0.514823	0.505573	0.678411	0.296913	0.337384	0.980651
protein_co zinc_finger_	339	257	197	474	350	457	6.161001	5.50417	4.717943	7.452345	7.146094	8.254247
protein_co protein_ph	7	0	0	5	1	2	0.494116	0	0	0.305326	0.079301	0.140304
protein_co serine_pept	12	8	4	3978	3271	3157	0.207883	0.163319	0.091313	59.61651	63.66025	54.35293
protein_co fibrillin_1	17523	14798	17315	1998	2058	1489	78.91162	78.53127	102.7519	7.783788	10.41183	6.664029
protein_co arginine_va	1	0	1	4	14	0	0.034715	0	0.045746	0.120128	0.546008	0
protein_co chromoson	0	0	0	0	0	1	0	0	0	0	0	0.049264
protein_co DEP_domai	10	3	4	45	42	18	0.226534	0.080087	0.119407	0.881879	1.068887	0.405243
protein_co leucine-rich	0	0	0	0	1	0	0	0	0	0	0.014921	0
protein_co bromodom	732	615	565	2154	1711	1767	7.216538	7.144963	7.340085	18.37073	18.95033	17.31267
protein_co creatine_ki	1105	794	637	1071	531	785	34.23043	28.98529	26.00305	28.70136	18.47964	24.16737
protein_co tRNA_meth	502	356	262	971	615	891	8.230529	6.8783	5.66057	13.77229	11.32787	14.51815
protein_co beta-transd	454	397	433	531	542	483	3.918359	4.03781	4.924601	3.964659	5.25529	4.142906
protein_co polymerase	338	251	220	445	277	362	6.140719	5.373823	5.26696	6.993999	5.653682	6.536131
protein_co BCL2-assoc	610	439	485	1058	891	964	6.6353	5.62733	6.951961	9.955875	10.88824	10.42119
protein_co deleted_in_	618	604	402	409	311	419	21.82624	25.13822	18.70903	12.49617	12.33957	14.70666
protein_co La_ribonuc	954	784	676	270	208	329	24.3401	23.57204	22.7277	5.959376	5.961923	8.34218
protein_co apoptosis_i	1203	955	1030	3465	2537	2553	17.14809	16.04208	19.34738	42.72838	40.62746	36.16685
protein_co asparaginas	0	0	0	0	5	5	0	0	0	0	0.137867	0.121961
protein_co zinc_finger_	171	144	111	204	159	208	2.144731	2.128366	1.834571	2.213451	2.240386	2.592685
protein_co Hermansky	510	425	350	867	591	762	10.20405	10.0207	9.227947	15.00667	13.2843	15.15189
protein_co SUMO/sent	24	18	16	37	31	48	0.692794	0.612311	0.608622	0.923969	1.005318	1.377031
protein_co nucleolar_a	1752	1441	1385	5536	4573	4770	23.38694	22.66786	24.36262	63.92908	68.57876	63.28014
protein_co alkB_alkyla	205	160	165	417	227	284	6.970394	6.41107	7.393026	12.26599	8.671184	9.596911
protein_co COP9_signa	1649	1399	1320	2552	1634	1762	21.49709	21.49235	22.67607	28.78079	23.93096	22.82836
protein_co gamma-am	14	19	25	423	410	368	0.124903	0.199758	0.293913	3.264735	4.109391	3.262887
protein_co thymus_bra	26	11	13	0	0	0	0.86953	0.433522	0.572914	0	0	0
protein_co sphingosin	1607	1309	1031	1323	1036	1090	14.80873	14.21506	12.51975	10.5469	10.72534	9.982474
protein_co fibroblast_g	436	365	423	435	459	299	3.364272	3.31898	4.301103	2.903735	3.978931	2.292902
protein_co chaperonin	3426	2835	2501	10074	6619	7373	82.85786	80.79909	79.7067	210.7712	179.8406	177.2149
protein_co pterin-4_al	363	312	235	817	653	876	19.10296	19.34888	16.29659	37.19454	38.60614	45.81502
protein_co ariadne_ho	837	750	866	1475	1076	1038	7.327867	7.737853	9.990905	11.17139	10.58311	9.031484
protein_co chromoson	14	15	17	7	8	8	0.200047	0.252582	0.320101	0.08653	0.128423	0.113607
protein_co CXADR-like_	629	496	514	204	285	259	12.75858	11.85606	13.73882	3.579685	6.494497	5.221088
protein_co sodium_ch	14	0	3	25	4	22	0.122286	0	0.034531	0.188908	0.039252	0.190977
protein_co cytochrom	683	578	558	869	667	724	11.14633	11.11594	11.99997	12.26857	12.22886	11.74247
protein_co zinc_finger_	172	156	153	355	281	316	2.204807	2.356534	2.584451	3.93671	4.046667	4.025676
protein_co family_with	52	56	24	61	57	66	1.249062	1.585169	0.759673	1.267574	1.53817	1.575557
protein_co syntaxin_bi	237	225	258	191	134	180	2.009773	2.248477	2.883057	1.401184	1.276593	1.516984

protein_co	cysteine/ty	178	191	170	350	268	310	3.038857	3.84265	3.824495	5.169177	5.140131	5.259708
protein_co	cullin_5	518	462	530	828	733	768	4.317971	4.538361	5.821845	5.970948	6.864407	6.362398
protein_co	myelin_reg	0	0	0	28	3	7	0	0	0	0.370092	0.051494	0.106291
protein_co	WW_doma	1259	982	1037	968	860	930	16.24091	14.92806	17.62781	10.80247	12.46328	11.92277
protein_co	chromoson	225	242	208	378	215	254	4.918135	6.233621	5.991231	7.147806	5.279654	5.517741
protein_co	complemer	5	9	6	0	4	1	0.092879	0.197014	0.14687	0	0.083475	0.018461
protein_co	pleckstrin_	279	257	155	199	123	165	7.08759	7.693688	5.188728	4.373312	3.510335	4.1657
protein_co	transmemb	493	401	362	49	50	83	13.30271	12.75101	12.87172	1.143805	1.515696	2.225773
protein_co	anaphase_p	822	645	596	1749	1104	1552	13.6205	12.59471	13.01375	25.07114	20.5513	25.55775
protein_co	sphingomy	2013	1594	1298	458	355	360	43.46257	40.55711	36.93016	8.554608	8.61091	7.724738
protein_co	amyloid_be	1508	1346	1021	736	664	723	30.21765	31.78421	26.96	12.75851	14.94777	14.39817
protein_co	synaptopoc	6	2	1	2	0	6	0.064549	0.025356	0.014177	0.018614	0	0.06415
protein_co	nudix_(nuc	114	114	91	200	144	219	2.820221	3.323458	2.966569	4.280272	4.002118	5.384335
protein_co	chromoson	22	9	9	13	7	10	0.434104	0.209277	0.234018	0.22191	0.155174	0.196102
protein_co	tripartite_r	822	635	905	556	782	705	13.67615	12.4501	19.84154	8.002574	14.61665	11.6571
protein_co	integrin-lin	40	22	20	9	19	15	1.021041	0.661779	0.672741	0.198742	0.544861	0.380526
protein_co	TAF10_RNA	1191	1082	800	1298	870	1398	11.69159	12.51688	10.34872	11.02299	9.594669	13.63887
protein_co	tripeptidyl_	2824	2419	2413	1963	1378	1302	42.28093	42.67984	47.60713	25.42513	23.17811	19.37316
protein_co	dachsous_1	4388	3759	3368	754	984	910	21.58367	21.78904	21.8306	3.208434	5.437546	4.448461
protein_co	neuropilin_	154	117	122	652	472	493	2.666093	2.386973	2.783231	9.764842	9.180063	8.482252
protein_co	MSS51_mit	100	84	75	81	63	74	2.186741	2.16463	2.161192	1.532305	1.5477	1.608195
protein_co	cytochrom	356	288	223	745	521	711	3.187383	3.038672	2.631018	5.770368	5.240479	6.326499
protein_co	ubiquitin_s	132	84	93	291	281	258	1.118651	0.838894	1.038576	2.133421	2.675321	2.172951
protein_co	recombinat	27	33	50	35	23	21	0.217765	0.313649	0.531408	0.244205	0.208401	0.168326
protein_co	chromoson	172	150	93	241	141	207	9.791238	10.06254	6.976328	11.86832	9.017316	11.71087
protein_co	WD_repeat	17	18	6	21	25	14	0.490462	0.611978	0.228109	0.524129	0.810299	0.401415
protein_co	olfactory_r	0	3	0	0	0	0	0	0.177574	0	0	0	0
protein_co	olfactory_r	2	0	0	0	0	0	0.095389	0	0	0	0	0
protein_co	ATPase_cla	345	297	288	332	309	266	2.483972	2.519945	2.732466	2.067896	2.499396	1.903351
protein_co	PTPRF_inte	836	618	639	587	611	586	12.4427	10.83936	12.53268	7.558043	10.21641	8.667932
protein_co	cytochrom	1001	865	785	941	710	834	7.100889	7.231058	7.338091	5.774725	5.658301	5.879689
protein_co	serpin_pep	256	241	227	300	151	178	6.152017	6.824985	7.1885	6.236801	4.076652	4.251158
protein_co	KIAA0355	278	210	238	574	582	497	2.196001	1.954853	2.477419	3.922497	5.164874	3.901698
protein_co	serpin_pep	165	177	136	472	282	285	2.512299	3.175907	2.728733	6.217165	4.823759	4.312627
protein_co	tubby_hom	570	459	514	471	546	487	4.700369	4.460431	5.585409	3.360013	5.058232	3.991128
protein_co	resistance_	0	2	1	53	55	57	0	0.023668	0.013233	0.460421	0.620481	0.568854
protein_co	LIM_domai	0	0	0	43	16	9	0	0	0	1.53976	0.74403	0.370232
pseudogen	olfactory_r	0	0	0	5	5	0	0	0	0	0.247562	0.321491	0
protein_co	isocitrate_d	179	146	153	206	233	221	2.295649	2.206543	2.585703	2.285507	3.357047	2.816789
protein_co	WD_repeat	4	12	20	102	44	100	0.028209	0.099727	0.185862	0.622284	0.3486	0.700867
protein_co	cellular_ret	176	158	129	24	11	6	12.06945	12.76847	11.65734	1.4238	0.847455	0.408917
protein_co	phospholip	3	3	0	1	2	3	0.079135	0.093255	0	0.02282	0.059268	0.078646
protein_co	zinc_finger_	8	6	4	23	10	8	0.073606	0.065055	0.048497	0.183068	0.103364	0.073151
protein_co	X-ray_radia	91	82	113	53	50	73	0.848025	0.900509	1.387652	0.427274	0.523463	0.676083

protein_co	tripartite_r	298	250	211	200	258	162	1.564655	1.546854	1.459888	0.908438	1.521847	0.845331
protein_co	ring_finger_	170	156	211	91	163	79	1.15045	1.244086	1.881638	0.53275	1.23924	0.531319
protein_co	ribosomal_	32662	28327	19904	19709	16906	23058	351.741	359.4909	282.459	183.6149	204.5362	246.7809
protein_co	suppressior	603	448	503	588	685	668	7.023855	6.14955	7.720777	5.925139	8.963917	7.732934
protein_co	chromodor	11	11	18	11	12	9	0.247493	0.291655	0.533676	0.214105	0.30332	0.201244
protein_co	transmemb	37	28	46	6	2	4	0.503422	0.448948	0.824752	0.070623	0.030571	0.054088
protein_co	protogenin	17	6	5	8431	8762	7179	0.075207	0.03128	0.029148	32.26628	43.54709	31.56315
protein_co	centromere	98	67	113	871	585	605	2.09118	1.684796	3.177449	16.07854	14.02395	12.83011
protein_co	A_kinase_(A	332	321	279	488	305	481	12.36904	14.09322	13.69737	15.72827	12.76577	17.80954
protein_co	ATM_intera	715	673	704	1728	1333	1247	7.084561	7.858308	9.192093	14.812	14.83837	12.27957
protein_co	chromoson	37	10	13	30	27	41	1.054829	0.33596	0.488381	0.739885	0.864755	1.161646
protein_co	transmemb	432	356	323	1581	1100	1333	5.763737	5.597286	5.678816	18.248	16.48778	17.67503
polymorph	Homo_sapi	0	0	0	4	3	5	0	0	0	0.024827	0.02418	0.035651
protein_co	Leo1_Paf1/	515	497	433	634	491	467	12.43256	14.13894	13.77451	13.24054	13.31631	11.20418
protein_co	zinc_finger_	234	240	225	385	232	301	4.203662	5.080779	5.326345	5.98323	4.68219	5.373882
protein_co	thioredoxir	1023	897	955	1064	864	907	10.99221	11.35819	13.52221	9.890407	10.42971	9.685598
protein_co	microfibrill	1218	1043	761	8	15	11	33.37584	33.68033	27.47922	0.189644	0.46177	0.299562
protein_co	WEE1_hom	536	479	479	2535	2092	2120	5.470671	5.761273	6.442377	22.38292	23.98759	21.5041
protein_co	mitogen-ac	1171	895	761	932	619	819	13.67613	12.31789	11.71186	9.416409	8.121684	9.506046
pseudogen	family_witl	2	1	0	142	124	166	0.109044	0.064251	0	6.697677	7.595277	8.994781
protein_co	protein_kir	0	0	0	22	9	5	0	0	0	0.126437	0.067171	0.033012
protein_co	Hepatoma-	708	556	627	1327	1206	1091	15.47573	14.32187	18.06011	25.09296	29.61518	23.70022
protein_co	N-deacetyla	391	357	320	292	312	282	3.557911	3.828192	3.8371	2.298604	3.189496	2.550217
protein_co	minichrom	827	705	629	9965	6546	8211	14.80629	14.87431	14.83974	154.3409	131.6636	146.0987
protein_co	coiled-coil_	0	1	4	13	20	20	0	0.015099	0.067535	0.144091	0.28788	0.254666
protein_co	C-type_lect	0	0	0	2	3	0	0	0	0	0.042426	0.082644	0
protein_co	zinc_finger_	696	571	482	772	642	694	10.60954	10.25724	9.682091	10.18046	10.9944	10.51372
protein_co	C-type_lect	0	0	0	0	3	0	0	0	0	0	0.092163	0
protein_co	zinc_finger_	86	81	81	72	96	71	2.270786	2.520402	2.818367	1.644649	2.847725	1.863141
protein_co	ribosomal_	520	399	478	1031	894	913	4.72201	4.269761	5.719871	8.099258	9.120321	8.239559
protein_co	alpha-2-ma	3	0	1	28	44	43	0.030114	0	0.013228	0.243149	0.496197	0.428973
protein_co	brain_expr	6	7	8	25	19	18	0.108449	0.1491	0.190545	0.390909	0.385812	0.323337
protein_co	thymidine_	268	230	174	146	125	160	2.774381	2.805862	2.373643	1.307517	1.453752	1.646118
protein_co	transmemb	5634	4638	3882	2653	1892	2268	201.1258	195.1142	182.617	81.93155	75.87892	80.46437
protein_co	solute_carr	4	0	0	6	0	4	0.161899	0	0	0.210087	0	0.160899
protein_co	SEC11_hon	288	212	229	474	315	460	12.6847	11.00349	13.29101	18.06047	15.58645	20.13516
protein_co	complexin_	0	1	1	0	0	0	0	0.031733	0.035485	0	0	0
protein_co	galanin_rec	0	0	0	1	4	1	0	0	0	0.043618	0.226575	0.050109
protein_co	transmemb	188	190	190	331	325	298	2.527401	3.010073	3.365928	3.849527	4.9085	3.981459
protein_co	IQ_motif_c	20	20	14	31	29	37	0.565609	0.666536	0.521734	0.758422	0.921368	1.039914
protein_co	nudE_nucle	1338	1095	946	1215	959	1185	18.03796	17.39612	16.80572	14.17002	14.52442	15.87666
protein_co	centromere	166	148	102	1219	695	814	4.965088	5.216601	4.020257	31.54173	23.35354	24.19652
protein_co	cadherin_1	0	0	0	1	0	3	0	0	0	0.012941	0	0.044601
protein_co	Ras-related	24	19	25	19	12	23	0.809805	0.755492	1.111588	0.554608	0.454883	0.77127

protein_co	family_with	780	586	509	1181	900	1299	57.5125	50.91812	49.45614	75.33218	74.55199	95.18893
protein_co	WD_repeat	6	5	0	5	4	4	0.140179	0.13766	0	0.101057	0.104988	0.092876
protein_co	heat_shock	23765	20551	18398	24658	18102	18999	414.9547	422.8662	423.3195	372.4635	355.0901	329.6881
protein_co	bladder_ca	1505	1291	1188	1290	918	1133	36.13433	36.52724	37.58675	26.79392	24.7614	27.03479
protein_co	serpin_pep	0	0	0	2	1	0	0	0	0	0.071673	0.046538	0
protein_co	CHRNA7_(c	3	7	5	6	5	6	0.056844	0.156304	0.124845	0.098351	0.106435	0.112987
pseudogen	speedy_hor	105	112	93	101	107	145	1.767505	2.221757	2.062952	1.470807	2.023505	2.425767
protein_co	activating_	62	74	52	325	235	290	0.895591	1.25967	0.98982	4.061294	3.813599	4.163185
protein_co	matrix_met	1	1	3	31	22	39	0.030114	0.035488	0.11905	0.807603	0.744295	1.167206
protein_co	trans-golgi_	9	6	9	5	20	8	0.129581	0.101802	0.170756	0.062278	0.323502	0.114472
protein_co	nerve_grow	4413	3930	3499	3222	2706	4589	253.6684	266.2147	265.0399	160.2216	174.7468	262.1562
protein_co	transmemb	9	7	3	6	3	8	0.213472	0.19566	0.093768	0.123115	0.079941	0.188581
protein_co	componen	436	371	301	457	371	318	5.69792	5.713613	5.183596	5.16665	5.446943	4.130157
protein_co	pleckstrin_	17	20	11	1263	1331	1444	0.187343	0.259732	0.159741	12.0408	16.47844	15.81488
protein_co	zinc_finger_	167	164	147	189	126	156	2.081249	2.408566	2.414125	2.037663	1.764116	1.932154
protein_co	zinc_finger_	37	41	24	18	12	17	1.569565	2.049597	1.341602	0.660561	0.571884	0.716698
protein_co	beta-2-micr	18905	17337	13974	2969	2023	2115	429.7336	464.4122	418.5797	58.38426	51.66156	47.77961
protein_co	zinc_finger_	747	631	664	1452	1043	1265	5.030775	5.007843	5.892739	8.459485	7.891284	8.466706
protein_co	cancer_sus	1651	1470	1304	798	579	664	22.06097	23.14739	22.96096	9.224515	8.69171	8.8177
protein_co	nicotinami	3710	3229	2394	1404	760	944	105.2014	107.9004	89.45544	34.44117	24.21087	26.60293
protein_co	acyl-CoA_sy	0	0	0	1	7	2	0	0	0	0.021332	0.193913	0.049012
protein_co	adaptor-rel	1409	1146	1191	1874	1774	1746	10.71905	10.27394	11.93966	12.33326	15.1617	13.20077
protein_co	schlafen_fa	1259	1041	1112	1194	1115	1086	6.293335	6.132152	7.324782	5.163242	6.26151	5.395039
protein_co	cation_cha	11	28	17	51	33	50	0.114839	0.34448	0.233874	0.460608	0.387045	0.518774
pseudogen	stereocilin_	0	0	0	4	1	0	0	0	0	0.034384	0.011163	0
lincRNA	-	0	1	0	0	0	0	0	0.041018	0	0	0	0
protein_co	chromoson	387	312	284	40	57	34	8.522531	8.09691	8.241586	0.762045	1.410203	0.744126
protein_co	KIAA0430	715	600	680	446	500	358	4.888649	4.834384	6.126699	2.638036	3.840625	2.432627
protein_co	serum_amy	224	230	163	766	631	668	7.49607	9.070277	7.187999	22.1757	23.7227	22.2163
protein_co	yippee-like_	36	42	33	23	49	60	0.476469	0.655071	0.575547	0.263344	0.72858	0.789211
protein_co	peptidylpro	6753	5664	4306	3285	2964	3584	295.9524	292.5199	248.6761	124.5442	145.9326	156.1
protein_co	lactate_deh	2	0	0	0	0	0	0.051878	0	0	0	0	0
protein_co	family_with	553	436	406	1052	654	895	19.06014	17.70902	18.44003	31.36748	25.32373	30.65728
protein_co	lactate_deh	12	6	8	5	6	6	0.251501	0.148189	0.220945	0.090655	0.141273	0.124974
protein_co	family_with	74	86	66	475	420	393	0.632999	0.866916	0.743961	3.515023	4.036175	3.340979
protein_co	KIAA0101	361	327	300	1226	918	1254	12.64838	13.50151	13.85108	37.16046	36.13428	43.66513
protein_co	kinesin_fam	405	402	305	422	423	582	4.711295	5.510848	4.675412	4.246789	5.528085	6.728494
protein_co	lactate_deh	5	13	3	0	7	0	0.128062	0.392376	0.101253	0	0.201418	0
protein_co	perilipin_1	8	12	6	7	9	1	0.143423	0.253523	0.141747	0.108565	0.181268	0.017817
protein_co	peroxisoma	109	92	119	71	41	62	2.106047	2.09477	3.029865	1.18676	0.889968	1.190537
protein_co	transmemb	255	223	192	1116	739	901	2.722314	2.805498	2.701059	10.30683	8.863219	9.559439
protein_co	mesoderm_	4	3	0	3	7	3	0.08939	0.079005	0	0.057998	0.175741	0.066628
protein_co	alanyl_(mer	4483	3642	3166	29	30	34	64.52813	61.77708	60.05181	0.361112	0.485122	0.486372
protein_co	sodium_ch	4	0	0	0	0	0	0.060383	0	0	0	0	0

protein_co	RNA_bindi	25	17	11	587	452	511	0.659126	0.528183	0.382169	13.38843	13.38801	13.38933
protein_co	neuron_na	240	211	237	857	1060	892	1.155076	1.19671	1.503082	3.568151	5.731316	4.266521
protein_co	ankyrin_re	127	155	89	118	61	87	2.159816	3.10636	1.994517	1.736033	1.165445	1.470422
protein_co	glycine-N-a	0	3	1	6	7	4	0	0.082053	0.030585	0.120471	0.182521	0.092265
protein_co	chromoson	159	127	158	558	545	508	1.607336	1.512935	2.104754	4.879853	6.189493	5.103673
protein_co	dynactin_5	1082	849	970	1625	1271	1314	16.70034	15.44233	19.72897	21.69773	22.03904	20.15594
protein_co	telomeric_	901	796	710	781	442	614	22.52117	23.44695	23.38618	16.88808	12.41188	15.25261
protein_co	polo-like_k	696	601	471	5441	3085	3302	8.910987	9.067721	7.946434	60.26405	44.37321	42.0149
protein_co	ClpX_casei	788	742	668	880	681	778	8.885517	9.859786	9.925851	8.584246	8.626858	8.71858
protein_co	G_protein-	0	0	0	1	0	1	0	0	0	0.027036	0	0.031059
protein_co	zinc_finger_	169	164	186	522	449	433	1.450086	1.65828	2.103075	3.874721	4.32815	3.692364
protein_co	tachykinin_	0	0	0	445	232	395	0	0	0	16.47576	11.15474	16.80077
protein_co	myosin_IA	1	3	0	0	1	2	0.014473	0.051165	0	0	0.016259	0.028767
protein_co	transmemb	261	209	239	1181	1066	976	2.471842	2.332564	2.982724	9.67594	11.34192	9.186281
protein_co	NGFI-A_bin	1399	1290	938	1216	1089	1441	27.31997	29.68653	24.13794	20.54278	23.89129	27.96638
protein_co	vacuolar_p	1186	1001	1010	1180	891	1200	12.96202	12.89226	14.54602	11.15663	10.93993	13.03403
protein_co	signal_tran	1805	1604	1245	1394	1390	1737	23.68827	24.80662	21.53081	15.82639	20.49368	22.65508
protein_co	protein_ass	702	489	595	1048	933	783	9.126861	7.492043	10.1938	11.78714	13.62746	10.11709
protein_co	XRCC6_bin	68	34	38	125	95	103	2.891556	1.703761	2.129321	4.598284	4.538323	4.352809
protein_co	extracellula	57	57	66	2	1	1	0.360961	0.425371	0.550763	0.010957	0.007114	0.006294
protein_co	syntaxin_3	109	87	76	3078	2329	2400	0.906894	0.853015	0.833256	22.15449	21.76951	19.845
protein_co	mitochond	441	411	332	1105	679	915	19.7521	21.6932	19.5951	42.81539	34.16595	40.72915
protein_co	phosphatid	225	222	221	925	711	821	4.073777	4.736688	5.272806	14.48837	14.46217	14.77296
protein_co	myotubula	242	217	334	867	701	622	2.255982	2.383895	4.103	6.992015	7.341542	5.762624
protein_co	tyrosine_3-	4240	3405	3311	10972	6735	7976	72.2	68.32751	74.29599	161.6293	128.8422	134.979
protein_co	chromoson	0	0	0	105	68	99	0	0	0	5.495869	4.622128	5.952904
protein_co	secretograr	19	12	6	72	71	62	0.812503	0.604728	0.33811	2.663587	3.410977	2.634952
protein_co	gremlin_1_	6700	5908	6253	1471	1315	1216	85.10189	88.43251	104.6617	16.16367	18.76459	15.34997
protein_co	neuronal_t	110	145	87	61	80	120	1.624863	2.524057	1.693473	0.779501	1.327587	1.761631
protein_co	TSC22_dom	2380	1916	1481	1432	988	1441	52.87435	50.16151	43.35687	27.52163	24.65892	31.81571
protein_co	membrane-	2	0	0	22	3	9	0.14892	0	0	1.417125	0.250953	0.666001
protein_co	membrane-	0	0	0	5	3	1	0	0	0	0.079761	0.062148	0.018326
protein_co	membrane-	0	0	0	0	1	1	0	0	0	0	0.019845	0.017556
protein_co	DIS3_mitot	213	156	139	986	647	583	2.99666	2.586363	2.576959	12.00046	10.22613	8.151473
protein_co	cyclin_D-ty	134	119	95	609	419	468	2.583428	2.70362	2.413515	10.15715	9.075167	8.966998
protein_co	erythrocyte	0	5	3	19	4	11	0	0.068513	0.045967	0.191122	0.052252	0.127115
protein_co	transglutan	2	0	0	0	1	0	0.046196	0	0	0	0.025949	0
protein_co	SMAD_fami	1319	1160	1211	2113	2015	1960	11.17803	11.58472	13.52382	15.49113	19.18424	16.50769
protein_co	membrane-	0	0	0	0	2	0	0	0	0	0	0.087917	0
protein_co	coiled-coil_	3	0	4	0	0	1	0.046837	0	0.082292	0	0	0.015516
protein_co	membrane-	1	0	0	0	0	0	0.025091	0	0	0	0	0
protein_co	microtubul	4562	3700	4341	441	700	555	22.88608	21.87384	28.69728	1.913893	3.945148	2.767061
protein_co	RCC1_dom	240	262	199	392	297	420	4.024656	5.177569	4.397495	5.686782	5.595295	6.999652
protein_co	AKT_intera	80	73	46	304	285	225	1.985598	2.135164	1.504506	6.527364	7.946853	5.550005

protein_co microtubul	586	400	422	1746	1398	1340	7.176364	5.772633	6.81011	18.49755	19.23371	16.30877
protein_co eva-1_hom	406	285	318	0	3	0	8.625218	7.135033	8.902377	0	0.0716	0
protein_co methionyl-	1833	1441	1302	5609	3934	4684	27.01582	25.02804	25.28725	71.51616	65.13871	68.60919
protein_co methyl-CpG	1222	983	746	1054	1271	1140	15.10834	14.32208	12.154	11.27325	17.65387	14.00748
protein_co canopy_4_l	296	241	255	295	249	321	10.43311	10.01028	11.84397	8.995125	9.859856	11.24441
protein_co protein_dis	10951	10241	7867	12421	8558	10105	155.5559	171.4282	147.2572	152.6343	136.5696	142.6523
protein_co nudix_(nuc	1060	964	1041	3214	2895	2921	12.65046	13.55766	16.37141	33.18253	38.81487	34.64509
protein_co N-acetyltra	2	5	3	2	0	0	0.036076	0.106282	0.071308	0.031209	0	0
protein_co NK3_home	6	0	0	32	31	26	0.09711	0	0	0.448048	0.563667	0.41821
protein_co small_G_pr	0	0	2	1	0	4	0	0	0.021004	0.006894	0	0.031681
protein_co HCG20182	0	0	0	0	0	2	0	0	0	0	0	0.054438
protein_co dual_specif	69	63	50	62	42	36	1.251003	1.346037	1.194577	0.972443	0.855476	0.648666
protein_co thyrotroph	203	152	149	221	203	229	2.44584	2.158155	2.365664	2.303495	2.747749	2.742061
protein_co meiosis_inh	3	1	0	0	2	1	0.039508	0.015519	0	0	0.02959	0.013088
protein_co pre-B-cell_l	527	463	414	706	441	490	9.614026	9.953659	9.952446	11.14198	9.038208	8.883833
protein_co guanine_nu	0	0	0	2	0	0	0	0	0	0.09978	0	0
protein_co prohibitin	1551	1186	943	3622	2451	2866	44.82068	40.38856	35.90981	90.54784	79.57176	82.30997
protein_co small_nucl	1076	932	643	3508	2360	2940	32.21975	32.88765	25.37205	90.87249	79.39093	87.49169
protein_co tetratricop	0	0	2	0	0	0	0	0	0.027151	0	0	0
protein_co sterile_alph	307	268	253	52	37	78	3.672968	3.778511	3.988726	0.538202	0.497313	0.927434
protein_co phosphatid	202	127	71	45	16	15	4.865369	3.604751	2.2535	0.937648	0.432946	0.359059
protein_co transmemb	50	24	28	26	9	7	0.957342	0.541521	0.706464	0.430659	0.193592	0.1332
protein_co family_with	905	677	680	427	440	429	11.10093	9.786027	10.99143	4.531078	6.063347	5.22971
protein_co acyl-CoA_sy	384	301	250	590	596	718	9.031249	8.342384	7.748032	12.00416	15.74751	16.78227
protein_co golgin_A2	3335	2742	2502	1264	1238	1675	41.44559	40.15661	40.97365	13.58916	17.28432	20.68745
protein_co TruB_pseuc	653	470	391	967	594	861	19.4544	16.50098	15.35028	24.92265	19.88109	25.4928
protein_co coenzyme_	774	684	510	1099	729	1059	13.10404	13.64669	11.37809	16.09626	13.86567	17.81845
protein_co solute_carr	446	304	312	1075	785	970	8.490357	6.819802	7.826733	17.70364	16.78842	18.35154
processed_ long_interg	1	0	0	0	0	0	0.019161	0	0	0	0	0
protein_co ubiquitin_r	1491	1186	887	2369	1414	1794	25.92283	24.29946	20.32185	35.6314	27.6187	30.99823
protein_co cerebral_er	3381	2836	2161	502	338	490	34.4417	34.04495	29.00875	4.423908	3.868166	4.960724
protein_co dolichyl_py	389	304	315	1105	741	876	9.459829	8.711929	10.09437	23.24657	20.24421	21.17129
protein_co endonuclea	102	74	68	161	121	187	4.607493	3.939157	4.047699	6.291488	6.140432	8.394904
protein_co paired_rela	283	221	165	127	154	154	12.1511	11.18223	9.335719	4.717324	7.42846	6.571422
protein_co chromoson	237	197	157	1067	957	951	2.777732	2.720917	2.424803	10.81856	12.60094	11.07726
protein_co immunoglo	67	51	64	192	198	252	0.73636	0.66053	0.926894	1.825491	2.444723	2.752489
protein_co Sp2_transc	284	253	218	470	368	406	4.831376	5.07201	4.887017	6.91693	7.033142	6.864172
protein_co proline_ric	5	0	0	4	9	7	0.174263	0	0	0.120603	0.352392	0.242461
protein_co coenzyme_	276	209	205	333	268	304	5.499328	4.907428	5.382564	5.739946	5.999076	6.019824
protein_co G_protein-r	32	26	17	555	491	557	0.367486	0.351861	0.257262	5.513751	6.334637	6.357056
protein_co v-crk_sarco	1678	1353	1447	2669	2195	2487	22.89562	21.75531	26.01739	31.50445	33.64681	33.72452
protein_co F-box_prot	733	575	627	1503	1351	1405	11.14147	10.29944	12.55859	19.76335	23.06976	21.22387
protein_co TBC1_dom	1598	1546	1302	256	327	345	13.90071	15.84808	14.92471	1.926474	3.195633	2.982558
protein_co nucleotide-	0	3	1	0	0	0	0	0.041722	0.015551	0	0	0

protein_co	sorting_nex	5	4	0	0	0	0	0.080117	0.07553	0	0	0	0
protein_co	katanin_p6	42	30	25	70	54	43	1.184615	0.99714	0.929186	1.708004	1.711081	1.20533
protein_co	haloacid_d	262	248	240	334	278	296	4.295615	4.791625	5.185255	4.737329	5.120565	4.82309
protein_co	chromoson	8	8	8	2	3	4	0.227459	0.268046	0.299735	0.049193	0.095826	0.113027
protein_co	zinc_finger_	420	409	389	679	489	607	4.050869	4.648676	4.944055	5.665414	5.298547	5.818315
protein_co	insulin-like_	9149	8143	5732	962	663	760	86.72465	90.96209	71.59949	7.888728	7.060436	7.159656
protein_co	ring_finger_	376	237	230	489	339	311	6.994313	5.195324	5.637932	7.869172	7.084447	5.749462
protein_co	cyclin-depe	969	873	915	1484	1550	1454	6.633026	7.042215	8.253608	8.787894	11.91979	9.891496
protein_co	dipeptidase	0	0	0	0	0	1	0	0	0	0	0	0.023405
protein_co	dihydrouri	137	174	106	366	241	298	3.139791	4.699335	3.201259	7.25645	6.205063	6.78744
protein_co	processing_	307	283	240	683	516	604	17.80163	19.33815	18.33865	34.26139	33.61399	34.8071
protein_co	endo-beta-l	327	285	262	182	241	288	3.742262	3.843602	3.951141	1.801859	3.098508	3.275583
protein_co	RNA_bindi	3	1	2	12	13	15	0.0517	0.020309	0.045419	0.178902	0.251688	0.256905
protein_co	ATP_syntha	419	335	308	936	574	800	14.02167	13.21106	13.58223	27.0972	21.57976	26.60635
protein_co	TBC1_dom	3057	2473	2386	1363	1931	1763	14.79889	14.10798	15.22085	5.708112	10.50183	8.481947
protein_co	ENTH_dom	102	66	65	98	98	157	1.482697	1.130585	1.245089	1.23237	1.600395	2.268096
protein_co	myosin_VB	6	18	12	579	690	528	0.033419	0.118146	0.088076	2.789854	4.317557	2.922695
protein_co	ADP-ribosy	9	12	11	41	28	85	0.316801	0.497774	0.510237	1.248507	1.107264	2.973533
protein_co	acetyl-CoA_	635	526	427	1583	772	969	16.65884	16.26162	14.76161	35.9265	22.75293	25.26413
protein_co	stromal_int	1419	1089	1189	1493	1319	1451	18.60408	16.82522	20.54199	16.93357	19.42762	18.90614
protein_co	ribonucleo	758	585	677	3191	2606	2381	12.67507	11.52774	14.9178	46.16055	48.95586	39.56856
protein_co	olfactory_r	0	0	0	0	4	0	0	0	0	0	0.085546	0
protein_co	tripartite_r	143	151	150	295	196	215	2.258521	2.810426	3.121865	4.030632	3.477709	3.374708
protein_co	olfactory_r	0	1	0	0	0	0	0	0.066019	0	0	0	0
protein_co	fructosamii	59	50	22	69	54	82	1.241956	1.240313	0.610255	1.256511	1.277018	1.715448
protein_co	proline-rich	143	144	128	14	17	13	2.523521	2.994611	2.976567	0.213728	0.33703	0.227994
protein_co	zinc_finger_	16	10	13	10	16	11	0.261276	0.192436	0.279742	0.141267	0.293527	0.178518
protein_co	immunity-r	856	780	683	2044	1614	1827	4.679142	5.024515	4.919806	9.665768	9.911629	9.925232
protein_co	zinc_finger_	472	338	351	282	257	250	4.184218	3.530987	4.100287	2.162641	2.559496	2.202531
protein_co	zinc_finger_	137	88	100	74	105	82	1.346374	1.019142	1.29503	0.629129	1.159267	0.800882
protein_co	zinc_finger_	111	109	110	192	188	175	1.79708	2.079591	2.346777	2.68911	3.419411	2.815737
protein_co	protein_ph	279	239	182	1489	860	1116	2.545767	2.569919	2.188369	11.75363	8.815803	10.12018
protein_co	zinc_finger_	309	262	204	403	324	372	5.709866	5.705265	4.967438	6.442219	6.726072	6.831563
protein_co	zinc_finger_	648	600	466	527	704	821	4.225889	4.611066	4.004643	2.973149	5.157803	5.321032
protein_co	vitamin_K_	77	88	49	20	13	45	3.785011	5.097605	3.174003	0.85049	0.717908	2.198359
protein_co	guanine_nu	0	0	1	9	13	7	0	0	0.322978	1.908288	3.579569	1.705085
protein_co	lactoperoxi	0	0	0	0	3	0	0	0	0	0	0.05293	0
protein_co	carbonic_a	1	1	0	1	6	6	0.045876	0.054062	0	0.039687	0.309234	0.273557
protein_co	smg-8_hom	376	246	215	529	442	360	5.724997	4.413972	4.313807	6.967967	7.560643	5.447529
protein_co	tropomyos	23318	20372	17212	32457	25142	26855	462.0053	475.6597	449.3883	556.323	559.6345	528.7988
protein_co	RAB8A_mer	231	185	180	568	439	434	4.325918	4.082678	4.441949	9.201902	9.235914	8.07729
protein_co	glutathione	2646	2190	1713	5016	2350	3127	120.8644	117.8854	103.11	198.2117	120.594	141.9535
protein_co	midnolin	2425	2048	1674	2879	3129	3309	33.87385	33.71242	30.81365	34.79025	49.10294	45.93665
protein_co	junctional_	8	2	1	1	2	7	0.372496	0.109741	0.061357	0.04028	0.104619	0.323921

protein_co	family_with	22	10	8	8	6	14	0.227703	0.12197	0.109112	0.071631	0.069766	0.144007
protein_co	kelch-like_f	73	43	53	190	177	203	1.210743	0.840436	1.15835	2.726125	3.298007	3.346069
protein_co	GATA_zinc_	1807	1489	1449	4501	4249	4412	16.56239	16.08299	17.50121	35.68921	43.75228	40.18926
pseudogen	nitric_oxid	0	0	0	0	1	2	0	0	0	0	0.174929	0.309494
protein_co	mevalonate	2179	1688	1490	2340	1899	2420	49.04695	44.77487	44.19528	45.56524	48.02073	54.1352
protein_co	chromatin_	323	301	246	2802	2156	2370	5.27776	5.795897	5.296842	39.60757	39.57718	38.4862
protein_co	trafficking_	750	616	531	1084	728	965	12.80005	12.38905	11.94207	16.00452	13.95824	16.36768
protein_co	ankyrin_rep	3439	2881	2709	3111	4652	4161	19.57468	19.3247	20.31918	15.31883	29.74755	23.53801
protein_co	chromoson	136	108	121	290	251	271	2.156327	2.017932	2.528109	3.977743	4.470936	4.270263
protein_co	uncharacte	7	8	2	9	28	13	0.124567	0.167765	0.0469	0.138551	0.559773	0.22991
protein_co	protein_int	68	60	45	148	155	223	1.13636	1.181586	0.990956	2.139595	2.909964	3.703577
protein_co	ribosomal_	36846	30947	19425	33883	21295	27070	817.8884	809.5233	568.1978	650.6517	531.0439	597.175
protein_co	zinc_finger_	35	30	28	211	161	158	0.380323	0.384161	0.400938	1.983491	1.96544	1.706285
protein_co	calcium_ch	730	572	520	748	734	734	9.592188	8.85723	9.003948	8.50275	10.83528	9.585186
protein_co	dehydroger	51	25	46	145	137	146	1.325474	0.765682	1.57541	3.260109	4.000099	3.771061
protein_co	tumor_pro	658	541	350	723	508	614	14.11474	13.67575	9.893496	13.41678	12.24221	13.08956
protein_co	myeloid/ly	3764	3141	3209	1649	4927	4429	10.26159	10.09114	11.52842	3.889098	15.09026	11.99998
protein_co	coronin_6	50	38	16	90	55	81	0.650541	0.582633	0.274321	1.013001	0.803926	1.047367
protein_co	Ras_homol	2	11	3	15	27	21	0.083967	0.544223	0.165971	0.544793	1.273473	0.876205
protein_co	tubulin_alp	11677	10239	8690	9324	5162	5826	322.8157	333.5707	316.5759	222.9916	160.321	160.0676
protein_co	tubulin_alp	2311	1852	1582	10741	5957	6319	67.97035	64.19004	61.31417	273.2922	196.8322	184.7045
protein_co	zinc_finger_	73	50	61	68	60	46	1.419277	1.14557	1.56282	1.143711	1.310523	0.888816
protein_co	zinc_finger_	5	4	7	40	27	41	0.055044	0.051892	0.101548	0.380943	0.333926	0.448571
protein_co	zinc_finger_	124	84	75	110	178	137	1.185389	0.946293	0.94479	0.909693	1.911649	1.301575
protein_co	SERTA_dom	355	310	218	734	457	622	10.83855	11.15352	8.770701	19.38662	15.67503	18.87309
protein_co	NCK-associ	2173	1887	1526	1118	1279	1579	23.47771	24.02564	21.72628	10.44963	15.52443	16.95461
protein_co	RAB4B_mer	29	30	20	36	36	43	0.774616	0.944315	0.703969	0.831867	1.080289	1.141475
protein_co	glycerol-3-p	2	1	0	6	7	8	0.034355	0.020243	0	0.089161	0.135085	0.136571
protein_co	chromoson	523	471	337	1126	853	900	7.676224	8.146554	6.517945	14.29708	14.06514	13.12799
protein_co	cytochrom	2	4	5	1262	848	1045	0.03806	0.089702	0.125383	20.77578	18.12925	19.76337
protein_co	AXL_recept	670	532	423	4317	2952	3676	7.48796	7.006602	6.229653	41.7382	37.06416	40.82948
protein_co	nuclear_fac	49	46	26	87	54	79	1.414454	1.564796	0.989011	2.172576	1.751199	2.266363
protein_co	transmemb	26	24	15	59	38	48	0.570674	0.620773	0.433851	1.120288	0.937017	1.047046
protein_co	ankyrin_rep	0	0	0	1	0	0	0	0	0	0.013799	0	0
protein_co	tweety_hor	97	79	51	36	40	59	1.395835	1.339666	0.967091	0.448155	0.646653	0.84377
protein_co	leukocyte_	4492	4127	2582	3715	3314	4822	41.0727	44.46877	31.11033	29.38565	34.042	43.81778
protein_co	CDC42_effe	1227	1012	696	146	145	164	75.18356	73.07452	56.1982	7.739167	9.981491	9.986926
protein_co	transmemb	4	12	4	3	0	4	0.105303	0.372279	0.138763	0.068323	0	0.104653
protein_co	zinc_finger_	503	397	336	724	617	641	6.619269	6.156582	5.826613	8.242209	9.12171	8.383198
protein_co	trafficking_	196	152	144	565	436	492	0.351541	0.32127	0.340343	0.87666	0.878528	0.87699
protein_co	NLR_family	1	0	0	8	6	3	0.013837	0	0	0.095764	0.093271	0.041255
protein_co	zinc_finger_	1878	1597	1524	2337	1708	1690	26.30243	26.35799	28.12678	28.31535	26.8743	23.52321
protein_co	zinc_finger_	167	178	141	108	111	102	3.101068	3.89513	3.450236	1.734929	2.315618	1.882369
protein_co	protein_ph	0	1	2	162	108	234	0	0.06574	0.147025	7.818148	6.768598	12.97333

protein_co	serine_pept	1	4	0	4539	3344	3974	0.013906	0.065551	0	54.605	52.24257	54.92205
protein_co	chromoson	1	0	0	2	0	7	0.10181	0	0	0.17615	0	0.708266
protein_co	Yip1_intera	1382	1030	724	1216	802	1090	38.16612	33.52079	26.34774	29.05137	24.88247	29.91618
protein_co	dynein_axo	0	0	1	7	0	0	0	0	0.031312	0.143892	0	0
protein_co	prostate_st	12	16	13	23	7	16	0.622835	0.978631	0.88914	1.03272	0.408168	0.825318
protein_co	ataxia_cere	13	15	4	32	26	36	0.135746	0.184579	0.05504	0.289066	0.305005	0.373591
protein_co	lymphocyt	0	0	0	0	0	1	0	0	0	0	0	0.036974
protein_co	death-assoc	1381	1030	868	3193	2160	2851	32.39323	28.47114	26.82965	64.79216	56.9198	66.46108
protein_co	eukaryotic_	179520	147607	108157	80636	69605	84025	3003.782	2910.514	2384.762	1167.206	1308.414	1397.249
protein_co	transmemb	0	0	0	13	2	11	0	0	0	0.47178	0.094257	0.458601
protein_co	chromatin_	328	190	215	1790	1768	2083	5.200553	3.550065	4.492095	24.55227	31.49249	32.82272
protein_co	UBX_doma	2566	2042	1521	1426	1133	1245	29.54471	27.70677	23.07741	14.20384	14.65555	14.2463
protein_co	Hepatoma-	2257	1813	1533	2933	2684	3512	38.35885	36.31106	34.33294	43.12301	51.24667	59.3196
protein_co	perilipin_4	30	33	23	39	9	16	0.25047	0.32468	0.253045	0.281684	0.084416	0.132759
protein_co	sema_dom	127	98	79	10	12	2	1.68678	1.533868	1.382664	0.114899	0.179054	0.026399
protein_co	zinc_finger_	853	756	549	1374	1053	1196	8.114765	8.475314	6.882308	11.30776	11.25393	11.30753
protein_co	nucleoredo	3085	2626	1995	3360	2680	3058	53.79544	53.96251	45.84247	50.68654	52.5018	52.99531
protein_co	family_with	521	421	414	872	612	609	11.46395	10.91656	12.00416	16.59877	15.12854	13.31752
protein_co	glyoxalase_	792	673	558	2033	1566	1714	15.31943	15.3405	14.22284	34.0187	34.0297	32.94866
protein_co	major_facil	395	258	252	533	372	529	13.50885	10.39795	11.35681	15.76926	14.29266	17.97987
protein_co	glutamic-p	20	44	29	14	9	16	0.561708	1.456265	1.073281	0.340151	0.28397	0.446591
protein_co	kinesin_fam	387	374	233	308	253	443	5.619354	6.399619	4.458268	3.868915	4.1271	6.392766
protein_co	solute_carr	381	321	300	289	203	235	6.198684	6.154413	6.431772	4.067573	3.710391	3.799724
protein_co	Rab_intera	29	27	11	61	47	79	0.866905	0.95114	0.433312	1.577489	1.578412	2.346985
protein_co	serpin_pep	12	5	1	16	2	3	0.278149	0.136576	0.030544	0.320833	0.05208	0.069108
protein_co	WD_repeat	485	353	295	350	414	565	3.813513	3.270885	3.056612	2.380754	3.657067	4.41511
protein_co	serine_race	57	65	49	180	101	119	1.106172	1.486511	1.253079	3.021922	2.202004	2.295114
protein_co	TSR1_20S_	780	743	666	1504	1354	1375	8.203015	9.208201	9.229707	13.68326	15.9973	14.37114
protein_co	transient_r	26	12	10	4	9	16	0.272567	0.148248	0.138145	0.036276	0.105997	0.166698
protein_co	hydroxyste	306	204	163	123	86	75	8.598696	6.755359	6.035783	2.990056	2.71493	2.094508
protein_co	cytochrom	493	363	334	257	160	222	13.66487	11.85693	12.19944	6.162471	4.982276	6.11535
protein_co	gamma-glu	0	0	0	2	0	1	0	0	0	0.036148	0	0.020763
protein_co	chromoson	1465	1256	902	4203	2730	3653	42.05995	42.49403	34.12499	104.3887	88.05274	104.2295
protein_co	kallikrein_1	0	0	0	1	1	0	0	0	0	0.024703	0.03208	0
protein_co	kallikrein-r	0	0	0	1	1	1	0	0	0	0.026814	0.034822	0.030804
protein_co	kallikrein-r	0	0	0	0	1	0	0	0	0	0	0.03685	0
protein_co	HCG20081	11	17	7	19	21	8	0.342358	0.623511	0.287092	0.511569	0.734271	0.24745
protein_co	zinc_finger_	460	399	298	645	506	576	5.482408	5.603941	4.680202	6.650224	6.775059	6.822533
protein_co	keratin_80	25	43	32	118	107	107	0.339888	0.688925	0.573299	1.387846	1.634289	1.445738
protein_co	keratin_1	0	0	0	6	0	0	0	0	0	0.112115	0	0
protein_co	alkaline_ce	0	0	0	0	0	1	0	0	0	0	0	0.036411
protein_co	OTU_doma	1206	998	713	4585	2549	2859	25.61044	24.97511	19.95235	84.23104	60.81192	60.33838
protein_co	REST_corep	256	213	122	531	388	546	5.204645	5.103144	3.268479	9.339178	8.862003	11.03198
protein_co	angiopoieti	1546	1223	830	180	129	169	43.55869	40.60681	30.81614	4.387335	4.083232	4.732184

protein_co	CD320_mo	1731	1604	1048	2019	926	1238	53.00223	57.87734	42.28567	53.48062	31.8535	37.67276
protein_co	SPRY_doma	882	712	641	443	405	368	17.66035	16.80033	16.91311	7.673568	9.110343	7.322984
protein_co	insulin-like	2514	2069	1455	137	65	96	113.0787	109.6688	86.24093	5.330884	3.284566	4.291375
protein_co	sterol_O-ac	3	2	3	0	0	1	0.077702	0.061045	0.102392	0	0	0.025741
protein_co	zinc_finger_	2	0	0	20	17	35	0.030269	0	0	0.261858	0.289048	0.526441
protein_co	NADH_deh	2322	2066	1465	2731	2115	2824	70.32551	73.73744	58.46865	71.55424	71.96314	85.00119
protein_co	cyclin-depe	747	525	432	1540	851	968	23.37289	19.35789	17.8119	41.68458	29.91371	30.10071
protein_co	nudix_(nuc	103	116	71	100	55	76	3.722131	4.939916	3.381019	3.126205	2.232884	2.729466
protein_co	T-box_10	25	8	13	7	6	9	0.85499	0.322417	0.585867	0.207101	0.230527	0.305896
protein_co	peroxiredo	1921	1641	1256	1956	1199	1477	59.23101	59.62625	51.03243	52.17394	41.53269	45.25973
protein_co	zinc_finger_	69	49	58	290	232	245	1.532269	1.282298	1.697261	5.571176	5.787925	5.407065
protein_co	MIS12_MIN	192	147	116	547	439	540	4.057753	3.661076	3.230555	10.0008	10.42312	11.34195
protein_co	CD300c_m	0	0	0	0	0	3	0	0	0	0	0	0.104049
protein_co	HID1_doma	3	0	0	327	324	296	0.048555	0	0	4.57849	5.891225	4.761161
protein_co	immature_	245	194	175	732	492	627	14.57364	13.59912	13.7175	37.66831	32.87882	37.0663
protein_co	ATP_syntha	485	412	364	391	323	533	11.71902	11.73151	11.59007	8.17315	8.768015	12.79931
protein_co	transmemb	11	12	6	123	81	103	0.665544	0.855603	0.478377	6.438018	5.505771	6.193425
protein_co	envoplakin	1	2	0	0	3	2	0.008004	0.018865	0	0	0.026977	0.01591
protein_co	signal_reco	2074	1547	1546	2788	2265	2445	41.44946	36.43406	40.715	48.20209	50.85427	48.56223
protein_co	mannosyl_(	416	369	326	245	142	144	4.902817	5.124905	5.062963	2.497937	1.880138	1.686648
protein_co	transmemb	0	0	0	15	16	7	0	0	0	0.155743	0.215737	0.083495
protein_co	thymidine_	577	463	389	3677	2292	2930	18.17189	17.18353	16.14391	100.18	81.09387	91.70682
protein_co	transmemb	218	237	184	575	361	535	4.459481	5.71325	4.959986	10.17557	8.296293	10.87655
protein_co	cytochrom	0	0	1	0	1	0	0	0	0.023649	0	0.020161	0
processed_	-	63	75	69	88	77	65	3.015626	4.230633	4.35232	3.644036	4.140728	3.092146
protein_co	gasdermin_	1	1	1	0	0	0	0.024464	0.02883	0.032238	0	0	0
protein_co	transmemb	167	132	151	436	282	309	4.295989	4.001545	5.118686	9.702781	8.149761	7.899777
protein_co	GH3_doma	40	26	21	53	28	43	0.799109	0.612106	0.552841	0.915978	0.628425	0.853737
protein_co	integrin_al	830	805	610	764	618	684	13.67601	15.63091	13.24482	10.89025	11.43981	11.20075
protein_co	proline_ric	10	4	8	0	1	2	0.437891	0.206411	0.461626	0	0.049194	0.087037
protein_co	zinc_finger_	830	726	574	1249	964	1092	9.858879	10.16233	8.984547	12.83438	12.86399	12.89086
protein_co	RAB26_mer	30	31	25	18	20	28	0.826342	1.006254	0.907431	0.428918	0.618896	0.76649
protein_co	MTOR_asso	1301	984	635	1692	1082	1153	32.5502	29.01206	20.93558	36.62181	30.41254	28.66919
protein_co	E4F_transcr	453	355	277	830	579	814	4.043546	3.734217	3.258208	6.409221	5.806197	7.221014
protein_co	deoxyribon	4	7	7	16	19	18	0.09652	0.199049	0.222581	0.333994	0.51506	0.431656
protein_co	enoyl-CoA_	353	282	216	1061	668	1063	12.1273	11.41683	9.77863	31.53319	25.7819	36.29379
protein_co	CASK_inter	22	19	8	30	18	24	0.202346	0.205936	0.096961	0.238702	0.185991	0.219378
protein_co	ATP-bindin	13	15	12	195	154	134	0.104136	0.141597	0.12667	1.351307	1.385882	1.06677
protein_co	potassium_	758	658	555	1431	1034	1207	16.16812	16.53954	15.59977	26.40541	24.77764	25.58628
protein_co	serine/argi	11481	10056	9148	12649	13680	13073	64.98616	67.07698	68.2342	61.93845	86.9914	73.54041
protein_co	zinc_finger_	10	30	17	15	36	17	0.289137	1.022191	0.64772	0.375196	1.169379	0.488497
polymorph	NLR_family	35	33	21	29	25	28	0.28062	0.311797	0.221873	0.201146	0.225185	0.22311
protein_co	succinate_(	75	53	59	143	99	164	1.953062	1.626439	2.024611	3.221468	2.896269	4.244321
protein_co	damage-spe	7982	7062	6228	10341	10681	12234	93.78052	97.77677	96.42382	105.1057	140.9814	142.8496

protein_co	vacuolar_p	648	454	422	1039	771	920	11.97409	9.886223	10.27578	16.6091	16.00556	16.89526
protein_co	von_Willeb	789	624	537	876	602	702	11.4754	10.69504	10.292	11.02193	9.836402	10.147
protein_co	RAB3A_inte	473	360	345	88	88	82	10.9637	9.833442	10.5378	1.764581	2.291541	1.888946
protein_co	bestrophin	69	37	40	1	2	6	0.632871	0.399921	0.48346	0.007935	0.020608	0.054692
protein_co	ferritin_hea	10012	8800	7842	4744	4166	4114	431.2817	446.7144	445.1454	176.786	201.6084	176.1222
protein_co	Berardinell	27	40	30	26	32	25	0.701377	1.224489	1.026937	0.584284	0.933871	0.645413
protein_co	polymerase	827	905	627	1473	1024	1363	28.13766	36.28592	28.11155	43.3559	39.14096	46.08801
protein_co	solute_carr	4011	3102	2740	8950	6169	8098	88.58837	80.73706	79.7461	171.0055	153.0692	177.7508
protein_co	HRAS-like_s	0	0	0	40	23	22	0	0	0	0.604207	0.45117	0.381764
protein_co	chromoson	758	632	488	2767	1900	2735	19.82672	19.48075	16.8204	62.61145	55.83214	71.09655
protein_co	autophagy_	104	97	73	136	89	144	1.202942	1.322178	1.112676	1.360859	1.156512	1.655325
protein_co	C2_calcium	461	328	403	1051	921	852	3.348305	2.807405	3.857128	6.603738	7.515067	6.149975
protein_co	tetratricop	71	96	63	41	42	47	0.358631	0.571436	0.419338	0.179158	0.238335	0.235937
protein_co	tetratricop	35	56	46	19	39	64	0.435166	0.820506	0.753666	0.204363	0.544754	0.790817
protein_co	ribosomal_	25819	23021	17707	37900	22386	28696	664.1805	697.8756	600.2422	843.4298	646.9523	733.6311
protein_co	ectonucleo	2	0	0	36	26	24	0.03756	0	0	0.584874	0.548554	0.447938
protein_co	catenin_(ca	4722	4166	4327	9194	8439	7618	67.03872	69.69892	80.95085	112.919	134.5984	107.4856
protein_co	unc-51-like	101	107	67	120	88	73	1.159124	1.447103	1.013254	1.191387	1.134594	0.832609
protein_co	Fas_(TNFRS	193	138	174	284	256	315	5.550034	4.676538	6.593596	7.065122	8.270415	9.002404
protein_co	latent_tran	3765	2687	2276	191	142	176	44.86222	37.73032	35.73739	1.968848	1.900873	2.084194
protein_co	N-acetylate	6	0	1	1	0	3	0.11769	0	0.025848	0.016969	0	0.058482
protein_co	SAC3_dom	398	220	255	1137	651	824	13.45499	8.76456	11.35992	33.25246	24.72466	27.68453
protein_co	basic_leuci	0	0	0	0	2	0	0	0	0	0	0.046303	0
protein_co	solute_carr	0	0	0	0	0	4	0	0	0	0	0	0.054522
protein_co	splicing_fac	3995	3314	2798	9568	6819	7275	60.9508	59.58298	56.25293	126.2836	116.8779	110.3076
protein_co	mitogen-ac	329	251	275	281	188	243	5.496241	4.941407	6.053929	4.061058	3.528391	4.034463
protein_co	chromoson	0	0	0	2	0	0	0	0	0	0.044769	0	0
protein_co	coiled-coil_	14	5	10	13	23	25	0.14158	0.059587	0.133263	0.113732	0.261308	0.251261
protein_co	scavenger_	1675	1300	1312	1055	1030	1278	25.26386	23.10657	26.07676	13.76577	17.45305	19.15691
protein_co	PDZ_bindir	168	87	116	1051	775	801	4.199286	2.562669	3.820841	22.72646	21.76291	19.89795
protein_co	scavenger_	41	32	12	1	0	2	0.539141	0.495879	0.207938	0.011376	0	0.026137
protein_co	prepronoci	0	0	1	0	5	0	0	0	0.053254	0	0.227007	0
protein_co	COP9_signa	2785	2212	1883	2827	2115	2526	102.9614	96.36987	91.73482	90.41446	87.84327	92.80942
protein_co	platelet-act	1465	1223	1111	3358	2486	2567	18.48833	18.18837	18.47604	36.66096	35.24604	32.19553
protein_co	ankyrin_rep	375	357	255	457	309	447	6.408287	7.18929	5.742297	6.756004	5.932233	7.591504
protein_co	nudix_(nuc	496	430	347	884	602	878	12.87193	13.15035	11.8666	19.84619	17.55123	22.64467
protein_co	KIAA1586	298	252	256	442	312	360	5.378935	5.360282	6.089124	6.901847	6.326794	6.457913
protein_co	RAB4A_mer	559	467	400	633	461	566	9.977753	9.823017	9.408399	9.774345	9.244234	10.04031
pseudogen	olfactory_r	0	0	0	4	2	9	0	0	0	0.195097	0.126679	0.504288
protein_co	olfactory_r	7	0	0	13	9	10	0.305765	0	0	0.491242	0.441653	0.434109
protein_co	potassium_	9	3	3	4	2	0	0.230736	0.090636	0.101351	0.088715	0.057604	0
protein_co	SET_domai	2473	2126	2078	2529	2508	2610	19.06832	19.31784	21.11391	16.86942	21.72525	20.00039
protein_co	vasorin	1374	1089	923	896	731	844	25.92335	24.21249	22.94779	14.62431	15.49426	15.82547
protein_co	family_with	5	3	6	120	143	97	0.083582	0.059098	0.132169	1.735355	2.685525	1.611482

protein_co	histone_clu	5	2	4	6	0	2	0.550322	0.259408	0.580152	0.571296	0	0.218769
protein_co	THAP_dom	35	44	26	112	73	66	0.48659	0.720867	0.476325	1.347027	1.140163	0.911903
protein_co	ring_finger_	2810	2309	1868	2562	1676	2074	49.30865	47.74719	43.1945	38.89188	33.03999	36.16889
protein_co	hook_hom	1790	1441	1636	1829	1696	1576	6.581774	6.243973	7.926985	5.817905	7.005914	5.759115
protein_co	mitogen-ac	1206	1111	1052	2215	1849	1882	25.52852	27.71402	29.34465	40.56161	43.9708	39.59202
protein_co	DNA-damag	1954	1472	1234	695	753	795	59.18004	52.53704	49.24936	18.20952	25.62092	23.92916
protein_co	recombinat	3728	3114	3405	1660	1277	1246	35.56749	35.01088	42.80843	13.70088	13.68729	11.81422
protein_co	LMBR1_dor	605	552	561	854	655	613	14.49946	15.58987	17.71716	17.70587	17.63546	14.60046
protein_co	zinc_finger_	199	184	168	441	285	362	3.782857	4.121846	4.208342	7.252179	6.086404	6.838882
protein_co	tetratricop	319	251	218	395	253	299	4.102059	3.803575	3.694048	4.394114	3.654945	3.821132
protein_co	glycerate_k	62	80	47	69	55	87	0.906224	1.377973	0.905266	0.872481	0.903141	1.263783
protein_co	histone_clu	0	1	3	7	11	5	0	0.130246	0.436931	0.669295	1.365835	0.549207
protein_co	guanine_nu	508	448	356	393	314	279	5.269206	5.476039	4.865934	3.526444	3.658981	2.876042
protein_co	ubiquitin_c	982	894	873	1390	1262	1214	15.74918	16.89628	18.44997	19.28521	22.73814	19.34973
protein_co	polymerase	133	141	94	146	100	165	2.757991	3.445621	2.568644	2.619131	2.329648	3.400438
protein_co	NFKB_inhib	1307	1128	808	1509	1219	1413	16.4239	16.70386	13.37971	16.40412	17.20891	17.64625
protein_co	DnaJ_(Hsp4	1003	976	721	2128	1348	1530	20.70976	23.74822	19.61752	38.01095	31.26893	31.39606
protein_co	chromoson	0	1	0	1	5	8	0	0.063987	0	0.046973	0.305005	0.431705
protein_co	potassium_	5	7	13	7	8	7	0.121091	0.199778	0.414878	0.146657	0.217661	0.16848
protein_co	interferon_	1052	854	945	1369	907	956	11.9438	11.42593	14.13817	13.446	11.56866	10.78684
protein_co	5'-nucleoti	4729	3797	3218	3650	2009	2250	122.3048	115.7236	109.6718	81.6639	58.37182	57.83176
protein_co	small_integ	116	78	79	135	143	259	3.469579	2.74929	3.113728	3.493137	4.805116	7.698892
protein_co	histone_clu	50	30	24	13	20	47	4.839213	3.42163	3.060912	1.088457	2.174622	4.520768
protein_co	cytochrom	89	71	71	253	101	231	4.651282	4.372684	4.889628	11.43842	5.929978	11.99787
protein_co	kinesin_fam	52	34	62	619	616	617	0.397191	0.306043	0.624055	4.09025	5.285985	4.683721
protein_co	BMI1_polyc	372	318	297	344	196	231	5.745055	5.787426	6.044252	4.595923	3.400607	3.545463
protein_co	THAP_dom	349	281	253	454	293	352	9.801807	9.30024	9.363454	11.03061	9.244798	9.825011
protein_co	methylmal	1144	981	861	2849	1734	2040	35.08951	35.45907	34.8008	75.59738	59.75159	62.18578
protein_co	pyruvate_d	1008	1026	820	2201	1325	1631	11.96782	14.35519	12.82931	22.60673	17.67338	19.24501
protein_co	PX_domain	985	974	899	155	149	164	18.47215	21.5252	22.2165	2.514641	3.139182	3.056573
protein_co	histone_clu	24	51	81	33	134	85	1.618578	4.053216	7.198504	1.925304	10.15258	5.697063
protein_co	protein-L-is	321	280	241	146	177	130	3.996721	4.108317	3.954128	1.572587	2.475832	1.608614
protein_co	potassium_	199	139	123	250	169	174	4.344436	3.576039	3.538509	4.721537	4.14492	3.775194
protein_co	M-phase_sp	364	299	214	672	525	662	20.32755	19.67714	15.74825	32.46505	32.93761	36.74104
protein_co	acyl-CoA_o	120	90	63	6	4	11	2.618681	2.314466	1.81166	0.11327	0.098064	0.238563
protein_co	family_with	33	31	36	0	0	0	0.5042	0.558159	0.724813	0	0	0
protein_co	interferon_	219	188	199	170	150	158	5.034337	5.092876	6.028178	3.380727	3.873811	3.609648
protein_co	myelin-assc	0	0	0	2	6	5	0	0	0	0.016141	0.062882	0.046356
protein_co	chemokine_	1	0	0	1	0	0	0.016265	0	0	0.01407	0	0
protein_co	chromoson	0	0	0	0	0	1	0	0	0	0	0	0.035099
protein_co	xin_actin-b	0	0	0	3	0	3	0	0	0	0.021269	0	0.024434
protein_co	insulinoma	0	0	5	0	0	0	0	0	0.11577	0	0	0
protein_co	delta(4)-des	5	0	0	2	3	3	0.140056	0	0	0.048464	0.094406	0.083514
protein_co	sodium_ch	2	0	0	4	3	1	0.01629	0	0	0.028184	0.02745	0.008094

protein_co	ADP-ribosy	5034	4502	4042	6061	4441	4975	160.5452	169.1985	169.8694	167.2212	159.116	157.6837
protein_co	septin_2	9596	8168	8030	11677	9147	9753	137.2661	137.6879	151.3643	144.4998	146.9944	138.6503
protein_co	filamin_A_i	1145	1080	967	1246	722	808	14.36773	15.97031	15.98983	13.52582	10.17815	10.07636
protein_co	major_facil	44	50	49	51	9	37	0.957814	1.282642	1.405592	0.960421	0.2201	0.80046
protein_co	deoxythym	754	682	532	2591	1820	2477	32.40058	34.53606	30.12505	96.31896	87.86215	105.7833
protein_co	transporter	197	151	175	368	318	292	3.524629	3.183693	4.125912	5.695842	6.391802	5.192059
protein_co	inhibitor_c	604	522	434	797	636	795	6.154034	6.267589	5.827033	7.024967	7.279962	8.050071
protein_co	autophagy_	970	825	684	1914	1301	1594	15.58979	15.62534	14.48636	26.61175	23.49064	25.46047
protein_co	bradykinin_	97	52	74	3	11	8	0.750223	0.473946	0.754198	0.020073	0.095579	0.061492
protein_co	mixed_line	5	3	1	39	17	39	0.068188	0.048213	0.017971	0.460113	0.260456	0.52858
pseudogen	cytidine_m	0	0	1	5	0	0	0	0	0.030814	0.101146	0	0
protein_co	ring_finger_	449	427	383	2889	2213	2499	4.795341	5.37413	5.390223	26.69216	26.55239	26.52461
protein_co	melatonin_	0	0	0	2	10	11	0	0	0	0.071061	0.461411	0.448995
protein_co	ras_homol	0	1	1	2	4	0	0	0.031209	0.034899	0.045822	0.119011	0
protein_co	kelch-like_f	0	0	1	4	0	0	0	0	0.018723	0.049167	0	0
protein_co	componen	404	353	276	324	143	190	7.309693	7.526613	6.580542	5.071376	2.906718	3.416497
protein_co	cell_divisio	241	249	226	328	272	271	3.248989	3.95583	4.014897	3.825322	4.119544	3.630865
protein_co	stress-indu	3392	2767	2523	9548	6563	8278	65.46695	62.93359	64.16798	159.4196	142.3042	158.782
protein_co	sodium_ch	1	0	0	0	0	0	0.020385	0	0	0	0	0
protein_co	hair_growt	5	10	3	115	91	144	0.041778	0.098465	0.033032	0.831262	0.854215	1.195774
protein_co	thioredoxir	0	5	2	6	3	4	0	0.166545	0.074494	0.146713	0.095263	0.112363
protein_co	RAB31_mer	2022	1632	1797	2833	2620	2447	26.39869	25.10895	30.91606	31.99711	38.42834	31.75008
protein_co	receptor_a	544	446	342	1523	1004	1456	16.84205	16.27189	13.95266	40.79049	34.92036	44.79886
protein_co	tenascin_X	45	49	42	4	12	9	0.181415	0.23279	0.223124	0.01395	0.054349	0.036059
protein_co	leucine-rich	3	0	6	0	0	0	0.035933	0	0.094701	0	0	0
protein_co	bone_morp	3166	2812	2001	1293	1067	1277	38.68248	40.48795	32.21702	13.66674	14.64593	15.50615
protein_co	ataxin_2-lik	3285	2624	2278	5341	4647	4938	38.02168	35.79042	34.74437	53.47878	60.42514	56.80109
protein_co	phytanoyl-(	0	3	1	6	0	3	0	0.058488	0.021801	0.085873	0	0.049326
protein_co	coiled-coil_	31	15	23	7	4	7	0.566312	0.322918	0.553677	0.110625	0.082092	0.127087
protein_co	polymerase	1115	982	787	861	719	839	20.59637	21.3764	19.15691	13.75885	14.92086	15.40237
protein_co	flap_struct	500	385	380	2783	2324	2787	11.52896	10.46136	11.54619	55.51322	60.20123	63.86557
protein_co	serum_dep	228	188	207	33	15	24	3.738169	3.632361	4.472282	0.468059	0.276289	0.391061
protein_co	SOGA_fami	2593	2138	2104	1064	1394	1222	22.53012	21.89151	24.09026	7.997708	13.60732	10.55217
protein_co	gastrulatio	3	2	0	86	52	54	0.074811	0.058773	0	1.855255	1.456782	1.338275
protein_co	hemochror	0	0	1	0	0	0	0	0	0.032783	0	0	0
protein_co	hexamethy	48	28	24	25	24	32	1.663068	1.143231	1.095758	0.749328	0.934177	1.101865
protein_co	farnesyltra	605	503	483	1111	708	716	4.371407	4.28293	4.598835	6.944532	5.747093	5.141485
protein_co	serine_incc	617	425	393	1453	915	1046	11.63683	9.445951	9.767357	23.70709	19.38741	19.60609
protein_co	myosin_lig	2	0	0	65	55	56	0.09942	0	0	2.795238	3.071526	2.76656
protein_co	trafficking_	526	415	435	467	411	411	6.117523	5.687809	6.666746	4.698614	5.37008	4.750522
protein_co	cholinergic	0	1	0	0	0	2	0	0.021048	0	0	0	0.035502
protein_co	collagen_ty	334685	293383	269097	32716	34434	35406	3196.564	3302.093	3386.81	270.3152	369.4739	336.0731
protein_co	GDNF_fami	17	13	16	29	38	26	0.182889	0.164812	0.226826	0.269898	0.459273	0.277985
protein_co	inhibitor_c	160	197	138	379	200	284	7.124103	10.33674	8.097	14.59864	10.00436	12.56719

protein_co	CDKN2A_in	143	109	140	499	318	350	2.782272	2.499178	3.589438	8.398991	6.950879	6.767702
protein_co	small_nucl	421	390	413	807	684	578	5.34104	5.830629	6.904442	8.85687	9.748748	7.287544
protein_co	transmemb	175	130	112	315	254	298	7.19307	6.296898	6.066372	11.20082	11.72895	12.17313
protein_co	solute_carr	982	914	936	4304	3091	3094	14.21604	15.59267	17.85574	53.90169	50.27073	44.51405
protein_co	dynein_ligh	4	2	1	0	0	0	0.218089	0.128502	0.071847	0	0	0
protein_co	transmemb	945	793	693	1060	720	856	20.69034	20.46049	19.99419	20.07727	17.70995	18.62598
protein_co	ADAM_met	0	0	0	0	0	1	0	0	0	0	0	0.015824
protein_co	signal_tran	2909	2274	2486	2064	1725	1820	30.51424	28.10971	34.36329	18.72973	20.32811	18.97317
protein_co	zinc_finger_	222	184	164	437	299	350	4.244457	4.145663	4.131881	7.227924	6.422282	6.650386
protein_co	neuroblast	467	320	369	313	257	278	6.718327	5.42502	6.995286	3.895396	4.153617	3.974648
protein_co	ADAM_met	5473	4530	5417	5250	4593	4178	75.47436	73.6172	98.4391	62.632	71.1573	57.26009
protein_co	ADAM_met	0	0	0	2	7	11	0	0	0	0.038358	0.174343	0.24236
protein_co	glial_cell_d	18	12	19	381	337	384	0.250115	0.196497	0.347901	4.579891	5.260731	5.302833
protein_co	diffuse_pan	0	0	0	0	1	0	0	0	0	0	0.011192	0
protein_co	axin_2	2397	2085	1846	860	1032	891	29.79562	30.54201	30.23785	9.247959	14.41163	11.00707
protein_co	NADH_dehy	2543	2128	1683	3020	2206	2948	245.6733	242.2648	214.2548	252.3954	239.4231	283.0405
protein_co	von_Willeb	2	0	0	0	0	2	0.019888	0	0	0	0	0.019765
protein_co	zinc_finger_	38	49	35	86	90	92	0.758868	1.153149	0.921054	1.485743	2.019175	1.825912
protein_co	UDP_glycos	1	0	3	156	112	130	0.02248	0	0.08887	3.033813	2.828579	2.904385
protein_co	family_with	15	12	8	8335	7207	7207	0.146949	0.138537	0.103277	70.63913	79.31957	70.16829
protein_co	low_densit	20	13	19	3	3	8	0.1219	0.093373	0.152602	0.015818	0.020542	0.048459
protein_co	potassium_	0	1	0	1	0	0	0	0.012698	0	0.009322	0	0
protein_co	solute_carr	95	103	72	177	133	142	1.910864	2.441465	1.908418	3.079942	3.005432	2.8386
protein_co	interleukin	447	382	425	10	12	20	5.115569	5.151775	6.409294	0.099003	0.154283	0.227471
protein_co	transmemb	763	564	565	643	434	716	26.48785	23.07323	25.84672	19.31062	16.92626	24.70273
protein_co	low_densit	222	223	263	38	69	15	0.710789	0.841395	1.109631	0.105253	0.248191	0.04773
protein_co	adenosylho	1834	1551	1658	2050	1702	1667	24.18276	24.10047	28.80885	23.38425	25.21246	21.84499
protein_co	DnaJ_(Hsp4	919	716	746	1550	1135	1169	7.837109	7.195492	8.383281	11.43497	10.8739	9.90751
protein_co	protein_kir	798	645	410	556	380	563	28.37268	27.02491	19.2095	17.10154	15.17854	19.89369
protein_co	nephronect	22	14	12	562	479	500	0.253306	0.189958	0.18207	5.597865	6.195947	5.721406
protein_co	family_with	0	2	0	12	2	2	0	0.04337	0	0.191028	0.041346	0.036576
protein_co	sema_dom	941	792	676	1504	1447	1914	13.19319	13.08556	12.4894	18.24194	22.79175	26.6693
protein_co	cyclin_M3	140	111	115	341	302	302	2.1502	2.009004	2.327467	4.53073	5.210829	4.609644
protein_co	glutathione	139	100	98	62	41	52	1.84431	1.563602	1.713484	0.711662	0.611156	0.685697
protein_co	tet_methyl	528	461	565	133	220	168	2.74964	2.829111	3.877263	0.599179	1.287104	0.869483
protein_co	CXXC_finge	24	25	24	4	6	6	0.228317	0.280268	0.300866	0.032919	0.064125	0.056727
protein_co	tectonic_fa	355	373	336	315	255	290	6.440731	7.974854	8.033058	4.944022	5.197518	5.228949
protein_co	short_statu	611	552	541	80	76	89	7.932062	8.444832	9.255011	0.898458	1.108428	1.148271
protein_co	diphosphoi	76	45	58	172	117	158	0.706252	0.492794	0.710246	1.38273	1.221464	1.459193
protein_co	tetraspanin	3111	2576	2398	862	669	641	40.54639	39.56445	41.18472	9.719019	9.795517	8.30271
protein_co	abhydrolas	76	83	80	87	65	51	1.120132	1.441587	1.553748	1.109272	1.076262	0.747026
protein_co	zinc_finger_	283	307	226	592	516	480	3.238016	4.139406	3.4075	5.859726	6.632715	5.458125
protein_co	CTF8_chron	104	133	122	159	213	234	1.896612	2.858274	2.931836	2.508448	4.363889	4.241022
protein_co	adenosine_	107	140	82	220	155	167	1.57659	2.430916	1.592148	2.804275	2.565758	2.445462

protein_co	leucine_car	136	94	132	418	299	314	2.544161	2.072243	3.253976	6.764644	6.283851	5.837743
protein_co	syntrophin_	2977	2415	2864	996	978	1017	16.10025	15.3914	20.41087	4.659895	5.942124	5.466185
protein_co	interleukin_	8	2	0	13	2	5	0.221859	0.065362	0	0.311884	0.062311	0.137805
protein_co	zinc_finger_	340	345	396	511	521	419	2.357247	2.818723	3.617897	3.064856	4.058008	2.88702
protein_co	syntaxin_1	555	456	428	764	680	750	8.402131	8.135203	8.538371	10.00582	11.56523	11.28411
protein_co	Neuron-spe	20	16	24	1350	1010	1120	0.253792	0.239263	0.401323	14.81988	14.39853	14.12458
protein_co	zinc_finger_	53	48	31	99	47	73	0.971226	1.036556	0.748585	1.569433	0.96759	1.329465
protein_co	G_elongati	451	392	420	1069	908	873	6.416659	6.572424	7.874383	13.15749	14.51334	12.34401
protein_co	5-hydroxyt	0	0	0	70	45	71	0	0	0	1.572302	1.312612	1.832073
protein_co	follistatin-l	260	244	247	376	297	236	2.849236	3.151026	3.566866	3.56456	3.656458	2.570258
pseudogen	transmemb	5	0	0	0	7	7	0.354832	0	0	0	0.558085	0.493698
protein_co	DEAD_(Asp	931	751	699	1657	1263	1445	9.843832	9.357536	9.739272	15.15654	15.00261	15.1842
protein_co	atonal_hon	609	459	400	173	137	154	10.4037	9.24039	9.004619	2.556699	2.6293	2.614574
protein_co	SRY_(sex_d	0	0	0	76	81	42	0	0	0	4.255155	5.889425	2.701455
protein_co	ankyrin_rep	112	101	100	251	142	152	1.975147	2.098988	2.323893	3.829289	2.813318	2.664003
protein_co	surfactant_	1	1	0	0	4	9	0.014449	0.017027	0	0	0.06493	0.129238
protein_co	ubiquitin_s	746	549	513	2428	1647	1808	18.14147	15.73306	16.4394	51.07935	44.99625	43.696
protein_co	TNFAIP3_in	613	454	419	850	620	776	16.17788	14.11966	14.57169	19.40632	18.38239	20.35319
protein_co	chromoson	334	257	251	449	450	529	6.232743	5.65162	6.172218	7.248399	9.433966	9.810657
protein_co	transmemb	293	251	183	432	250	338	6.677448	6.74099	5.495773	8.517059	6.400766	7.655424
protein_co	ring_finger_	786	674	482	976	610	888	49.30287	49.82148	39.84112	52.96177	42.98615	55.35696
protein_co	vesicle-assc	80	51	79	163	98	150	6.146995	4.61796	7.998983	10.83486	8.459564	11.45444
protein_co	leucine_ric	209	203	131	354	191	211	1.853068	2.121037	1.530563	2.715259	1.902512	1.859247
protein_co	methionine	5909	5414	5443	6238	4655	5372	110.9714	119.8181	134.7008	101.3457	98.21227	100.2635
protein_co	phospholip	1	0	0	4	1	6	0.015135	0	0	0.052372	0.017003	0.090247
protein_co	energy_hor	0	3	3	2	8	17	0	0.172979	0.193429	0.084656	0.439748	0.826653
protein_co	zinc_finger_	541	471	482	863	1104	924	4.807163	4.93196	5.643824	6.633846	11.02071	8.159681
protein_co	solute_carr	147	93	113	296	205	256	2.743153	2.045139	2.778728	4.778455	4.297696	4.74769
protein_co	inositol_pc	123	152	100	780	850	850	1.377272	2.005697	1.475535	7.555657	10.69258	9.458956
protein_co	leucine_zip	860	710	562	1899	1587	1701	8.335638	8.109719	7.178133	15.92313	17.2809	16.3853
protein_co	chymotryp	1	2	2	0	4	0	0.061703	0.145426	0.162618	0	0.277277	0
protein_co	chymotryp	0	0	0	0	0	2	0	0	0	0	0	0.04681
protein_co	tripartite_r	0	0	0	8	0	5	0	0	0	0.16939	0	0.121623
protein_co	transmemb	648	473	403	761	510	736	12.20846	10.50156	10.0052	12.40319	10.79456	13.78076
protein_co	peptidylpro	352	356	260	203	158	197	13.50379	16.09423	13.14381	6.737085	6.809562	7.510846
protein_co	sprouty_ho	95	92	83	35	54	24	0.557644	0.636398	0.642017	0.177732	0.356104	0.140009
protein_co	centrosom	329	288	295	504	427	369	3.55461	3.666871	4.200034	4.710745	5.182901	3.96216
protein_co	syntaxin_bi	80	67	60	201	145	161	1.024995	1.011611	1.01302	2.227875	2.087127	2.050063
protein_co	transmemb	0	1	0	6	2	0	0	0.027172	0	0.119684	0.051808	0
protein_co	mitochond	801	677	648	1346	825	922	12.03341	11.98538	12.82821	17.493	13.92385	13.76565
protein_co	lectin_gala	68	38	24	29	19	50	1.156065	0.761315	0.537675	0.426515	0.362891	0.844798
protein_co	JMJD7-PLA	19	31	14	7	22	50	0.139183	0.26761	0.135144	0.04436	0.181053	0.36401
protein_co	complexin_	27	25	12	17	28	22	0.655391	0.715128	0.383842	0.356984	0.763561	0.530724
protein_co	PX_domain	403	331	253	273	162	186	9.74211	9.429378	8.059411	5.709179	4.399588	4.468591

protein_co	E2F_transcr	195	195	208	438	364	426	3.132128	3.691022	4.402537	6.086141	6.568336	6.800238
protein_co	fem-1_hom	979	871	1049	1232	1162	944	7.277342	7.629839	10.27544	7.922529	9.703878	6.973836
protein_co	COMM_dor	167	181	188	675	432	506	6.328666	8.083163	9.38833	22.12903	18.39198	19.05706
protein_co	ATP_syntha	8	8	8	7	9	16	0.853887	1.006254	1.125214	0.646356	1.0792	1.697227
protein_co	ubiquinol-c	1182	1019	860	2793	1967	2362	40.89951	41.55104	39.21335	83.60545	76.46348	81.22509
protein_co	major_facil	6	13	6	16	7	13	0.149621	0.382026	0.197164	0.345164	0.196105	0.322177
protein_co	collagen_ty	6	8	15	5	12	25	0.03923	0.06164	0.129239	0.028281	0.088145	0.162449
protein_co	mitogen-ac	992	737	753	1637	1072	1322	15.40102	13.4838	15.40521	21.98616	18.69741	20.39759
protein_co	heterogene	4918	4138	4013	9257	8778	10015	46.79436	46.39835	50.31633	76.19706	93.8317	94.7034
protein_co	insulin_rec	1692	1425	1476	2692	3385	2964	14.97679	14.86416	17.21629	20.61372	33.66092	26.07391
protein_co	methyl_Cp	1177	1053	1038	970	1006	1012	5.931609	6.25362	6.893316	4.228933	5.695647	5.068579
protein_co	variable_ch	0	1	1	0	0	0	0	0.062701	0.070114	0	0	0
protein_co	UPF3_regul	1093	863	779	1118	1021	1265	24.33327	22.64113	22.85349	21.53203	25.53613	27.98855
protein_co	zinc_finger_	0	3	0	4	3	3	0	0.057589	0	0.056368	0.054901	0.048567
protein_co	actin_beta-	0	1	0	93	95	115	0	0.022353	0	1.526083	2.02444	2.167902
protein_co	receptor_ty	2538	2147	1789	663	730	660	30.81749	30.72166	28.62535	6.964375	9.958124	7.964512
pseudogen	bromodom	0	18	4	1	0	4	0	0.760311	0.188932	0.031008	0	0.142489
protein_co	androgen_r	164	105	141	182	246	168	0.862625	0.650841	0.97731	0.828157	1.453659	0.878208
protein_co	dehydroger	381	313	258	351	213	217	7.845398	7.595239	7.000749	6.252593	4.92741	4.440781
protein_co	chromoson	7	6	0	59	24	50	0.10549	0.106555	0	0.769182	0.406326	0.748848
protein_co	HSPB_(heat	23	38	40	105	93	83	0.407784	0.79395	0.934538	1.610477	1.852398	1.46248
protein_co	acetylserot	1229	956	773	797	741	844	31.76977	29.1224	26.33155	17.82311	21.51936	21.68274
protein_co	solute_carr	30040	25136	18237	18215	13670	16922	771.2645	760.5131	617.0092	404.5718	394.2948	431.7822
protein_co	carbohydra	329	337	234	731	498	688	7.938736	9.582801	7.440569	15.25934	13.5	16.49885
protein_co	prostate_ar	2	1	4	116	142	99	0.02113	0.01245	0.055688	1.060202	1.685408	1.039471
protein_co	casein_kina	516	483	492	554	569	489	3.369625	3.716945	4.233815	3.129714	4.174392	3.173587
protein_co	family_with	755	608	560	703	567	509	11.62608	11.03308	11.36342	9.36493	9.808855	7.789573
protein_co	armadillo_r	94	88	80	20	20	12	1.393184	1.536988	1.562448	0.256433	0.333012	0.176755
protein_co	actin_filam	13	15	7	694	712	726	0.173621	0.236079	0.123194	8.018275	10.68286	9.636176
protein_co	zinc_finger_	201	179	128	290	214	223	4.283873	4.495734	3.594887	5.346893	5.123932	4.723403
protein_co	activating_	405	452	297	1395	743	1266	10.36303	13.62941	10.01435	30.8794	21.35844	32.194
protein_co	ubiquitin-c	780	638	598	1864	1248	1389	9.44294	9.102074	9.540005	19.52188	16.97369	16.71185
protein_co	zinc_finger_	255	175	214	389	296	306	2.263194	1.830319	2.502824	2.986718	2.951362	2.699061
protein_co	carnitine_p	247	177	175	16	9	25	4.432687	3.743264	4.1385	0.248401	0.181452	0.445882
protein_co	proprotein	29	49	38	113	99	93	0.394574	0.785659	0.681317	1.330063	1.513265	1.257545
protein_co	exportin_6	2309	1782	1747	4098	2758	2877	27.64377	25.14132	27.56139	42.44322	37.09511	34.23126
protein_co	GSG1-like	0	0	0	1	0	0	0	0	0	0.009204	0	0
protein_co	meningiom	520	510	428	81	95	66	3.643372	4.210924	3.951652	0.490962	0.747778	0.459572
protein_co	APEX_nucle	518	393	378	1292	764	858	8.450981	7.55574	8.126509	18.23488	14.00296	13.91151
protein_co	non-SMC_e	473	440	278	647	437	552	13.51381	14.81414	10.46637	15.99131	14.02643	15.67348
protein_co	coiled-coil_	57	62	58	301	187	210	1.220233	1.564108	1.636179	5.574392	4.49737	4.467833
protein_co	interleukin	0	7	0	0	0	0	0	0.279586	0	0	0	0
protein_co	Uncharacte	5	9	8	28	11	19	0.098918	0.209824	0.20856	0.479211	0.244482	0.373568
protein_co	RAB3B_mer	386	299	299	878	732	742	1.591033	1.452346	1.624044	3.130757	3.389627	3.039522

protein_co	olfactory_r	0	0	0	0	2	0	0	0	0	0	0.112113	0
protein_co	CD2_(cytop	1709	1508	1237	2005	1934	2560	26.44728	27.50093	25.22572	26.84209	33.62363	39.3721
protein_co	regulator_c	150	122	101	166	139	143	3.28826	3.151678	2.917636	3.148082	3.423252	3.115449
protein_co	TBC1_doma	2005	1813	1409	2220	1799	2105	23.00535	24.51429	21.30396	22.03588	23.18968	24.00359
protein_co	lectin_man	4666	3810	2866	4584	3326	4015	137.2348	132.054	111.0786	116.6345	109.8983	117.3586
protein_co	germinal_c	0	0	0	1	2	2	0	0	0	0.011089	0.028802	0.025479
protein_co	RAB24_mer	129	83	89	18	33	61	3.752411	2.845155	3.411501	0.452956	1.078409	1.763438
protein_co	PRELI_dom	1386	1011	786	2977	2496	2911	58.18891	50.01903	43.48449	108.1232	117.7255	121.4588
protein_co	thrombosp	326	290	250	336	261	348	4.101417	4.299535	4.144682	3.656947	3.688977	4.351162
protein_co	carbonic_a	135	110	127	239	236	238	1.181328	1.134322	1.464452	1.809246	2.320052	2.069776
protein_co	solute_carr	261	209	194	373	201	320	10.62892	10.03003	10.41083	13.14076	9.195892	12.95115
protein_co	ephrin-A1	28	14	16	463	320	492	0.769651	0.453493	0.57955	11.00981	9.881772	13.44035
protein_co	chemokine	0	2	0	1	0	0	0	0.106373	0	0.039044	0	0
protein_co	nuclear_po	82	60	40	218	178	146	1.239978	1.069198	0.797067	2.851803	3.023911	2.194131
protein_co	SH3_domai	12	10	13	87	38	65	0.086741	0.085183	0.123829	0.544034	0.308586	0.466946
protein_co	chemokine_	0	0	0	3	3	1	0	0	0	0.085552	0.111101	0.032761
protein_co	zinc_finger_	128	143	107	189	156	212	4.544901	5.983531	5.006486	5.805495	6.222832	7.481005
protein_co	NMD3_hon	852	690	732	1249	1027	971	14.73562	14.06323	16.68302	18.68763	19.95484	16.69005
protein_co	adrenocept	3	7	9	54	18	40	0.077816	0.213971	0.307628	1.21173	0.52453	1.031143
protein_co	beta-13-N-a	46	76	52	304	240	268	0.675343	1.314883	1.006015	3.861028	3.958464	3.910307
protein_co	G_protein_	318	268	226	396	277	330	3.997919	3.970532	3.744123	4.306903	3.912332	4.123162
protein_co	heat_shock	1	7	1	6	0	0	0.069385	0.572364	0.091433	0.360149	0	0
protein_co	potassium_	108	69	103	54	49	48	1.399321	1.053537	1.758595	0.605272	0.713245	0.61808
protein_co	mitochond	418	375	277	1048	642	807	14.8519	15.70161	12.96942	32.21292	25.62654	28.49633
protein_co	Src_homol	2	1	0	4	2	1	0.015446	0.009101	0	0.026724	0.017353	0.007675
protein_co	nuclear_rec	3	0	0	112	106	116	0.078586	0	0	2.538089	3.119469	3.019906
protein_co	phosphoglu	507	399	348	1168	830	973	8.223371	7.626441	7.437997	16.38882	15.12408	15.68427
protein_co	serine/thre	0	0	0	1	5	2	0	0	0	0.008492	0.055142	0.019512
protein_co	interleukin	11	7	6	0	3	1	0.158809	0.119093	0.114148	0	0.048658	0.014348
protein_co	chromoson	5	1	2	2	6	3	0.130977	0.03087	0.069038	0.045323	0.176574	0.078101
protein_co	KIAA1024	70	81	67	27	24	17	0.550486	0.750654	0.694317	0.183685	0.212035	0.132864
protein_co	solute_carr	444	382	470	619	470	431	6.310282	6.397883	8.802347	7.61061	7.504344	6.087693
protein_co	snurportin_	167	138	122	153	159	143	4.578532	4.458574	4.407623	3.62881	4.897292	3.896328
protein_co	CASP2_and	141	154	131	139	88	93	5.078014	6.535857	6.217	4.330645	3.560463	3.328644
protein_co	SIN3_transc	921	767	821	1127	1196	1103	7.237443	7.102774	8.501656	7.661476	10.55859	8.614116
protein_co	ADP-ribosy	138	126	131	336	307	271	1.870419	2.012507	2.339731	3.939691	4.67463	3.650386
protein_co	ribonuclea	0	1	0	0	0	0	0	0.082633	0	0	0	0
protein_co	epididymal	0	0	0	1	1	0	0	0	0	0.043535	0.056536	0
protein_co	protein_tyr	1262	1046	1188	3033	2409	2396	13.48366	13.17004	16.72629	28.03392	28.91574	25.44163
protein_co	radial_spok	0	0	0	0	0	7	0	0	0	0	0	0.114378
protein_co	platelet-act	2	0	1	28	19	29	0.023576	0	0.015534	0.285542	0.251624	0.339748
protein_co	protein_tyr	950	826	748	1054	718	912	12.75525	13.0693	13.23432	12.24247	10.83026	12.16942
protein_co	ribonuclea	0	0	0	11	5	15	0	0	0	0.474824	0.280282	0.743837
protein_co	natriuretic_	1	1	1	8	2	7	0.012498	0.014728	0.016469	0.086495	0.028081	0.086945

protein_co potassium_	0	0	0	0	0	2	0	0	0	0	0	0.032121
protein_co interleukin	57	39	35	11	2	2	1.769875	1.427051	1.432091	0.295477	0.069766	0.061717
protein_co sodium_ch	13	20	21	22	18	22	0.070321	0.127491	0.149691	0.10295	0.109387	0.11827
protein_co Ras_associa	5	0	1	7	8	11	0.044162	0	0.011639	0.053486	0.079381	0.096556
protein_co collagen_ty	8	9	3	10	9	15	0.066739	0.088479	0.03298	0.07217	0.08435	0.124363
protein_co syndecan_2	3640	3094	3004	4659	3248	3623	51.37436	51.46031	55.87014	56.88539	51.50034	50.81864
protein_co CD52_mole	0	0	0	0	1	0	0	0	0	0	0.102368	0
protein_co membrane_	582	515	477	887	699	601	8.242819	8.59542	8.902377	10.86774	11.1219	8.459348
protein_co small_proli	0	0	0	2	0	0	0	0	0	0.147738	0	0
protein_co TM2_doma	1791	1550	1401	1915	1450	1726	27.6033	28.15167	28.45367	25.53272	25.10628	26.43722
protein_co HtrA_serine	5	4	3	19	27	25	0.126351	0.119117	0.0999	0.41536	0.766515	0.627853
protein_co pleckstrin_	1213	1149	858	149	100	105	11.39011	12.71435	10.61669	1.210365	1.054912	0.979864
protein_co chloride_in	6992	5847	6653	7926	6924	6276	85.17336	83.9349	106.7959	83.52557	94.75639	75.97924
protein_co solute_carr	1	0	2	0	3	3	0.014167	0	0.037337	0	0.047746	0.042238
protein_co G_protein-(	1	1	3	7	2	13	0.031142	0.036699	0.123112	0.188584	0.069972	0.402343
protein_co coiled-coil_	928	815	628	275	264	417	15.29077	15.82509	13.63565	3.919919	4.88691	6.828528
protein_co methyltran	201	171	188	296	259	272	2.409678	2.415829	2.969995	3.069854	3.488284	3.24072
protein_co mucin_15_	0	0	0	31	21	34	0	0	0	0.436582	0.38407	0.550085
protein_co chromoson	0	0	2	0	0	0	0	0	0.080745	0	0	0
protein_co zinc_finger_	1286	1084	1230	672	771	563	10.8411	10.76884	13.66383	4.900775	7.3019	4.716833
protein_co gap_junctio	2	0	0	0	0	2	0.05561	0	0	0	0	0.055267
protein_co poly(rC)_bi	1755	1441	1325	2984	2481	2882	53.153	51.43062	52.88121	78.18303	84.41633	86.74696
protein_co histidine_tr	2320	2036	1393	3968	2512	4047	113.6199	117.5036	89.89848	168.1129	138.2086	196.9742
protein_co DTW_doma	56	59	68	177	109	139	0.679197	0.843271	1.086805	1.857138	1.485195	1.675453
protein_co chloride_in	3	1	1	7	2	2	0.156168	0.061345	0.068597	0.315233	0.116963	0.103469
protein_co INO80_com	772	674	402	915	640	1040	9.145323	9.409114	6.275417	9.377041	8.517473	12.24404
protein_co basonuclin_	41	32	41	997	826	675	0.470842	0.43306	0.620454	9.904883	10.65664	7.703793
protein_co DNA_fragm	157	160	147	324	179	250	2.636972	3.16689	3.253554	4.707755	3.377598	4.173069
protein_co NFU1_iron-	323	294	229	448	318	385	11.6564	12.50306	10.89011	13.98631	12.89253	13.80805
protein_co anthrax_to	3024	2690	2686	1078	855	836	27.32438	28.64362	31.98228	8.426561	8.679281	7.507313
protein_co gastrokine_	0	0	1	0	1	0	0	0	0.085704	0	0.073066	0
protein_co cytoskeletc	165	140	155	561	567	468	1.84405	1.843843	2.282734	5.423936	7.11903	5.198095
protein_co chromoson	241	189	168	318	263	286	6.782977	6.268624	6.230851	7.742718	8.315878	7.999797
protein_co family_with	33	37	33	92	43	61	1.114192	1.472159	1.468232	2.687181	1.631036	2.046848
protein_co aprataxin_a	54	40	44	67	82	33	0.731903	0.638891	0.785864	0.785593	1.248598	0.444512
protein_co bolA_homc	15	9	6	31	10	18	0.784699	0.554832	0.413616	1.402931	0.587707	0.935823
protein_co RANBP2-lik	26	22	31	67	51	45	0.246855	0.24615	0.387852	0.55031	0.543987	0.424611
protein_co hypermeth	362	387	261	1731	2261	2653	2.761475	3.47897	2.623662	11.42333	19.37681	20.11312
protein_co leucine_zip	520	376	495	1311	1159	1106	3.093877	2.636299	3.880965	6.74785	7.746976	6.5398
protein_co hexosamini	288	258	165	256	199	252	6.67265	7.044216	5.037611	5.131081	5.179741	5.802512
protein_co dopamine_	0	0	0	2	2	4	0	0	0	0.038567	0.050085	0.088613
protein_co BUB1_mitc	232	206	235	2283	1725	1651	3.477438	3.638695	4.641668	29.60331	29.04755	24.59394
protein_co spinster_ho	16	13	19	16	14	19	0.375968	0.359982	0.588328	0.325247	0.36958	0.443705
protein_co leucine_ric	287	285	156	728	603	876	5.625348	6.582933	4.029275	12.34417	13.27804	17.06402

protein_co cholinergic	32	29	23	71	61	77	0.467599	0.499377	0.44288	0.897522	1.001389	1.118212
protein_co stimulated_	772	508	469	1187	1058	1627	45.71638	35.45075	36.59841	60.80906	70.38649	95.75286
protein_co 1-acylglyce	381	259	233	577	419	550	13.34029	10.68679	10.75056	17.47749	16.48175	19.13871
protein_co alveolar_so	403	358	240	621	487	633	3.877016	4.05866	3.042556	5.168294	5.263451	6.052098
protein_co fatty_acid_	12845	10623	9923	12722	14479	14572	79.44241	77.42346	80.87162	68.06702	100.6018	89.56682
protein_co CCHC-type_	3646	3262	2753	8101	5341	6318	115.9993	122.3009	115.4197	222.9669	190.902	199.769
protein_co metallothic	605	508	415	227	278	328	43.93594	43.47458	39.71435	14.26111	22.6808	23.67271
protein_co dihydrouri	657	570	417	2494	1606	2155	7.805708	7.980477	6.528566	25.63341	21.43589	25.44508
protein_co G_protein_	1731	1297	1145	3942	2234	2888	22.48304	19.85203	19.59739	44.29325	32.59794	37.27904
protein_co RFNG_O-fu	755	622	456	551	319	442	12.86464	12.48959	10.23883	8.122046	6.106475	7.484844
protein_co dicarbonyl,	845	739	432	899	583	813	35.7595	36.85414	24.09092	32.91224	27.71739	34.19282
protein_co zinc_finger_	216	202	141	111	63	107	9.521444	10.49319	8.19036	4.232871	3.119886	4.687513
protein_co LIM_domai	315	239	231	242	135	165	6.135546	5.485897	5.929109	4.077754	2.954102	3.19401
protein_co ras-related_	1155	980	674	758	656	738	56.09803	56.09172	43.13803	31.84915	35.79468	35.62309
protein_co neuregulin_	63	55	67	135	102	193	0.979237	1.007435	1.372325	1.815283	1.781134	2.98136
protein_co LIM_and_se	1160	1082	1103	1531	1100	1138	13.98259	15.36965	17.52024	15.96496	14.89606	13.63269
protein_co chromoson	44	33	22	127	98	140	0.924367	0.816982	0.609045	2.308119	2.312952	2.923003
protein_co neuroligin_	104	79	83	12	14	12	0.668025	0.59799	0.702542	0.066681	0.101027	0.076604
protein_co transmemb	123	114	122	197	161	166	1.418371	1.549162	1.853871	1.965233	2.085738	1.902403
protein_co UDP-glucos	2099	1987	1797	4056	3000	3137	25.27249	28.19295	28.5114	42.24707	40.57943	37.53702
protein_co taste_recep	0	0	2	0	0	0	0	0	0.102972	0	0	0
protein_co leucine_ric	13	9	8	243	115	184	0.225281	0.183794	0.182686	3.642924	2.238864	3.168899
protein_co heterogene	2971	2625	2334	6689	5923	6914	57.09172	59.44384	59.10254	111.1974	127.8678	132.0412
protein_co biotinidase	133	104	117	150	114	88	3.293336	3.034763	3.817729	3.213207	3.171307	2.165592
protein_co chondroiti	551	567	500	367	298	271	7.820506	9.483604	9.351646	4.506219	4.751695	3.822629
protein_co tachykinin_	0	0	0	1	0	0	0	0	0	0.008824	0	0
protein_co protocadhe	1594	1313	1621	5609	5907	5371	12.47789	12.11224	16.72132	37.98404	51.94799	41.78472
protein_co roundabou	3674	3073	3862	1196	1241	970	25.8995	25.52829	35.87561	7.293674	9.828178	6.79569
protein_co one_cut_ho	3	5	5	4	12	10	0.075919	0.14911	0.166738	0.08757	0.341162	0.251501
protein_co apoptosis_(	463	318	352	385	319	412	15.27207	12.36093	15.30011	10.98603	11.82107	13.50591
protein_co purinergic_	0	0	3	30	82	46	0	0	0.067382	0.442359	1.570195	0.779216
protein_co catenin_(ca	0	2	1	75	80	61	0	0.022765	0.012728	0.626695	0.868103	0.58556
protein_co tripartite_r	456	369	341	242	349	388	6.681731	6.371733	6.584356	3.067627	5.745114	5.650222
protein_co mucin_17_	0	0	0	1	0	0	0	0	0	0.003216	0	0
protein_co wingless-ty	4	3	1	13	1	11	0.093124	0.082306	0.030679	0.261823	0.026155	0.254509
protein_co calmodulin	10	11	5	6	13	33	0.281302	0.364647	0.185343	0.146011	0.410833	0.922563
protein_co RALBP1_ass	11	14	13	18	7	1	0.073298	0.109934	0.11415	0.103761	0.052402	0.006622
protein_co mucin_3A_	0	0	0	37	21	16	0	0	0	0.399849	0.294713	0.198637
protein_co synapse_ass	1363	1238	1034	1719	1223	1523	11.7733	12.60173	11.76949	12.84521	11.86801	13.07411
protein_co integrin_alp	3	0	0	0	0	0	0.033663	0	0	0	0	0
protein_co PYD_(pyrin_	2	0	0	0	0	0	0.130236	0	0	0	0	0
protein_co tyrosylprot	279	234	243	227	218	225	6.980405	6.89921	8.011568	4.91321	6.127481	5.594594
protein_co transmemb	1	2	2	0	0	0	0.025198	0.059389	0.06641	0	0	0
protein_co torsin_A_in	1399	1451	1074	2290	1692	2210	9.369317	11.45156	9.478275	13.26749	12.73033	14.7093

protein_co	transmemb	1738	1568	1475	384	152	197	29.53819	31.40416	33.03398	5.645836	2.902196	3.327438
protein_co	OTU_doma	416	314	333	570	523	559	3.442778	3.062333	3.631573	4.080878	4.862577	4.597664
protein_co	OTU_doma	10	2	3	6	12	10	0.154302	0.036367	0.061	0.080091	0.208018	0.153349
protein_co	glucuronid	507	519	335	1135	761	965	10.50532	12.67289	9.147045	20.34511	17.71474	19.87184
protein_co	bromodom	623	531	477	834	910	913	5.835499	5.861268	5.887666	6.758013	9.575917	8.49905
protein_co	Kruppel-lik	1132	1008	932	1269	1528	1370	8.780836	9.214188	9.526649	8.515577	13.31563	10.56136
protein_co	FERM_and_	4	0	8	3	2	1	0.025016	0	0.065931	0.016231	0.014052	0.006215
protein_co	zinc_finger_	106	66	84	69	38	30	1.193988	0.876083	1.246833	0.672367	0.480869	0.335834
protein_co	zinc_finger_	177	176	115	238	132	167	3.155069	3.697051	2.701272	3.670081	2.643374	2.958433
protein_co	zinc_finger_	64	52	40	91	64	70	0.860829	0.824228	0.708976	1.058867	0.967088	0.935717
protein_co	zinc_finger_	707	647	478	1404	1046	1216	16.18914	17.45885	14.42338	27.81214	26.90822	27.67244
protein_co	taste_recep	22	22	6	9	14	13	0.339266	0.399805	0.121928	0.120067	0.242547	0.199238
protein_co	transmemb	223	176	147	81	84	72	3.844299	3.575461	3.339369	1.207982	1.626824	1.233543
protein_co	mitogen-ac	578	513	560	455	453	363	2.783833	2.911654	3.55417	1.895788	2.451109	1.737527
protein_co	pseudourid	185	138	115	300	242	263	5.493036	4.828663	4.499595	7.705929	8.072446	7.760794
protein_co	splicing_fac	1879	1544	1027	2839	1566	1963	134.9744	130.701	97.21423	176.4221	126.3762	140.1376
protein_co	zinc_finger_	87	95	84	256	194	208	1.730878	2.227296	2.202223	4.406058	4.336087	4.112635
protein_co	tigger_tran	8	1	2	9	7	3	0.17133	0.025238	0.056443	0.166744	0.168419	0.063852
protein_co	intermedia	514	371	401	641	605	867	4.39749	3.740441	4.520859	4.744198	5.814953	7.371749
protein_co	neuroligin_	4086	3698	2866	307	364	411	46.59994	49.70052	43.07229	3.028924	4.663773	4.658418
protein_co	myosin_VII	0	0	0	5	10	10	0	0	0	0.034087	0.088532	0.078318
protein_co	chromodor	10419	8591	7360	1783	2290	2313	74.98535	72.86202	69.80122	11.10107	18.51548	16.54381
protein_co	transmemb	92	82	87	261	193	187	0.455279	0.478201	0.56734	1.11736	1.07299	0.919688
protein_co	myosin_VII	7	6	3	4	6	0	0.072993	0.07373	0.041223	0.036083	0.070289	0
protein_co	activated_l	2424	2096	2728	3891	3344	2910	27.29823	27.81635	40.48378	37.90758	42.30748	32.569
protein_co	tyrosine_3-	5822	4763	5191	7934	8430	7928	82.30239	79.34653	96.69992	97.02764	133.8804	111.3816
protein_co	ubiquitin-c	1534	1241	978	2919	1844	2028	51.72706	49.31412	43.45764	85.15096	69.85579	67.96261
protein_co	centrobin_	810	699	545	963	827	983	11.37761	11.57045	10.08782	11.70187	13.0503	13.72237
protein_co	trafficking_	1233	1050	801	1533	1010	1232	80.48859	80.77326	68.90307	86.57179	74.06988	79.92665
protein_co	zona_pellu	12	8	2	0	0	0	0.175544	0.137912	0.038554	0	0	0
protein_co	potassium_	98	74	51	15	14	24	2.110748	1.878231	1.447489	0.279489	0.338756	0.513725
protein_co	G_protein-r	0	0	0	0	4	1	0	0	0	0	0.094858	0.020978
protein_co	SUMO-inte	183	137	137	260	189	168	2.712263	2.39281	2.675691	3.333627	3.146962	2.474569
protein_co	transmemb	441	370	365	808	546	692	5.140242	5.082224	5.606252	8.147405	7.149681	8.016055
pseudogen	-	153	158	110	576	272	417	5.159218	6.27851	4.887873	16.80266	10.30411	13.97456
protein_co	Neuron-spe	0	6	0	1	2	3	0	0.152662	0	0.018678	0.048512	0.064373
pseudogen	-	37	49	37	50	38	55	0.734464	1.146231	0.967845	0.858622	0.847426	1.085029
protein_co	serpin_pep	1	0	0	0	0	2	0.032903	0	0	0	0	0.0654
protein_co	zinc_finger_	46	37	88	45	67	61	0.835432	0.791885	2.106061	0.707016	1.367028	1.101014
protein_co	non_impri	84	79	95	543	414	417	0.584138	0.647397	0.870552	3.266624	3.23434	2.88192
protein_co	forkhead_b	3	1	5	4	4	20	0.072821	0.028605	0.159934	0.083996	0.10908	0.482476
protein_co	ubiquitin-c	1537	1354	1204	2105	1631	1873	53.85196	55.90535	55.58901	63.80324	64.19935	65.21914
protein_co	heterogene	6087	5126	4877	10923	11112	13223	56.65468	56.22354	59.81637	87.95032	116.1913	122.3129
protein_co	salt-induci	1090	933	860	772	1062	840	5.962563	6.01444	6.199258	3.653312	6.526496	4.566626

protein_co	ring_finger_	76	62	98	7	46	20	0.887214	0.85293	1.507564	0.070693	0.603284	0.232036
protein_co	coiled-coil_	0	0	0	0	1	0	0	0	0	0	0.006674	0
lincRNA	-	23	12	5	10	11	11	0.479198	0.294629	0.137275	0.18024	0.257472	0.227766
protein_co	homeobox_	14	12	5	0	2	0	0.506266	0.511375	0.238263	0	0.081251	0
protein_co	cholinergic	104	87	83	131	110	192	2.153251	2.122696	2.26451	2.346366	2.558604	3.950683
protein_co	homeobox_	3	0	4	0	0	0	0.087991	0	0.1546	0	0	0
protein_co	ubiquitin_s	289	235	230	636	513	495	2.1829	2.091756	2.289279	4.155814	4.353138	3.715788
protein_co	solute_carr	49	56	39	239	164	158	1.264802	1.703419	1.326557	5.336879	4.755754	4.053155
protein_co	N-acetylneu	142	169	166	262	212	177	1.896474	2.65982	2.921469	3.027072	3.180851	2.349316
protein_co	ankyrin_rep	0	2	3	11	8	12	0	0.049066	0.0823	0.198108	0.187105	0.248277
protein_co	adrenocept	17	5	2	175	128	129	0.517835	0.179481	0.08028	4.611512	4.380275	3.905186
protein_co	ADP-ribose	135	89	104	101	66	103	5.596738	4.348088	5.681583	3.62231	3.073932	4.243733
protein_co	PWWP_dor	164	172	217	332	282	276	2.175476	2.688722	3.793193	3.809881	4.202508	3.638556
protein_co	ubiquitin_s	2	0	0	0	7	0	0.076394	0	0	0	0.300383	0
protein_co	ubiquitin_s	1118	962	1051	1529	1298	1140	7.612609	7.719228	9.430381	9.006627	9.929227	7.714472
protein_co	programme	2511	2155	2115	3287	2274	2148	21.57683	21.82203	23.94893	24.43451	21.95232	18.34361
protein_co	MAS-relate	0	0	0	8	0	4	0	0	0	0.306091	0	0.17582
protein_co	zinc_finger_	204	162	122	355	256	352	3.843403	3.59673	3.028868	5.785983	5.418447	6.590799
protein_co	melanocort	12	1	8	2	1	0	0.635292	0.062388	0.558106	0.091598	0.059476	0
protein_co	family_with	100	69	60	263	233	198	1.314651	1.068973	1.039433	2.991088	3.441244	2.586934
protein_co	zinc_finger_	1086	858	809	1144	948	1301	15.4512	14.38556	15.16756	14.08061	15.15269	18.39583
protein_co	galactosida	1691	1450	1342	3126	1987	2261	34.22141	34.58035	35.78835	54.72759	45.17532	45.47415
protein_co	chromoson	94	79	86	283	167	209	4.312351	4.27091	5.198997	11.23145	8.607	9.528888
protein_co	fatty_acid_	128	89	83	88	50	67	1.775333	1.454679	1.51699	1.055883	0.779092	0.923537
protein_co	cartilage_a	6318	5367	4313	6536	3939	4315	132.8361	132.9765	119.4952	118.8807	93.04036	90.16268
protein_co	cyclic_nucl	1	1	2	0	0	0	0.012179	0.014352	0.032097	0	0	0
protein_co	sarcolipin	0	0	1	8	10	26	0	0	0.077001	0.404405	0.656467	1.509895
protein_co	elongator_	429	380	322	936	613	798	10.28143	10.73216	10.16921	19.40596	16.50463	19.0068
protein_co	CKLF-like_M	194	176	180	105	55	100	8.748341	9.352845	10.69624	4.096154	2.78635	4.481606
protein_co	GABA(A)_re	31	27	18	13	14	14	1.004389	1.030887	0.768506	0.364373	0.509586	0.450794
protein_co	syntaxin_8	377	365	282	448	291	388	16.03113	18.29038	15.8018	16.48025	13.9016	16.39699
protein_co	cyclin-depe	414	323	395	2967	2099	2413	11.25132	10.34458	14.14605	69.75634	64.08622	65.17336
protein_co	ubiquitin_E	2143	1747	1878	1316	1294	1911	92.61433	88.97254	106.9514	49.20111	62.82599	82.07792
protein_co	nuclear_fac	370	422	344	999	788	876	3.846096	5.169374	4.712069	8.983528	9.202243	9.049658
protein_co	fatty_acid_	20	14	11	5	3	4	1.125207	0.928192	0.815511	0.243352	0.189615	0.223652
protein_co	FERM_and_	3	0	0	38	18	17	0.031784	0	0	0.348281	0.214242	0.178995
protein_co	PR_domain	189	139	167	290	295	227	1.582703	1.371701	1.842845	2.100867	2.775292	1.889179
protein_co	UDP-GlcNA	86	79	70	2253	1970	1748	1.64782	1.783797	1.767437	37.34525	42.40592	33.28605
protein_co	FBJ_murine	105	99	85	63	58	60	2.575906	2.862088	2.747859	1.337039	1.598519	1.462856
protein_co	transmemb	7334	6023	6030	5402	4388	4477	94.08026	91.0495	101.9318	59.94807	63.2373	57.07611
pseudogen	olfactory_r	0	0	0	1	0	4	0	0	0	0.015722	0	0.072247
protein_co	SET_domai	124	144	124	348	224	273	2.68714	3.677377	3.540993	6.523954	5.453379	5.879507
protein_co	SMAD_fami	766	652	653	224	222	194	12.31485	12.35251	13.83402	3.115383	4.009612	3.099643
protein_co	empty_spir	0	0	1	53	46	64	0	0	0.02409	0.838171	0.944714	1.162741

protein_co	cystatin_SN	0	0	0	2	3	8	0	0	0	0.120523	0.234773	0.553832
protein_co	Sp7_transc	0	0	1	3	1	2	0	0	0.022161	0.043646	0.018893	0.033427
protein_co	family_with	297	222	164	52	42	35	2.8239	2.487442	2.054809	0.42772	0.448633	0.330728
protein_co	sema_dom	56	26	42	23	41	37	0.457797	0.250476	0.452449	0.162658	0.376546	0.300605
protein_co	leucine_ric	31	11	8	61	19	58	0.325888	0.136272	0.110823	0.554752	0.224393	0.60596
protein_co	solute_carr	294	238	328	1058	1007	859	2.843378	2.71251	4.180189	8.851889	10.94122	8.256388
protein_co	doublecort	97	66	63	141	165	143	1.204051	0.965437	1.030501	1.514102	2.300944	1.764082
protein_co	zinc_finger_	29	53	74	410	359	279	0.327354	0.705021	1.100743	4.003742	4.552634	3.129919
pseudogen	-	2	3	2	0	4	0	0.319885	0.565448	0.42153	0	0.718742	0
protein_co	G_protein-	6	1	11	616	510	637	0.106307	0.020879	0.256826	9.441809	10.15151	11.21658
protein_co	transmemb	70	52	45	86	49	96	1.031414	0.902912	0.87374	1.096216	0.81111	1.405775
protein_co	V-set_and_	0	0	0	1	5	4	0	0	0	0.013466	0.087439	0.061881
protein_co	keratin_8	236	197	149	144824	100206	124984	4.365505	4.294334	3.631981	2317.533	2082.405	2297.664
protein_co	keratin_78	0	2	0	0	0	0	0	0.048855	0	0	0	0
protein_co	adenosine_	116	115	74	189	143	150	3.275283	3.826447	2.753324	4.61653	4.53603	4.209124
protein_co	short_chair	0	0	0	0	0	2	0	0	0	0	0	0.059619
protein_co	O-6-methyl	253	228	136	331	197	297	7.614594	8.086641	5.393864	8.618214	6.661032	8.883669
protein_co	methyltran	1	0	0	0	0	1	0.035153	0	0	0	0	0.034936
protein_co	keratin_86	0	2	0	2	1	5	0	0.059673	0	0.043806	0.028444	0.125811
protein_co	histidyl-tRN	1833	1567	1328	1975	1685	2043	27.77357	27.97984	26.51564	25.88805	28.68258	30.76431
protein_co	nuclear_tra	218	168	211	314	250	240	2.986064	2.711808	3.808552	3.720791	3.847084	3.267108
protein_co	DENN/MAD	165	146	175	423	409	381	0.922414	0.961838	1.289184	2.045717	2.568706	2.116785
protein_co	CD14_mole	4	3	0	4	0	9	0.112282	0.099238	0	0.097134	0	0.251074
protein_co	DnaJ_(Hsp4	498	419	378	172	119	149	5.166493	5.122567	5.167651	1.543682	1.386956	1.536252
protein_co	spermatoge	86	65	51	44	43	62	5.008719	4.461169	3.914112	2.216889	2.813492	3.588637
protein_co	Ral_GTPase	910	813	1002	1019	972	876	5.562441	5.856278	8.070986	5.388418	6.674817	5.321546
protein_co	within_bgc	392	336	232	1227	921	1196	16.9273	17.09811	13.20153	45.83626	44.67971	51.32659
protein_co	marginal_z	0	0	3	0	0	0	0	0	0.110911	0	0	0
protein_co	solute_carr	11	12	11	15	5	7	0.252866	0.325077	0.333216	0.298299	0.129127	0.159921
protein_co	neuronal_P	795	611	623	71	67	74	5.272215	4.77501	5.444385	0.407331	0.499172	0.487716
protein_co	keratin_72	0	0	0	0	4	1	0	0	0	0	0.118066	0.026111
protein_co	KiSS-1_met	1	0	0	29	12	15	0.07467	0	0	1.873298	1.006645	1.113132
protein_co	LON_peptic	1	4	5	25	65	46	0.003805	0.017938	0.025073	0.082301	0.277885	0.173968
protein_co	nudix_(nuc	674	533	430	484	428	574	14.51677	13.52834	12.20432	9.018173	10.35626	12.2866
protein_co	hydroxyste	4	1	0	0	4	9	0.088345	0.026027	0	0	0.099251	0.19755
protein_co	proliferatic	1660	1349	1090	5492	3535	4390	34.10246	32.65854	29.50795	97.60481	81.5861	89.62968
protein_co	ELOVL_fatty	623	638	699	1402	1298	1192	5.110356	6.167241	7.555707	9.948879	11.96153	9.717376
protein_co	6-phospho	1545	1381	1131	1716	1883	1842	18.24533	19.2187	17.60033	17.53088	24.98174	21.61835
protein_co	transmemb	0	4	4	36	14	11	0	0.055468	0.062026	0.366473	0.185077	0.128641
protein_co	ADP-ribosy	1412	1125	1170	7721	4645	5325	31.05637	29.1592	33.91069	146.9104	114.7759	116.3979
protein_co	serpin_pep	30	44	27	562	413	387	0.38568	0.6666	0.457409	6.250361	5.964923	4.944545
protein_co	small_cell_	277	204	178	568	370	423	6.240279	5.415786	5.284198	11.06969	9.364293	9.470529
protein_co	iroquois_h	11	0	7	3	15	12	0.313429	0	0.262833	0.073949	0.480161	0.339811
protein_co	cadherin_2	1823	1605	1734	2115	1748	1662	22.27872	23.11457	27.92464	22.36027	23.99905	20.18572

protein_co	iroquois_h	119	125	105	279	216	269	2.395429	2.965196	2.785226	4.858515	4.884714	5.381437
protein_co	embigin	360	400	391	951	623	710	4.451941	5.829267	6.371746	10.17397	8.655337	8.725993
protein_co	SIX_homeo	562	443	356	10	33	33	13.49335	12.53413	11.26337	0.207705	0.890116	0.787421
protein_co	discs_large	5	10	6	207	211	173	0.039609	0.093353	0.062634	1.41858	1.877812	1.361998
protein_co	signal_tran	2822	2410	2010	912	999	1063	45.57641	45.86773	42.77736	12.7421	18.12582	17.06185
protein_co	NudC_dom	229	218	207	741	477	610	11.62367	13.03981	13.84564	32.53786	27.2004	30.7714
lincRNA	long_interg	0	0	2	0	0	0	0	0	0.191921	0	0	0
protein_co	interferon_	754	614	524	801	716	759	15.89706	15.2553	14.55833	14.60969	16.95928	15.90365
protein_co	heat_shock	2696	1971	2299	6407	5194	5504	29.58112	25.48523	33.24058	60.81525	64.02444	60.01818
protein_co	forkhead_b	0	0	1	0	0	0	0	0	0.035075	0	0	0
protein_co	solute_carr	3	7	3	0	3	7	0.059064	0.162408	0.077832	0	0.066355	0.136965
protein_co	COMM_dor	186	150	130	456	190	260	6.260029	5.949243	5.76556	13.27673	7.183995	8.696537
protein_co	sarcoglycar	496	480	508	17	32	17	2.691823	3.069822	3.632983	0.079814	0.195103	0.09169
pseudogen	dpy-19-like	26	19	33	8	6	17	0.337535	0.290674	0.564539	0.089846	0.087507	0.219333
protein_co	zinc_finger_	147	83	89	84	90	67	2.974895	1.979427	2.373445	1.470607	2.04619	1.347531
protein_co	armadillo_	559	425	401	790	628	740	11.25676	10.0855	10.64096	13.76232	14.20726	14.80958
protein_co	ring_finger_	450	336	345	1102	800	931	11.53119	10.14631	11.64973	24.42904	23.03036	23.70943
protein_co	acylphosph	87	51	33	45	39	76	2.407667	1.663238	1.203444	1.07734	1.212525	2.09026
protein_co	TraB_doma	674	543	437	1469	1019	1388	14.84286	14.09174	12.68159	27.9861	25.21047	30.37783
protein_co	transmemb	74	64	94	245	192	236	2.114211	2.154784	3.53899	6.055441	6.162642	6.70098
protein_co	activating_	539	476	420	432	314	399	4.271736	4.445593	4.386314	2.961845	2.795724	3.142666
protein_co	RAS_p21_p	33	15	20	6	1	7	0.489508	0.262207	0.39094	0.076995	0.016665	0.103194
protein_co	suppressor_	297	281	256	455	392	411	2.688693	2.997769	3.053933	3.563355	3.986758	3.697738
protein_co	muscle-rela	36	19	29	75	61	62	0.728824	0.453295	0.773665	1.313544	1.387392	1.247446
protein_co	olfactory_r	0	0	0	5	5	9	0	0	0	0.215829	0.280282	0.446302
protein_co	zinc_finger_	19	22	2	128	81	96	0.576765	0.787001	0.080004	3.361388	2.762356	2.896186
pseudogen	olfactory_r	0	0	0	14	22	31	0	0	0	0.691677	1.41151	1.759477
protein_co	homeobox_	12	0	1	1257	830	971	0.234858	0	0.02579	21.28252	18.24954	18.8866
protein_co	tubulin_tyr	0	3	0	0	0	0	0	0.042154	0	0	0	0
protein_co	block_of_p	268	214	201	455	638	735	6.07371	5.715314	6.002748	8.920592	16.24385	16.55451
protein_co	polymerase	730	704	683	1178	787	846	10.91721	12.40705	13.45998	15.24043	13.22247	12.57387
protein_co	synaptotag	3	0	3	10	22	19	0.040158	0	0.052918	0.1158	0.330839	0.25276
protein_co	potassium_	0	1	0	46	39	41	0	0.026027	0	0.878911	0.967693	0.899948
protein_co	RNA_bindir	0	3	0	0	0	0	0	0.084498	0	0	0	0
protein_co	kinesin_fan	2064	1851	2186	4052	3810	3206	18.59286	19.64943	25.94904	31.57685	38.55764	28.70183
protein_co	G_protein-r	97	71	77	951	861	768	1.69986	1.466246	1.778144	14.41733	16.95093	13.37557
protein_co	A_kinase_(P	2846	2584	2821	1439	2172	1933	11.40144	12.19901	14.89234	4.987107	9.775383	7.696024
protein_co	cell_divisio	324	312	244	1271	1009	1300	6.825659	7.745711	6.773673	23.16371	23.8803	27.21777
protein_co	olfactory_r	2	0	0	0	0	0	0.106414	0	0	0	0	0
protein_co	short_chair	0	0	0	39	20	17	0	0	0	0.744542	0.495839	0.372838
protein_co	olfactory_r	2	0	0	0	1	0	0.100553	0	0	0	0.056482	0
protein_co	coiled-coil-	500	425	417	637	552	596	8.3847	8.398728	9.214852	9.241021	10.39934	9.932839
protein_co	HtrA_serine	21	32	16	61	59	39	0.437529	0.785678	0.439281	1.099462	1.380984	0.807536
protein_co	forkhead_b	145	117	128	382	265	246	1.419461	1.349735	1.651202	3.235056	2.914408	2.393317

protein_co	leiomodin_	0	0	0	4	1	3	0	0	0	0.078089	0.025352	0.067281
protein_co	beaded_fila	0	0	0	0	0	1	0	0	0	0	0	0.03377
protein_co	follicle_stir	0	0	0	2	0	0	0	0	0	0.032902	0	0
pseudogen	carboxyl_es	1	0	0	0	0	1	0.042387	0	0	0	0	0.042125
protein_co	ubiquitin_s	587	512	604	523	627	497	6.00974	6.177242	8.148718	4.632146	7.211642	5.056891
protein_co	carboxyl_es	27	25	11	99	46	67	0.599583	0.654234	0.321894	1.901884	1.147606	1.478667
protein_co	protein_ph	228	199	250	526	407	400	4.028887	4.143911	5.821369	8.040796	8.079672	7.024573
protein_co	G_protein-	6	7	4	18	30	19	0.12981	0.178469	0.114039	0.336894	0.729169	0.408528
processed_	-	315	241	212	544	396	460	7.216103	6.506033	6.399747	10.78088	10.19146	10.47272
protein_co	pregnancy_	0	0	0	7	10	4	0	0	0	0.138127	0.256251	0.090675
protein_co	kelch_repe	501	386	378	849	640	702	7.08236	6.430351	7.041528	10.38272	10.16411	9.8625
protein_co	MYC_induc	395	320	303	460	413	353	7.154188	6.829994	7.231705	7.207491	8.403542	6.354006
protein_co	TP53_regul	697	590	560	1731	1163	1584	31.21817	31.14108	33.05198	67.07099	58.51987	70.50817
protein_co	LSM3_hom	719	649	464	2111	1529	1886	9.977608	10.61327	8.484971	25.34246	23.83714	26.01051
protein_co	KIAA0232	564	438	589	747	798	571	3.808025	3.484992	5.240476	4.363191	6.053027	3.831478
protein_co	metastasis_	12	17	42	119	89	93	0.128498	0.214521	0.592649	1.10236	1.070663	0.989706
protein_co	transmemb	2337	2048	1809	2111	1576	1564	37.03176	38.24306	37.77365	28.93789	28.05569	24.62986
protein_co	ring_finger_	477	391	397	549	417	397	9.576357	9.250513	10.50285	9.534926	9.405179	7.921038
protein_co	ribosomal_	25736	22326	15971	24421	17718	25756	571.514	584.2569	467.3613	469.1506	442.0278	568.426
protein_co	phospholip	0	5	0	0	0	0	0	0.552104	0	0	0	0
protein_co	cytokine-lik	1022	910	692	4	4	12	53.94386	56.60302	48.1318	0.182648	0.237192	0.62948
protein_co	tRNA_splici	1539	1309	922	3403	2101	2446	34.34915	34.42898	27.11709	65.7056	52.68082	54.25547
protein_co	thyrotropir	1	0	0	2	3	0	0.026765	0	0	0.046308	0.090206	0
protein_co	glutathione	995	951	856	365	279	323	31.11417	35.04473	35.27311	9.873952	9.801406	10.038
protein_co	Myb/SANT-	261	218	249	434	342	317	3.380866	3.327753	4.25032	4.863402	4.976942	4.080904
protein_co	NADH_dehy	560	464	355	756	570	732	30.78604	30.06013	25.71751	35.95428	35.20381	39.99323
protein_co	osteoclast_	9	6	9	9	0	11	0.231858	0.182154	0.305533	0.200579	0	0.281632
protein_co	progestin_a	100	94	89	1223	1111	1058	1.11737	1.237747	1.310454	11.82188	13.94634	11.74877
protein_co	nudix_(nuc	32	21	18	53	53	59	0.319282	0.246917	0.236664	0.457471	0.594087	0.585041
processed_	TPT1_antis	340	348	244	200	166	223	6.273941	7.567421	5.933162	3.192674	3.44127	4.089555
protein_co	tetratricop	989	840	1014	902	1046	772	4.46708	4.471094	6.035318	3.524496	5.307722	3.465408
protein_co	polycystic_	0	0	0	2	3	1	0	0	0	0.005626	0.010959	0.003231
protein_co	DnaJ_(Hsp4	221	178	162	255	182	192	4.26228	4.045543	4.117177	4.254543	3.943394	3.680108
protein_co	zinc_finger_	487	366	330	435	406	342	5.49963	4.870714	4.910811	4.249685	5.150858	3.838312
protein_co	phosphogly	0	0	0	4	0	0	0	0	0	0.108528	0	0
protein_co	zinc_finger_	27	31	16	166	85	97	0.543501	0.735369	0.424415	2.890729	1.922225	1.940518
protein_co	protein_kir	1731	1289	970	1301	935	1149	78.05865	68.49896	57.64087	50.7533	47.36796	51.49365
protein_co	doublecort	4	3	1	0	1	2	0.039567	0.034971	0.013035	0	0.011113	0.019661
protein_co	hyaluronan	455	430	453	233	219	249	5.748962	6.402559	7.542426	2.546813	3.108646	3.126706
protein_co	platelet_de	726	676	842	598	502	498	9.485479	10.40822	14.49671	6.759068	7.368438	6.466386
protein_co	placenta-sp	5	1	4	10	0	8	0.232605	0.054822	0.245214	0.402451	0	0.36987
protein_co	DNA-damag	0	6	6	2	1	10	0	0.143146	0.160069	0.035028	0.022744	0.201201
protein_co	sphingosin	564	513	396	85	72	61	10.26426	11.00203	9.496824	1.338229	1.472075	1.103285
protein_co	heparan_su	78	91	111	627	748	607	0.929835	1.27838	1.743689	6.466092	10.01756	7.191337

protein_co	pygopus_h	272	230	286	230	214	185	1.696507	1.690525	2.350648	1.241017	1.499511	1.146748
protein_co	leucine_ric	3	2	11	2	2	5	0.044179	0.034708	0.213462	0.025479	0.033088	0.073177
protein_co	protein_kir	197	187	184	367	279	285	2.505255	2.802427	3.08346	4.037521	3.986015	3.601971
protein_co	XK_Kell_blc	105	95	57	196	193	176	1.643644	1.752464	1.175786	2.654224	3.394102	2.738046
protein_co	t-SNARE_dc	125	117	75	79	67	76	3.15125	3.475888	2.491546	1.722911	1.897565	1.904128
protein_co	formyl_pep	0	0	1	0	0	2	0	0	0.026617	0	0	0.040148
protein_co	formyl_pep	0	0	0	2	0	7	0	0	0	0.046615	0	0.187429
protein_co	prostate_ar	0	0	0	0	3	0	0	0	0	0	0.116849	0
protein_co	olfactory_r	0	0	0	2	6	0	0	0	0	0.084734	0.330116	0
protein_co	fasciculatic	718	633	671	1292	627	797	8.456426	8.785636	10.41405	13.164	8.296196	9.328898
protein_co	SRY_(sex_d	3	9	2	851	493	646	0.049385	0.174593	0.043385	12.11905	9.117421	10.56862
protein_co	chromoson	1337	1047	907	1821	1218	1472	34.31028	31.6626	30.6715	40.42647	35.11472	37.54139
pseudogen	family_with	25	17	8	27	9	22	0.657816	0.527133	0.277389	0.614598	0.266045	0.575303
protein_co	anaplastic_	75	84	88	25	15	19	0.638356	0.842535	0.987005	0.184079	0.143431	0.160718
protein_co	cysteine_cc	82	77	56	194	141	141	1.743438	1.929259	1.568973	3.568268	3.367913	2.97935
protein_co	myotubula	86	70	106	262	216	187	1.267165	1.215458	2.058143	3.339636	3.575507	2.738332
protein_co	tRNA_meth	102	97	104	251	195	249	2.941166	3.296084	3.951733	6.261179	6.316887	7.135566
protein_co	insulin_rec	52	45	57	37	30	32	0.307453	0.313541	0.444104	0.189252	0.199272	0.188033
protein_co	mitofusin_	577	517	605	951	725	806	5.847426	6.174283	8.0794	8.337435	8.254219	8.117711
protein_co	heat_shock	0	0	1	0	0	0	0	0	0.035539	0	0	0
protein_co	neurturin	3	3	0	24	8	7	0.143213	0.168768	0	0.99114	0.429042	0.3321
protein_co	potassium_	26	15	27	30	20	20	0.669813	0.455385	0.916598	0.668597	0.578841	0.512059
protein_co	potassium_	2	0	0	0	2	1	0.027689	0	0	0	0.031107	0.013759
protein_co	ATPase_H+_	44	51	24	954	731	804	0.855769	1.16891	0.615106	16.05149	15.97241	15.54067
protein_co	protein_kir	442	339	332	214	177	182	4.141579	3.743264	4.099365	1.734684	1.863228	1.694824
protein_co	jagunal_ho	690	520	529	1260	785	922	21.57666	19.16221	21.79845	34.08542	27.57743	28.65337
protein_co	transcriptic	2088	1647	1408	2518	1736	2117	43.28144	40.23202	38.45995	45.15335	40.42686	43.61157
protein_co	suppressor_	608	582	661	401	388	324	6.74662	7.610492	9.66538	3.849374	4.836859	3.573035
protein_co	C1GALT1-sp	173	180	162	639	398	503	5.67811	6.962053	7.006604	18.14352	14.6754	16.40723
protein_co	chromoson	1078	852	602	796	504	657	36.35057	33.85627	26.75	23.22034	19.09291	22.01747
protein_co	MORN_repe	191	143	126	237	190	213	4.352876	3.840484	3.783975	4.672553	4.864582	4.824276
protein_co	zinc_finger_	330	272	192	1443	1116	1256	5.844941	5.677304	4.481281	22.11034	22.20646	22.10881
protein_co	zinc_finger_	493	432	253	821	517	821	9.652334	9.96727	6.527408	13.90566	11.37169	15.9749
protein_co	nuclear_ap	165	149	134	206	150	212	2.569951	2.734855	2.750303	2.775691	2.624709	3.281606
protein_co	ribokinase	25	33	24	45	22	43	0.615307	0.957134	0.778391	0.958136	0.608308	1.051792
protein_co	glutamate_	11	23	17	3	11	6	0.160693	0.395949	0.327256	0.037913	0.180528	0.087109
protein_co	mucin_7_s	0	0	0	0	0	2	0	0	0	0	0	0.041428
protein_co	transmemb	358	326	222	536	359	409	25.64665	27.52152	20.95731	33.21815	28.8929	29.11928
protein_co	transmemb	364	346	279	928	566	780	13.88366	15.55198	14.02302	30.62059	24.25315	29.56697
protein_co	tripartite_r	1233	1083	874	1233	777	844	23.80607	24.64111	22.23673	20.59447	16.85368	16.19484
protein_co	neuropilin_	1051	755	928	2574	1852	1939	7.43764	6.296315	8.653967	15.7581	14.72389	13.63703
protein_co	claudin_20	3	8	11	7	7	5	0.131367	0.412822	0.634736	0.265171	0.34436	0.217593
protein_co	CDC42_bin	51	58	48	820	1153	1351	0.470218	0.630179	0.583183	6.540422	11.94283	12.37924
protein_co	SCAN_dom	1345	1016	626	1595	977	1342	41.23083	36.70291	25.28767	42.29835	33.64677	40.8848

protein_co	jun_B_prot	2246	1955	1415	186	156	207	65.51266	67.20001	54.38845	4.693442	5.11198	6.000611
protein_co	chromoson	0	3	0	102	65	110	0	0.176237	0	4.398765	3.64024	5.449666
protein_co	transmemb	60	51	68	55	58	95	1.881789	1.884937	2.810369	1.492263	2.043604	2.961099
protein_co	UDP_glucu	1	3	0	0	0	1	0.028056	0.099186	0	0	0	0.027882
protein_co	leucine-rich	0	0	0	4	5	6	0	0	0	0.060341	0.097951	0.10398
protein_co	SHC_SH2-d	294	228	201	1053	770	887	4.497155	4.109911	4.051551	13.93419	13.23215	13.48416
protein_co	sclerostin_	1	0	1	122	112	103	0.021958	0	0.028935	2.317489	2.76288	2.247718
protein_co	neuronal_p	1402	850	1248	140	244	217	14.49107	10.35329	16.99816	1.251825	2.833292	2.229061
protein_co	family_with	508	445	370	1260	1058	1086	6.128994	6.326923	5.882501	13.15101	14.34036	13.02162
protein_co	BAH_and_c	1112	994	872	652	1177	1218	5.69291	5.996848	5.882756	2.887621	6.769476	6.197071
protein_co	zinc_finger_	0	1	1	20	27	27	0	0.023794	0.026607	0.349343	0.612452	0.541792
protein_co	zinc_finger_	236	226	204	431	299	347	2.982591	3.365869	3.3974	4.712181	4.245237	4.358337
protein_co	glucosidase	3118	2594	1947	1104	997	1008	45.524	44.63149	37.45977	13.94429	16.35342	14.6263
protein_co	calcium_ac	1561	1277	1265	2701	2260	2264	23.38452	22.54361	24.97186	35.00363	38.03497	33.70634
protein_co	potassium_	1	0	0	4	0	10	0.008592	0	0	0.02973	0	0.085385
protein_co	zinc_finger_	818	751	623	1623	1018	1172	22.10604	23.91689	22.18608	37.94366	30.90683	31.47711
protein_co	carbohydra	265	198	225	438	309	301	2.457412	2.163736	2.749472	3.513736	3.219138	2.774011
protein_co	exosome_c	390	342	240	903	527	599	9.771409	10.09778	7.923894	19.57237	14.83379	14.9152
protein_co	phosphogly	7507	6376	4864	9983	6839	7474	217.1738	217.3684	185.4255	249.8418	222.2709	214.8838
protein_co	chromodor	117	75	95	1818	2105	1706	0.592963	0.44793	0.634455	7.970746	11.98514	8.592722
protein_co	establishm	58	45	38	479	344	339	0.782911	0.71582	0.675932	5.593492	5.216654	4.547721
protein_co	keratin_19	1197	977	795	26281	17106	20071	45.59019	43.85094	39.90058	865.9288	731.9389	759.7242
protein_co	keratin_15	1	1	2	45	38	37	0.010109	0.011913	0.026642	0.393537	0.431561	0.371724
protein_co	leucine_ric	20	21	14	1	0	0	0.5711	0.706657	0.526799	0.024703	0	0
protein_co	chloride_ch	203	141	172	1542	1602	1643	1.063219	0.870268	1.187108	6.986734	9.426239	8.552125
protein_co	tubulin_po	30	18	21	15	31	46	0.310444	0.219503	0.286362	0.134281	0.36039	0.473074
protein_co	potassium_	11	5	17	0	2	1	0.078739	0.042177	0.160354	0	0.016083	0.007114
protein_co	apelin	110	34	41	31	25	14	1.808543	0.658752	0.88829	0.440921	0.46177	0.228757
protein_co	keratin_9	0	0	0	58	35	53	0	0	0	1.161494	0.910213	1.219302
protein_co	phosphodi	487	456	412	3	3	3	4.783351	5.278071	5.332555	0.025491	0.033103	0.029284
protein_co	mitochond	419	285	223	796	540	775	27.97261	22.42182	19.61817	45.97217	40.50062	51.41978
protein_co	zinc_finger_	1142	999	692	880	669	764	45.66361	47.07352	36.46238	30.44036	30.05241	30.36037
protein_co	N-acetyltra	37	15	48	79	67	62	0.839973	0.401293	1.435951	1.551507	1.708785	1.39883
protein_co	keratin_20	2	8	1	0	2	0	0.060957	0.287336	0.040163	0	0.068481	0
protein_co	kinase_sup	0	0	0	39	35	44	0	0	0	0.105019	0.122393	0.136113
protein_co	zinc_finger_	208	199	127	220	108	144	8.739466	9.8533	7.031696	7.996634	5.097936	6.013034
protein_co	mutated_in	992	773	835	462	527	453	1.772442	1.627598	1.965992	0.714111	1.05784	0.804393
protein_co	zinc_finger_	125	111	137	136	149	126	1.48945	1.55864	2.151152	1.401902	1.994578	1.492093
protein_co	cyclin-depe	0	2	0	2	6	0	0	0.04991	0	0.036639	0.142742	0
protein_co	dermatan_s	713	604	617	160	112	132	3.960437	3.953645	4.516204	0.768841	0.698909	0.728681
protein_co	polymerase	550	389	373	919	659	841	15.4716	12.89523	13.82662	22.36408	20.82605	23.51138
protein_co	additional_	1709	1411	1444	1715	1724	1898	12.86818	12.52014	14.32772	11.17126	14.58348	14.20302
protein_co	olfactory_r	0	0	2	0	0	0	0	0	0.133646	0	0	0
protein_co	delta-like_2	48	31	20	208	188	210	1.246893	0.948979	0.684625	4.674275	5.486493	5.421467

protein_co	zinc_finger_	477	421	374	897	624	726	4.425667	4.60309	4.572637	7.199723	6.504201	6.694322
protein_co	zinc_finger_	477	354	447	385	441	352	3.154241	2.758588	3.895102	2.202421	3.276153	2.313283
protein_co	zinc_finger_	711	522	626	1565	1101	1128	8.020679	6.939355	9.305735	15.27281	13.95333	12.64621
protein_co	microtubul	7	2	4	2	0	5	0.445417	0.149971	0.3354	0.110094	0	0.31619
protein_co	WAS/WASL	1494	1221	1165	1121	1170	1409	10.58253	10.19205	10.87426	6.869223	9.31052	9.918811
protein_co	HOP_home	23	15	18	27	14	17	0.380157	0.292169	0.392051	0.386066	0.259963	0.27925
protein_co	leucine_ric	98	104	94	298	257	251	0.718789	0.898909	0.908527	1.890839	2.117666	1.82961
protein_co	ribosomal_	3645	3044	2558	6079	4141	4882	46.67874	45.93813	43.16751	67.34677	59.57663	62.13396
protein_co	leucine_ric	179	171	127	1423	923	1028	2.399098	2.700836	2.243022	16.4992	13.89779	13.69297
protein_co	maestro_he	0	1	0	0	0	0	0	0.011908	0	0	0	0
protein_co	olfactory_r	0	0	0	1	0	0	0	0	0	0.043166	0	0
protein_co	peptidylpro	499	426	401	1142	843	1002	14.49125	14.57881	15.34563	28.69026	27.50313	28.91897
protein_co	collagen_ty	31	29	28	5	6	9	0.240465	0.265091	0.286208	0.033552	0.052287	0.069381
protein_co	electron-tra	320	235	188	255	197	189	5.161828	4.467129	3.99619	3.558416	3.570005	3.029877
protein_co	relaxin/insu	0	0	0	1	0	0	0	0	0	0.011921	0	0
protein_co	lysophosph	1	0	2	261	205	236	0.015827	0	0.041712	3.573547	3.645011	3.712082
protein_co	prostaglanc	112	116	77	64	62	54	1.540902	1.880711	1.395991	0.761728	0.958292	0.738347
protein_co	tubulin_fol	1795	1621	1266	2783	1951	3155	41.29904	43.95068	38.38345	55.39259	50.42917	72.14139
protein_co	neuronal_d	1	1	1	0	0	0	0.008481	0.009995	0.011176	0	0	0
protein_co	microtubul	12	12	4	4	7	9	0.146753	0.172939	0.064461	0.042318	0.096173	0.109385
protein_co	orthopedia	1	0	0	10	0	0	0.014433	0	0	0.124861	0	0
protein_co	endothelin_	0	0	2	8	11	5	0	0	0.047058	0.123572	0.220653	0.088725
protein_co	BCL2-like_1	2184	1745	1716	3696	2957	3781	44.30005	41.71134	45.86735	64.85546	67.38325	76.21982
protein_co	fibrinogen_	6	1	0	0	1	3	0.156399	0.030718	0	0	0.029284	0.077716
protein_co	fibrinogen_	2	1	0	0	2	4	0.028788	0.016962	0	0	0.032341	0.05722
protein_co	fibrinogen_	0	1	0	0	0	4	0	0.031589	0	0	0	0.10656
protein_co	pleiotropic	995	808	840	1794	1193	1337	15.71957	15.04306	17.48766	24.51902	21.17421	20.99224
protein_co	zinc_finger_	233	195	153	180	140	147	4.553434	4.490811	3.940119	3.043117	3.073691	2.855026
protein_co	Down_syndc	0	0	0	0	3	0	0	0	0	0	0.020864	0
protein_co	neuromedi	0	0	0	0	4	0	0	0	0	0	0.072136	0
protein_co	calsyntenin	5266	4276	4065	4261	4005	3730	53.39729	51.09556	54.31675	37.37773	45.62364	37.58866
protein_co	CXXC_finge	2903	2471	2112	1308	891	1053	57.82081	57.99852	55.43268	22.53761	19.93719	20.84372
protein_co	zinc_finger_	278	274	265	572	509	602	3.033305	3.523132	3.810237	5.399211	6.239333	6.527959
protein_co	phosphatid	412	359	311	346	319	296	3.978058	4.084843	3.957027	2.890101	3.460299	2.840372
protein_co	pre_T-cell_a	0	0	0	1	0	0	0	0	0	0.042406	0	0
protein_co	solute_carr	167	119	122	561	447	436	6.105764	5.127168	5.877846	17.74391	18.36031	15.84235
protein_co	ectodermal	2060	1714	1948	8488	9031	8841	19.76771	19.38238	24.63275	70.46241	97.35853	84.31409
protein_co	splA/ryanoc	237	177	136	956	820	1187	4.021479	3.539304	3.040964	14.03325	15.63149	20.01695
protein_co	pyrimidine	5	2	5	2054	1615	1771	0.110386	0.052033	0.145461	39.22892	40.05572	38.85717
protein_co	bromodom	1037	914	958	1170	1209	979	4.861832	5.049804	5.918635	4.74537	6.367905	4.561562
protein_co	S100_calci	0	0	0	2	0	0	0	0	0	0.062396	0	0
protein_co	zinc_finger_	122	99	112	196	220	187	1.544798	1.477251	1.868808	2.146995	3.129563	2.353223
protein_co	G_protein-r	5	7	8	1	2	2	0.07904	0.130401	0.166649	0.013675	0.035519	0.031421
pseudogen	-	7	7	8	4	1	4	0.207148	0.244111	0.311965	0.102401	0.033245	0.117639

protein_co	G_protein-	2	6	3	0	0	2	0.055032	0.194556	0.108779	0	0	0.054692
antisense	SHANK2_ar	0	0	0	0	2	0	0	0	0	0	0.070678	0
protein_co	pleckstrin_	1170	1017	712	385	263	342	11.86381	12.15252	9.513782	3.377242	2.99601	3.446467
protein_co	activating_	1024	781	1019	965	957	715	11.18456	10.05257	14.66655	9.118206	11.74303	7.761305
protein_co	chromoson	8	2	2	3	2	0	0.487935	0.143751	0.160745	0.158291	0.137041	0
protein_co	regulator_c	225	214	147	349	254	283	7.477542	8.381026	6.437666	10.03378	9.483291	9.347003
protein_co	transcriptic	527	424	314	662	422	563	11.83704	11.22291	9.293878	12.86333	10.64864	12.56755
protein_co	anoctamin_	4	0	1	47	37	51	0.031839	0	0.010489	0.323643	0.330869	0.403446
protein_co	histone_de	933	774	675	1366	966	1156	25.21386	24.64936	24.03788	31.93533	29.32809	31.04739
protein_co	chromoson	0	1	3	0	6	1	0	0.052471	0.176022	0	0.300131	0.044251
protein_co	gephyrin	240	289	242	342	381	298	2.956909	4.195963	3.928954	3.645154	5.273522	3.648822
protein_co	vesicle_ami	424	266	334	88	53	62	5.868492	4.338598	6.091748	1.053674	0.824111	0.852829
protein_co	transmemb	86	62	35	282	246	266	2.344452	1.991781	1.25732	6.65051	7.534025	7.206662
protein_co	calmodulin	314	265	207	991	697	1036	1.968673	1.957929	1.710208	5.375025	4.909369	6.455253
protein_co	lectin_gala	2	0	2	2	1	9	0.068978	0	0.090897	0.059673	0.038747	0.308486
protein_co	leucine_ric	29	30	30	115	83	104	0.40541	0.494225	0.552653	1.390777	1.303539	1.444907
protein_co	phenylalan	0	1	0	0	1	0	0	0.015135	0	0	0.014429	0
protein_co	spermatoge	133	133	124	417	329	340	2.739748	3.228626	3.36601	7.431184	7.613843	6.960614
protein_co	glycine_am	1	2	2	148	82	70	0.013536	0.031904	0.035675	1.733121	1.247002	0.941699
protein_co	synaptoner	2	0	0	0	0	0	0.042712	0	0	0	0	0
protein_co	RAS_guanyl	2	4	3	0	0	0	0.03196	0.075325	0.063172	0	0	0
protein_co	nescient_h	13	11	8	19	17	15	0.268526	0.267758	0.217755	0.339516	0.394495	0.307925
protein_co	schlafen-lik	51	44	26	105	87	82	0.626448	0.636905	0.420846	1.115751	1.200558	1.00101
protein_co	B-cell_CLL/	33	30	42	93	110	102	0.234158	0.250855	0.392717	0.570875	0.876873	0.719291
protein_co	RAD9-HUS1	183	138	137	1070	595	692	5.180857	4.604014	5.111	26.20579	18.92416	19.47001
protein_co	CTP_syntha	492	389	362	2928	2076	2513	8.142222	7.586379	7.894438	41.9191	38.59706	41.33139
protein_co	undifferent	0	0	0	0	3	1	0	0	0	0	0.154216	0.045475
protein_co	kinase_non	0	0	0	4	4	7	0	0	0	0.026968	0.035022	0.054217
protein_co	methyltran	35	32	33	161	117	126	1.218235	1.312562	1.513602	4.847879	4.575071	4.35856
protein_co	tetratricop	20	3	4	7	6	11	0.127908	0.02261	0.03371	0.038728	0.043109	0.069915
protein_co	collagen_ty	510	460	388	5	0	4	5.781565	6.145258	5.796178	0.049035	0	0.045066
protein_co	PWWP_dor	120	104	108	630	504	739	2.396424	2.447501	2.84211	10.88393	11.30738	14.66684
protein_co	zinc_finger_	20	12	11	16	7	13	0.336454	0.237894	0.24385	0.232851	0.132295	0.217344
protein_co	angiopoieti	5	6	4	2	0	1	0.118277	0.167259	0.124689	0.040928	0	0.023509
protein_co	F-box_and_	238	194	154	539	543	467	5.968715	5.733406	5.089316	11.6938	15.29864	11.63939
protein_co	exosome_c	726	541	505	1865	1133	1118	11.52824	10.1235	10.56702	25.61936	20.21182	17.64322
protein_co	zinc_finger_	38	27	65	46	40	26	0.895308	0.749652	2.018074	0.937583	1.058761	0.608796
protein_co	ninjurin_2	2	0	1	5	2	1	0.08457	0	0.055721	0.182903	0.095009	0.042024
protein_co	myeloid/ly	493	419	439	277	225	260	3.854092	3.86008	4.522457	1.873346	1.97609	2.020031
protein_co	family_with	4	0	0	7	3	0	0.084267	0	0	0.127574	0.071002	0
protein_co	ribonucleo	663	500	510	8441	5812	6622	9.556188	8.492748	9.686707	105.2514	94.11218	94.85713
protein_co	trafficking_	968	794	691	1252	971	1069	15.06818	14.56509	14.17419	16.85981	16.98063	16.53761
protein_co	ribosomal_	5536	4578	3316	5193	4221	6637	292.4963	285.0409	230.8733	237.359	250.5468	348.5024
protein_co	complemer	192	141	163	71	45	57	4.868137	4.212964	5.44608	1.557338	1.281809	1.436303

protein_co	RNA_methy	250	240	198	501	396	498	7.316334	8.276979	7.635782	12.68394	13.0196	14.48413
protein_co	phosphatas	2236	1880	1705	1788	1331	1264	13.11356	12.99312	13.17674	9.071501	8.769519	7.367249
protein_co	ribosomal_	13313	11420	7775	16811	10926	13915	129.822	131.2337	99.90966	141.8172	119.6968	134.8544
protein_co	ribonuclea	362	317	355	919	839	911	9.039924	9.328731	11.68206	19.85339	23.53787	22.60915
protein_co	prion_prot	2360	2024	1754	2787	2413	2407	47.02324	47.52456	46.05374	48.03972	54.01407	47.66354
protein_co	Kruppel-lik	3	4	3	0	0	0	0.050726	0.079703	0.066844	0	0	0
protein_co	adrenocept	53	29	26	50	49	42	1.048141	0.675848	0.677566	0.855415	1.088651	0.825473
protein_co	FERM_dom	196	143	141	435	249	344	2.070731	1.780372	1.963006	3.975758	2.955399	3.6119
protein_co	aquaporin_	0	0	0	1	2	2	0	0	0	0.008684	0.022554	0.019952
processed_	MIR31_hos	9	16	10	1	7	5	0.639556	1.339871	0.93642	0.061475	0.558834	0.353114
protein_co	talin_2	294	254	240	1683	2040	1882	1.310156	1.333879	1.409359	6.488178	10.21304	8.334987
protein_co	trans-golgi_	540	487	435	1149	734	873	8.668325	9.2125	9.201646	15.95602	13.23691	13.92725
protein_co	F-box_and_	0	0	3	6	2	6	0	0	0.060558	0.079512	0.034419	0.091344
protein_co	zinc_finger_	588	568	606	731	839	752	5.370825	6.113911	7.294091	5.776225	8.609437	6.826392
pseudogen	SLIT-ROBO_	61	38	57	111	80	87	3.332715	2.446578	4.103722	5.246314	4.910292	4.723862
protein_co	secretogran	1152	922	925	23	12	12	23.67548	22.32977	25.05087	0.408919	0.277062	0.245097
protein_co	ATP_syntha	263	267	177	557	417	418	8.015821	9.589824	7.108866	14.68624	14.27833	12.6613
protein_co	forkhead_b	0	3	0	0	2	1	0	0.11194	0	0	0.071143	0.031468
protein_co	peptidylpro	314	295	225	1047	831	973	12.67999	14.03843	11.9731	36.57624	37.69984	39.04918
protein_co	leucine_ric	84	70	60	87	59	63	0.766071	0.752307	0.721068	0.686392	0.604493	0.571005
protein_co	zinc_finger_	14	24	25	50	25	32	0.370032	0.747531	0.870735	1.143258	0.742335	0.840564
protein_co	chromoson	14	18	11	33	16	40	0.642265	0.973119	0.664988	1.309674	0.824623	1.823711
protein_co	jumonji_do	573	524	610	656	620	529	3.500483	3.772348	4.91064	3.466892	4.255143	3.211728
protein_co	lactate_deh	6	9	5	1	2	2	0.190893	0.337434	0.209625	0.027523	0.071485	0.063238
protein_co	synaptopod	174	180	101	75	57	41	1.304224	1.589946	0.997606	0.486326	0.479984	0.305419
pseudogen	olfactory_r	0	0	1	0	0	0	0	0	0.073051	0	0	0
protein_co	zinc_finger_	2	1	0	0	0	0	0.064444	0.037972	0	0	0	0
protein_co	mal_T-cell_	0	0	0	0	0	2	0	0	0	0	0	0.094971
protein_co	zinc_finger_	92	78	77	147	117	142	1.208878	1.207804	1.333277	1.670995	1.727149	1.854355
protein_co	RAB33B_m	218	186	167	313	254	273	2.529841	2.543647	2.553807	3.142275	3.311461	3.148539
protein_co	thimet_olig	1917	1601	1163	4270	2909	3982	34.09066	33.55148	27.25385	65.69074	58.11738	70.37593
protein_co	ankyrin_rep	0	0	0	2	0	0	0	0	0	0.022141	0	0
protein_co	growth_ass	1522	1268	1028	1125	989	1133	42.38621	41.6137	37.72575	27.10351	30.94249	31.35808
protein_co	epoxide_hy	8	32	5	37	21	26	0.294731	1.389288	0.242739	1.179234	0.869168	0.951959
protein_co	laminin_be	6012	5048	4450	2592	2378	2598	56.09469	55.50463	54.71389	20.92188	24.92664	24.09082
protein_co	ubiquitin_s	913	890	783	1233	1061	1292	10.24266	11.76628	11.57547	11.96653	13.37231	14.40503
protein_co	glutaminyl-	4796	3658	3255	4364	3390	3915	91.89468	82.59657	82.18584	72.33674	72.97262	74.55085
protein_co	ORM1-like_	930	700	643	919	746	943	22.07853	19.58359	20.1156	18.87408	19.89643	22.2489
protein_co	small_EDRK	0	0	1	0	1	0	0	0	0.036931	0	0.031485	0
protein_co	Kruppel-lik	76	82	82	182	165	95	0.997648	1.268483	1.418445	2.066799	2.433307	1.239359
protein_co	leucine_ric	45	28	31	9	4	2	0.404954	0.296933	0.367612	0.070065	0.040439	0.017887
protein_co	survival_of	189	149	130	528	342	459	6.455386	5.997272	5.851114	15.60118	13.12307	15.58055
protein_co	eukaryotic_	219	217	238	276	243	224	2.495497	2.913934	3.573754	2.720727	3.110772	2.536708
protein_co	testis_expr	0	0	0	30	2	1	0	0	0	1.728261	0.149625	0.066181

protein_co	MOB_kinas	1587	1278	990	1849	1350	1445	24.77657	23.51269	20.36734	24.97263	23.67812	22.42032
protein_co	lysine-rich_	259	244	236	339	251	308	7.821858	8.683746	9.391976	8.856719	8.515947	9.244226
protein_co	NME/NM23	222	180	193	553	322	408	5.864721	5.603688	6.718719	12.63812	9.55651	10.71184
protein_co	cytochrom	1541	1373	1280	5595	4427	6127	19.90778	20.90248	21.79039	62.52925	64.25083	78.6643
protein_co	CD8b_mole	0	0	0	0	2	1	0	0	0	0	0.083946	0.037131
protein_co	schlafen_fa	39	24	20	327	313	255	0.813194	0.589723	0.549534	5.898481	7.332006	5.2842
protein_co	calbindin_2	13	3	8	899	604	774	0.469463	0.127669	0.3807	28.08541	24.5044	27.7785
protein_co	solute_carr	2	0	1	4	4	1	0.025379	0	0.016722	0.043911	0.057024	0.012611
protein_co	chemokine_	5	0	0	0	0	0	0.245324	0	0	0	0	0
protein_co	FERM_dom	10	7	6	11	27	15	0.099945	0.082446	0.079022	0.095108	0.303162	0.148992
protein_co	syntrophin_	882	927	803	625	571	548	9.042207	11.19935	10.84816	5.543051	6.576442	5.583366
protein_co	Mdm2_trar	51	58	102	228	211	182	0.799997	1.072145	2.108401	3.09397	3.718346	2.837261
protein_co	transcriptic	131	119	111	376	177	305	3.288416	3.520218	3.671752	8.165191	4.991578	7.608955
protein_co	mitochond	399	354	272	1046	680	896	8.920379	9.326544	8.01335	20.23043	17.07923	19.90802
protein_co	mucosa_ass	366	304	390	3203	2531	2353	3.852168	3.770551	5.409082	29.1638	29.92715	24.6125
protein_co	interferon_	34	20	15	46	58	49	0.319488	0.221469	0.185738	0.373935	0.612283	0.457595
protein_co	membrane_	67	30	21	493	328	373	1.101909	0.581433	0.455119	7.014247	6.060298	6.096627
protein_co	inhibitor_c	700	549	562	1992	1464	1621	15.81002	14.61214	16.72652	38.92125	37.14707	36.3854
protein_co	G_protein-r	0	0	2	0	0	3	0	0	0.047523	0	0	0.053761
protein_co	chemokine_	6	3	7	40	31	13	0.113243	0.066725	0.174097	0.653104	0.65731	0.243844
protein_co	CCAAT/enh	962	792	678	883	479	673	27.72414	26.8977	25.74823	22.01439	15.50842	19.27559
protein_co	azurocidin_	4	2	0	0	1	0	0.123622	0.07284	0	0	0.03472	0
protein_co	poly(A)_bin	1602	1332	1262	2506	1897	1972	30.48579	29.87076	31.64675	41.25523	40.55565	37.29508
protein_co	C-type_lect	0	0	2	30	23	30	0	0	0.037457	0.36885	0.367234	0.423737
protein_co	chromoson	28	28	33	182	114	165	0.591284	0.696792	0.918304	3.324851	2.704529	3.462831
protein_co	C1q_and_tr	18	8	1	94	41	29	0.572679	0.299941	0.041925	2.587198	1.465452	0.916952
processed_	serine_hydr	46	29	31	58	42	58	1.42248	1.056801	1.263237	1.551598	1.459105	1.782485
protein_co	neuronal_g	436	443	445	48	26	27	3.973536	4.757749	5.344235	0.378438	0.266203	0.244548
protein_co	zinc_finger_	511	471	437	661	576	530	8.099655	8.797791	9.127711	9.063795	10.25692	8.348936
protein_co	MACRO_do	10	15	8	13	10	8	0.106009	0.187388	0.111755	0.11922	0.119095	0.084284
protein_co	dolichyl-ph	888	747	579	1257	817	935	14.35907	14.23446	12.33749	17.58376	14.84173	15.0257
protein_co	basigin_(Ok	11302	9073	7565	10996	7556	9698	279.2063	264.1362	246.2712	234.9999	209.706	238.1013
protein_co	histone_H4	307	246	241	515	407	432	4.662331	4.402576	4.822992	6.766046	6.943975	6.520158
protein_co	ceramide_s	341	280	377	255	280	223	2.502478	2.421481	3.645794	1.618897	2.308464	1.626412
protein_co	serine_paln	104	73	59	175	146	138	1.437562	1.189113	1.074682	2.092639	2.267228	1.895754
protein_co	coordinato	825	604	576	889	604	781	41.12648	35.48229	37.83771	38.33826	33.82623	38.69263
protein_co	TP53_regul	604	420	489	662	524	543	9.097115	7.454579	9.705333	8.625569	8.866396	8.12786
protein_co	UDP-Gal:be	4	9	17	15	13	10	0.097677	0.25899	0.547037	0.316874	0.356636	0.242685
protein_co	23-bisphos	277	223	177	308	221	241	7.150003	6.783259	6.020527	6.877651	6.408668	6.182343
protein_co	processing_	414	437	223	1202	872	1364	23.64355	29.4104	16.78232	59.38542	55.94714	77.41701
protein_co	ALG14_UDI	92	65	82	135	81	97	4.714977	3.925656	5.53784	5.985336	4.663649	4.940526
protein_co	succinate-C	744	664	544	543	473	494	16.74664	17.61286	16.13573	10.57347	11.96093	11.05074
protein_co	StAR-relate	31	35	20	25	10	17	0.336927	0.44828	0.286443	0.235059	0.122102	0.183625
protein_co	cold_shock	541	469	315	8	20	19	10.31368	10.53649	7.913372	0.131938	0.428347	0.359981

protein_co	regulator_c	1026	922	844	109	90	86	16.32626	17.2893	17.69769	1.500475	1.608907	1.360027
protein_co	interleukin	1	7	1	5	6	2	0.006362	0.052483	0.008384	0.02752	0.042886	0.012646
protein_co	ATP-bindin	1	8	3	6	0	5	0.013754	0.129671	0.054375	0.071393	0	0.068348
protein_co	guanine_nu	6197	4992	3844	8108	5146	6593	174.694	165.8358	142.7956	197.7303	162.9729	184.7095
protein_co	coiled-coil_	13	24	7	31	20	32	0.371817	0.808917	0.263827	0.767027	0.642636	0.909589
protein_co	family_with	189	168	85	295	165	279	5.790421	6.065474	3.431643	7.818679	5.679124	8.494977
protein_co	PDZ_domai	0	0	0	0	2	0	0	0	0	0	0.039704	0
protein_co	C2CD2-like	106	94	87	224	130	187	0.946172	0.988779	1.023336	1.729718	1.303637	1.658882
protein_co	aryl-hydroc	364	297	294	58	45	54	2.880497	2.769679	3.06583	0.397061	0.400062	0.424687
protein_co	guanine_nu	2813	2579	2923	2002	1710	1497	33.8154	36.5345	46.30292	20.81958	23.09351	17.88448
protein_co	protease_se	20	12	11	24	21	14	0.295842	0.209179	0.214416	0.307118	0.348979	0.205811
protein_co	myozenin_	0	2	1	11	14	12	0	0.048046	0.026863	0.193988	0.320625	0.243115
protein_co	synaptopoc	84	74	95	383	484	431	0.609602	0.632857	0.908501	2.404521	3.946038	3.10852
protein_co	DnaJ_(Hsp4	14	3	1	3	5	12	0.2875	0.0726	0.027061	0.053296	0.115353	0.244906
protein_co	cleavage_ar	222	172	183	592	400	515	4.826653	4.406854	5.24299	11.13468	9.770171	11.12782
protein_co	EF-hand_ca	0	2	0	0	0	1	0	0.073788	0	0	0	0.031114
protein_co	tetratricop	1	0	2	0	6	0	0.052469	0	0.138282	0	0.353672	0
protein_co	radial_spok	34	53	32	14	6	17	0.696053	1.278635	0.863273	0.247945	0.137995	0.345877
protein_co	myeloma_c	688	652	450	915	585	1072	39.50478	44.118	34.04932	45.45119	37.73689	61.17382
protein_co	GTP_bindir	728	600	534	1049	882	1044	13.14049	12.76258	12.70153	16.38017	17.88536	18.72795
protein_co	FGGY_carb	209	150	142	110	77	106	4.452583	3.765859	3.986473	2.027316	1.842916	2.244302
protein_co	interleukin	694	657	486	77	40	82	19.74264	22.02511	18.21868	1.894957	1.278365	2.318298
protein_co	fucosyltran	0	0	0	14	22	11	0	0	0	0.236164	0.481941	0.213169
protein_co	transcriptic	296	233	231	215	113	137	13.04791	12.10353	13.41825	8.198805	5.595986	6.001769
protein_co	zinc_finger_	945	898	1021	1522	1430	1294	6.743394	7.551446	9.600797	9.395597	11.46388	9.176787
protein_co	heat_shock	0	0	0	1	0	0	0	0	0	0.031029	0	0
protein_co	mannosida	176	196	172	418	341	315	2.036637	2.672786	2.622794	4.184468	4.433068	3.622607
protein_co	RAB40A_m	20	32	25	52	27	34	0.338714	0.638646	0.557928	0.76185	0.513708	0.572258
protein_co	chromosom	0	0	0	15	7	20	0	0	0	0.340597	0.206411	0.521706
protein_co	AF4/FMR2_	1456	1151	1453	664	754	682	8.208955	7.647314	10.79511	3.238602	4.775808	3.821383
protein_co	acyl-CoA_th	0	0	0	0	0	2	0	0	0	0	0	0.050445
protein_co	fibroblast_g	1298	954	754	1527	957	1162	49.8675	43.1915	38.17236	50.75104	41.30512	44.36686
protein_co	carnosine_s	30	38	28	4	6	1	0.31357	0.468062	0.385661	0.036169	0.070455	0.010388
protein_co	BTG3_assoc	473	344	318	732	508	589	10.27116	8.802863	9.099559	13.75094	12.39285	12.71111
protein_co	protein_ph	2243	1649	1563	4885	3550	4417	70.80897	61.34607	65.02088	133.4095	125.9031	138.5786
protein_co	host_cell_fa	2618	1905	1965	4547	5993	5927	15.62741	13.40045	15.45663	23.48039	40.18933	35.16106
protein_co	cathepsin_L	2	1	12	10	3	2	0.078957	0.046523	0.62428	0.341528	0.133056	0.07847
protein_co	NIPA-like_d	4	4	1	1074	763	919	0.064681	0.076222	0.021308	15.02383	13.86076	14.76857
protein_co	syntrophin_	0	0	0	5	0	2	0	0	0	0.121289	0	0.055735
protein_co	fibronectin	5	2	0	0	1	2	0.124567	0.058718	0	0	0.027989	0.049519
protein_co	phosphodi	69	53	75	231	323	215	0.482171	0.436451	0.690634	1.396456	2.535734	1.493139
protein_co	RAS_guanyl	4	10	7	77	28	39	0.042159	0.124204	0.097221	0.702074	0.33154	0.40851
protein_co	kelch-like_f	2	0	0	0	0	0	0.016812	0	0	0	0	0
protein_co	coiled-coil-	392	362	334	683	659	740	17.26528	18.78898	19.38514	26.02384	32.60784	32.39135

protein_co	mitochond	720	611	588	1746	1168	1972	18.87006	18.87074	20.30733	39.58658	34.39004	51.36382
protein_co	sphingomy	110	94	84	105	103	80	3.146142	3.168259	3.165919	2.597993	3.309573	2.273973
protein_co	Rho_family	0	1	0	9	19	18	0	0.029208	0	0.192973	0.529046	0.443377
protein_co	RAD9_hom	172	113	93	385	219	348	4.29724	3.326953	3.061815	8.321179	6.146874	8.640722
protein_co	EGF_contai	5821	4902	3716	183	99	110	135.3402	134.3103	113.8517	3.680808	2.585909	2.541742
protein_co	olfactory_r	0	0	0	0	2	0	0	0	0	0	0.10913	0
protein_co	ArfGAP_wit	4	6	0	0	1	8	0.087146	0.154044	0	0	0.024476	0.173215
protein_co	chromoson	5	10	5	0	6	2	0.101497	0.239217	0.133749	0	0.136831	0.040348
protein_co	TAF15_RNA	4289	3705	3371	3030	5118	6965	103.6348	105.4982	107.3355	63.33669	138.931	167.2555
protein_co	family_witl	454	385	416	253	340	263	5.184472	5.181034	6.260036	2.499379	4.361909	2.984792
protein_co	transmemb	442	373	272	391	341	341	12.54015	12.47086	10.16914	9.596662	10.86886	9.614893
protein_co	zinc_finger_	3835	3335	4107	1691	1695	1440	21.58502	22.12025	30.46117	8.233675	10.71781	8.054883
protein_co	zinc_finger_	51	40	49	94	42	91	0.82695	0.764321	1.046983	1.31856	0.765081	1.466425
protein_co	zinc_finger_	132	108	108	884	573	751	2.861675	2.759162	3.085354	16.57913	13.95565	16.18065
protein_co	membrane-	0	1	0	0	0	0	0	0.027172	0	0	0	0
protein_co	schlafen_fa	194	203	202	39	27	48	2.041859	2.517835	2.801627	0.355101	0.319254	0.502082
protein_co	family_witl	1	2	1	0	1	0	0.024785	0.058415	0.032661	0	0.027845	0
protein_co	chemokine_	0	2	0	0	0	0	0	0.181624	0	0	0	0
protein_co	coronin_ac	2132	1530	1411	3837	2627	3217	57.76366	48.85017	50.37666	89.93367	79.96071	86.62201
protein_co	fucosyltran	111	113	89	298	219	253	1.536327	1.843088	1.62325	3.568124	3.405288	3.480093
protein_co	leucine_ric	182	133	143	474	263	345	2.822279	2.430453	2.922129	6.358723	4.581771	5.316886
protein_co	MUS81_en	602	512	371	966	795	1080	9.318853	9.339917	7.567888	12.93618	13.82554	16.61496
protein_co	purine-rich	101	47	67	9	10	6	1.85984	1.019904	1.625788	0.14337	0.206873	0.109803
protein_co	transmemb	12	6	5	27	18	30	0.410926	0.242126	0.225625	0.799852	0.692475	1.020971
pseudogen	-	0	0	0	2	0	0	0	0	0	0.184301	0	0
protein_co	zinc_finger_	72	75	82	92	77	76	1.329063	1.631478	1.994627	1.469142	1.596808	1.394236
protein_co	collagen_ty	0	0	0	10	10	12	0	0	0	0.049641	0.064466	0.068434
protein_co	cofilin_1_(r	16620	13995	11832	24983	18309	25167	502.2142	498.354	471.1411	653.0788	621.5437	755.7864
protein_co	transmemb	286	241	219	471	458	430	2.52689	2.509253	2.549759	3.600014	4.546056	3.775708
protein_co	N(alpha)-ac	196	157	170	407	303	237	2.387034	2.253249	2.728263	4.28805	4.145664	2.868537
protein_co	EF-hand_ca	8	5	8	14	13	16	0.075536	0.055634	0.099537	0.114354	0.137897	0.150138
protein_co	family_witl	970	776	648	1753	1278	1532	18.03117	16.9989	15.87311	28.19013	26.68898	28.30222
protein_co	RAB43_mer	74	43	36	47	48	73	0.877017	0.600553	0.562229	0.481878	0.639096	0.859822
protein_co	fatty_acid_	0	0	0	0	1	0	0	0	0	0	0.028322	0
protein_co	COBW_dor	117	138	109	443	355	463	1.696083	2.357477	2.082201	5.555563	5.781476	6.670401
protein_co	homeobox_	58	46	37	22	23	17	1.701151	1.589937	1.430051	0.558214	0.757865	0.495534
protein_co	RAB37_mer	0	0	0	9	7	17	0	0	0	0.108357	0.109446	0.235131
protein_co	DCP2_deca	611	508	497	1960	1663	1759	3.615396	3.542301	3.875305	10.03307	11.05493	10.34404
protein_co	sorting_nex	122	125	97	9	10	21	2.673345	3.227842	2.800926	0.170609	0.246175	0.457324
protein_co	ribosomal_	5417	5570	4255	4491	4107	6503	117.0536	141.8366	121.1603	83.9522	99.70106	139.6527
protein_co	cytochrom	32	34	46	24	8	2	0.769351	0.963298	1.457362	0.499171	0.21608	0.047788
protein_co	ovo-like_1(	0	0	0	138	131	143	0	0	0	2.083141	2.568011	2.479832
protein_co	retinoic_ac	982	800	703	972	888	932	17.56947	16.86725	16.57438	15.04445	17.84881	16.57191
protein_co	carboxylest	12	11	9	19	10	21	0.185812	0.200721	0.183641	0.254513	0.173957	0.323163

protein_co	carboxylest	3	8	1	0	2	5	0.041425	0.130178	0.018196	0	0.031026	0.068615
protein_co	slingshot_p	233	180	143	311	285	327	4.125502	3.755783	3.336505	4.763699	5.669109	5.754112
protein_co	carboxylest	982	795	663	653	573	708	13.23862	12.63006	11.77822	7.615657	8.678304	9.485803
protein_co	pyruvate_d	193	118	166	148	209	241	2.553126	1.839518	2.893729	1.693713	3.106064	3.168412
protein_co	Sp3_transc	1253	1034	1163	1660	1596	1482	10.43168	10.14451	12.75903	11.95568	14.92744	12.26199
protein_co	Dmx-like_1	282	266	383	317	320	232	1.348389	1.498838	2.413235	1.311258	1.718957	1.102462
protein_co	methionyl_	172	168	137	220	153	154	2.663308	3.065557	2.795428	2.94699	2.661543	2.369864
protein_co	zinc_finger_	805	695	636	788	713	631	6.681954	6.798287	6.95664	5.658441	6.648844	5.20531
protein_co	EGF-like-do	310	226	204	240	180	225	7.723157	6.635119	6.697275	5.172582	5.03796	5.570899
protein_co	NAD_synth	1671	1374	1019	1802	1299	1500	24.46471	23.70596	19.65951	22.82346	21.36593	21.82552
protein_co	7-dehydroc	2457	2046	2089	3079	2131	2474	48.79071	47.87896	54.66448	52.89378	47.54058	48.82489
pseudogen	-	0	2	0	0	2	0	0	0.057713	0	0	0.055019	0
protein_co	Aminopept	4	9	4	2	1	3	0.046227	0.122569	0.060915	0.019995	0.012983	0.034456
pseudogen	cytochrom	0	0	0	0	1	0	0	0	0	0	0.228754	0
protein_co	neurobeach	114	92	91	95	93	80	0.542789	0.516204	0.570956	0.391303	0.49746	0.378552
protein_co	ribonuclea	726	546	410	815	545	772	13.75632	12.19173	10.23727	13.35938	11.60142	14.5376
protein_co	myeloma_c	4	8	1	59	42	48	0.085804	0.202229	0.028267	1.094868	1.012151	1.023288
protein_co	ankyrin_rep	608	503	399	903	565	810	11.17255	10.89241	9.661767	14.35488	11.66397	14.79257
protein_co	MAS-relate	1030	793	620	115	74	68	23.76001	21.55707	18.84673	2.294934	1.917742	1.558935
protein_co	myeloid_di	620	549	528	1264	875	990	9.904471	10.3352	11.11497	17.46826	15.70351	15.71753
protein_co	oxidative-st	1331	1314	1226	2128	2056	1914	15.47649	18.00516	18.78537	21.40568	26.85756	22.11801
protein_co	solute_carr	25	15	6	7	3	0	0.518014	0.366268	0.163828	0.125476	0.069835	0
protein_co	PHD_finger	461	352	345	796	655	615	4.026031	3.622646	3.970362	6.013845	6.426382	5.337783
protein_co	lysocardiol	213	174	152	348	379	347	2.228544	2.145349	2.095656	3.149806	4.454817	3.608118
protein_co	alcohol_de	16	14	3	12	11	6	0.253838	0.261741	0.062718	0.164695	0.196055	0.094601
processed_	-	266	200	175	501	275	451	8.873538	7.862348	7.692863	14.45826	10.30616	14.95207
protein_co	XK_Kell_blo	0	0	0	0	0	1	0	0	0	0	0	0.031133
protein_co	FSHD_regio	3	3	5	1	0	0	0.076431	0.090069	0.167862	0.02204	0	0
pseudogen	unc-93_hor	1	0	0	0	0	0	0.077061	0	0	0	0	0
pseudogen	-	16	24	21	37	20	47	0.672267	1.188338	1.162721	1.344888	0.944062	1.962588
protein_co	K(lysine)_ac	281	246	153	297	279	304	6.479277	6.6844	4.64886	5.924336	7.227256	6.96632
protein_co	SH3_domai	599	444	409	118	123	104	10.138	8.855547	9.121861	1.727708	2.338727	1.749316
protein_co	glucoside_x	1036	883	772	289	248	239	16.82419	16.89827	16.52063	4.060087	4.524548	3.857288
protein_co	heparanase	0	0	0	6	0	3	0	0	0	0.119736	0	0.068777
protein_co	dephospho	531	479	424	852	579	622	13.74654	14.61307	14.46437	19.08101	16.83939	16.0029
protein_co	cAMP-regul	0	1	0	1	5	6	0	0.018173	0	0.013341	0.086624	0.091956
protein_co	transcriptio	301	323	260	472	392	411	4.173714	5.277956	4.750774	5.661887	6.106485	5.663796
protein_co	coiled-coil_	44	39	37	47	46	51	1.083444	1.131684	1.200577	1.001185	1.272508	1.248054
protein_co	adrenergic_	1046	961	755	2095	1412	1669	12.32501	13.344	11.72296	21.35515	18.6913	19.54437
protein_co	v-rel_reticu	1815	1434	1312	2089	1327	1556	30.18784	28.10682	28.75571	30.05778	24.79565	25.72022
protein_co	Ellis_van_C	215	166	161	156	147	180	2.357563	2.145063	2.326406	1.479832	1.810886	1.961584
protein_co	zinc_finger_	68	52	72	239	206	149	1.19126	1.073515	1.66213	3.622084	4.054282	2.594141
protein_co	HECT_dom	1049	878	1032	732	842	652	3.605005	3.555756	4.673529	2.176228	3.25081	2.226833
protein_co	family_with	443	376	325	1306	1065	1107	5.588006	5.589179	5.402208	14.25146	15.09217	13.87747

protein_co basonuclin	1734	1526	1817	400	413	430	7.147281	7.412307	9.869191	1.426313	1.912454	1.761448
protein_co deleted_in_	1	4	1	1	3	6	0.019933	0.093957	0.026266	0.017244	0.067179	0.118857
protein_co relaxin/insu	5	11	4	0	0	0	0.230982	0.598835	0.243502	0	0	0
protein_co heparanase	44	29	14	643	408	502	0.500732	0.388917	0.20995	6.33033	5.216289	5.677612
protein_co coenzyme_	183	125	89	676	488	604	5.90384	4.752265	3.783627	18.86658	17.68693	19.36556
protein_co chromoson	0	0	0	7	5	12	0	0	0	0.258334	0.239629	0.508758
protein_co heat_shock	1	2	2	1	7	8	0.020008	0.047156	0.052731	0.017309	0.157344	0.159075
protein_co tRNA_meth	1707	1461	1274	1987	1636	2701	81.70911	82.41272	80.36024	82.28067	87.97703	128.4906
protein_co leucine_ric	125	94	108	31	9	9	1.776543	1.574348	2.022667	0.381145	0.1437	0.127121
protein_co lysine_(K)-s	1868	1678	1581	1817	2018	1939	15.18872	16.07842	16.93991	12.78093	18.43379	15.66866
protein_co chromoson	0	0	0	7	5	1	0	0	0	0.138965	0.128903	0.022806
protein_co aarF_doma	131	119	79	307	222	321	3.421446	3.662624	2.718944	6.936489	6.513889	8.332072
protein_co mitochond	516	443	346	1664	971	1289	12.16276	12.30533	10.74715	33.93116	25.71287	30.19569
protein_co nucleolar_(	388	272	303	846	613	582	5.945327	4.911567	6.118169	11.21444	10.55246	8.862917
protein_co estrogen-re	1040	882	731	876	827	1307	24.11679	24.10249	22.3377	17.5733	21.54471	30.12114
protein_co ras_homol(	250	227	205	438	255	285	11.72298	12.54386	12.66738	17.76787	13.43344	13.28167
protein_co ADAM_met	8	0	1	26	34	30	0.069705	0	0.011482	0.19598	0.332815	0.25978
protein_co copper_me	356	331	269	482	399	495	20.68825	22.66777	20.5997	24.23169	26.04928	28.58831
protein_co Ras_associa	759	638	707	595	785	641	4.096882	4.058256	5.028817	2.77838	4.760256	3.438581
protein_co metaxin_1	294	246	221	421	390	526	6.03515	5.950904	5.978164	7.476285	8.994032	10.7309
protein_co adenylate_(	71	35	39	31	42	22	0.514131	0.298669	0.372147	0.194196	0.341675	0.158324
protein_co poly_(ADP-	316	182	235	181	144	178	1.982856	1.345806	1.943152	0.98253	1.015116	1.110027
protein_co cysteinyl_le	1	0	2	0	0	4	0.017449	0	0.045988	0	0	0.069366
protein_co poly_(ADP-	1	0	0	2	5	5	0.011926	0	0	0.020635	0.066992	0.059263
protein_co CDC28_prc	401	320	310	3142	2149	3056	18.20698	17.12185	18.5477	123.4135	109.6173	137.8975
protein_co ATP-bindin	0	0	0	2	2	0	0	0	0	0.014684	0.019069	0
protein_co AHA1_activ	514	465	398	398	293	398	9.312687	9.928232	9.502322	6.238181	5.963875	7.166459
protein_co actin_bindi	41	49	48	7	8	3	0.475067	0.669074	0.732904	0.070167	0.104138	0.034546
protein_co mab-21-like	0	0	0	1	1	2	0	0	0	0.014184	0.018419	0.032588
protein_co Tubulin_be	1	0	0	3	1	4	0.027416	0	0	0.071153	0.030801	0.108988
protein_co KIAA1919	237	191	167	799	614	798	2.105911	2.000009	1.955433	6.141881	6.129274	7.046998
protein_co VANGL_pla	274	255	308	816	778	761	1.669064	1.830499	2.472338	4.30007	5.324159	4.606983
protein_co glutaredoxi	595	507	415	213	165	180	9.245639	9.283997	8.497729	2.863272	2.880401	2.779727
protein_co IQ_motif_c	340	281	280	1183	772	910	6.939066	6.75827	7.530347	20.8867	17.70062	18.45751
protein_co synaptotag	3	3	5	1	1	0	0.026348	0.031049	0.057866	0.007598	0.009867	0
protein_co golgin_B1	1679	1417	1847	972	971	993	7.93784	7.894572	11.50677	3.975401	5.157271	4.665632
protein_co chromoson	0	3	1	0	0	0	0	0.157677	0.058773	0	0	0
protein_co lipase_fami	0	1	0	2	4	7	0	0.042967	0	0.063084	0.163846	0.253649
protein_co G_protein-(	0	0	1	0	0	0	0	0	0.022592	0	0	0
protein_co doublesex_	3	1	0	15	5	3	0.064588	0.025371	0	0.279375	0.120935	0.06419
protein_co zinc_finger_	4	6	5	23	21	15	0.057938	0.102415	0.095435	0.288201	0.341722	0.215926
protein_co PLAC8-like_	8	7	7	28	15	17	0.663837	0.684505	0.765428	2.009983	1.398337	1.401942
protein_co solute_carr	0	0	0	112	94	82	0	0	0	1.24351	1.35533	1.045904
protein_co G_protein-(	834	713	613	770	612	876	23.95702	24.13589	23.20396	19.13465	19.75001	25.00809

protein_co	synuclein_g	5	7	7	32	14	30	0.333382	0.550018	0.615042	1.8458	1.048694	1.987936
protein_co	multimerin	15	9	6	2	10	10	0.192419	0.136053	0.101425	0.022195	0.144114	0.127487
protein_co	mitotic_spi	1119	996	648	1089	937	1273	20.96284	21.98803	15.99668	17.64862	19.72008	23.70053
protein_co	tankyrase_T	1151	1112	1332	827	777	690	6.334208	7.211555	9.659531	3.937182	4.803824	3.773773
protein_co	zinc_finger_	256	225	261	149	130	110	3.592074	3.720445	4.825925	1.80865	2.049263	1.533937
protein_co	zinc_finger_	190	191	202	259	233	169	1.350354	1.599685	1.891822	1.592417	1.860369	1.193687
protein_co	protein_ph	400	382	311	478	348	311	3.816943	4.295622	3.910667	3.945904	3.730645	2.949346
pseudogen	family_witl	57	63	50	128	87	105	1.06668	1.389334	1.233003	2.072202	1.829058	1.952801
protein_co	storkhead_	20	18	13	45	96	82	0.101245	0.10738	0.08672	0.197069	0.545964	0.412541
protein_co	mitogen-ac	1781	1525	1184	2409	2138	2689	16.82211	16.97436	14.73679	19.68413	22.6868	25.2416
protein_co	tribbles_ho	89	86	100	363	287	260	1.296217	1.476023	1.91921	4.573591	4.695898	3.763316
protein_co	potassium_	8	8	1	0	0	0	0.270971	0.319323	0.044634	0	0	0
protein_co	neuron-der	245	172	215	185	173	176	4.495856	3.719476	5.198997	2.936845	3.566493	3.209731
protein_co	oxidized_lo	0	0	0	22	10	19	0	0	0	0.409584	0.241772	0.406369
protein_co	GLI_pathog	11	5	0	0	2	1	0.514444	0.275564	0	0	0.105081	0.046479
protein_co	dystroglyca	1798	1425	1520	8178	9399	10138	16.33847	15.25961	18.2012	64.28827	95.95162	91.55531
protein_co	Dab_reelin_	17	7	19	81	68	56	0.169875	0.08243	0.250189	0.70021	0.763375	0.556132
protein_co	ARV1_hom	173	166	103	391	238	293	6.860518	7.757575	5.382485	13.41376	10.6032	11.5475
protein_co	N(alpha)-ac	866	762	613	1394	1091	1292	28.58286	29.63806	26.6614	39.80279	40.45401	42.3799
protein_co	coiled-coil_	2	0	2	7	0	0	0.037243	0	0.049077	0.112766	0	0
protein_co	serum_amy	0	5	1	0	0	2	0	0.462131	0.103353	0	0	0.155893
protein_co	mitochond	67	74	71	88	62	58	0.955562	1.243721	1.334373	1.08575	0.993402	0.822095
protein_co	EH_domain	572	479	431	72	59	70	5.840357	5.763495	5.799031	0.635973	0.676775	0.710315
protein_co	THAP_dom	100	128	94	108	70	79	0.925704	1.396333	1.14666	0.864886	0.727979	0.72679
protein_co	transmemb	2	1	8	2	1	2	0.026118	0.015389	0.137668	0.022594	0.014671	0.025957
protein_co	ring_finger_	546	448	390	1620	1302	1249	10.37165	10.0286	9.762354	26.62154	27.7853	23.5791
protein_co	protein_ph	5158	4270	3249	6414	5370	6266	278.075	271.2786	230.8156	299.1387	325.24	335.7226
protein_co	Sjogren_syn	305	274	201	690	496	574	14.99257	15.87209	13.01989	29.34192	27.39095	28.04129
protein_co	SWI/SNF_re	2737	2251	2420	4420	4949	4886	22.72933	22.02898	26.48269	31.75391	46.17197	40.32506
protein_co	zinc_finger_	238	191	153	206	214	255	3.502907	3.312776	2.967412	2.622901	3.538462	3.729937
protein_co	protein_tyr	1090	832	932	530	504	440	9.467709	8.516258	10.66766	3.982514	4.918107	3.798225
protein_co	FK506_bin	1372	1132	856	795	845	1462	72.49006	70.48195	59.59817	36.33745	50.15684	76.7682
protein_co	vascular_er	1108	974	746	741	520	619	42.69186	44.22536	37.8773	24.69941	22.50908	23.70313
protein_co	Homo_sapi	1737	1484	1748	582	725	646	7.849638	7.902978	10.40941	2.275285	3.680755	2.901295
protein_co	tumor_nec	4992	3983	4347	2307	1663	2020	74.69798	70.23469	85.71537	29.86379	27.95603	30.03968
protein_co	macrophag	90	73	41	36	41	38	1.147565	1.096894	0.688896	0.3971	0.58731	0.481535
protein_co	tumor_nec	75	39	44	421	589	467	2.311161	1.416252	1.78672	11.22313	20.39075	14.30196
protein_co	MOB_kinas	836	744	894	1016	888	797	6.356265	6.66616	8.957112	6.682707	7.585037	6.022318
protein_co	zinc_finger_	673	535	526	1050	714	820	20.97074	19.64534	21.59829	28.30421	24.99459	25.39348
protein_co	chondroitin	1990	1735	1551	96	125	137	12.70839	13.05702	13.05221	0.530361	0.896802	0.869496
protein_co	sorting_nex	1195	987	905	469	392	524	7.900161	7.689397	7.884087	2.682279	2.911409	3.442778
protein_co	nucleic_aci	896	727	780	1103	824	863	14.00506	13.39117	16.06595	14.91473	14.46949	13.40594
protein_co	nudix_(nuc	140	129	97	80	75	61	4.220808	4.583153	3.853666	2.08651	2.540258	1.827709
protein_co	G_protein-r	12	10	4	28	38	43	0.158348	0.155503	0.069555	0.319633	0.563331	0.563909

protein_co	chromodor	2380	2139	2135	2185	2212	2127	12.78275	13.53833	15.11054	10.15224	13.34693	11.35336
protein_co	chemokine	0	0	0	13	5	21	0	0	0	0.112741	0.056311	0.209221
protein_co	coiled-coil_	430	391	257	417	315	357	10.52943	11.28289	8.29286	8.833554	8.665548	8.687889
protein_co	chemokine	0	0	1	0	0	0	0	0	0.027177	0	0	0
protein_co	coiled-coil_	180	152	121	223	230	230	2.993836	2.979244	2.652013	3.208657	4.297663	3.801832
protein_co	sulfotransfe	4	0	8	0	0	0	0.14819	0	0.390557	0	0	0
protein_co	nudix_(nuc	1155	1001	975	3140	2700	2454	12.59461	12.86305	14.01013	29.62071	33.07621	26.59421
protein_co	pyruvate_c	723	542	538	235	205	219	9.130806	8.066352	8.953398	2.567448	2.908531	2.748682
protein_co	suppressor_	41	36	44	86	62	47	0.839358	0.868507	1.187001	1.523088	1.42595	0.956249
protein_co	nicotinami	318	243	254	264	227	245	4.452588	4.009579	4.686557	3.197808	3.570757	3.409268
protein_co	leucine_ric	494	422	368	661	395	543	10.75806	10.82996	10.56063	12.45293	9.663919	11.75213
protein_co	BET3_like_(	2	1	0	0	0	0	0.043735	0.025769	0	0	0	0
protein_co	apolipopro	4	0	0	10	3	1	0.079971	0	0	0.172957	0.067382	0.019869
protein_co	solute_carr	679	556	369	1137	840	1116	9.432415	9.101962	6.754828	13.66396	13.10936	15.40732
protein_co	heat_shock	153	152	93	9	5	7	2.80082	3.279023	2.243425	0.142528	0.102828	0.127351
protein_co	RCE1_hom	210	194	145	663	414	527	4.088859	4.45135	3.720366	11.16759	9.055914	10.19772
protein_co	ubiquinol-c	3769	3148	2366	3538	3076	4866	290.4434	285.8757	240.2619	235.861	266.2997	372.6637
protein_co	eukaryotic_	1445	1296	1263	2990	2685	2871	17.28027	18.26395	19.9031	30.93262	36.07247	34.12129
protein_co	Putative_sp	9	14	5	8	4	15	0.273518	0.501394	0.200239	0.210328	0.136569	0.453049
protein_co	chromoson	91	95	65	134	112	131	0.737995	0.90791	0.694641	0.940112	1.02042	1.055827
protein_co	proteasom	1656	1430	1447	5125	4011	4038	26.35908	26.82335	30.35101	70.57107	71.72517	63.87719
protein_co	G_protein-r	29	12	29	12	9	17	0.265254	0.129346	0.34954	0.094953	0.092482	0.154533
protein_co	spermatoge	0	0	0	4	0	0	0	0	0	0.113223	0	0
protein_co	sushi_dom	161	145	137	235	223	195	1.702997	1.807437	1.909604	2.150398	2.649976	2.049898
protein_co	heart_deve	962	712	1047	1810	1939	1553	5.562389	4.85147	7.977518	9.053737	12.59544	8.924161
protein_co	WAP_follist	6	3	0	0	0	1	0.08853	0.052164	0	0	0	0.014664
protein_co	chromoson	79	94	73	585	303	401	1.800404	2.524514	2.192303	11.53352	7.757728	9.082322
protein_co	translocase	4698	4212	4043	4844	4101	4163	73.43277	77.58403	83.27515	65.50041	72.0138	64.66852
protein_co	Uncharacte	2	4	6	3	0	0	0.152788	0.360102	0.604011	0.198264	0	0
protein_co	chromoson	2	0	5	1	8	1	0.1259	0	0.414764	0.054458	0.565764	0.062561
protein_co	ArfGAP_wit	476	372	482	1818	1260	1222	6.113516	5.630334	8.157667	20.19952	18.18041	15.59786
protein_co	signal_tran	570	518	541	796	674	719	5.913456	6.332911	7.396029	7.144019	7.85553	7.413189
protein_co	CD7_molec	38	21	12	1	0	1	0.995427	0.648264	0.41423	0.022662	0	0.026034
protein_co	2'3'-cyclic_	2421	2050	1702	2873	2249	2892	48.18427	48.08077	44.63801	49.46626	50.28622	57.20294
protein_co	junction_p	543	419	391	11846	8813	9658	8.220463	7.47511	7.800241	155.1426	149.8888	145.3093
protein_co	huntingtin-	5	1	6	137	152	171	0.046578	0.010978	0.073655	1.104074	1.590769	1.583143
protein_co	tudor_dom	0	1	0	0	2	2	0	0.015859	0	0	0.030237	0.026748
antisense	CCDC13_ar	3	0	0	5	0	5	0.077512	0	0	0.111759	0	0.12839
protein_co	eukaryotic_	10606	9272	7043	10908	7555	9220	240.9838	248.2657	210.8767	214.4096	192.85	208.1981
protein_co	endonuclea	510	407	298	344	259	415	9.591441	9.02018	7.385243	5.59674	5.472207	7.756601
protein_co	ring_finger_	1698	1383	1516	878	1286	1147	4.269476	4.097945	5.023089	1.909828	3.632678	2.866223
protein_co	tigger_tran	8	0	2	8	7	9	0.210501	0	0.069347	0.182103	0.206924	0.235351
protein_co	potassium_	0	5	0	0	0	0	0	0.081638	0	0	0	0
protein_co	membrane-	7	2	1	12	2	4	0.111021	0.03738	0.0209	0.164646	0.035636	0.063049

protein_co	polo-like_k	300	245	244	471	300	416	6.373314	6.133625	6.830755	8.656214	7.160022	8.783084
protein_co	neuroepith	621	477	552	4517	3945	3937	9.663832	8.747486	11.31962	60.80942	68.96899	60.88816
protein_co	dpy-19-like	674	629	663	1845	1397	1489	7.326947	8.057881	9.497547	17.35092	17.06116	16.08672
protein_co	HCG16436	6	1	6	4	6	4	0.300232	0.058968	0.395633	0.173153	0.337293	0.198919
processed_	-	0	0	3	1	1	0	0	0	0.349983	0.076587	0.099458	0
protein_co	phosphatas	3	2	1	1	3	3	0.073089	0.057421	0.032105	0.021076	0.082111	0.072638
protein_co	zinc_finger_	398	352	331	467	279	371	4.626815	4.82224	5.070629	4.69655	3.643781	4.286301
protein_co	tubulin_be	4	5	3	10	6	9	0.107604	0.158505	0.106346	0.232718	0.181329	0.240613
protein_co	polyhomec	187	183	239	179	270	143	1.968184	2.269772	3.314796	1.629822	3.192544	1.495787
protein_co	G_protein-r	9	7	12	64	39	53	0.233678	0.214181	0.410574	1.437533	1.137597	1.367604
protein_co	chromobo	348	307	255	899	947	1029	3.967155	4.124253	3.830671	8.865895	12.12827	11.65802
protein_co	spectrin_be	564	450	378	704	771	886	3.673563	3.454045	3.244405	3.966834	5.641724	5.735242
protein_co	golgi_integ	1975	1480	1826	1205	1502	1271	23.91001	21.11453	29.13052	12.6201	20.42827	15.29212
protein_co	RNA_bindir	517	469	393	528	435	484	11.70179	12.50955	11.72166	10.33853	11.06115	10.88722
protein_co	up-regulate	967	940	632	1598	1148	1811	64.88459	74.32759	55.88136	92.75875	86.53784	120.7656
protein_co	homeobox_	154	135	73	112	99	82	3.074251	3.175846	1.920332	1.934192	2.220255	1.62683
protein_co	C1q_and_t	276	241	209	100	86	119	4.713456	4.850143	4.703395	1.477384	1.649977	2.019701
protein_co	membrane-	124	96	97	88	67	52	1.56451	1.427365	1.612736	0.960511	0.949687	0.652033
protein_co	SWIM-type	14	2	9	27	22	31	0.440127	0.074095	0.372844	0.734305	0.777001	0.968548
protein_co	solute_carr	4	0	5	13	10	12	0.039701	0	0.065395	0.111621	0.111503	0.118367
protein_co	RNA_bindir	98	66	87	105	78	88	2.235337	1.774059	2.614996	2.071902	1.99876	1.994846
protein_co	primary_cil	3	11	14	367	330	438	0.042083	0.18184	0.258793	4.453683	5.200597	6.106241
protein_co	xyloside_xy	599	445	504	1171	787	756	11.62877	10.18062	12.89354	19.66649	17.16448	14.58607
protein_co	UBX_doma	461	405	317	1297	836	984	4.023376	4.165353	3.645724	9.792479	8.196813	8.534821
protein_co	retina_and_	1	0	0	0	0	8	0.021804	0	0	0	0	0.173358
protein_co	leucine_ric	3	1	0	5	0	9	0.068252	0.02681	0	0.098408	0	0.203492
protein_co	titin-cap	21	14	17	13	13	17	0.523674	0.411412	0.558632	0.280445	0.364195	0.421309
protein_co	copper_cha	750	580	490	357	282	481	27.76626	25.30411	23.9049	11.43371	11.72882	17.69745
protein_co	leucine_ric	0	0	0	11	0	4	0	0	0	0.196485	0	0.082081
protein_co	centrosom	62	58	38	95	81	88	1.491296	1.64402	1.204455	1.976781	2.1888	2.103606
protein_co	kelch-like_f	134	159	140	147	135	91	1.131074	1.581577	1.557216	1.073412	1.280174	0.763373
protein_co	F-box_prot	216	225	222	593	475	528	1.938507	2.379596	2.625436	4.603958	4.789127	4.70931
protein_co	spermatid_	2	4	1	0	0	0	0.057482	0.135478	0.037874	0	0	0
protein_co	family_with	0	0	0	1	0	0	0	0	0	0.014745	0	0
protein_co	guanine_nu	2061	1643	1142	4057	2550	3467	118.5993	111.4163	86.59747	201.9632	164.8517	198.2749
pseudogen	family_with	91	71	64	79	103	148	7.074347	6.504448	6.556314	5.312942	8.995623	11.43448
protein_co	solute_carr	394	304	385	158	176	159	3.452864	3.139525	4.446096	1.197853	1.732786	1.384809
protein_co	chromoson	23	14	8	9	5	13	0.357185	0.256212	0.163716	0.120912	0.087234	0.20064
protein_co	CD34_mole	3	7	4	10	0	0	0.055262	0.151953	0.097096	0.159356	0	0
protein_co	cathepsin_l	2	0	1	19	22	9	0.05203	0	0.034282	0.427606	0.642983	0.232691
protein_co	TBC1_doma	284	337	271	252	250	284	2.949243	4.124101	3.708484	2.263893	2.91663	2.93103
protein_co	methionine	708	551	593	913	811	829	8.485901	7.782576	9.366001	9.466697	10.9203	9.874813
protein_co	mitochond	1036	872	694	1850	957	1203	32.16825	31.90739	28.39632	49.69383	33.38326	37.12299
protein_co	LEM_doma	376	306	392	604	587	516	4.178382	4.007272	5.740388	5.806578	7.328372	5.698751

protein_co	chromoson	164	130	116	293	231	338	8.106744	7.57274	7.55606	12.52949	12.82814	16.60462
protein_co	suppressor_	118	98	100	52	132	95	3.045849	2.980984	3.401428	1.161162	3.827802	2.437023
protein_co	toll-like_re	13	5	6	8	0	5	0.24174	0.109567	0.147025	0.128694	0	0.092403
protein_co	toll-like_re	133	86	115	49	35	42	1.197679	0.912629	1.36465	0.381722	0.354084	0.375879
protein_co	family_witl	152	131	119	145	125	162	5.934389	6.027133	6.122294	4.897376	5.482662	6.285749
protein_co	RGM_doma	775	664	694	483	325	340	8.958356	9.044859	10.57112	4.829885	4.220453	3.905847
protein_co	family_witl	30	34	26	22	12	31	0.56682	0.757025	0.64734	0.359592	0.254715	0.582097
protein_co	cytochrom	321	289	243	247	181	227	3.347264	3.55132	3.339074	2.228152	2.120374	2.35245
protein_co	zinc_finger_	478	310	273	248	184	278	13.0375	9.964037	9.812146	5.851689	5.638109	7.535655
processed_	-	14	7	8	23	30	35	0.255577	0.150591	0.19245	0.363233	0.615268	0.634997
protein_co	tRNA_meth	361	326	286	1059	741	809	10.50671	11.18109	10.96883	26.66357	24.22851	23.40009
protein_co	cytosolic_t	318	269	180	859	472	626	8.837394	8.809606	6.591806	20.65158	14.73629	17.28945
protein_co	ArfGAP_wit	23	27	20	37	19	21	0.434407	0.600952	0.497776	0.604552	0.403155	0.394183
protein_co	MGA_MAX_	458	339	502	682	786	681	2.013534	1.756306	2.908252	2.593826	3.882085	2.975433
protein_co	chromoson	62	63	58	99	73	67	1.216583	1.456793	1.49973	1.680538	1.609245	1.306576
protein_co	ADP-ribosy	2	4	2	0	1	1	0.068978	0.162574	0.090897	0	0.038747	0.034276
protein_co	sorting_nex	1	0	1	1	0	0	0.0216	0	0.028463	0.018686	0	0
protein_co	phosphatid	1096	928	904	1157	1062	1103	16.48858	16.45235	17.92157	15.05807	17.94925	16.49142
protein_co	PRP8_pre-r	4622	3827	3950	8764	7476	7088	32.86679	32.06956	37.01343	53.91291	59.72357	50.09112
protein_co	adenylate_(	1460	1232	1232	768	779	915	11.95759	11.89073	13.29647	5.441454	7.167658	7.447688
protein_co	RAB15_effe	13	5	3	6	4	7	0.604243	0.273871	0.183749	0.241259	0.208871	0.323352
protein_co	phosphatid	1552	1072	1156	2258	1744	2005	21.00318	17.09602	20.61512	26.43505	26.51483	26.96605
protein_co	DEAD_(Asp-	1347	1106	1048	2633	2085	2180	25.18062	24.3647	25.81636	42.58069	43.78788	40.50093
protein_co	zinc_finger_	0	0	1	0	0	0	0	0	0.023737	0	0	0
protein_co	zinc_finger_	85	67	42	182	105	137	3.47221	3.225292	2.260847	6.431636	4.818651	5.561825
protein_co	zinc_finger_	1716	1293	1356	899	1049	1077	15.25298	13.54388	15.88298	6.912897	10.47519	9.513991
protein_co	tyrosine_ki	58	55	52	89	84	103	0.983529	1.099079	1.161977	1.305606	1.600249	1.735825
protein_co	zinc_finger:	984	863	1039	452	436	410	5.193812	5.367957	7.226725	2.063919	2.585394	2.150724
protein_co	pleckstrin_	2324	1879	1394	2808	2363	3211	80.36242	76.56861	63.52058	83.99956	91.79725	110.3486
protein_co	disrupted_i	10	10	6	0	0	0	0.510521	0.601617	0.403645	0	0	0
protein_co	solute_carr	11	16	8	5	15	3	0.32299	0.553635	0.309543	0.127008	0.494808	0.087544
protein_co	solute_carr	81	65	68	115	135	165	2.453215	2.31991	2.713903	3.013086	4.593392	4.966429
protein_co	GLIS_family	526	452	286	8	13	5	9.902903	10.02818	7.095412	0.130296	0.27496	0.093553
protein_co	cholinergic	0	0	3	0	1	0	0	0	0.091955	0	0.026132	0
protein_co	podocan	42	43	46	1	2	2	0.676459	0.816146	0.976304	0.013933	0.036189	0.032013
protein_co	stromal_an	54	49	42	144	99	166	1.33777	1.430509	1.371108	3.086122	2.755319	4.087006
processed_	small_nucl	105	95	93	254	150	227	2.09608	2.234855	2.44645	4.386471	3.364022	4.50354
pseudogen	postmeioti	2	0	3	3	0	2	0.098863	0	0.195415	0.128288	0	0.098252
protein_co	chromoson	10	10	9	34	35	18	0.146084	0.172152	0.173253	0.429681	0.574409	0.261328
protein_co	exonucleas	80	75	71	709	549	624	1.219487	1.347273	1.4262	9.349676	9.40175	9.453259
protein_co	Ral_GTPase	226	176	259	345	394	270	1.494836	1.371844	2.257458	1.974091	2.927725	1.774837
protein_co	Williams-B	464	388	349	776	619	747	10.47532	10.32258	10.38268	15.15563	15.69961	16.76021
protein_co	ligase_IV_D	130	102	99	390	355	379	1.67739	1.55095	1.683296	4.353296	5.145979	4.860035
protein_co	chromoson	0	0	0	0	0	2	0	0	0	0	0	0.086253

protein_co	GTF2I_repe	159	119	117	159	100	121	2.374504	2.094257	2.302483	2.054168	1.677741	1.795853
protein_co	actin-bindi	1	2	3	0	2	0	0.019216	0.045291	0.075967	0	0.043177	0
protein_co	ATPase_Ca+	4464	3776	4032	7014	5926	6255	28.71899	28.62754	34.18223	39.03676	42.83076	39.99282
protein_co	zwilch_kine	211	170	212	1078	710	821	3.095192	2.93874	4.098037	13.68003	11.70072	11.969
protein_co	ribosomal_	46552	39967	30044	53033	31864	37251	890.6791	901.1386	757.4875	877.793	684.9081	708.3216
protein_co	small_nucl	78	83	77	251	161	264	2.371854	2.974257	3.085452	6.602829	5.50007	7.978236
protein_co	StAR-relate	0	4	0	0	0	0	0	0.219869	0	0	0	0
protein_co	chromoson	174	175	107	260	180	205	4.179552	4.953654	3.386874	5.402775	4.85738	4.893775
protein_co	zinc_finger_	35	25	29	0	2	5	0.83054	0.699101	0.906829	0	0.053318	0.117916
protein_co	contactin_	179	215	210	308	245	244	0.957796	1.355707	1.480725	1.425719	1.472771	1.297537
protein_co	UDP-N-acet	17	17	26	23	1	12	0.229474	0.270421	0.46248	0.268581	0.015165	0.160981
protein_co	leucine_ric	11	5	11	34	20	15	0.191311	0.102477	0.252101	0.511552	0.390775	0.259268
protein_co	Bardet-Biec	15	20	11	8	17	24	0.22151	0.348049	0.214057	0.102201	0.282034	0.352228
protein_co	DENN/MAD	193	195	218	78	108	57	1.424653	1.696264	2.120524	0.498092	0.895622	0.418154
protein_co	immunoglc	229	187	187	6027	6190	6278	2.70674	2.604712	2.912644	61.6276	82.19601	73.7466
protein_co	germinal_c	3	7	10	33	32	34	0.047609	0.13091	0.209123	0.453047	0.570512	0.536234
protein_co	ankyrin_rep	65	75	101	4	27	16	0.633965	0.862026	1.298101	0.03375	0.295846	0.155089
protein_co	solute_carr	1	0	0	0	4	0	0.011032	0	0	0	0.049574	0
protein_co	major_facil	2	4	3	16	20	13	0.025856	0.06094	0.051109	0.178946	0.290481	0.167029
protein_co	pellino_E3_	155	152	110	105	98	80	2.948564	3.407451	2.757442	1.72795	2.094373	1.512441
protein_co	tetratricop	8	6	6	2	0	0	0.182319	0.161139	0.180189	0.039431	0	0
protein_co	myosin_IH	31	35	38	8	6	15	0.37607	0.50036	0.607471	0.083958	0.081773	0.180846
protein_co	transmemb	40	27	31	69	60	63	1.525677	1.213594	1.558114	2.276747	2.571005	2.388102
protein_co	mitochond	633	566	412	1894	1397	1588	15.17051	15.98527	13.01153	39.26805	37.61333	37.82305
protein_co	interleukin	14	17	9	66	21	46	0.362078	0.51812	0.306727	1.476662	0.610158	1.182338
protein_co	golgi_trans	0	0	0	9	9	9	0	0	0	0.466807	0.60621	0.53627
pseudogen	-	1	0	0	0	0	0	0.079016	0	0	0	0	0
protein_co	akirin_1	1121	911	1003	4293	3087	3428	21.65153	20.73521	25.52812	71.73101	66.98364	65.80115
protein_co	neuronal_P	0	6	5	9	5	4	0	0.113329	0.105606	0.124793	0.090033	0.063717
protein_co	male-specif	261	238	263	486	438	417	2.944927	3.164595	3.910431	4.743876	5.5521	4.676057
protein_co	zinc_finger_	91	54	32	52	18	37	1.389167	0.971435	0.643721	0.686719	0.308699	0.561338
protein_co	Kruppel-lik	21	14	8	0	3	1	0.747151	0.586981	0.375071	0	0.119911	0.035359
protein_co	translocati	91	62	41	78	51	42	2.386147	1.915819	1.416689	1.769348	1.502363	1.094497
protein_co	chemokine	0	1	0	7	15	18	0	0.011809	0	0.060684	0.16887	0.179264
protein_co	angel_hom	375	296	334	702	498	483	4.270353	3.972202	5.012032	6.915645	6.371049	5.466248
protein_co	UDP_glycos	2	0	1	469	375	347	0.025926	0	0.017082	5.259473	5.461182	4.470391
protein_co	kyphoscoli	3	3	3	3	1	0	0.039283	0.046293	0.051766	0.033984	0.014711	0
protein_co	IQ_motif_c	66	53	47	135	77	94	1.343887	1.27175	1.261105	2.37802	1.761402	1.9022
protein_co	solute_carr	38	5	10	543	347	418	0.476381	0.073867	0.165198	5.888895	4.887081	5.207832
protein_co	zinc_finger_	338	317	310	539	370	418	4.065907	4.493731	4.914024	5.609091	5.000248	4.997199
protein_co	solute_carr	342	244	188	645	423	638	7.201997	6.055134	5.216984	11.75032	10.00728	13.35233
protein_co	BR_serine/t	53	44	22	309	259	293	0.6862	0.671328	0.375347	3.460959	3.767244	3.770095
pseudogen	family_with	0	3	4	0	0	0	0	0.056889	0.084819	0	0	0
antisense	GRIK1_anti	0	2	0	0	0	2	0	0.152537	0	0	0	0.128641

protein_co	UDP-GlcNA	1248	1025	829	883	688	730	31.88724	30.86266	27.91205	19.51758	19.74876	18.5368
protein_co	transmemb	1721	1437	1643	2675	2308	2332	19.6785	19.3631	24.75617	26.46049	29.64804	26.50021
protein_co	SH3_and_P	7563	6595	6812	2093	2352	2065	51.48421	52.90563	61.10679	12.32572	17.98732	13.97043
pseudogen	-	0	5	0	0	5	0	0	0.618926	0	0	0.590039	0
protein_co	KIAA1551	207	182	237	1230	932	909	1.7596	1.823148	2.654768	9.045063	8.900378	7.679218
protein_co	La_ribonuc	333	301	260	903	527	554	7.559756	8.052619	7.778067	17.73431	13.44074	12.49922
protein_co	fibroblast_	17	25	21	468	368	446	0.353633	0.612846	0.57565	8.42196	8.600054	9.22038
protein_co	nuclear_rec	56	55	62	609	582	620	0.563845	0.652591	0.822618	5.30459	6.583299	6.204015
protein_co	poly(A)_bin	6	6	0	46	35	30	0.098617	0.116214	0	0.654067	0.646277	0.490041
protein_co	breast_can	1069	792	698	2081	1434	1803	31.1469	27.19377	26.79954	52.45323	46.93917	52.20866
protein_co	ribosomal_	38005	32517	24535	29630	21391	25738	737.0046	743.0996	626.9751	497.0775	466.0254	496.0368
protein_co	chromoson	47	19	32	389	280	394	0.912776	0.434837	0.818938	6.5355	6.109045	7.604525
protein_co	v-Ha-ras_Ha	729	657	495	1870	1221	1642	31.30088	33.2431	28.00716	69.45982	58.89708	70.06672
protein_co	WD_repeat	0	0	0	1	0	0	0	0	0	0.017656	0	0
protein_co	signal_reco	2083	1759	1775	2692	2023	2140	27.68669	27.5521	31.08959	30.95422	30.20833	28.26866
protein_co	Purkinje_ce	5	3	0	3	11	12	0.341115	0.24119	0	0.177058	0.843086	0.813619
protein_co	Ras_and_Ra	2494	2154	1579	399	288	335	29.89919	30.43097	24.9448	4.13808	3.878864	3.991329
protein_co	chromoson	1	0	0	8	0	3	0.02825	0	0	0.195513	0	0.084227
protein_co	THAP_dom	152	112	125	217	138	134	2.267408	1.968844	2.457146	2.800328	2.312673	1.986555
protein_co	centrosoma	199	144	190	284	277	230	1.894149	1.615216	2.38314	2.338527	2.962033	2.175698
protein_co	frizzled_fam	83	65	87	180	166	142	0.595165	0.549262	0.822078	1.116593	1.337262	1.011946
protein_co	CD248_mo	7325	5934	4746	337	255	310	151.6	144.7259	129.4357	6.03371	5.928991	6.376214
protein_co	betacellulin	0	0	0	12	1	11	0	0	0	0.195166	0.021121	0.205524
protein_co	PDZ_domai	7	8	17	12	3	8	0.177825	0.239492	0.569086	0.263717	0.085618	0.201973
protein_co	DENN/MAD	387	330	288	521	449	390	4.401324	4.422761	4.316182	5.125935	5.736775	4.408051
protein_co	phosphodi	347	365	328	946	769	829	4.727361	5.859887	5.888409	11.14919	11.76968	11.22415
protein_co	glomulin_F	154	173	138	566	302	357	4.086673	5.410064	4.825731	12.99357	9.003372	9.415146
protein_co	dynein_axo	1	6	2	12	2	3	0.005548	0.039229	0.014622	0.057597	0.012466	0.016542
protein_co	Yip1_intera	2356	1926	1472	1786	1223	1430	110.9688	106.9028	91.36259	72.77299	64.71445	66.9378
protein_co	cornichon_	226	197	175	78	85	76	7.85083	8.064556	8.010876	2.344038	3.317226	2.623798
protein_co	NLR_family	2	2	2	0	0	0	0.036063	0.042498	0.047523	0	0	0
protein_co	NADH_dehy	121	79	63	189	130	198	2.662452	2.048475	1.826719	3.59767	3.213578	4.329835
protein_co	arginine/se	300	220	232	452	325	317	6.587432	5.692783	6.713016	8.586108	8.017285	6.917733
protein_co	catsper_cha	3	0	0	0	0	1	0.063125	0	0	0	0	0.020912
protein_co	chromoson	0	0	0	7	11	11	0	0	0	0.216033	0.440859	0.389996
protein_co	RAB1B_mer	1693	1455	1063	2053	1634	1876	44.65825	45.22877	36.94986	46.84861	48.42235	49.17985
pseudogen	methyltran	6	5	5	2	1	1	0.303967	0.298506	0.333796	0.087653	0.056915	0.050348
protein_co	phosphatid	1240	940	752	1577	1037	1182	20.98684	18.74823	16.77174	23.08979	19.71756	19.88165
protein_co	chromoson	778	629	466	633	525	778	45.96885	43.79674	36.28314	32.3557	34.84917	45.68497
protein_co	chromoson	24	25	14	44	22	34	0.657993	0.807713	0.505793	1.043579	0.677613	0.9264
protein_co	seizure_rela	2101	1727	1160	578	458	506	29.2631	28.34612	21.29056	6.964422	7.166527	7.004133
protein_co	aspartate_b	281	242	234	58	77	95	8.589157	8.716992	9.425293	1.533682	2.644137	2.885875
protein_co	potassium_	442	355	265	337	220	314	9.256297	8.760935	7.313002	6.105313	5.175911	6.535131
protein_co	purinergic_	0	0	0	2	6	3	0	0	0	0.03645	0.142004	0.06281

protein_co	archaelysin	4	1	1	33	22	39	0.038391	0.01131	0.012647	0.273996	0.237214	0.371999
protein_co	G_protein-	0	0	0	1	3	4	0	0	0	0.025643	0.099904	0.117837
protein_co	G_protein-	0	0	0	3	6	3	0	0	0	0.059146	0.153618	0.067948
protein_co	CD164_sial	0	0	0	3	2	1	0	0	0	0.094301	0.081642	0.036111
protein_co	fucosyltran	0	0	0	86	99	84	0	0	0	0.927627	1.386744	1.040881
protein_co	DEAH_(Asp	873	815	853	1777	1393	1353	6.864323	7.55176	8.838271	12.08743	12.30506	10.57282
protein_co	Zic_family_	522	426	471	56	77	76	6.380789	6.136498	7.586817	0.592182	1.057411	0.923267
pseudogen	-	60	59	61	143	65	120	2.356424	2.73062	3.156944	4.858489	2.867904	4.683743
protein_co	F-box_and_	834	645	582	734	604	650	9.499309	8.657505	8.73542	7.232443	7.728798	7.357817
protein_co	carbonic_a	1	0	0	0	0	0	0.048392	0	0	0	0	0
protein_co	zymogen_g	0	0	0	3	3	1	0	0	0	0.071043	0.092258	0.027205
protein_co	kinesin_ligh	426	425	289	1151	847	1111	6.006089	7.061194	5.369265	14.03849	13.41574	15.56703
protein_co	solute_carr	5	7	27	17	6	21	0.135886	0.224186	0.966945	0.399682	0.183191	0.567195
protein_co	testis_expr	3	2	0	0	0	0	0.172259	0.135331	0	0	0	0
protein_co	C-terminal_	1473	1098	1073	3114	2336	2416	21.25432	18.67041	20.40229	38.87103	37.86747	34.64583
protein_co	carbohydra	2169	1705	1751	234	165	183	32.56637	30.16763	34.64422	3.039406	2.78319	2.730678
protein_co	zinc_finger_	184	95	139	520	381	359	1.319938	0.803094	1.31397	3.227023	3.070505	2.55941
protein_co	ataxia_telan	384	283	397	470	468	372	2.464461	2.140348	3.357501	2.609466	3.374316	2.372703
processed_	C17orf76_a	5643	4927	3907	3702	3179	4381	179.7509	184.9485	163.9983	102.0142	113.7629	138.6896
protein_co	ubiquitin-c	577	456	413	3390	2268	3069	21.12514	19.67414	19.92547	107.3709	93.28588	111.6684
protein_co	desmoglein	1	2	0	1	0	3	0.011697	0.027569	0	0.010119	0	0.034875
protein_co	glycerol_ki	307	267	232	126	128	104	3.628686	3.719027	3.613548	1.288382	1.699691	1.22167
protein_co	valosin_cor	350	338	347	395	415	334	1.863745	2.121007	2.434908	1.819611	2.48265	1.767561
protein_co	receptor_(c	0	0	1	0	0	0	0	0	0.031467	0	0	0
protein_co	desmin	5	4	2	0	0	0	0.117751	0.11101	0.062067	0	0	0
protein_co	PDLIM1_in	67	46	83	77	101	109	0.828943	0.670679	1.353202	0.824145	1.403848	1.34025
protein_co	splA/ryanoc	9	11	6	1509	1277	1521	0.163848	0.235992	0.143941	23.76566	26.11786	27.51925
protein_co	recombinat	0	0	0	0	0	1	0	0	0	0	0	0.022033
protein_co	TNF_recept	253	178	216	309	316	288	2.894764	2.400047	3.256726	3.058539	4.061895	3.274875
protein_co	zinc_finger_	278	262	254	253	209	154	2.963672	3.291499	3.568239	2.333291	2.503115	1.631608
protein_co	trans-golgi_	161	134	131	129	88	139	2.851623	2.796907	3.057541	1.9766	1.751047	2.446756
protein_co	mitochond	413	403	344	845	576	683	10.12251	11.63993	11.11045	17.9167	15.86024	16.63676
protein_co	phosphofur	1845	1502	1297	1791	1545	1716	22.23956	21.33569	20.60177	18.67619	20.9222	20.55686
protein_co	MARCKS-lik	6899	5334	4798	11487	9505	11491	214.9735	195.8659	197.0125	309.648	332.7361	355.8494
protein_co	SH3-bindin	1229	1103	930	1281	1304	1361	15.78469	16.69424	15.7399	14.23299	18.81528	17.37208
processed_	TMEM51_a	0	0	0	5	2	0	0	0	0	0.077311	0.040159	0
protein_co	yippee-like_	113	95	101	25	30	33	1.1467	1.136062	1.350602	0.21947	0.342012	0.332809
protein_co	cell_adhesi	9	4	7	4	1	7	0.050218	0.026302	0.05147	0.019308	0.006269	0.038817
protein_co	proteasom	4194	3182	3310	9660	7065	8323	64.37649	57.55806	66.95171	128.2741	121.8316	126.9663
protein_co	family_with	0	1	0	0	4	2	0	0.037113	0	0	0.141525	0.062599
protein_co	protein_ph	0	5	9	9	20	12	0	0.104397	0.21013	0.137949	0.398099	0.211301
protein_co	family_with	141	123	84	140	168	177	2.030101	2.086943	1.593722	1.743771	2.71742	2.532686
protein_co	cysteine_ar	719	713	545	1606	1306	1758	7.495978	8.759837	7.487394	14.48465	15.29648	18.21495
protein_co	inhibin_bet	0	0	2	0	1	0	0	0	0.070043	0	0.029857	0

protein_co presenilin_	498	397	354	1176	658	855	18.64541	17.51622	17.46549	38.09018	27.67691	31.81401
protein_co DNA-damag	123	109	86	133	66	82	5.657465	5.908134	5.212548	5.292141	3.410435	3.748351
protein_co propionyl_	292	221	271	598	444	500	6.205849	5.535001	7.589663	10.99468	10.60109	10.56083
protein_co HIG1_hypo	0	10	1	0	5	2	0	0.55903	0.062512	0	0.266469	0.09429
protein_co dynactin_2	3145	2711	2211	3669	2527	2954	80.78575	82.06363	74.84067	81.53138	72.92365	75.41092
protein_co natriuretic_	2	7	1	15	2	6	0.123839	0.510777	0.081594	0.80349	0.139125	0.369221
protein_co zinc_finger_	274	221	202	521	327	384	5.940144	5.646064	5.770755	9.771183	7.96422	8.273462
protein_co CTD_(carbo	6353	5049	5433	1411	1332	1312	70.14268	65.69252	79.04565	13.47701	16.52178	14.39617
protein_co cytoskeletc	1810	1446	1604	4443	3543	3127	13.45642	12.66854	15.71413	28.57528	29.5918	23.10408
protein_co Rho_GTPas	2588	2285	1746	3098	2227	2594	40.59594	42.2388	36.09087	42.04	39.24529	40.43877
protein_co mediator_c	1442	1155	775	1792	1062	1203	24.4604	23.08806	17.32347	26.29658	20.2382	20.28026
protein_co autophagy_	872	709	654	1192	1060	1057	9.764075	9.35552	9.649997	11.54659	13.33428	11.76249
protein_co galactose-3	4	1	2	4	2	0	0.09928	0.029249	0.065413	0.085886	0.055767	0
protein_co carbohydra	281	236	229	23	6	8	5.473296	5.417036	5.877775	0.387555	0.131293	0.154861
protein_co golgin_A8_	1095	1048	795	468	299	356	8.94881	10.09298	8.561564	3.30872	2.745184	2.891417
protein_co von_Willeb	1	0	0	0	0	4	0.011363	0	0	0	0	0.045172
protein_co tumor_pro	923	750	711	1318	1020	1284	13.19593	12.63592	13.395	16.3011	16.38278	18.24371
protein_co apoptosis-i	39	39	30	62	44	44	1.405513	1.656311	1.42471	1.932969	1.781443	1.575914
protein_co dolichol_ki	301	246	223	672	442	551	7.624516	7.343245	7.443642	14.72577	12.57816	13.87098
protein_co phytanoyl-(	15	4	4	199	112	127	0.3723	0.116995	0.130827	4.272847	3.122974	3.13267
protein_co cation_cha	0	1	0	0	0	0	0	0.023821	0	0	0	0
protein_co cyclin_E2	41	18	11	104	92	75	0.651826	0.337231	0.230449	1.430356	1.643178	1.185001
protein_co alanine-gly(	983	998	714	316	255	400	18.71978	22.39675	17.91762	5.205919	5.455525	7.570367
protein_co cystatin_E/	0	0	0	4	4	12	0	0	0	0.241364	0.313444	0.831843
protein_co GRAM_dom	7	0	1	142	125	118	0.112949	0	0.021263	1.982153	2.265922	1.892246
protein_co zinc_finger_	52	59	38	296	228	251	0.423724	0.56655	0.408035	2.086575	2.087195	2.03265
protein_co LSM1_hom	251	203	155	324	337	401	8.474611	8.076983	6.896243	9.463549	12.78277	13.45551
protein_co barrier_to_	1982	1729	1349	3983	2979	3855	90.84766	93.39254	81.4811	157.9368	153.4015	175.6079
protein_co apolipopro	2	0	0	0	1	0	0.061739	0	0	0	0.03468	0
protein_co cholinergic	4	11	19	26	48	32	0.037355	0.121056	0.233816	0.21005	0.503589	0.296992
protein_co TMEM9_do	596	533	487	870	552	687	15.14778	15.96383	16.31047	19.12868	15.76126	17.35279
protein_co nuclear_rec	70	86	57	55	24	45	0.972925	1.408597	1.043977	0.661313	0.37475	0.621589
protein_co protein_tyr	450	400	338	921	595	648	7.027566	7.361384	6.955749	12.44271	10.43899	10.0572
protein_co signal_pept	10	13	13	19	4	20	0.113049	0.173188	0.193663	0.185817	0.050802	0.224702
protein_co eukaryotic_	382	347	293	768	512	588	7.005009	7.498629	7.080236	12.18343	10.54786	10.71599
protein_co SMAD_fami	1238	1047	1069	2086	1635	1616	5.427822	5.40952	6.176145	7.911927	8.053261	7.04135
protein_co eukaryotic_	6865	5691	4136	8858	5558	6230	48.20158	47.08867	38.26803	53.8046	43.8418	43.47288
protein_co olfactory_r	0	0	0	0	0	2	0	0	0	0	0	0.102163
protein_co zinc_finger_	195	180	157	9	35	21	2.4942	2.713165	2.646252	0.099587	0.502937	0.266947
protein_co ADP-ribosy	1865	1516	1528	458	486	506	9.104191	8.721051	9.829257	1.934154	2.665311	2.454837
protein_co clathrin_lig	882	663	531	2976	2092	2901	31.35927	27.77909	24.87865	91.53629	83.56187	102.5073
protein_co proprotein_	7	2	13	5	5	1	0.072864	0.024533	0.178317	0.045024	0.05847	0.010345
protein_co lipoprotein	0	0	0	402	435	388	0	0	0	4.787093	6.726995	5.307918
protein_co Rieske_(Fe-S	6	5	9	10	10	7	0.113933	0.111886	0.225204	0.164272	0.213328	0.132101

protein_co	coiled-coil_	677	650	694	1197	997	1141	4.5271	5.122145	6.115412	6.924503	7.489894	7.58275
protein_co	TBC1_dom	26	34	10	2	5	21	0.307247	0.473478	0.155722	0.020446	0.066379	0.246628
protein_co	squamous_	1820	1574	1233	1909	1833	2517	29.25983	29.82031	26.12151	26.55029	33.10639	40.21548
protein_co	protein_ph	472	438	336	1119	732	800	4.868137	5.323558	4.56662	9.984215	8.481662	8.200125
protein_co	multiple_C	338	324	333	159	127	110	3.31617	3.746039	4.305258	1.349523	1.399822	1.072562
protein_co	polymerase	34	18	20	8	22	24	1.003901	0.626313	0.778174	0.204345	0.729766	0.704259
protein_co	olfactory_r	0	0	1	0	1	0	0	0	0.062624	0	0.05339	0
protein_co	leucine_ric	4	0	0	0	0	0	0.087687	0	0	0	0	0
protein_co	dipeptidyl-	0	0	0	105	114	87	0	0	0	0.76599	1.080002	0.729121
protein_co	cardiotropl	77	52	52	85	42	62	2.21066	1.759307	1.967294	2.111121	1.354658	1.769019
processed_	testis_speci	2	0	0	0	1	0	0.055004	0	0	0	0.030897	0
protein_co	ubiquilin-li	5	11	4	10	1	3	0.114442	0.296699	0.120646	0.198007	0.025714	0.068241
protein_co	lipoyl(octa	2	0	9	34	17	22	0.10401	0	0.616768	1.529629	0.993213	1.137042
protein_co	potassium_	5	8	14	17	23	12	0.08422	0.158798	0.31075	0.247719	0.435236	0.200881
protein_co	ALG10B_al	29	23	36	93	81	69	0.493503	0.46124	0.80729	1.369109	1.548553	1.166946
protein_co	DR1-associ	2890	2308	1877	2814	2109	3237	154.7012	145.5924	132.4021	130.3115	126.8298	172.2059
protein_co	LON_peptic	0	5	1	13	4	5	0	0.078515	0.017559	0.149858	0.05988	0.066215
protein_co	uncoupling	21	25	9	45	35	47	0.423851	0.594622	0.239371	0.785723	0.793617	0.94276
protein_co	uncoupling	111	86	90	1497	933	1090	2.781093	2.539207	2.97146	32.44721	26.26173	27.14118
protein_co	chromoson	1034	748	607	837	492	523	33.8116	28.82398	26.15584	23.67738	18.07421	16.99639
protein_co	proteasom	326	260	243	568	367	491	8.543943	8.030104	8.392316	12.87811	10.80577	12.78886
protein_co	mitochond	409	326	273	576	375	450	11.2658	10.58189	9.909145	13.72537	11.6043	12.31859
protein_co	RAB6A_me	1915	1759	1665	3402	2161	2273	32.34908	35.01596	37.06313	49.71534	41.01068	38.15946
protein_co	purinergic_	0	0	0	80	107	82	0	0	0	1.377411	2.392452	1.621937
protein_co	FOS-like_an	501	420	330	2318	1322	1544	15.89181	15.69973	13.79382	63.60807	47.11034	48.67351
protein_co	excision_re	146	117	124	247	184	177	1.143739	1.080107	1.28006	1.673917	1.61935	1.378024
protein_co	chromoson	1626	1467	1265	115	100	126	50.07682	53.24188	51.33831	3.063917	3.459914	3.856527
protein_co	coiled-coil_	1261	1108	701	1114	774	1014	54.23119	56.15402	39.7271	41.44596	37.39591	43.33927
protein_co	-	2	0	2	0	0	0	0.053638	0	0.070682	0	0	0
protein_co	transmemb	296	227	219	872	468	663	7.765379	7.017847	7.570941	19.79021	13.79323	17.28598
processed_	long_interg	80	61	72	117	100	103	1.499214	1.347133	1.778038	1.896804	2.105342	1.918318
protein_co	ribosomal_	597	452	348	902	655	796	5.717398	5.101167	4.391755	7.472976	7.047165	7.576119
protein_co	RMI2_RecC	46	67	46	731	433	640	1.305783	2.241275	1.720703	17.95121	13.80862	18.05522
protein_co	target_of_r	844	708	705	1720	1626	1769	7.990379	7.898876	8.795264	14.08693	17.29396	16.64418
protein_co	testis_expr	0	0	0	0	1	0	0	0	0	0	0.040241	0
protein_co	zinc_finger_	43	23	41	59	50	64	1.137094	0.716742	1.428719	1.349718	1.485413	1.681968
protein_co	G_protein-	5	3	8	21	17	6	0.059591	0.042135	0.125643	0.216519	0.227621	0.071068
lincRNA	long_interg	96	79	62	194	137	238	2.477979	2.403038	2.108885	4.332027	3.972794	6.105385
protein_co	chromoson	2	4	4	274	171	233	0.059053	0.139181	0.155635	6.998829	5.672271	6.837186
protein_co	UDP-GlcNA	139	113	95	176	124	149	2.213838	2.120882	1.993836	2.424972	2.218717	2.358452
protein_co	RNA_bindi	1	0	0	0	3	1	0.015261	0	0	0	0.051435	0.015167
protein_co	MLX_intera	747	694	554	591	739	690	6.819611	7.466302	6.664745	4.667555	7.579359	6.260337
protein_co	chromoson	5	5	10	0	0	0	0.074628	0.087944	0.196682	0	0	0
pseudogen	BCL2-antag	13	8	5	16	10	20	0.328669	0.238349	0.166579	0.349944	0.28403	0.502522

pseudogen	RWD_dom	42	33	26	63	64	67	3.949417	3.65683	3.22175	5.124922	6.761028	6.261352
protein_co	nuclear_rec	1878	1457	1410	262	350	256	26.64073	24.35662	26.35751	3.21525	5.577859	3.60911
protein_co	chromoson	0	0	1	0	4	0	0	0	0.022665	0	0.077292	0
pseudogen	eukaryotic_	0	0	0	0	0	3	0	0	0	0	0	0.240613
protein_co	aurora_kin	1676	1316	997	3310	2665	3632	82.76969	76.58792	64.88246	141.4127	147.8576	178.2595
protein_co	tubulin_tyr	129	68	90	64	34	70	2.10135	1.305343	1.931906	0.901886	0.62221	1.133226
protein_co	translocase	21	22	22	31	31	58	0.362019	0.446933	0.49977	0.462314	0.600376	0.993688
processed_	-	7	5	4	1	0	1	0.151693	0.127687	0.114226	0.018747	0	0.021537
lincRNA	-	0	1	0	1	3	0	0	0.093255	0	0.068459	0.266708	0
protein_co	solute_carr	320	293	249	639	434	482	3.378763	3.645713	3.464511	5.836757	5.148095	5.057833
protein_co	proline_ric	0	0	0	4	6	8	0	0	0	0.049366	0.096162	0.113423
protein_co	zinc_finger_	71	41	26	71	49	45	1.383951	0.941788	0.667837	1.197247	1.073019	0.871735
protein_co	RuvB-like_1	1167	1044	963	3003	2208	2747	15.20978	16.03466	16.53915	33.85872	32.3296	35.58119
protein_co	stratifin	14	12	2	1081	879	1073	0.56363	0.569318	0.106104	37.64914	39.75615	42.93146
pseudogen	olfactory_r	0	0	1	1	0	0	0	0	0.074059	0.048619	0	0
protein_co	methionine	127	88	74	247	172	244	3.941094	3.218124	3.026074	6.630908	5.9964	7.525104
protein_co	coiled-coil_	0	2	1	1	3	3	0	0.016955	0.00948	0.006224	0.024246	0.021449
protein_co	CTD_nuclea	1156	945	694	1113	855	1044	35.49872	34.19745	28.08336	29.56739	29.49647	31.86141
protein_co	ets_variant	279	195	169	1507	1302	1671	6.080913	5.008484	4.853847	28.41455	31.88046	36.19517
protein_co	SWI5_reco	329	309	216	296	197	316	16.61983	18.39486	14.37869	12.93557	11.18011	15.86454
protein_co	BAI1-associ	616	504	401	951	800	877	8.840242	8.523561	7.583377	11.80666	12.898	12.50814
protein_co	calcitonin-	0	0	0	40	29	36	0	0	0	0.811318	0.763863	0.838842
lincRNA	-	40	41	36	71	88	99	1.024499	1.237492	1.215035	1.57316	2.532115	2.519976
protein_co	cellular_rep	7	10	6	24	13	21	0.116281	0.195757	0.13134	0.344893	0.242607	0.346688
protein_co	homeobox_	150	91	134	6	14	2	3.07439	2.197942	3.619156	0.106385	0.322363	0.040739
pseudogen	ribosomal_	2	2	3	5	3	3	0.131694	0.155193	0.260311	0.284819	0.221925	0.196321
protein_co	zinc_finger_	83	81	96	275	274	170	0.935114	1.075422	1.425255	2.680293	3.468057	1.903466
protein_co	thrombosp	9	1	3	2	1	0	0.120108	0.015727	0.052758	0.02309	0.014993	0
protein_co	pleckstrin_	92	85	68	399	326	327	1.690584	1.840665	1.646617	6.342854	6.730007	5.971813
lincRNA	-	966	925	545	140	117	168	29.05739	32.78901	21.60283	3.643095	3.953797	5.02225
protein_co	alpha-2-ma	766	622	618	2830	2286	1997	8.371759	8.010976	8.900435	26.757	28.06811	21.6908
protein_co	ADP-ribosy	530	464	342	120	55	122	17.40616	17.95776	14.80089	3.409348	2.029265	3.981957
protein_co	Uncharacte	98	77	43	78	61	61	2.885549	2.671777	1.668421	1.986827	2.017815	1.785015
protein_co	docking_pr	14	8	13	2	2	16	0.289295	0.194809	0.35399	0.035752	0.046429	0.328581
protein_co	leucine_ric	3	6	1	8684	6555	6388	0.041544	0.097914	0.018248	104.0329	101.9787	87.91487
protein_co	ubiquitin-c	896	810	685	1043	1020	1194	8.726109	9.296185	8.790995	8.787391	11.15994	11.55651
protein_co	ORAI_calciu	141	82	57	41	53	40	3.383808	2.319036	1.802587	0.851204	1.428932	0.954017
protein_co	kelch-like_f	1	3	0	0	0	0	0.026711	0.094431	0	0	0	0
antisense	-	4	0	4	1	0	0	0.093909	0	0.123749	0.02031	0	0
protein_co	unc-119_h	1058	871	968	963	1146	1044	12.71834	12.33872	15.33398	10.01461	15.4767	12.47254
protein_co	DENN/MAD	58	47	43	57	30	44	0.498228	0.475779	0.486747	0.423582	0.289514	0.375632
protein_co	pleckstrin_	1	0	2	0	1	1	0.013239	0	0.03489	0	0.014873	0.013157
protein_co	achaete-scu	0	0	1	3	0	2	0	0	0.107328	0.21138	0	0.161889
protein_co	tubulin_be	3520	2951	2440	13313	9200	10057	86.15455	85.11613	78.69737	281.8867	252.972	244.6322

protein_co	LysM_putat	375	339	369	331	301	290	4.661393	4.965823	6.044295	3.559389	4.203393	3.582549
protein_co	UDP-Gal:be	1057	902	720	1133	828	814	20.03531	20.14813	17.98409	18.57865	17.63196	15.33399
protein_co	zinc_finger_	24	40	42	112	41	94	0.46885	0.920852	1.081202	1.892796	0.89982	1.824989
protein_co	chromoson	1	4	1	11	9	4	0.027747	0.130792	0.036564	0.26404	0.280547	0.110302
protein_co	calponin_h	0	0	1	0	1	0	0	0	0.03563	0	0.030376	0
protein_co	nuclear_pr	1299	1107	697	32	40	60	75.24108	75.56151	53.20023	1.603463	2.602885	3.453876
protein_co	janus_kinas	277	245	211	82	66	57	2.443702	2.547074	2.452933	0.625814	0.654126	0.49975
pseudogen	ribosomal_	6	4	3	5	14	16	0.754503	0.592758	0.497126	0.54393	1.977821	1.999584
protein_co	metallo-be	129	105	98	96	92	83	1.595651	1.53054	1.597384	1.027265	1.278454	1.020319
protein_co	taperin	568	467	345	635	411	605	8.976264	8.697036	7.184577	8.681285	7.296896	9.50194
protein_co	KCNE1-like	7	2	4	8	4	2	0.25296	0.085171	0.19048	0.250096	0.162392	0.071828
protein_co	zinc_finger_	0	0	0	3	0	0	0	0	0	0.080255	0	0
protein_co	solute_carr	1705	1411	1297	3455	2445	2441	24.9556	24.3376	25.01603	43.74764	40.20421	35.50757
protein_co	absent_in_	0	0	0	843	952	1098	0	0	0	15.30261	22.44196	22.89743
protein_co	inositol_he	1290	1119	996	1311	1315	1577	15.32628	15.66694	15.59341	13.4745	17.5518	18.62037
protein_co	Sjogren_syr	827	652	501	1737	1191	1597	37.42069	34.7665	29.873	67.99376	60.54343	71.81593
protein_co	cleavage_st	537	419	447	982	881	948	10.16422	9.345892	11.14916	16.07956	18.73374	17.83272
protein_co	v-yes-1_Yan	1071	821	983	1964	1770	1560	12.22242	11.04124	14.78278	19.38975	22.6929	17.69302
protein_co	charged_m	182	158	91	264	179	286	5.790421	5.923835	3.815179	7.266172	6.39795	9.04304
pseudogen	aquaporin_	0	1	0	0	0	0	0	0.059873	0	0	0	0
protein_co	deleted_in_	250	218	157	289	171	212	5.424282	5.573986	4.488867	5.424542	4.168189	4.571385
protein_co	UFM1-spec	23	26	17	23	23	41	1.224993	1.631872	1.193135	1.059733	1.376203	2.170197
protein_co	Protein_LO	0	0	0	1	0	1	0	0	0	0.047411	0	0.054466
protein_co	transmemb	905	749	811	711	556	605	10.90635	10.63702	12.87913	7.412479	7.527569	7.24596
protein_co	t-complex_	278	219	231	314	288	256	4.341474	4.030358	4.753781	4.24214	5.052821	3.973214
protein_co	glutathione	8	6	5	5	2	7	0.373481	0.330094	0.307598	0.201935	0.104896	0.324778
protein_co	coiled-coil_	671	540	430	687	777	893	6.604091	6.26313	5.576912	5.849386	8.591334	8.734774
protein_co	heat_shock	4	1	0	1	0	0	0.051725	0.015239	0	0.011187	0	0
protein_co	forkhead_b	4	0	2	24	9	15	0.076893	0	0.050663	0.399119	0.194366	0.286569
protein_co	sphingosin	870	654	530	2248	1470	1973	18.40874	16.30758	14.77799	41.14946	34.94388	41.48982
protein_co	BCL2/aden	3875	3938	2670	1071	795	830	127.658	152.8829	115.9104	30.5231	29.42337	27.17465
protein_co	Myb-relate	237	171	175	182	148	161	6.638633	5.644604	6.459563	4.410265	4.657373	4.481938
protein_co	cell_death-	0	2	0	11	2	1	0	0.069013	0	0.278644	0.065792	0.029101
protein_co	leucine_ric	0	0	0	26	21	27	0	0	0	0.329306	0.345408	0.392859
protein_co	ATPase_fam	118	118	115	550	509	461	0.909454	1.071736	1.167969	3.667113	4.407227	3.531093
protein_co	small_integ	74	112	86	270	96	204	2.672328	4.76632	4.092525	8.434996	3.894739	7.321464
protein_co	zinc_finger_	86	98	53	47	17	40	2.459711	3.303078	1.997544	1.162911	0.54624	1.136986
protein_co	rotatin	95	80	94	394	261	229	0.686513	0.681275	0.895134	2.463113	2.118921	1.644638
protein_co	chromoson	3	4	0	25	4	5	0.092662	0.145596	0	0.668012	0.1388	0.153483
protein_co	acyl-CoA_b	3	2	3	22	13	25	0.120138	0.094384	0.158313	0.76216	0.584862	0.994971
protein_co	anaphase_p	1021	755	552	1516	1193	1431	20.53676	17.89618	14.63121	26.37961	26.9585	28.60589
protein_co	zinc_finger_	305	235	246	575	400	598	10.08557	9.157474	10.7194	16.4487	14.85969	19.65222
pseudogen	cytochrom	0	10	1	5	0	7	0	2.052228	0.229484	0.753271	0	1.211508
protein_co	solute_carr	76	81	67	191	172	213	1.15287	1.447967	1.339295	2.506473	2.931191	3.211115

protein_co	solute_carr	65	56	62	57	61	61	0.552886	0.561329	0.694943	0.419431	0.58291	0.515658
pseudogen	iduronate_	3	2	3	0	3	1	0.422402	0.33185	0.556622	0	0.474542	0.139931
protein_co	zinc_finger_	14	7	30	77	56	71	0.221312	0.130401	0.624932	1.053006	0.994521	1.115437
protein_co	forkhead_b	0	0	0	1	0	0	0	0	0	0.039516	0	0
protein_co	cytochrom	114	125	125	182	110	148	11.90389	15.38159	17.20002	16.44063	12.90405	15.35874
pseudogen	ribosomal_	1	0	0	1	1	0	0.191815	0	0	0.165938	0.215492	0
protein_co	Protein_LO	12	9	3	1	3	2	0.141775	0.125305	0.046706	0.010221	0.039819	0.023483
protein_co	tachykinin_	4	5	0	7	12	5	0.313724	0.462131	0	0.474952	1.05735	0.389734
protein_co	zinc_finger_	246	208	258	134	137	154	3.415548	3.403265	4.720411	1.609508	2.136953	2.124984
pseudogen	profilin_1_	0	0	1	0	0	0	0	0	0.213343	0	0	0
protein_co	proline_ric	0	3	0	0	0	6	0	0.069217	0	0	0	0.116747
protein_co	UDP-GlcNA	31	14	11	8	8	7	0.558601	0.297287	0.261197	0.124708	0.161949	0.125357
protein_co	cell_divisio	118	107	82	231	139	208	7.164034	7.655375	6.560309	12.13251	9.480679	12.55014
protein_co	hydroxyste	40	9	11	6	0	13	1.114547	0.295521	0.403893	0.144628	0	0.359991
protein_co	cytokine_re	197	194	142	543	474	548	3.527012	4.093074	3.350147	8.410147	9.533847	9.750592
protein_co	arginyl_am	1617	1301	1152	3729	2311	2746	35.27218	33.44311	33.11384	70.3684	56.63323	59.52954
processed_	carcinoemb	0	0	0	0	2	0	0	0	0	0	0.056109	0
protein_co	EP300_inte	379	249	254	647	511	531	10.12854	7.841769	8.944913	14.95805	15.34184	14.10301
protein_co	DMRT-like_	27	7	13	51	39	27	0.620941	0.189711	0.393972	1.014659	1.007628	0.617107
protein_co	EP300_inte	51	21	19	40	25	22	1.447716	0.702489	0.710725	0.982282	0.797264	0.620648
protein_co	gap_junctio	0	0	2	3	0	4	0	0	0.125024	0.123115	0	0.188581
protein_co	regulating_	48	35	61	478	362	359	0.317567	0.272878	0.531812	2.735801	2.690613	2.360465
protein_co	potassium_	867	629	653	1828	1167	1320	12.99175	11.10724	12.89426	23.69669	19.64574	19.65767
protein_co	DnaJ_(Hsp4	135	160	108	170	120	174	6.041449	8.437901	6.368922	6.581415	6.03306	7.738668
protein_co	SPRY_doma	119	81	73	211	168	214	2.998562	2.405238	2.42395	4.599509	4.755809	5.35907
protein_co	vacuolar_p	180	172	151	5	8	25	5.867844	6.607567	6.486611	0.141006	0.292985	0.809945
protein_co	C-type_lect	3	1	0	6	9	5	0.070059	0.02752	0	0.121215	0.23612	0.116043
protein_co	spectrin_re	483	423	398	51	94	91	4.655107	4.804298	5.054758	0.425222	1.017793	0.871633
protein_co	CDC-like_ki	732	695	463	1120	824	1047	14.34227	16.04718	11.95426	18.984	18.13773	20.38746
protein_co	lysophosph	599	518	471	1055	702	917	16.05653	16.36296	16.63722	24.46473	21.1403	24.4289
protein_co	solute_carr	39	32	21	57	38	40	0.403656	0.390304	0.286418	0.510369	0.441854	0.411449
protein_co	zinc_finger_	70	56	42	30	31	29	1.621825	1.528977	1.282301	0.601299	0.806894	0.667749
protein_co	WD_repeat	360	255	210	245	183	202	8.977276	7.49358	6.900749	5.285319	5.126751	5.006141
protein_co	coiled-coil_	190	184	110	279	191	246	8.724015	9.956064	6.655647	11.0823	9.852472	11.22555
protein_co	phospholip	1	2	4	641	469	529	0.020409	0.048102	0.107576	11.31731	10.75336	10.7297
protein_co	DIRAS_fami	307	270	269	61	57	37	4.746754	4.919593	5.480819	0.815927	0.990107	0.568551
pseudogen	olfactory_r	1	5	1	2	0	2	0.079135	0.466276	0.10428	0.136918	0	0.157292
protein_co	pleckstrin_	195	195	147	414	338	513	3.984367	4.695333	3.958009	7.317926	7.758726	10.41722
protein_co	proline_ric	62	34	39	761	758	753	1.956103	1.264114	1.621435	20.77054	26.86695	23.61048
protein_co	guanine_nu	26	18	20	17	34	33	0.327107	0.266868	0.331575	0.185024	0.480556	0.41261
protein_co	KIAA2018	281	302	271	222	285	233	1.085236	1.37446	1.379184	0.74171	1.236551	0.894301
protein_co	cyclin_N-te	10	20	16	19	7	12	0.199251	0.46961	0.420103	0.327504	0.156692	0.237625
protein_co	HCG18115	170	107	95	167	133	168	1.397945	1.036888	1.029436	1.188011	1.228689	1.372967
protein_co	kelch_repe	1069	852	759	53	61	50	8.434266	7.921661	7.891256	0.36175	0.54069	0.392057

protein_co	UDP-GlcNA	437	418	452	146	255	169	5.611257	6.325023	7.648073	1.62179	3.678477	2.156627
protein_co	lamin_B2	3573	2908	2655	11877	12730	15991	40.49629	38.8404	39.6535	116.4534	162.0913	180.1223
protein_co	regulator_c	678	583	534	649	439	513	11.71857	11.87465	12.16245	9.704045	8.524299	8.811952
protein_co	mex-3_hon	773	742	744	1612	1474	1306	10.62945	12.02382	13.48153	19.17606	22.77078	17.84778
protein_co	ring_finger_	185	159	146	1030	1123	1104	1.030848	1.044064	1.072039	4.965043	7.029939	6.113663
pseudogen	Nanog_hon	0	0	0	1	1	0	0	0	0	0.050053	0.065001	0
protein_co	myosin_ID	459	435	369	1214	873	1097	4.368132	4.878422	4.627476	9.994584	9.333539	10.37527
protein_co	chromoson	14	8	8	6	0	4	0.271294	0.182687	0.204285	0.100583	0	0.077034
protein_co	forkhead_b	71	68	69	6	11	7	1.17868	1.330312	1.50946	0.086169	0.205154	0.11549
protein_co	TGFB-induc	0	0	0	11	0	0	0	0	0	0.556672	0	0
protein_co	leucine_ric	15	21	22	24	23	13	0.153393	0.25307	0.296464	0.212319	0.264235	0.13212
protein_co	forkhead_b	360	309	242	8	4	1	11.32428	11.45443	10.03132	0.217701	0.141357	0.031262
protein_co	brain-deriv	607	485	541	234	124	158	6.74259	6.34873	7.918996	2.248624	1.547422	1.744234
pseudogen	SCAN_dom	233	239	159	361	215	286	3.114176	3.764369	2.800394	4.174048	3.228307	3.798944
protein_co	coiled-coil_	13	2	19	60	36	40	0.293865	0.053277	0.56597	1.173328	0.914233	0.898617
protein_co	acyl-CoA_s	409	332	291	553	583	586	3.084454	2.950531	2.891897	3.607806	4.939382	4.391999
protein_co	olfactory_r	6	0	1	0	4	0	0.311418	0	0.068395	0	0.233239	0
protein_co	BCL2-relate	588	491	362	2182	1313	1892	11.74691	11.55939	9.529928	37.71065	29.46863	37.56445
protein_co	zinc_finger_	21	18	23	4	11	3	0.514466	0.519657	0.742506	0.084774	0.302746	0.073041
processed_	testis-speci	40	23	12	134	91	125	1.416481	0.959811	0.559973	4.105052	3.620273	4.399168
protein_co	chromoson	104	82	88	130	78	100	6.454705	5.997414	7.19715	6.979904	5.438595	6.168118
protein_co	profilin_far	5	7	7	4	14	14	0.271771	0.448372	0.501379	0.188086	0.85489	0.756259
protein_co	cyclin-depe	161	98	112	387	317	373	1.970751	1.413641	1.806587	4.098075	4.359275	4.537582
protein_co	chromoson	3	2	3	17	5	7	0.0746	0.058608	0.098304	0.365703	0.13968	0.172991
pseudogen	zinc_finger_	4	3	3	5	4	2	0.119844	0.105921	0.118444	0.129595	0.134637	0.059552
protein_co	transcriptic	0	0	0	263	265	274	0	0	0	2.741264	3.586964	3.280894
protein_co	NCK-associa	108	96	101	56	81	81	0.753112	0.788886	0.928094	0.337821	0.634556	0.561346
protein_co	RUN_and_F	653	666	593	829	586	772	12.47581	14.99467	14.92949	13.70166	12.57773	14.65826
protein_co	brain_abun	5762	4636	4162	5318	4473	4831	162.4313	154.0093	154.6085	129.6904	141.6591	135.3453
protein_co	leucine_ric	71	63	54	85	61	64	0.663515	0.693809	0.664999	0.687186	0.640429	0.594404
pseudogen	-	3	6	2	0	5	4	0.053548	0.126206	0.047042	0	0.100263	0.070956
pseudogen	FK506_bin	36	40	26	16	11	12	0.777591	1.01816	0.740043	0.298973	0.266926	0.257596
protein_co	V-set_and_i	128	83	107	425	346	362	1.370086	1.046943	1.509234	3.935409	4.160669	3.850846
lincRNA	MIR7-3_ho	2	0	0	0	0	2	0.120457	0	0	0	0	0.119713
protein_co	iroquois_h	125	104	89	57	34	39	2.756195	2.702342	2.585978	1.087271	0.842225	0.854622
protein_co	meteorin_g	836	813	503	1478	1242	1455	23.29404	26.69538	18.46891	35.62673	38.87847	40.29129
protein_co	family_with	1033	931	1188	1047	931	863	9.923434	10.53946	15.03879	8.701044	10.04756	8.239144
pseudogen	-	0	8	3	0	0	1	0	0.435516	0.182626	0	0	0.045911
protein_co	WD_repeat	925	681	667	1938	1272	1345	18.50734	16.05671	17.58583	33.54432	28.5916	26.74448
protein_co	glutamate_	0	0	1	5	4	5	0	0	0.013567	0.044534	0.046267	0.051161
protein_co	SRY_(sex_d	1689	1453	1529	2675	3000	3156	10.25663	10.39795	12.23538	14.05277	20.46659	19.04679
protein_co	thymidylat	497	452	354	3056	2080	2205	15.83133	16.96706	14.85933	84.21267	74.43436	69.80384
protein_co	peroxisoma	16	6	8	44	27	25	0.80672	0.356501	0.53153	1.919192	1.529381	1.252715
protein_co	transcriptic	14	23	41	24	16	23	0.24805	0.480227	0.957261	0.367863	0.318479	0.404994

protein_co	olfactory_r	0	0	0	0	1	0	0	0	0	0	0.055846	0
protein_co	paraneopla	1261	1083	1084	1212	931	1156	25.33533	25.64171	28.69958	21.06576	21.01407	23.08229
protein_co	chromoson	191	176	111	1150	1092	1149	5.516492	5.990311	4.224618	28.73363	35.43246	32.98066
protein_co	MEF2_activ	35	41	40	7	17	14	1.008674	1.392432	1.51907	0.17452	0.550403	0.400978
protein_co	chromoson	18	8	5	25	24	22	1.129073	0.591353	0.41329	1.356603	1.691258	1.371456
protein_co	ankyrin_rep	1497	1387	1242	1986	1683	1997	7.277564	7.945985	7.956473	8.352307	9.191733	9.648325
protein_co	complemer	2	0	1	1	4	7	0.123839	0	0.081594	0.053566	0.27825	0.430758
protein_co	fucosyltran	43	28	31	15	6	28	0.731746	0.56151	0.695166	0.220824	0.114708	0.473543
protein_co	EF-hand_ca	1	7	4	17	14	12	0.010316	0.085096	0.054375	0.151711	0.162249	0.123026
protein_co	glucosamin	18	25	39	79	163	121	0.277339	0.453927	0.791842	1.053002	2.821471	1.852823
pseudogen	transducer_	2	6	5	1	9	1	0.092716	0.327781	0.305443	0.040104	0.468724	0.046072
protein_co	mucin_20_	7	4	6	14	7	6	0.05984	0.040296	0.067589	0.103534	0.067226	0.050974
protein_co	THAP_dom	1144	910	692	1796	1070	1303	25.58703	23.98514	20.39552	34.75067	26.88603	28.96329
protein_co	nuclear_fac	637	540	493	1668	1312	1710	7.380918	7.373468	7.527533	16.71976	17.07866	19.6914
protein_co	lymphocyt	0	0	0	11	7	17	0	0	0	0.316649	0.261679	0.562187
protein_co	fin_bud_ini	472	462	414	28	18	27	8.321062	9.598112	9.617715	0.427029	0.356499	0.473053
protein_co	family_with	18	16	18	12	9	5	0.676322	0.708448	0.891227	0.390055	0.379903	0.186707
protein_co	serine_hydr	178	150	147	979	841	972	3.419266	3.395559	3.721046	16.26891	18.14922	18.55619
protein_co	dipeptidyl-	501	416	250	309	197	336	16.68141	16.32283	10.96907	8.900542	7.369029	11.11844
protein_co	Uncharacte	0	0	0	4	0	1	0	0	0	0.088032	0	0.025283
protein_co	SEC24_fam	2284	2172	1975	2726	2731	2889	25.90343	29.02874	29.51638	26.74546	34.79621	32.56255
protein_co	fragile_X_m	0	0	0	1	0	0	0	0	0	0.044857	0	0
protein_co	Smith-Mag	254	202	269	113	316	214	3.923844	3.677363	5.476021	1.510148	5.484211	3.285499
protein_co	methylenet	649	484	421	240	233	245	4.868741	4.278824	4.161874	1.557565	1.963708	1.826618
protein_co	chromoson	7	8	7	30	11	10	0.405013	0.545466	0.533708	1.501603	0.715011	0.575017
protein_co	DEAF1_tran	1230	989	780	858	661	706	26.04697	24.68059	21.76614	15.71818	15.72543	14.85821
protein_co	metaxin_3	190	135	220	136	222	159	2.096018	1.755021	3.19815	1.297906	2.751334	1.743204
protein_co	transmemb	375	340	312	300	239	361	9.698521	10.3624	10.63319	6.712101	6.944184	9.278785
protein_co	SIX_homeo	73	46	30	90	80	90	1.299056	0.964651	0.703495	1.385513	1.599352	1.591686
protein_co	interferon_	0	0	0	0	1	0	0	0	0	0	0.039284	0
protein_co	F-box_prot	535	477	361	871	642	756	9.437998	9.916344	8.392051	13.29252	12.72361	13.25432
protein_co	zinc_finger_	136	148	136	474	301	304	1.142128	1.464687	1.505045	3.443636	2.839824	2.537226
protein_co	solute_carr	133	139	123	385	278	380	1.746318	2.150767	2.128195	4.373159	4.10077	4.958665
protein_co	alkaline_ce	35	9	19	53	99	79	0.827942	0.250889	0.592271	1.084603	2.630972	1.857243
protein_co	WD_repeat	621	551	428	926	716	766	6.48321	6.778868	5.888126	8.3632	8.397704	7.947616
protein_co	polymerase	687	656	506	2665	2607	2871	4.540065	5.108769	4.406469	15.23581	19.3551	18.85594
protein_co	family_with	119	136	91	49	43	41	2.698064	3.633718	2.718826	0.961091	1.095274	0.923844
protein_co	sodium_ch	7	4	3	9	13	22	0.082647	0.055654	0.046675	0.091925	0.172432	0.258142
protein_co	Down_syno	0	0	0	0	1	3	0	0	0	0	0.008621	0.022879
protein_co	ras_homol	1114	952	807	1564	891	1020	44.71286	45.0289	42.68307	54.3059	40.17668	40.68714
protein_co	EPS8-like_2	203	179	123	4651	3620	4659	2.795791	2.905152	2.23228	55.41382	56.0101	63.76921
protein_co	zinc_finger_	0	0	4	20	20	13	0	0	0.081882	0.268773	0.349037	0.200699
antisense	MRVI1_ant	14	1	8	0	2	4	0.894058	0.075257	0.673228	0	0.143488	0.253868
protein_co	anoctamin_	1091	902	1152	2506	2325	2301	9.666715	9.418198	13.45059	19.20871	23.14335	20.26191

protein_co	zinc_finger_	459	356	381	397	480	380	3.701998	3.383612	4.049331	2.769983	4.349244	3.045908
lincRNA	-	0	0	1	0	0	0	0	0	0.016426	0	0	0
pseudogen	nudix_(nuc	2	2	3	10	9	6	0.194994	0.229789	0.385432	0.843442	0.985789	0.581371
protein_co	family_witl	313	243	270	523	368	401	3.818095	3.493138	4.340112	5.519085	5.043119	4.861344
protein_co	transaldola	2153	1646	1389	4981	3075	3906	84.68199	76.29287	71.99198	169.4832	135.8755	152.6824
protein_co	unc-51-like	867	735	567	674	833	898	8.644038	8.63559	7.4493	5.81327	9.330215	8.897819
pseudogen	nucleosom	7	2	1	0	11	11	0.3203	0.107844	0.060297	0	0.565458	0.50022
protein_co	ribosomal_	0	0	0	11	10	21	0	0	0	0.333634	0.39388	0.731719
protein_co	clavesin_1	0	1	0	6	0	0	0	0.017225	0	0.075868	0	0
protein_co	ribosomal_	589	528	588	1074	1037	1037	3.938147	4.160233	5.180703	6.212178	7.789407	6.890726
protein_co	UDP-GlcNA	10	25	5	30	33	25	0.282503	0.83228	0.186135	0.733174	1.047335	0.701895
protein_co	pseudourid	368	343	272	1516	1002	1491	9.057316	9.948392	8.821763	32.27854	27.70566	36.47027
pseudogen	PEST_conta	2	0	0	0	0	1	0.220129	0	0	0	0	0.109385
protein_co	chromodor	866	875	1086	580	599	464	3.497094	4.163941	5.779018	2.026191	2.717473	1.86216
protein_co	sperm_acro	0	0	0	8	7	7	0	0	0	0.377334	0.428766	0.379298
protein_co	olfactory_r	0	0	0	6	0	2	0	0	0	0.25778	0	0.098713
protein_co	Parkinson_	1764	1478	1116	1817	1369	1847	21.43399	21.16343	17.86914	19.09952	18.68775	22.30391
protein_co	chromoson	46	46	29	23	17	22	1.275687	1.503319	1.059788	0.551794	0.529644	0.606343
pseudogen	-	76	36	60	96	68	95	6.326282	3.531381	6.581442	6.913042	6.35906	7.859017
protein_co	mannosida	3565	2915	2200	1574	1238	1658	37.388	36.02619	30.40397	14.2804	14.58621	17.28092
pseudogen	endosulfine	0	0	1	0	0	0	0	0	0.209499	0	0	0
protein_co	potassium_	0	0	0	7	10	3	0	0	0	0.095814	0.177752	0.047173
protein_co	frizzled_fan	66	44	58	79	58	81	1.096706	0.861601	1.270016	1.135629	1.082738	1.337645
protein_co	gap_junctic	0	1	0	0	0	0	0	0.039486	0	0	0	0
protein_co	potassium_	0	0	0	8	5	6	0	0	0	0.106324	0.086297	0.091609
protein_co	topoisomer	852	838	646	1669	1383	1714	11.12074	12.88977	11.11121	18.84575	20.27988	22.23385
protein_co	CASK_inter	428	345	323	642	551	717	4.518195	4.291878	4.493228	5.86299	6.534642	7.522288
protein_co	zinc_finger_	626	575	665	376	456	363	4.313557	4.669132	6.038342	2.241363	3.530004	2.485865
protein_co	chromoson	3	3	0	6	10	4	0.084706	0.09982	0	0.146556	0.317205	0.112243
antisense	DLGAP1_ar	24	24	16	26	15	29	0.646279	0.7616	0.567758	0.605682	0.453784	0.776097
lincRNA	long_interg	0	0	0	0	0	2	0	0	0	0	0	0.148627
protein_co	-	2	9	3	5	26	24	0.064958	0.344472	0.128399	0.140487	0.948696	0.774685
protein_co	coiled-coil_	488	318	299	760	529	679	14.50601	11.13941	11.71208	19.54361	17.66578	20.05892
pseudogen	-	94	51	58	51	22	25	1.124114	0.71872	0.913998	0.527613	0.295566	0.29712
protein_co	LRRN4_C-te	188	143	107	5	23	17	3.850254	3.451236	2.887687	0.088586	0.529186	0.346011
protein_co	translocase	516	481	342	1181	835	958	16.16423	17.75651	14.11778	32.00503	29.38603	29.82501
protein_co	hypermeth	784	651	498	37	25	20	13.15137	12.86895	11.00827	0.536933	0.471134	0.333422
protein_co	protein_tyr	200	148	101	56	70	84	2.237101	1.950852	1.488716	0.541884	0.879635	0.93378
protein_co	melanoma_	745	650	578	1576	1454	1672	23.46284	24.12375	23.98761	42.93818	51.44437	52.33236
protein_co	uromodulir	0	2	0	0	1	0	0	0.022928	0	0	0.010929	0
antisense	-	1	5	11	41	26	32	0.022644	0.133421	0.328228	0.803146	0.661409	0.720124
protein_co	sterile_alpl	79	86	72	2	0	0	0.586254	0.752081	0.704087	0.01284	0	0
antisense	ZNFX1_anti	2449	2353	1534	2329	1706	2478	120.607	136.5566	99.55058	99.22386	94.3869	121.2815
protein_co	ubiquitin-c	0	0	0	1	0	2	0	0	0	0.02951	0	0.067802

pseudogen	-	0	1	0	0	0	0	0	0.120906	0	0	0	0
protein_co	PRKC_apop	287	218	240	2956	2368	2451	1.664373	1.489815	1.834066	14.82984	15.42765	14.12609
protein_co	TGFB-induc	703	604	466	1195	904	974	12.28301	12.43637	10.72927	18.0626	17.74463	16.9129
protein_co	Smith-Mag	179	147	119	246	190	273	2.817015	2.726218	2.467845	3.349147	3.359222	4.269808
protein_co	nucleosom	201	227	186	66	55	55	4.584722	6.101687	5.590681	1.302339	1.409382	1.246778
pseudogen	-	4	3	4	3	2	4	0.36261	0.320485	0.477831	0.235268	0.203685	0.36037
protein_co	Serine/thre	85	64	57	7	2	2	1.536355	1.363201	1.357633	0.109455	0.040612	0.035926
protein_co	CD19_mole	0	0	0	0	0	1	0	0	0	0	0	0.022659
protein_co	chromoson	4	7	5	76	93	65	0.120252	0.247992	0.198079	1.976557	3.140977	1.942029
protein_co	olfactory_r	0	0	0	12	0	6	0	0	0	0.58529	0	0.336192
protein_co	nuclear_rec	89	99	136	143	101	101	1.42435	1.867106	2.86814	1.97982	1.815921	1.606414
protein_co	G_protein-r	2	0	6	19	7	14	0.034738	0	0.137329	0.285492	0.136592	0.241666
protein_co	acyl-CoA_th	8	6	2	46	41	45	0.179309	0.158479	0.059071	0.891935	1.032393	1.002385
protein_co	oligodendr	0	0	0	6	4	8	0	0	0	0.125134	0.108335	0.191672
protein_co	polymerase	13634	11152	10174	6525	5951	6615	188.5573	181.7523	185.4158	78.06632	92.46112	90.92005
protein_co	ariadne_ho	742	650	663	1468	1191	1337	7.96315	8.22056	9.376253	13.62919	14.35958	14.26008
protein_co	RNA_bindir	5	20	18	10	6	10	0.049404	0.232877	0.234367	0.085478	0.066602	0.098197
protein_co	zinc_finger_	344	331	377	672	508	437	3.494857	3.962836	5.047161	5.906134	5.798074	4.41227
protein_co	zinc_finger_	1	1	5	136	53	78	0.022908	0.026996	0.150937	2.695219	1.364008	1.77581
protein_co	variable_ch	0	0	0	0	3	2	0	0	0	0	0.22001	0.129751
protein_co	iroquois_h	47	30	14	294	250	279	0.956642	0.719582	0.375504	5.176808	5.716639	5.643722
protein_co	ST8_alpha-l	0	0	0	8	3	11	0	0	0	0.030964	0.015079	0.04891
protein_co	reprimo_TF	0	0	0	174	140	224	0	0	0	5.41741	5.660522	8.011929
protein_co	solute_carr	971	725	578	1109	847	1034	17.76286	15.62927	13.93337	17.55044	17.40708	18.79852
protein_co	rabaptin_R	694	606	441	633	523	694	13.02412	13.40197	10.90592	10.27675	11.02655	12.94369
protein_co	nescient_h	0	0	0	75	81	90	0	0	0	0.475355	0.666697	0.655309
protein_co	ATX1_antic	1765	1395	1028	915	714	1128	21.52519	20.04858	16.52077	9.653536	9.782494	13.67165
protein_co	transducin_	1190	1082	1130	1115	840	867	7.926495	8.493146	9.918534	6.424985	6.285829	5.739353
protein_co	sterile_alph	0	0	5	60	54	38	0	0	0.039343	0.309941	0.362249	0.225506
protein_co	CD163_mo	7	7	5	12	2	4	0.069764	0.082213	0.065666	0.103461	0.022393	0.039619
protein_co	chromoson	22	10	3	9	2	7	1.032537	0.553083	0.185541	0.365417	0.105454	0.326506
protein_co	p53-induce	597	568	370	1136	864	1294	7.029754	7.881724	5.741195	11.57197	11.42954	15.14292
protein_co	zinc_finger_	81	73	72	14	20	11	1.735419	1.843102	2.032763	0.259484	0.481391	0.234219
protein_co	ribosomal_	13947	12351	9540	12141	9337	14716	945.4136	986.6208	852.1661	711.9648	711.0456	991.3807
protein_co	germ_cell_	68	50	44	416	389	391	1.260059	1.09184	1.074408	6.668654	8.098051	7.200593
protein_co	jun_proto-r	5951	5070	4210	2004	1555	1808	94.86656	95.24414	88.43825	27.63656	27.84856	28.64384
protein_co	cleavage_st	620	520	489	1142	827	1100	7.988176	7.895259	8.302323	12.72873	11.97045	14.08505
protein_co	piggyBac_tr	23	28	14	176	131	209	0.353658	0.507365	0.283673	2.341158	2.262952	3.193824
protein_co	glucosidase	1361	1081	908	821	747	787	30.02196	28.10047	26.39378	15.66704	18.51188	17.25302
antisense	cancer_sus	8	5	9	27	19	24	0.129599	0.095452	0.192127	0.378388	0.34579	0.386394
protein_co	acyl-CoA_d	767	658	532	946	827	984	16.54676	16.72825	15.12391	17.65516	20.04343	21.09708
protein_co	interleukin_	321	234	209	535	522	422	1.974446	1.696146	1.694031	2.846801	3.607114	2.579659
protein_co	patatin-like	519	462	305	635	418	543	10.07937	10.57342	7.805503	10.66849	9.119932	10.48035
protein_co	membrane_	0	1	1	0	2	1	0	0.041262	0.04614	0	0.078672	0.034798

protein_co	angiotensir	417	306	225	959	543	624	19.78172	17.10631	14.06518	39.35587	28.93855	29.41861
protein_co	CD163_mo	23	3	13	3	6	1	0.263845	0.040555	0.196516	0.029772	0.077325	0.011401
protein_co	serine/argi	276	246	171	16	20	22	4.043086	4.246647	3.300919	0.202762	0.329142	0.320285
protein_co	THAP_dom	174	181	165	318	186	254	2.786368	3.415662	3.481833	4.405339	3.346195	4.042338
protein_co	EF-hand_ca	79	64	52	48	21	29	1.714073	1.636399	1.486758	0.900962	0.511883	0.625331
protein_co	SMT3_supp	0	0	1	2	0	0	0	0	0.102142	0.134111	0	0
protein_co	DnaJ_(Hsp4	12	13	22	35	13	19	0.390949	0.499102	0.944488	0.986438	0.475807	0.61518
protein_co	N-acetylate	46	41	72	21	18	19	0.491679	0.516434	1.014124	0.194181	0.216145	0.201831
protein_co	CD151_mo	7489	6397	5477	2812	2528	3638	219.8975	221.3501	211.921	71.42902	83.39164	106.1619
antisense	-	0	0	0	1	0	0	0	0	0	0.024105	0	0
protein_co	polymerase	2172	1616	1658	1777	1660	2884	128.9101	113.0253	129.6721	91.2384	110.6839	170.1109
protein_co	family_witl	552	444	405	307	319	261	10.62284	10.06912	10.27049	5.110965	6.896699	4.991736
protein_co	poliovirus_	368	353	389	1123	906	883	5.317218	6.010608	7.406637	14.03716	14.70665	12.67964
protein_co	solute_carr	4	2	4	5	1	3	0.160306	0.094455	0.211244	0.173349	0.045023	0.119487
protein_co	annexin_A2	54	52	43	10	23	17	1.279684	1.452176	1.342803	0.205009	0.61233	0.400375
pseudogen	-	5	4	2	3	0	3	0.111784	0.105385	0.058922	0.058022	0	0.066656
protein_co	KIAA0195	1281	1157	942	1279	1105	1186	12.04144	12.81651	11.6685	10.40071	11.66919	11.07959
protein_co	flightless_I	2484	2080	1873	5745	4495	5233	30.31476	29.9139	30.1214	60.65346	61.62846	63.46918
protein_co	SRY_(sex_d	3243	2518	2099	1850	1630	1819	37.10561	33.95122	31.64753	18.31164	20.95218	20.68402
protein_co	heterogene	5873	4987	4287	10048	9387	13019	104.8642	104.9334	100.8685	155.2065	188.2969	231.0227
pseudogen	-	0	5	0	0	0	1	0	0.570272	0	0	0	0.096187
processed_	-	185	177	100	64	61	100	4.101375	4.624216	2.92141	1.227441	1.519276	2.203268
protein_co	Yip1_doma	0	0	1	0	0	3	0	0	0.062456	0	0	0.141309
lincRNA	family_witl	3	7	8	0	5	0	0.081699	0.224647	0.287092	0	0.152973	0
protein_co	zinc_finger_	69	72	35	110	85	99	1.131288	1.391117	0.756183	1.560198	1.56564	1.613128
pseudogen	CDKN2A_in	0	0	0	0	0	1	0	0	0	0	0	0.174219
processed_	-	6	10	9	3	0	7	0.365952	0.718753	0.723352	0.158291	0	0.424307
protein_co	myozenin_	0	0	0	19	26	24	0	0	0	0.564685	1.003487	0.819427
protein_co	transmemb	2	1	0	0	1	0	0.048681	0.028684	0	0	0.027345	0
pseudogen	-	0	0	1	0	0	0	0	0	0.106185	0	0	0
protein_co	potassium_	2	0	0	4	0	1	0.020004	0	0	0.034611	0	0.00994
processed_	-	222	192	255	213	167	232	5.200399	5.300196	7.871521	4.316446	4.394902	5.401088
protein_co	chitinase_d	2289	1990	1476	1779	1494	1788	34.26122	35.10081	29.11241	23.03541	25.12214	26.59709
pseudogen	protocadhe	103	81	84	20	15	18	1.293081	1.198341	1.389641	0.217211	0.211558	0.22458
protein_co	zinc_finger_	3	5	4	293	289	340	0.04826	0.094785	0.084793	4.077508	5.222893	5.435666
processed_	zinc_finger_	235	244	225	602	538	452	1.501827	1.837591	1.894826	3.328216	3.862632	2.870781
protein_co	transmemb	177	166	122	131	115	146	4.984338	5.508704	4.527192	3.191307	3.638155	4.085985
pseudogen	calcyclin_b	7	7	3	37	21	41	0.546588	0.644121	0.308687	2.49935	1.842174	3.181676
protein_co	coiled-coil_	108	68	59	141	101	126	8.075745	5.992042	5.813607	9.120968	8.484559	9.363517
protein_co	zinc_finger_	26	11	27	20	11	8	0.331439	0.165246	0.453554	0.220558	0.157533	0.101351
protein_co	chromoson	21	30	22	17	7	10	0.474301	0.798478	0.654775	0.332159	0.177616	0.224463
protein_co	adaptor-rel	1498	1328	1147	1737	1253	1437	45.84139	47.8907	46.25346	45.98422	43.07707	43.70312
protein_co	growth_fac	1403	899	986	1507	1432	1430	19.91853	15.04065	18.44639	18.5087	22.83977	20.17648
protein_co	zinc_finger_	76	59	114	15	37	17	1.064704	0.974034	2.104529	0.18179	0.582326	0.236687

protein_co	ubiquitin-c	1294	1149	1112	5166	3276	4118	18.6613	19.52697	21.13233	64.45033	53.0763	59.02061
protein_co	ADP-ribosy	274	228	230	1072	766	865	5.17142	5.071088	5.72034	17.50318	16.24191	16.22501
protein_co	zinc_finger_	150	109	163	91	158	95	1.467594	1.256748	2.101537	0.770227	1.736684	0.923736
protein_co	MAM_dom	197	185	105	219	173	407	2.537561	2.808207	1.782274	2.44038	2.503488	5.210199
protein_co	CENPB_DN/	54	33	25	69	28	46	1.044506	0.752209	0.637224	1.154594	0.608449	0.88427
protein_co	outer_dens	4	3	2	0	0	5	0.069363	0.061305	0.045701	0	0	0.086168
protein_co	Bet1_golgi_	593	570	471	458	368	450	10.76612	12.19513	11.26835	7.193381	7.505877	8.119452
protein_co	ribosomal_	13265	12333	9351	11168	7448	11162	1123.62	1231.085	1043.77	818.3715	708.7626	939.6448
protein_co	resistance_	2178	1766	1646	3633	2642	3053	31.1384	29.75337	31.01009	44.93314	42.43461	43.37853
protein_co	IMP3_U3_s	617	522	394	1678	762	886	16.1068	16.05838	13.55362	37.89476	22.34746	22.98622
protein_co	ankyrin_rep	312	257	239	309	193	264	6.316478	6.131414	6.376071	5.411802	4.389618	5.311705
protein_co	lipocalin_1	0	0	0	1	1	2	0	0	0	0.015875	0.020616	0.036474
protein_co	outer_dens	14	21	4	3	5	10	0.430415	0.760826	0.162052	0.079789	0.172694	0.30554
protein_co	dpy-19-like	110	110	76	166	108	122	1.434362	1.690308	1.305914	1.872566	1.582118	1.581013
processed_	ZNRF3_anti	3	3	5	2	5	8	0.07319	0.08625	0.160745	0.042211	0.137041	0.193969
protein_co	chromoson	3	4	1	0	0	0	0.082677	0.129907	0.036316	0	0	0
protein_co	G_protein-r	2	2	0	4	4	2	0.051275	0.060424	0	0.088715	0.115208	0.050958
protein_co	TSPY-like_6	1	2	1	0	0	0	0.017105	0.040315	0.022541	0	0	0
protein_co	family_with	104	92	42	102	55	65	1.870834	1.950279	0.995602	1.587322	1.111511	1.16205
protein_co	DNA_methy	709	607	461	993	590	802	8.245862	8.319278	7.065218	9.990842	7.708873	9.269874
protein_co	ADAMTS-like	1552	1332	1359	14	22	15	10.23218	10.34875	11.80676	0.079849	0.162948	0.098283
protein_co	family_with	351	231	322	25	22	34	1.899253	1.472973	2.295971	0.117025	0.133736	0.182837
protein_co	IMP_(inosi	4732	4166	3004	6786	4554	5430	152.4752	158.1907	127.5526	189.1609	164.8529	173.8858
protein_co	ALS2_C-ter	4	2	4	272	244	315	0.03212	0.018925	0.042326	1.889474	2.201141	2.513791
protein_co	myeloid_le	206	174	90	148	141	140	3.578033	3.561504	2.059939	2.223831	2.751347	2.416656
protein_co	protease_se	0	2	0	0	0	0	0	0.097481	0	0	0	0
protein_co	NADH_dehy	646	459	374	737	385	561	16.99795	14.23259	12.96793	16.77624	11.38083	14.67022
protein_co	chromoson	188	171	222	555	473	467	2.669771	2.861669	4.154359	6.818238	7.546167	6.590869
protein_co	GRAM_dom	90	59	64	53	25	40	1.140697	0.881225	1.068913	0.581121	0.355973	0.503845
protein_co	signal_tran	18	7	4	582	312	437	0.46644	0.213761	0.13659	13.04697	9.082959	11.2542
pseudogen	unc-51-like	4	1	4	4	0	0	0.18287	0.053875	0.240979	0.1582	0	0
pseudogen	twinfilin_1	6	2	1	0	1	2	0.30252	0.118834	0.066441	0	0.056644	0.100217
protein_co	testis-speci	53	29	24	96	40	74	1.116543	0.719954	0.666263	1.74958	0.946692	1.549319
protein_co	bolA_homo	109	126	53	181	103	176	5.265117	7.172312	3.373589	7.563505	5.589434	8.448972
protein_co	phosphodi	2647	2067	2425	713	759	660	15.8811	14.61417	19.17225	3.70066	5.115846	3.935321
protein_co	DEAD_(Asp	804	647	594	878	723	812	6.346289	6.018318	6.178528	5.995443	6.411374	6.369854
protein_co	golgin_A8_	1	4	0	3	0	0	0.027878	0.131412	0	0.072352	0	0
protein_co	protein_ph	1	0	0	0	0	5	0.041296	0	0	0	0	0.205203
protein_co	NADH_dehy	11	6	21	24	21	11	0.618207	0.397374	1.555232	1.166851	1.325896	0.614389
pseudogen	-	0	0	0	1	0	1	0	0	0	0.029171	0	0.033512
protein_co	DALR_antic	434	403	223	668	367	452	7.69213	8.417226	5.208307	10.24227	7.307553	7.961684
protein_co	zinc_finger_	32	20	26	588	363	469	0.683661	0.503533	0.73198	10.86754	8.712574	9.958026
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.03954
protein_co	zinc_finger_	344	310	391	733	727	571	2.641674	2.805366	3.956693	4.869538	6.271974	4.357793

protein_co	APC_memb	0	0	0	0	2	1	0	0	0	0	0.019273	0.008525
protein_co	zinc_finger_	0	0	0	2	0	0	0	0	0	0.023916	0	0
protein_co	ligand_dep	85	84	103	138	181	154	0.89838	1.046231	1.434541	1.261779	2.14916	1.617601
protein_co	par-6_parti	532	436	445	488	397	425	7.28144	7.032329	8.026024	5.778145	6.104431	5.781016
protein_co	zinc_finger_	5	2	1	9	19	9	0.11351	0.053506	0.029916	0.176754	0.484581	0.203056
protein_co	SH2B_adap	1313	1121	818	981	1081	1445	11.50282	11.57317	9.443383	7.434838	10.63933	12.58105
antisense	-	0	0	2	0	0	0	0	0	0.17311	0	0	0
protein_co	zinc_finger_	51	46	26	4	2	1	0.886405	0.942165	0.595484	0.060143	0.039052	0.017273
protein_co	vomeronas	3	11	5	4	0	3	0.120962	0.522669	0.265664	0.139524	0	0.120215
protein_co	KDEL_(Lys-/	940	913	934	1818	1458	1373	11.37735	13.0224	14.89687	19.03576	19.82531	16.51557
protein_co	cytochrom	0	0	0	0	1	0	0	0	0	0	0.026445	0
protein_co	plectin	46570	39972	34965	9536	15211	16781	161.6802	163.5361	159.9628	28.64046	59.32771	57.89995
protein_co	SH2_domai	1	0	0	1	0	0	0.013292	0	0	0.011499	0	0
protein_co	ring_finger_	2	2	6	0	0	8	0.045404	0.053506	0.179494	0	0	0.180494
protein_co	protease_se	1	4	1	11	9	11	0.018641	0.08787	0.024565	0.17739	0.18848	0.203787
protein_co	zinc_finger_	110	92	89	222	162	187	1.591558	1.568645	1.696893	2.778726	2.63326	2.688939
protein_co	transmemb	31	16	16	12	14	8	0.335275	0.203923	0.228031	0.112275	0.170105	0.085988
protein_co	UDP-N-acet	675	597	532	779	593	596	9.250627	9.641593	9.607576	9.235658	9.130007	8.117518
protein_co	SLIT_and_N	9	5	10	12	12	4	0.091894	0.060162	0.134548	0.105996	0.137649	0.040589
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.033342
protein_co	WD_repeat	3063	2624	2316	3200	2954	3383	36.84578	37.19732	36.71251	33.30073	39.9209	40.44384
protein_co	Gen_endon	216	185	187	1058	700	745	1.796019	1.812742	2.048961	7.610373	6.538895	6.156348
protein_co	transmemb	55	47	39	38	25	59	0.874138	0.880283	0.816802	0.522473	0.446382	0.931921
protein_co	aquaporin_	25	28	23	65	30	36	0.615021	0.811736	0.745611	1.383331	0.829125	0.880161
protein_co	transmemb	381	302	231	1039	591	781	9.627933	8.993362	7.692276	22.71363	16.77817	19.61412
protein_co	zinc_finger_	82	106	113	198	115	132	1.549308	2.360135	2.813437	3.236325	2.441017	2.478606
protein_co	potassium_	2	3	7	0	9	3	0.068844	0.121693	0.317518	0	0.348039	0.102628
protein_co	shisa_homo	29	37	18	1	6	1	0.778939	1.171155	0.637108	0.023236	0.181053	0.026694
protein_co	olfactory_r	0	0	0	0	0	1	0	0	0	0	0	0.049636
protein_co	calmodulin	0	0	0	1	0	0	0	0	0	0.052282	0	0
protein_co	zinc_finger_	147	94	92	271	143	166	7.179268	5.410006	5.920869	11.44973	7.845993	8.057133
protein_co	pleckstrin_	21	12	18	11	23	11	0.301372	0.202942	0.340401	0.136565	0.370818	0.156887
protein_co	zinc_finger_	13	8	8	14	18	6	0.284629	0.206411	0.230813	0.265171	0.442749	0.130556
protein_co	5-hydroxyt	7	4	3	0	0	0	0.231907	0.156165	0.13097	0	0	0
protein_co	family_with	428	339	297	410	364	388	10.2343	9.552593	9.358489	8.481279	9.778335	9.220529
protein_co	DnaJ_(Hsp4	18	4	18	0	1	6	0.36261	0.094958	0.477831	0	0.022632	0.120123
protein_co	differential	38	24	21	3	20	40	0.962564	0.716414	0.700971	0.06574	0.569148	1.006967
protein_co	BEN_domai	86	71	67	374	429	396	0.685269	0.666696	0.703513	2.578084	3.840332	3.135937
lincRNA	-	0	3	2	4	0	7	0	0.168464	0.125586	0.164893	0	0.331502
protein_co	5'-nucleoti	203	144	135	501	417	498	3.446768	2.881281	3.02054	7.358965	7.954284	8.403399
pseudogen	ribosomal_	11	6	1	19	3	12	0.740904	0.476242	0.088757	1.107098	0.227007	0.803268
pseudogen	-	4	0	2	4	2	2	0.12842	0	0.084613	0.111095	0.072136	0.063813
lincRNA	long_interg	28	17	23	31	34	29	2.63763	1.887173	2.855081	2.526274	3.598187	2.71496
protein_co	glycine_del	56	41	57	524	441	446	0.787018	0.679028	1.055616	6.370753	6.962803	6.229325

protein_co	cytochrom	336	300	238	437	332	635	24.0706	25.32655	22.46774	27.08271	26.7199	45.20964
pseudogen	H3_histone	14	7	8	24	15	14	1.803343	1.062565	1.357923	2.674389	2.170654	1.792206
protein_co	minichrom	16	10	12	22	13	18	0.16622	0.122425	0.164278	0.197719	0.151724	0.185842
pseudogen	-	18	11	16	45	12	30	1.477423	1.063977	1.730562	3.195272	1.106529	2.447165
protein_co	prolyl_4-hy	213	188	121	387	307	365	2.133667	2.21928	1.597229	3.353676	3.454892	3.633705
protein_co	deltex_hon	436	363	329	254	221	218	7.215465	7.07932	7.17478	3.636424	4.10884	3.585453
protein_co	kelch-like_f	55	29	58	33	66	57	1.221886	0.75923	1.697973	0.634227	1.647256	1.258498
protein_co	ameloblast	0	0	0	13	8	3	0	0	0	0.296951	0.23731	0.078724
protein_co	cortexin_1	1794	1380	936	1926	1402	1449	74.66678	67.6848	51.33525	69.34646	65.55443	59.93534
protein_co	solute_carr	281	240	243	291	228	218	7.9172	7.96863	9.022074	7.092859	7.216876	6.104238
protein_co	carbonic_a	7	6	11	809	672	757	0.097216	0.098197	0.201311	9.719652	10.48474	10.44828
protein_co	EPM2A_(laf	784	700	767	730	551	551	5.579478	5.870602	7.192961	4.494314	4.405327	3.897075
protein_co	v-erb-a_ery	0	0	0	71	111	70	0	0	0	0.268029	0.544166	0.303576
protein_co	v-maf_musc	379	277	259	55	56	58	3.142957	2.706986	2.830309	0.394571	0.521719	0.47801
protein_co	catenin_be	2036	1695	1457	1582	1234	1388	35.92929	35.24907	33.8817	24.15129	24.46443	24.34277
protein_co	prosaposin	0	4	6	0	0	0	0	0.053334	0.089459	0	0	0
protein_co	otospiralin	3	5	4	0	0	0	0.247388	0.485886	0.434662	0	0	0
protein_co	GTP_bindir	1023	747	554	1770	1177	1401	26.8644	23.11688	19.17106	40.21035	34.72379	36.56363
protein_co	endoplasm	78	81	90	22	79	55	1.025937	1.255505	1.559924	0.250329	1.167353	0.71895
protein_co	G_protein-r	11	9	12	20	21	11	0.258938	0.249662	0.372236	0.407282	0.555355	0.257339
pseudogen	actin_gamr	5	3	2	7	12	1	0.23446	0.165778	0.123584	0.283961	0.632162	0.046602
protein_co	Uncharacte	0	0	1	2	10	6	0	0	0.033268	0.04368	0.283624	0.150541
pseudogen	-	9	4	3	21	22	14	0.153205	0.080241	0.067296	0.309253	0.42073	0.236848
pseudogen	armadillo_	1	0	0	1	0	1	0.061919	0	0	0.053566	0	0.061537
protein_co	cysteine-se	63	49	80	55	52	59	0.282939	0.259331	0.473453	0.213687	0.262364	0.263338
protein_co	zinc_finger_	35	18	32	89	54	48	0.521953	0.316332	0.628852	1.148198	0.904704	0.711401
protein_co	poly_(ADP-	96	86	50	60	52	47	1.453342	1.534271	0.997473	0.785798	0.8844	0.707138
protein_co	dynactin_a	0	0	0	11	9	8	0	0	0	0.248539	0.264077	0.207653
protein_co	suppressor_	550	505	569	1067	923	866	6.483533	7.01532	8.838857	10.88119	12.22362	10.14557
protein_co	NOP2/Sun_	103	113	115	142	84	97	1.657927	2.143452	2.439276	1.977332	1.518996	1.551707
protein_co	potassium_	26246	22418	25646	3957	4088	3692	223.6063	225.0737	287.9223	29.16419	39.12738	31.26023
protein_co	dihydrofola	254	230	211	118	118	102	3.330117	3.553536	3.645382	1.338353	1.738028	1.329032
protein_co	ribonuclea	46	40	38	462	297	334	0.798716	0.818468	0.869467	6.939683	5.793489	5.763559
protein_co	glutamate_	4704	3464	2838	3947	2263	2646	126.5419	109.8125	100.6038	91.8538	68.39126	70.74023
protein_co	chromoson	2	0	0	0	0	0	0.035651	0	0	0	0	0
pseudogen	glutamate-a	3	0	2	0	0	1	0.141553	0	0.124355	0	0	0.046893
protein_co	thrombom	0	0	0	137	92	70	0	0	0	1.527002	1.331658	0.896321
protein_co	glycoprotei	0	1	0	0	0	2	0	0.017654	0	0	0	0.029776
protein_co	chromoson	2	1	3	0	2	4	0.091752	0.054062	0.18136	0	0.103078	0.182371
protein_co	cytochrom	1703	1493	1146	2800	1954	2692	71.10293	73.45811	63.05104	101.1332	91.65295	111.7011
protein_co	syntaxin_1	3	0	5	6	5	6	0.137153	0	0.301223	0.2373	0.256804	0.272612
protein_co	family_with	51	49	48	34	20	39	1.170347	1.325097	1.451512	0.674973	0.515613	0.889444
protein_co	family_with	667	493	476	562	473	537	7.503537	6.535731	7.05638	5.469398	5.977924	6.003771
protein_co	zinc_finger	177	145	120	718	749	658	2.027381	1.957209	1.811249	7.114585	9.638135	7.490274

protein_co	carboxypep	1	2	0	0	0	0	0.017484	0.041207	0	0	0	0
protein_co	copine_VII	81	54	46	229	144	281	1.613933	1.267948	1.207795	3.94729	3.223384	5.564376
protein_co	chromoson	0	2	0	14	12	28	0	0.217758	0	1.118996	1.245569	2.571018
protein_co	glyceropho	0	2	0	0	0	0	0	0.04926	0	0	0	0
protein_co	mannose_p	651	579	506	474	349	387	11.2409	11.78164	11.51344	7.080457	6.77009	6.641108
antisense	ADORA2A_	11	1	2	3	4	6	0.226772	0.024294	0.054333	0.053503	0.092642	0.12293
protein_co	H1_histone	0	1	0	0	0	1	0	0.05847	0	0	0	0.04931
protein_co	tripartite_r	4	1	0	0	4	7	0.054649	0.0161	0	0	0.061394	0.095045
processed_	5-oxoprolir	104	65	64	62	52	56	1.365203	1.005505	1.107079	0.704074	0.76686	0.73057
protein_co	transmemb	18	7	3	22	15	15	0.852359	0.390621	0.1872	0.901231	0.797977	0.705913
protein_co	transmemb	9	1	2	11	9	19	0.199945	0.02618	0.058551	0.211409	0.224626	0.419499
protein_co	ring_finger_	0	1	0	0	0	0	0	0.04995	0	0	0	0
protein_co	EF-hand_ca	45	43	40	22	37	22	0.60604	0.68244	0.709878	0.256315	0.559809	0.294457
protein_co	musculin	2	7	4	3	0	5	0.052339	0.215874	0.13794	0.067917	0	0.13004
protein_co	apolipopro	93	72	98	109	82	90	1.059731	0.966835	1.471546	1.07449	1.049726	1.019213
protein_co	family_witl	0	4	7	327	290	444	0	0.116178	0.227348	6.97218	8.029803	10.87553
protein_co	exosome_c	159	125	106	603	285	426	7.903867	7.322503	6.943575	25.93121	15.91609	21.04562
protein_co	dpy-19-like	796	660	755	775	628	617	7.00599	6.845536	8.756655	5.90094	6.209622	5.396986
protein_co	TAF7_RNA_	1086	1024	894	1727	1016	1161	25.28317	28.09368	27.42673	34.78219	26.57323	26.86232
protein_co	zinc_finger_	38	31	47	59	121	101	0.569097	0.547106	0.927546	0.764395	2.035809	1.503259
protein_co	forkhead_b	4	0	0	0	0	0	0.061363	0	0	0	0	0
protein_co	phosphorib	1008	862	740	2711	2491	2831	9.935677	10.0127	9.611772	23.11689	27.58416	27.73234
protein_co	hydroxypyr	151	99	94	145	107	170	3.678827	2.842331	3.017832	3.056071	2.928635	4.116148
protein_co	chromoson	1439	1282	864	1423	793	1095	17.60621	18.48419	13.93008	15.06167	10.90002	13.31463
protein_co	lectin_gala	0	1	5	1	0	0	0	0.11727	0.65567	0.086088	0	0
protein_co	zinc_finger_	113	95	61	346	326	426	2.543509	2.519913	1.809337	6.737424	8.243686	9.529586
lincRNA	long_interg	4	6	5	3	5	2	0.072696	0.128502	0.119745	0.047167	0.102087	0.036124
protein_co	cyclin_G_as	2257	1853	1498	2341	2392	2872	26.89956	26.02532	23.52665	24.1367	32.02755	34.01791
protein_co	zinc_finger_	1404	1068	959	799	738	890	13.70881	12.28884	12.33917	6.749046	8.095394	8.63639
protein_co	Tu_translat	4672	3562	2707	8623	5596	6685	119.4304	107.3033	91.18745	190.6924	160.7085	169.8334
protein_co	RMI1_RecC	138	116	98	554	442	402	2.138717	2.118553	2.001406	7.427574	7.695654	6.1917
protein_co	CTS_telome	106	90	84	300	277	263	1.169845	1.170501	1.221621	2.864222	3.434403	2.884614
pseudogen	-	14	7	18	11	6	6	0.290429	0.171126	0.492061	0.197409	0.139834	0.123701
protein_co	F-box_prot	342	260	236	345	310	267	5.226853	4.682682	4.752926	4.561381	5.322614	4.055413
lincRNA	long_interg	7	21	5	5	4	6	0.177996	0.629271	0.167539	0.109988	0.114267	0.151626
protein_co	selenoprot	2076	1863	1319	3975	2795	3852	43.90951	46.43561	36.76299	72.73298	66.41438	80.97056
protein_co	eukaryotic_	2376	1813	1351	3576	2309	3224	94.79111	85.23659	71.02501	123.4189	103.489	127.828
protein_co	Morf4_fam	859	748	696	1377	921	1078	21.3805	21.93983	22.82804	29.64978	25.75332	26.6657
protein_co	sorting_nex	1369	1118	1232	867	866	756	13.48395	12.97665	15.99039	7.38747	9.582538	7.400227
protein_co	exonucleas	2	0	1	0	0	0	0.03599	0	0.023713	0	0	0
protein_co	aurora_kina	316	202	166	2297	1637	2123	13.3942	10.08993	9.271981	84.22745	77.95202	89.43125
protein_co	chromoson	33	43	10	32	25	11	0.621064	0.95367	0.248003	0.520997	0.528581	0.205743
protein_co	Morf4_fam	7452	6017	5181	9721	7965	9386	192.5409	183.205	176.4	217.2822	231.1985	241.0129
protein_co	chromoson	269	220	244	481	369	336	5.408708	5.212799	6.46496	8.366606	8.335212	6.714136

protein_co	kelch_dom	0	0	0	5	2	10	0	0	0	0.045301	0.023532	0.104083
protein_co	transmemb	165	112	93	174	144	198	3.704522	2.963285	2.751478	3.379563	3.632117	4.417974
pseudogen	-	0	0	0	0	4	0	0	0	0	0	0.305789	0
protein_co	-	5	6	1	9	9	0	0.212103	0.299941	0.0559	0.330281	0.428913	0
protein_co	RRS1_ribos	327	232	214	2067	1774	2209	10.15945	8.494104	8.761351	55.55536	61.91918	68.20683
protein_co	exocyst_co	38	28	5	10	9	16	0.801497	0.695959	0.138971	0.182466	0.21326	0.335388
protein_co	tripartite_r	6	6	6	1419	944	1111	0.193805	0.228387	0.255387	39.6514	34.25581	35.66456
protein_co	regulator_c	2404	2008	1800	4458	5860	6362	31.14024	30.65196	30.7252	49.95633	85.27743	81.90129
protein_co	immunoglc	2	2	7	0	3	0	0.024716	0.029126	0.113992	0	0.04165	0
protein_co	chromoson	7	2	3	0	2	1	0.228757	0.077022	0.129191	0	0.073427	0.032478
protein_co	ZFP42_zinc	0	0	0	28	33	28	0	0	0	0.48373	0.740364	0.555712
protein_co	Uncharacte	0	0	0	0	0	1	0	0	0	0	0	0.041461
protein_co	coiled-coil_	5	8	2	2	2	2	0.109022	0.205561	0.057466	0.037726	0.048992	0.043339
processed_	chromoson	1	0	0	0	3	0	0.016833	0	0	0	0.056734	0
protein_co	family_witl	1	3	0	3	0	0	0.015498	0.05479	0	0.040222	0	0
protein_co	dolichyl-ph	488	389	305	394	313	443	49.97138	46.94164	41.15629	34.90284	36.00766	45.08322
protein_co	chromoson	0	0	0	2	0	4	0	0	0	0.043827	0	0.100697
protein_co	cytochrom	1827	1624	1135	3350	2069	2906	52.7965	55.30441	43.22125	83.748	67.17013	83.45875
protein_co	period_circ	2652	2173	1632	681	700	876	29.82781	28.80147	24.18816	6.6261	8.844942	9.79178
protein_co	5-hydroxyt	0	0	0	11	24	24	0	0	0	0.163887	0.464353	0.41078
pseudogen	-	0	2	2	5	0	1	0	0.311939	0.348816	0.572486	0	0.131535
protein_co	transmemb	329	310	334	352	405	371	2.804313	3.113862	3.75156	2.595591	3.87824	3.142781
protein_co	hairy_and_	15	12	21	26	8	9	0.474382	0.447224	0.875167	0.711333	0.284234	0.282871
protein_co	phenylalan	1296	1117	893	3408	1951	2494	33.35514	33.87802	30.28615	75.87879	56.41104	63.79166
protein_co	SPT2_Supp	509	444	479	483	466	461	4.683171	4.814069	5.807545	3.844434	4.816784	4.215342
pseudogen	-	0	0	0	3	1	1	0	0	0	0.378503	0.163846	0.144942
protein_co	chromoson	6	3	0	0	4	0	0.113486	0.066868	0	0	0.084996	0
protein_co	sterile_alpl	3001	2426	2296	2645	2641	2867	35.15732	33.49251	35.44512	26.8064	34.75899	33.38006
lincRNA	long_interg	0	0	2	0	0	0	0	0	0.047249	0	0	0
antisense	MTUS2_ant	0	0	0	0	1	0	0	0	0	0	0.05339	0
protein_co	arachidona	1	0	3	5	6	5	0.015747	0	0.062252	0.068113	0.106144	0.078248
protein_co	enhancer_c	809	704	595	1410	1234	1310	11.38168	11.67179	11.03087	17.1609	19.50393	18.31634
protein_co	T_cell_activ	348	355	352	592	462	515	4.996872	6.006955	6.66034	7.353662	7.452637	7.349128
pseudogen	-	0	0	0	2	0	0	0	0	0	0.123614	0	0
protein_co	fucosidase_	111	90	60	179	105	127	2.870762	2.742988	2.044845	4.004887	3.050792	3.264282
protein_co	peroxisom	0	0	0	0	1	3	0	0	0	0	0.028214	0.074878
protein_co	gametogen	29	27	10	8	11	11	0.685703	0.752331	0.311582	0.163641	0.2922	0.258488
protein_co	transmemb	0	0	2	145	76	99	0	0	0.07542	3.589644	2.443335	2.815563
protein_co	zinc_finger_	1808	1566	1670	2899	3042	3003	18.73871	19.1267	22.80828	25.99276	35.42007	30.93187
protein_co	calreticulin	34287	29341	24144	29253	24577	31065	953.8559	961.9119	885.1102	704.0228	768.1238	858.8836
lincRNA	long_interg	8	20	12	0	2	4	0.270452	0.796778	0.534585	0	0.075959	0.134391
protein_co	melanoma_	9299	7536	6869	5748	4628	4417	90.86347	86.77629	88.44666	48.58843	50.80372	42.89337
protein_co	Protein_LO	41	30	27	26	38	38	0.404733	0.34899	0.351223	0.222035	0.421422	0.372801
protein_co	low_densit	587	549	501	581	526	438	8.182297	9.018131	9.202581	7.006099	8.237054	6.067655

protein_co	cadherin_4	141	107	123	845	699	747	1.146472	1.025263	1.317906	5.943799	6.385143	6.036353
protein_co	Uncharacte	0	0	2	0	0	0	0	0	0.069763	0	0	0
protein_co	single-pass_	34	29	16	7	1	4	0.85551	0.859907	0.530519	0.152373	0.028268	0.100027
protein_co	RAD23_hor	1378	1251	1032	2840	1678	1997	41.78275	44.70049	41.23465	74.49536	57.15956	60.1777
protein_co	chromoson	0	0	1	0	0	0	0	0	0.009904	0	0	0
protein_co	growth_arr	2007	1473	1163	2739	1868	2419	143.0048	123.6839	109.1988	168.8334	149.5303	171.2966
protein_co	DAN_doma	0	0	0	1	2	1	0	0	0	0.024518	0.063679	0.028166
protein_co	transmemb	109	115	85	2	6	1	2.252369	2.800386	2.314551	0.035752	0.139288	0.020536
protein_co	chromoson	41	60	34	142	151	193	0.672631	1.159983	0.735033	2.015322	2.783038	3.146734
protein_co	protein_tyr	2164	1721	2274	3429	3545	2937	18.77796	17.59864	26.00257	25.74077	34.55862	25.32822
pseudogen	centaurin_	16	6	13	11	7	4	0.340868	0.150634	0.364959	0.202732	0.167538	0.084691
protein_co	NOP2/Sun_	8	6	4	160	160	187	0.114529	0.101224	0.075461	1.981564	2.573323	2.660581
protein_co	zinc_finger_	0	0	3	4	7	2	0	0	0.079037	0.069183	0.157225	0.039739
protein_co	family_with	77	61	79	35	73	80	1.383726	1.291803	1.870774	0.544115	1.473775	1.428759
protein_co	WSC_doma	2	2	4	91	69	72	0.017995	0.021206	0.047426	0.708311	0.697457	0.643816
protein_co	RAB39A_m	1	0	4	82	99	69	0.02893	0	0.152488	2.052191	3.21755	1.983808
protein_co	CDC-like_ki	950	823	704	1142	859	931	13.28068	13.55825	12.96893	13.81102	13.49084	12.93469
pseudogen	-	0	0	0	0	3	0	0	0	0	0	0.166911	0
protein_co	major_hist	0	0	0	13	8	10	0	0	0	0.128205	0.102456	0.113295
protein_co	GATA_bind	84	46	50	1775	1857	2371	1.320773	0.852342	1.035986	24.14406	32.80273	37.05017
protein_co	AT_rich_int	55	63	37	3420	2704	3202	0.68175	0.920259	0.604365	36.67344	37.65462	39.44514
pseudogen	high_mobil	6	6	2	6	4	3	0.165183	0.194658	0.072557	0.142898	0.123715	0.082081
protein_co	transmemb	0	2	0	2	2	5	0	0.171395	0	0.125821	0.163395	0.36136
protein_co	phosphofur	1503	1287	844	1746	1273	1704	12.56638	12.68051	9.298833	12.62869	11.95718	14.15893
protein_co	ELMO/CED-	410	398	452	735	626	613	4.923068	5.631734	7.151963	7.634882	8.444528	7.315131
protein_co	early_grow	30	30	27	0	2	5	0.366289	0.431649	0.434412	0	0.027434	0.060671
protein_co	chromoson	4	18	7	7	5	6	0.063536	0.336927	0.146518	0.096187	0.089223	0.094715
protein_co	glypican_5	5	0	0	165	96	182	0.091625	0	0	2.615721	1.976354	3.314558
protein_co	von_Willeb	526	510	301	1693	1236	1480	6.173124	7.053368	4.65501	17.18855	16.29622	17.26198
lincRNA	long_interg	136	80	69	129	112	123	1.531258	1.061467	1.023749	1.256499	1.416696	1.376335
protein_co	gem_(nucle	416	338	328	1454	982	1112	4.657106	4.459093	4.83873	14.08154	12.35047	12.37192
antisense	-	0	0	0	2	0	0	0	0	0	0.067154	0	0
protein_co	four_jointe	1137	816	797	2640	1917	2234	22.41859	18.96029	20.70813	45.03133	42.46381	43.77646
antisense	-	0	0	2	0	0	0	0	0	0.077991	0	0	0
protein_co	kelch-like_f	73	37	79	66	65	42	1.61365	0.963819	2.301169	1.262099	1.614169	0.922668
protein_co	makorin_ri	0	0	0	36	10	13	0	0	0	0.608174	0.219387	0.252299
protein_co	zinc_finger_	257	251	242	400	359	371	3.533066	4.0663	4.383982	4.757092	5.544496	5.068765
pseudogen	eukaryotic_	0	0	1	0	0	0	0	0	0.061465	0	0	0
pseudogen	-	0	2	0	3	0	2	0	0.282938	0	0.311557	0	0.238612
protein_co	chromoson	48	35	32	56	45	37	0.726463	0.624234	0.6382	0.733201	0.765128	0.556524
lincRNA	-	90	105	67	213	139	188	1.66423	2.288059	1.632602	3.407323	2.887584	3.454922
protein_co	SHANK-assc	1002	725	541	1395	935	1247	30.05489	25.62669	21.38353	36.198	31.50707	37.17265
protein_co	ladybird_h	7	3	7	20	12	15	0.255225	0.1289	0.336324	0.630839	0.491537	0.543534
protein_co	dynein_hea	174	164	136	151	159	166	0.619818	0.688439	0.638394	0.465323	0.636299	0.587669

protein_co	SLIT_and_N	2	1	0	71	71	41	0.012377	0.007293	0	0.380096	0.493605	0.252154
protein_co	5-hydroxyt	1	0	0	9	8	9	0.018674	0	0	0.145393	0.167833	0.167029
protein_co	GRIP_and_(	579	431	473	490	513	531	7.388006	6.480866	7.95325	5.408885	7.353855	6.733685
protein_co	leucine-rich	6	0	0	5	7	3	0.212614	0	0	0.153276	0.278669	0.105651
protein_co	ring_finger_	2	3	0	3	13	2	0.124129	0.219418	0	0.161075	0.906433	0.123362
protein_co	class_II_ma	11	2	5	10	11	17	0.061703	0.013221	0.036959	0.048526	0.069319	0.09477
protein_co	zinc_finger_	456	383	243	468	412	346	6.842714	6.772818	4.805124	6.075365	6.9456	5.159995
protein_co	phospholip	9	4	3	0	0	0	0.186121	0.097481	0.081754	0	0	0
protein_co	glutamate_	0	2	0	10	1	15	0	0.030756	0	0.112889	0.01466	0.194531
protein_co	CDC42_effe	1477	1171	960	739	628	770	23.89788	22.32764	20.46844	10.34395	11.4153	12.38167
pseudogen	diacylglyce	7	1	3	17	18	15	0.133497	0.022474	0.075393	0.280469	0.385651	0.284298
protein_co	zinc_finger_	71	77	64	151	120	149	0.989161	1.264172	1.174961	1.819904	1.878187	2.063025
protein_co	laccase_(m	568	483	583	378	302	267	7.055487	7.070219	9.542936	4.06194	4.214389	3.296094
protein_co	MAF1_hom	1003	714	601	1672	1164	1673	30.27356	25.39615	23.90407	43.65779	39.46976	50.18432
protein_co	tubulin_po	0	2	0	0	0	0	0	0.07357	0	0	0	0
protein_co	ADP-ribosy	0	0	0	1	0	1	0	0	0	0.035613	0	0.040913
protein_co	KIAA1875	16	8	1	27	11	20	0.118985	0.070108	0.0098	0.1737	0.0919	0.147813
protein_co	PC-esterase	4	4	5	20	26	40	0.090964	0.107195	0.149835	0.393461	0.66425	0.904021
processed_	-	57	28	23	91	54	69	1.222705	0.707802	0.650144	1.688695	1.301337	1.470976
protein_co	apolipopro	75	58	44	25	20	20	2.15324	1.962304	1.664634	0.620918	0.645075	0.570651
protein_co	pipecolic_a	0	1	1	3	3	6	0	0.025887	0.028947	0.057011	0.074036	0.130989
pseudogen	ATPase_clas	1	0	1	0	0	1	0.013362	0	0.017608	0	0	0.01328
protein_co	atonal_hon	0	0	4	1	0	1	0	0	0.187788	0.03082	0	0.035406
protein_co	cadherin_5	2	3	1	371	223	266	0.025718	0.045461	0.016945	4.12713	3.221552	3.399402
protein_co	leucine_ric	0	0	0	199	108	150	0	0	0	5.37381	3.787382	4.653365
protein_co	family_with	26	38	26	0	0	0	0.417111	0.718404	0.54965	0	0	0
antisense	PCBP1_ant	301	265	189	302	237	333	6.501526	6.745307	5.379543	5.643113	5.751037	7.148298
protein_co	myeloid-ass	2475	2238	1639	4883	3490	4163	41.12648	43.82415	35.88889	70.19336	65.15096	68.74836
protein_co	maestro_he	185	173	141	207	219	259	1.67937	1.850665	1.686664	1.625578	2.233406	2.336598
protein_co	SERTA_dom	664	542	580	1026	871	699	6.334983	6.093737	7.291891	8.468134	9.33565	6.627721
protein_co	RNA_bindi	2654	2104	1939	2340	2112	2106	21.2887	19.88845	20.49561	16.23779	19.03229	16.78867
protein_co	A_kinase_(P	3	5	12	90	104	59	0.061062	0.11993	0.321861	1.584737	2.378122	1.193475
protein_co	NTPase_KA	4	31	10	2	12	7	0.045181	0.412635	0.148844	0.019543	0.152275	0.078579
protein_co	GIPC_PDZ_	10	9	7	4	5	2	0.122125	0.129525	0.112651	0.04226	0.0686	0.024274
antisense	-	73	49	24	44	32	39	1.52815	1.208778	0.662048	0.796818	0.752562	0.811367
protein_co	Cbp/p300-i	48	26	44	72	34	45	1.969897	1.257427	2.379523	2.556218	1.567582	1.835374
protein_co	ATP-bindin	17	22	26	2	9	2	0.052374	0.079873	0.105554	0.00533	0.03115	0.006124
protein_co	tigger_tran	213	129	118	295	221	209	4.675138	3.336657	3.412963	5.601442	5.449493	4.559012
protein_co	pyridoxal-d	1778	1469	1590	1972	1700	1605	19.4965	18.98251	22.97507	18.7066	20.94222	17.49079
pseudogen	polyhomeo	40	22	33	27	31	33	0.596015	0.386302	0.647956	0.348036	0.518929	0.488675
protein_co	chromoson	1	1	3	6	3	1	0.055378	0.065259	0.218922	0.287441	0.18664	0.055036
protein_co	zinc_finger_	514	398	412	255	315	247	4.78489	4.366154	5.054066	2.053582	3.29434	2.285154
protein_co	R3H_doma	511	457	356	356	246	324	6.187751	6.521316	5.680633	3.72928	3.346541	3.89912
protein_co	UDP-GlcNA	0	0	0	0	2	0	0	0	0	0	0.053437	0

protein_co	neurexin_1	0	0	2	22	20	27	0	0	0.018412	0.132961	0.15697	0.187461
protein_co	selenophos	695	517	482	976	793	989	14.42336	12.64385	13.18146	17.52243	18.48859	20.398
protein_co	G_protein-	17	2	4	6	8	12	0.449324	0.062294	0.139318	0.137191	0.237547	0.315211
protein_co	zinc_finger_	206	131	107	199	161	201	5.396262	4.043935	3.693553	4.50964	4.738062	5.232768
protein_co	zinc_finger_	0	0	0	1	0	0	0	0	0	0.012551	0	0
protein_co	chromoson	651	633	463	1502	742	1016	9.432016	10.80773	8.839737	18.82593	12.07749	14.62941
processed_	long_interg	3	5	2	5	1	3	0.092716	0.182101	0.081452	0.13368	0.03472	0.092144
protein_co	Bardet-Biec	310	226	249	306	230	265	4.565148	3.92201	4.832005	3.898321	3.805135	3.878365
protein_co	FLT3-intera	384	295	259	644	452	540	4.338314	3.927525	3.855888	6.294173	5.7369	6.063079
protein_co	poly-U_bin	2199	1713	1474	5258	3330	4267	48.26586	44.3077	42.63312	99.83858	82.11227	93.07801
protein_co	scavenger_	302	323	180	17	35	28	3.299934	4.159182	2.591825	0.160698	0.429651	0.304065
protein_co	dCTP_pyro	392	341	227	1359	809	1089	16.98271	17.40934	12.9593	50.93348	39.37481	46.88764
protein_co	zinc_finger_	343	241	202	395	219	260	7.658693	6.341393	5.943561	7.629932	5.493558	5.769571
pseudogen	protein_ph	22	12	17	19	14	30	2.617308	1.682366	2.665114	1.955459	1.871152	3.547015
pseudogen	-	24	28	19	44	45	20	0.358517	0.492905	0.374013	0.568609	0.755196	0.296919
protein_co	cysteine-ric	97	99	83	175	130	132	1.156333	1.390765	1.30384	1.804731	1.74102	1.563849
protein_co	teashirt_zir	1320	1119	1109	90	94	82	9.870355	9.860433	10.92761	0.582189	0.789652	0.609372
protein_co	phosphoser	65	52	52	99	51	50	0.97263	0.916948	1.025351	1.281541	0.857341	0.743556
protein_co	suppressor_	385	358	453	852	682	591	3.00668	3.294705	4.661863	5.75611	5.983563	4.586946
protein_co	zinc_bindir	997	804	840	256	172	162	6.826458	6.487291	7.579043	1.516363	1.323055	1.102364
pseudogen	-	7	8	11	9	10	14	0.324223	0.43666	0.671388	0.360621	0.520349	0.644442
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.561094	0
protein_co	zinc_finger_	162	144	126	758	661	733	2.651961	2.777932	2.71805	10.73456	12.15633	11.9252
protein_co	chromoson	1	1	2	2	0	0	0.020544	0.024209	0.054143	0.035544	0	0
protein_co	NK2_home	2	0	0	2	0	0	0.116868	0	0	0.101101	0	0
protein_co	transmemb	1	2	0	0	3	0	0.044228	0.10424	0	0	0.149062	0
protein_co	chromoson	0	1	0	7	0	3	0	0.033796	0	0.173669	0	0.085505
protein_co	ankyrin_rep	0	0	0	17	41	40	0	0	0	0.19267	0.603443	0.520802
protein_co	transmemb	6	7	5	20	14	8	0.103772	0.14267	0.113955	0.299241	0.272023	0.137508
protein_co	septin_1	4	0	1	20	7	11	0.077343	0	0.02548	0.334543	0.152057	0.211379
protein_co	tRNA_selen	302	313	186	619	530	581	7.837343	9.572235	6.36077	13.89682	15.45208	14.98469
protein_co	exocyst_co	1443	1179	912	1080	848	1040	13.29051	12.79665	11.06891	8.605222	8.774457	9.519592
pseudogen	-	0	0	3	0	0	0	0	0	0.254301	0	0	0
protein_co	tudor_dom	3	0	3	1	0	1	0.017871	0	0.02355	0.005153	0	0.00592
protein_co	chromoson	0	2	2	0	0	0	0	0.040763	0.045582	0	0	0
protein_co	casein_kina	0	0	1	0	0	0	0	0	0.028996	0	0	0
antisense	ACTA2_anti	11	9	9	15	18	8	0.240442	0.231829	0.259236	0.283643	0.442018	0.173787
pseudogen	high_mobil	0	0	1	0	1	4	0	0	0.304643	0	0.25972	0.919023
pseudogen	-	0	0	1	0	0	0	0	0	0.087753	0	0	0
protein_co	Ly6/neurot	510	422	294	303	367	403	5.737337	5.59448	4.358352	2.948803	4.638262	4.505623
protein_co	tyrosine_hy	17	12	4	0	0	0	0.471203	0.391965	0.146101	0	0	0
pseudogen	-	1	7	2	3	8	2	0.013958	0.115137	0.036785	0.036224	0.125444	0.027743
protein_co	mediator_c	649	552	567	1344	937	821	4.303445	4.31338	4.954381	7.709635	6.980077	5.410338
protein_co	fumarylace	636	480	367	944	697	826	17.14382	15.24751	13.03621	22.01332	21.10729	22.12791

pseudogen	high_mobil	8	6	7	6	6	5	0.716629	0.633378	0.826299	0.464964	0.603816	0.445127
protein_co	chromoson	81	67	50	647	604	589	1.263099	1.231216	1.027442	8.728098	10.58128	9.128034
protein_co	regulator_c	999	743	614	2669	2030	2566	18.59636	16.2989	15.06141	42.98076	42.45292	47.47105
protein_co	myosin_ligl	3	0	0	5	7	6	0.232878	0	0	0.335769	0.610457	0.46288
protein_co	coagulation	1	0	2	19	6	6	0.02617	0	0.06897	0.430143	0.176399	0.156048
protein_co	family_witl	0	0	0	3	0	0	0	0	0	0.076502	0	0
pseudogen	-	0	1	0	0	0	1	0	0.125782	0	0	0	0.106077
protein_co	protein_kir	528	415	476	966	587	723	15.10148	13.98752	17.94021	23.90154	18.86135	20.55103
pseudogen	hect_doma	644	578	539	303	284	315	7.77869	8.227266	8.579149	3.166112	3.85379	3.781297
protein_co	zinc_and_ri	45	34	27	266	185	185	0.688539	0.613059	0.544396	3.520956	3.180071	2.813179
protein_co	retinal_pigi	6	0	3	2	3	2	0.218313	0	0.143842	0.062954	0.122631	0.072322
protein_co	solute_carr	2	0	2	2	2	2	0.025588	0	0.033718	0.022136	0.028746	0.02543
protein_co	zinc_finger_	70	51	59	154	110	78	1.374071	1.179746	1.526153	2.61514	2.425788	1.521652
protein_co	FYVE_RhoG	856	762	783	566	566	562	4.879144	5.118373	5.881207	2.790932	3.624394	3.183581
protein_co	G_protein-(	0	0	0	1	1	2	0	0	0	0.015836	0.020566	0.036386
lincRNA	-	3	6	3	0	2	4	0.169683	0.399921	0.2236	0	0.127085	0.224846
protein_co	phospholip	0	0	0	1117	820	757	0	0	0	18.07681	17.2333	14.07379
protein_co	ornithine_c	1759	1547	1384	1754	1474	1970	13.11225	13.58967	13.5951	11.31108	12.34406	14.59444
protein_co	patatin-like	0	0	4	1	0	0	0	0	0.112612	0.018482	0	0
protein_co	ALX_homec	43	51	30	44	22	27	1.575407	2.20192	1.448373	1.394569	0.905516	0.9831
protein_co	coiled-coil_	241	186	212	690	428	444	6.128136	5.573544	7.103658	15.17831	12.22656	11.22029
protein_co	chromoson	33	24	24	40	40	21	0.403663	0.345958	0.386857	0.42328	0.549685	0.25529
protein_co	frizzled_fan	1694	1206	1152	2076	1083	1085	45.22544	37.94231	40.52814	47.94681	32.48231	28.78782
pseudogen	-	1	2	1	0	0	0	0.127877	0.30139	0.16851	0	0	0
protein_co	tigger_tran	55	39	54	219	171	143	1.397866	1.168085	1.808554	4.815151	4.882564	3.612006
protein_co	coiled-coil_	0	0	1	0	2	0	0	0	0.015353	0	0.026178	0
protein_co	hematopoi	191	184	174	42	23	27	3.731266	4.23592	4.479266	0.709799	0.504777	0.524199
protein_co	chromoson	269	220	202	84	97	108	2.398708	2.311824	2.37362	0.647989	0.97173	0.957102
protein_co	zinc_finger_	1189	922	1155	1109	1348	1324	7.199685	6.579147	9.216126	5.809332	9.170026	7.967632
protein_co	p21_protei	1552	1286	1492	2792	2509	2239	13.38401	13.069	16.95501	20.82921	24.30772	19.18926
protein_co	coiled-coil_	111	89	109	236	209	229	1.883478	1.77965	2.437243	3.464276	3.984124	3.861736
pseudogen	-	55	69	69	183	244	223	1.010324	1.493669	1.670252	2.908119	5.035435	4.071108
protein_co	multiple_c	2143	1894	2004	3620	2969	3011	26.94835	28.06707	33.20799	39.38053	41.94394	37.62967
lincRNA	long_interg	15	12	14	2	5	6	0.354041	0.333773	0.435437	0.040837	0.132581	0.140742
protein_co	harbinger_t	50	32	28	84	75	104	1.345729	1.01495	0.993072	1.955825	2.267765	2.781831
protein_co	chromoson	12	18	16	35	24	13	0.440869	0.779305	0.77461	1.112395	0.990577	0.474658
protein_co	cytochrom	0	0	0	0	0	2	0	0	0	0	0	0.02664
protein_co	tetra-peptic	0	0	0	4	2	8	0	0	0	0.077956	0.050618	0.179112
protein_co	serine-rich_	4	2	4	9	6	11	0.066032	0.038907	0.087014	0.128528	0.111274	0.180466
protein_co	growth_arr	4675	3942	3510	907	952	906	87.57932	87.02492	86.64866	14.69908	20.03577	16.86777
protein_co	histocompa	95	60	36	525	425	577	1.179502	0.877876	0.588996	5.638937	5.928064	7.119678
antisense	-	0	0	0	1	2	1	0	0	0	0.014019	0.03641	0.016105
protein_co	zinc_finger_	51	22	29	59	32	21	0.702391	0.357058	0.52631	0.702949	0.495117	0.287434
protein_co	GLI_pathog	12	1	11	3	1	3	0.2435	0.023913	0.294134	0.052663	0.022796	0.060499

protein_co	family_with	247	227	213	253	244	195	2.472849	2.678142	2.810057	2.191211	2.74435	1.940193
protein_co	potassium_	0	5	1	80	42	56	0	0.093957	0.021013	1.103588	0.752406	0.887466
protein_co	proline_ric	42	28	32	5	21	23	0.988671	0.776726	0.99263	0.101821	0.555355	0.538072
protein_co	nuclear_rec	297	242	397	391	593	460	2.04973	1.96817	3.610484	2.334425	4.597734	3.15506
protein_co	zinc_finger_	0	1	0	2	1	6	0	0.027777	0	0.040783	0.026481	0.140554
protein_co	basic_helix	3	0	3	2	6	4	0.224962	0	0.296445	0.129742	0.505461	0.298097
protein_co	ring_finger_	130	111	120	290	145	164	1.857078	1.868602	2.25893	3.583832	2.327039	2.328307
protein_co	chromoson	0	1	0	4	0	5	0	0.016353	0	0.04802	0	0.068957
protein_co	TSPY-like_5	190	106	101	175	153	158	2.255334	1.482758	1.579841	1.797042	2.040317	1.863906
protein_co	histone_clu	1043	895	748	426	302	352	33.10399	33.47543	31.28473	11.69684	10.76842	11.1032
protein_co	Putative_eu	16	22	19	23	19	22	0.395451	0.64077	0.618815	0.491772	0.527564	0.540387
pseudogen	signal_reco	20	8	16	21	28	35	1.104087	0.52044	1.163934	1.002896	1.736523	1.920221
protein_co	SKI/DACH_(	77	74	56	319	302	333	0.617832	0.699711	0.59211	2.214285	2.722299	2.655423
protein_co	histone_clu	104	90	115	38	41	39	8.354876	8.520327	12.17417	2.640908	3.700323	3.11373
pseudogen	zinc_finger_	15	9	7	4	12	10	0.63025	0.445627	0.387574	0.145393	0.566437	0.417572
protein_co	Mab-21_do	80	99	91	469	356	396	1.257506	1.833844	1.884934	6.377579	6.286647	6.186213
protein_co	somatostat	1	5	4	18	17	5	0.025258	0.148826	0.133136	0.393311	0.482391	0.125511
protein_co	zinc_finger_	91	62	77	103	113	125	0.990874	0.795565	1.104848	0.970236	1.382307	1.352685
protein_co	polycomb_	378	284	333	1346	930	1093	2.851481	2.524667	3.310227	8.783888	7.881534	8.194237
protein_co	solute_carr	2	9	0	3	1	0	0.034002	0.180311	0	0.044122	0.0191	0
protein_co	perforin_1_	1	1	3	1	0	2	0.020901	0.02463	0.082625	0.018081	0	0.041543
protein_co	mab-21-like	214	242	202	0	0	0	3.897273	5.193612	4.847672	0	0	0
pseudogen	ribosomal_	2	1	0	0	3	2	0.19791	0.116613	0	0	0.33351	0.196688
protein_co	YOD1_OTU_	101	93	128	381	292	318	0.849951	0.922279	1.41944	2.773706	2.760605	2.659556
pseudogen	-	185	140	111	333	279	334	5.193046	4.631115	4.105898	8.086445	8.798399	9.317653
pseudogen	exocyst_co	3	0	0	0	0	0	0.080662	0	0	0	0	0
protein_co	transmemb	2122	1900	1944	1788	1501	1515	22.48165	23.72157	27.14025	16.38752	17.86539	15.95163
processed_	-	2	4	0	1	6	0	0.049179	0.115908	0	0.021272	0.165748	0
protein_co	cholinergic	8	6	13	7	6	7	0.288507	0.254991	0.617795	0.218387	0.24309	0.250884
protein_co	shisa_homo	96	112	119	26	38	29	1.77704	2.443156	2.902738	0.416354	0.790239	0.533499
protein_co	sphingosin	2	10	2	3	1	1	0.048326	0.284745	0.063682	0.06271	0.027146	0.024014
pseudogen	-	67	60	47	67	85	62	0.832249	0.878288	0.769328	0.719973	1.186169	0.765385
protein_co	G_protein-(	132	93	84	710	583	634	1.327296	1.102005	1.113032	6.176111	6.585842	6.335671
pseudogen	PIP5K1A_a	4	7	5	3	0	6	0.063213	0.130362	0.104124	0.041014	0	0.094234
processed_	WDFY3_ant	78	72	55	32	31	51	0.641809	0.698153	0.59636	0.227784	0.286564	0.417053
pseudogen	serine/argi	738	555	496	2079	1550	1701	9.021116	7.994733	7.989515	21.98474	21.28554	20.66417
protein_co	angiotensir	0	0	0	0	0	1	0	0	0	0	0	0.018256
protein_co	solute_carr	365	340	370	552	376	494	3.216289	3.530597	4.296341	4.207889	3.722195	4.326122
protein_co	zinc_finger_	290	185	324	189	323	197	8.214493	6.17535	12.0938	4.63135	10.27861	5.545729
protein_co	ankyrin_rep	0	0	0	2	1	8	0	0	0	0.021013	0.013644	0.096562
protein_co	ZFP3_zinc_	4	0	4	3	5	0	0.040677	0	0.053602	0.026392	0.057122	0
protein_co	arylsulfatas	739	610	682	1077	1053	1005	8.400987	8.171895	10.21657	10.59167	13.44817	11.35433
protein_co	homeobox_	93	98	96	4	0	2	3.247699	4.03298	4.417728	0.120841	0	0.069412
protein_co	mitogen-ac	3	6	1	37	22	37	0.033814	0.079695	0.014853	0.360775	0.278576	0.41446

protein_co	pyrophospl	1695	1649	1327	5166	2963	3505	69.34697	79.50337	71.54241	182.8417	136.1879	142.5133
protein_co	homeobox_	48	69	36	0	0	0	1.312587	2.22353	1.297251	0	0	0
protein_co	proteasom	316	253	206	395	340	371	3.634446	3.429089	3.122146	3.930169	4.393181	4.240672
protein_co	basic_helix	2	0	0	0	1	0	0.031438	0	0	0	0.017659	0
protein_co	MAP6_dom	46	41	32	79	52	67	1.153617	1.211699	1.05752	1.713933	1.465063	1.669892
antisense	CSNK1G2_a	6	13	8	1	9	17	0.24662	0.62969	0.433312	0.035558	0.415593	0.69444
protein_co	zinc_finger_	26	23	24	114	95	94	0.516885	0.538835	0.628734	1.960599	2.121747	1.857199
protein_co	chromoson	1	0	3	0	0	0	0.019251	0	0.076105	0	0	0
pseudogen	protein_dis	87	52	54	98	49	93	3.050243	2.148452	2.494846	2.972379	1.930013	3.240468
protein_co	chromoson	0	0	0	0	0	6	0	0	0	0	0	0.109461
protein_co	chemokine	0	0	0	7	2	15	0	0	0	0.111355	0.041317	0.274127
protein_co	gremlin_2_	293	299	264	29	53	39	3.719835	4.473365	4.416668	0.318506	0.755929	0.492074
protein_co	chromoson	5	5	1	0	0	1	0.231791	0.273151	0.061089	0	0	0.046072
protein_co	signal_sequ	4619	3666	2528	2845	1918	2349	98.52315	92.14884	71.05624	52.49713	45.96084	49.79468
protein_co	calcyphosir	16	21	12	8	13	8	0.221106	0.341984	0.218522	0.095639	0.201824	0.10987
protein_co	zinc_finger_	27	16	14	30	43	27	0.367646	0.25674	0.251205	0.353387	0.657784	0.365375
protein_co	CUE_domai	2018	1595	1362	1790	1398	1639	29.50426	27.48092	26.2407	22.64017	22.96253	23.81509
protein_co	scribbled_p	2087	1733	1360	5915	5237	6821	21.17437	20.72019	18.18284	51.91654	59.69248	68.77739
protein_co	potassium_	771	589	542	1114	747	921	11.22903	10.10904	10.40212	14.03576	12.22242	13.33082
protein_co	D-2-hydrox	598	524	319	282	277	465	6.959489	7.186452	4.892171	2.83915	3.621638	5.378222
protein_co	oxytocin_r	56	31	49	122	69	86	0.679353	0.443176	0.783318	1.280354	0.940385	1.036849
protein_co	FtsJ_methy	296	211	296	446	421	385	3.21843	2.703596	4.241103	4.195176	5.142609	4.160281
protein_co	olfactory_r	0	0	0	2	0	1	0	0	0	0.079512	0	0.045672
protein_co	family_with	20	22	14	2946	2832	3353	0.187269	0.242754	0.172742	23.86338	29.79055	31.20179
protein_co	G_protein-r	3	6	1	0	1	3	0.072855	0.171709	0.032002	0	0.027283	0.072405
protein_co	olfactory_r	0	0	0	0	0	4	0	0	0	0	0	0.196504
protein_co	zinc_finger_	2	1	1	4	14	7	0.03233	0.01905	0.021302	0.055938	0.254248	0.112458
protein_co	suppressor_	16	11	15	50	32	40	0.843681	0.683531	1.04228	2.280822	1.895647	2.096177
protein_co	phosphatid	1303	1101	1112	2290	1596	1699	23.57557	23.47536	26.51291	35.84398	32.44141	30.55067
protein_co	transcriptic	1360	1313	1127	1357	885	1212	58.9196	67.03362	64.33979	50.85852	43.0738	52.18349
protein_co	leucine_ric	120	124	120	440	306	343	2.398233	2.920377	3.160285	7.607217	6.870378	6.812616
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.104393
protein_co	olfactory_r	0	0	0	2	0	0	0	0	0	0.0885	0	0
protein_co	mitochond	672	469	440	1181	810	1091	37.21375	30.60653	32.10862	56.57794	50.39278	60.04386
protein_co	G_protein-r	64	53	60	81	57	48	0.626289	0.611192	0.773715	0.685714	0.626641	0.466816
protein_co	chromoson	0	2	1	166	110	131	0	0.126676	0.070826	7.718394	6.641981	6.997402
protein_co	Bardet-Biec	76	77	67	82	73	60	1.172695	1.400133	1.362326	1.094582	1.265445	0.920094
protein_co	ZFP82_zinc	100	121	77	168	114	103	0.925866	1.320202	0.93945	1.345613	1.185774	0.947752
protein_co	leucine-rich	12	13	17	33	22	21	0.339728	0.433711	0.634212	0.808216	0.699717	0.590853
protein_co	NAD(P)H_d	1840	1549	1439	6859	4371	5667	33.45173	33.18633	34.47437	107.8759	89.27515	102.3914
protein_co	apoptosis_(	937	811	785	3275	3303	4075	9.844356	10.04097	10.86806	29.76611	38.9857	42.54857
protein_co	fukutin_rel	550	458	376	1026	791	1028	8.73876	8.575504	7.872447	14.10254	14.11928	16.23267
protein_co	trafficking_	1	0	1	4	1	1	0.067014	0	0.088308	0.231893	0.075286	0.0666
protein_co	rabphilin_3	0	1	3	5	5	0	0	0.02221	0.074507	0.081522	0.105867	0

protein_co	solute_carr	212	134	182	36	60	57	3.597273	2.679473	4.069525	0.528449	1.143768	0.961218
protein_co	Fc_recepto	0	0	0	0	0	2	0	0	0	0	0	0.052693
protein_co	methyltran	170	129	107	210	150	158	7.601325	6.797312	6.304621	8.123117	7.534956	7.021132
protein_co	ankyrin_rep	152	101	106	14	9	10	2.228477	1.74499	2.047884	0.177564	0.148237	0.145705
protein_co	solute_carr	277	255	219	344	271	368	5.083069	5.51434	5.295722	5.460944	5.586819	6.711255
protein_co	HIG1_hypo	797	656	727	3585	2450	3206	30.73123	29.80798	36.93948	119.5842	106.1296	122.8555
protein_co	cholinergic	0	0	2	118	115	120	0	0	0.023577	0.913192	1.15575	1.066861
protein_co	mitogen-ac	20	28	14	39	27	21	0.472687	0.779847	0.436021	0.797392	0.716897	0.493257
protein_co	euchromat	1303	933	916	2186	2275	2260	8.796495	7.422565	8.148835	12.76669	17.25424	15.16294
antisense	-	10	12	22	8	15	20	0.269694	0.381382	0.781861	0.186649	0.454477	0.536058
protein_co	coagulation	1237	1046	1103	1143	732	784	17.13897	17.07866	20.13842	13.70012	11.39397	10.79545
protein_co	zinc_finger_	197	173	106	296	299	326	3.440903	3.560896	2.439758	4.472608	5.867139	5.658918
protein_co	mucin_16_	0	0	0	7	9	12	0	0	0	0.007317	0.012217	0.01441
protein_co	nucleophos	24511	21757	16320	48102	31667	36627	738.1324	772.1103	647.6318	1253.139	1071.345	1096.186
antisense	FER1L6_ant	1	1	0	0	0	0	0.022869	0.026949	0	0	0	0
protein_co	praja_ring_	606	480	418	806	745	808	11.6451	10.86973	10.58477	13.39888	16.08332	15.43091
protein_co	dehydroger	412	318	361	1566	1481	1377	4.227891	3.84557	4.881672	13.90213	17.07382	14.04333
protein_co	proenkepha	6	3	9	132	98	94	0.264926	0.156099	0.523661	5.042081	4.861251	4.124871
sense_intro	HECW1_int	10	1	0	0	0	0	0.287879	0.033925	0	0	0	0
protein_co	histone_clu	134	118	60	217	109	155	14.30261	14.84224	8.439107	20.03702	13.07031	16.44189
protein_co	zinc_finger_	592	568	506	847	713	843	6.204923	7.015686	6.988759	7.679999	8.39563	8.781161
protein_co	polymerase	4927	3941	4141	7261	6550	6285	38.64873	36.43059	42.80482	49.27335	57.72222	48.99679
pseudogen	-	8	16	14	2	2	6	0.312798	0.737226	0.721334	0.06765	0.087852	0.233149
protein_co	transmemb	0	0	0	81	110	76	0	0	0	0.749891	1.322489	0.808302
protein_co	solute_carr	5	5	3	22	7	9	0.162396	0.191373	0.128399	0.618145	0.255418	0.290507
protein_co	transmemb	271	208	241	264	227	259	3.462952	3.132186	4.058159	2.918395	3.258758	3.289172
protein_co	frequently_	77	45	59	139	146	147	1.849572	1.273797	1.867529	2.888406	3.939875	3.509195
protein_co	transmemb	42	43	27	168	88	152	1.126975	1.359692	0.954693	3.899755	2.652753	4.053389
protein_co	transmemb	0	0	0	70	41	52	0	0	0	0.733789	0.55814	0.626214
protein_co	zinc_finger_	168	91	170	87	108	109	3.056387	1.950956	4.075518	1.369246	2.207354	1.970767
protein_co	NME/NM23	7	16	28	9	4	3	0.17374	0.467981	0.915786	0.193244	0.111535	0.074
protein_co	hephaestin	1	1	3	10	7	8	0.009905	0.011672	0.039156	0.085686	0.077892	0.078749
protein_co	family_with	30	29	21	30	36	18	0.503082	0.57309	0.464057	0.435213	0.678218	0.299985
protein_co	orofacial_c	1	0	0	4	5	2	0.018401	0	0	0.063676	0.103364	0.036576
protein_co	coiled-coil_	2	0	0	4	6	1	0.017786	0	0	0.030774	0.059945	0.008838
protein_co	DEAD_(Asp	217	187	237	56	36	45	1.694174	1.72047	2.438268	0.378224	0.315755	0.349157
protein_co	spectrin_re	4	10	3	7	4	13	0.090536	0.266728	0.089478	0.137064	0.101712	0.292425
protein_co	2-oxoglutar	1114	975	681	785	764	966	13.757	14.18895	11.08206	8.386317	10.59939	11.85565
pseudogen	-	72	73	62	165	106	178	2.074987	2.479208	2.354558	4.113674	3.431926	5.09815
protein_co	urotensin_	0	0	0	4	1	0	0	0	0	0.139844	0.045401	0
protein_co	apoptosis-a	3	0	4	2	1	2	0.030212	0	0.053082	0.017424	0.011314	0.020017
protein_co	dendrin	14	14	7	21	10	7	0.197699	0.232976	0.13026	0.256542	0.158645	0.098239
protein_co	sarcoma_ar	0	0	0	6	3	1	0	0	0	0.090244	0.058597	0.017279
protein_co	zinc_finger_	104	114	72	37	39	41	2.156625	2.785821	1.967472	0.663752	0.908563	0.844957

protein_co	SRY_(sex_d	188	203	151	2	11	4	3.981163	5.065884	4.213702	0.036639	0.261694	0.084182
protein_co	zinc_finger_	57	53	78	107	156	69	0.988741	1.083404	1.782941	1.605663	3.040053	1.189505
protein_co	transmemb	2758	2606	1997	197	173	162	31.63841	35.22913	30.18793	1.955013	2.229541	1.846907
protein_co	RAP2B_mei	2592	2175	1920	2026	1909	1858	22.00145	21.75618	21.47595	14.87712	18.20419	15.67371
protein_co	zinc_finger_	238	193	174	789	593	614	4.077656	3.896709	3.928418	11.69428	11.41399	10.4547
protein_co	ring_finger_	217	180	176	218	144	216	3.972405	3.883054	4.245622	3.452338	2.961456	3.92968
protein_co	olfactory_r	0	0	0	0	1	0	0	0	0	0	0.054615	0
protein_co	acyl-CoA_b	38	21	37	54	40	65	0.897705	0.584624	1.151826	1.103588	1.061596	1.526066
protein_co	N-sulfogluc	556	575	389	538	458	542	5.292196	6.449648	4.879165	4.430027	4.897514	5.127079
pseudogen	ribosomal_	4	12	6	0	2	8	0.503002	1.778273	0.994251	0	0.282546	0.999792
protein_co	mab-21-lik	35	17	14	36	44	35	0.669655	0.3833	0.352976	0.595866	0.945768	0.665519
protein_co	Fanconi_an	30	14	21	124	123	92	0.528002	0.290368	0.487044	1.887987	2.432027	1.609206
protein_co	epididymal	0	0	0	7	2	2	0	0	0	0.357804	0.132759	0.117442
protein_co	SET_domai	861	722	847	948	1034	922	5.577851	5.511985	7.230727	5.312942	7.525465	5.936142
protein_co	epididymal	0	0	0	4	0	1	0	0	0	0.197622	0	0.056757
protein_co	chromoson	15	15	8	0	0	0	0.221758	0.261328	0.155852	0	0	0
protein_co	transmemb	0	0	0	5	0	3	0	0	0	0.125545	0	0.086536
protein_co	mex-3_hon	1623	1430	1007	5124	3708	4014	30.1485	31.30332	24.64969	82.34161	77.3813	74.10274
protein_co	mitochond	562	421	436	1201	762	1142	32.30493	28.51817	33.02583	59.72257	49.20809	65.23914
protein_co	G_protein-r	74	55	83	4	3	9	0.855752	0.749525	1.264821	0.040017	0.038975	0.103435
protein_co	purinergic_	0	0	0	0	3	5	0	0	0	0	0.064554	0.095177
protein_co	tumor_nec	1	0	0	229	183	177	0.018982	0	0	3.760469	3.902507	3.339077
protein_co	ZFP41_zinc	219	216	171	307	275	305	2.416943	2.809204	2.486871	2.931054	3.409605	3.345275
protein_co	pleckstrin_	363	306	267	1418	641	760	20.12312	19.9902	19.5045	68.00298	39.92048	41.87087
protein_co	autophagy_	19	10	5	15	11	15	0.220057	0.136486	0.076311	0.150292	0.143127	0.172656
protein_co	G_protein-r	7	2	9	0	0	0	0.106155	0.035742	0.179854	0	0	0
protein_co	HKR1_GLI-l	489	418	367	553	490	530	7.456263	7.510965	7.374172	7.294584	8.393779	8.031523
protein_co	pleiomorpl	257	212	278	141	158	110	1.858213	1.806364	2.648756	0.881951	1.283419	0.790432
protein_co	Yip1_doma	472	480	490	1085	934	938	3.706891	4.442384	5.071059	7.371579	8.240692	7.321166
protein_co	zinc_finger_	12	25	13	1	8	10	0.169864	0.41703	0.242493	0.012246	0.127221	0.140679
pseudogen	ferredoxin_	2	6	7	0	2	7	0.192163	0.679358	0.886285	0	0.215884	0.668418
protein_co	chromoson	1481	1428	1267	1015	732	708	18.04087	20.49924	20.33826	10.69625	10.01757	8.571272
protein_co	chromoson	316	282	295	1150	984	1008	5.486833	5.7702	6.749809	17.2741	19.19459	17.39422
protein_co	adhesion_r	10	8	25	32	40	23	0.104051	0.098094	0.342783	0.288043	0.467578	0.237839
protein_co	G_protein-r	29	14	19	168	108	145	0.725905	0.412968	0.626715	3.637927	3.037068	3.60711
protein_co	outer_dens	1	6	1	0	0	1	0.033006	0.233371	0.043493	0	0	0.032802
protein_co	siah_E3_ub	470	429	345	1849	1213	1298	9.885684	10.63343	9.562309	33.64409	28.66281	27.13271
protein_co	coatomer_	5602	4498	4191	3993	3194	3365	91.79061	86.85237	90.49146	56.60013	58.79483	54.79612
protein_co	brain-speci	56	51	15	15	7	14	0.475035	0.509818	0.167673	0.110076	0.066709	0.118025
processed_	long_interg	6	5	8	4	4	17	0.247774	0.243322	0.43534	0.142898	0.185572	0.69769
antisense	CELF2_anti	3	4	2	2	6	5	0.064353	0.101115	0.056534	0.037114	0.144593	0.106592
protein_co	solute_carr	232	220	164	20	11	5	3.386355	3.784202	3.154447	0.252544	0.180379	0.072531
protein_co	LSM10_U7_	424	417	305	764	545	530	22.3131	25.86052	21.1509	34.78167	32.22105	27.71913
pseudogen	potassium_	0	3	0	0	2	0	0	0.184761	0	0	0.117425	0

protein_co	RELT-like_1	88	60	63	93	110	101	3.450968	2.772788	3.25562	3.155036	4.846186	3.93631
protein_co	regulatory_	722	655	741	748	773	664	5.313233	5.680284	7.185793	4.761966	6.390726	4.856231
protein_co	solute_carr	1281	930	811	886	751	859	16.25927	13.91047	13.56462	9.728562	10.7088	10.83564
protein_co	T_cell_imm	1	0	2	0	0	2	0.01427	0	0.037608	0	0	0.028363
protein_co	ring_finger_	915	775	724	1033	771	773	14.81376	14.78608	15.44606	14.46797	14.02322	12.43751
protein_co	solute_carr	6	9	0	6	0	1	0.092716	0.163891	0	0.080208	0	0.015357
protein_co	IBA57_iron	465	371	323	416	451	420	2.508157	2.358212	2.295827	1.941146	2.732923	2.251442
protein_co	claudin_7	2	2	3	1725	1529	2384	0.055061	0.064886	0.108835	41.08326	47.29	65.22719
protein_co	zinc_finger_	244	188	223	256	218	242	3.788153	3.439558	4.562232	3.438276	3.802273	3.7339
protein_co	zinc_finger_	89	99	73	515	374	438	1.018316	1.334857	1.100653	5.097566	4.807433	4.980539
protein_co	chromoson	1400	1195	1490	1132	897	924	14.63325	14.71932	20.52266	10.23581	10.53305	9.598299
protein_co	HCG16520	0	0	0	15	5	11	0	0	0	0.29396	0.127248	0.247649
protein_co	2-aminoeth	379	282	313	684	527	508	5.389373	4.725581	5.865138	8.414303	8.418965	7.17914
protein_co	cytochrom	995	860	608	1670	1075	1354	50.74787	51.68926	40.86327	73.68417	61.59596	68.63143
protein_co	protein_kir	1122	1006	744	1028	695	847	28.6817	30.30519	25.06223	22.73359	19.95933	21.51816
protein_co	GINS_comp	81	82	46	500	395	460	1.339232	1.597687	1.002221	7.151609	7.336973	7.558546
protein_co	coiled-coil_	372	359	347	98	119	90	3.514284	3.996644	4.319746	0.800909	1.262961	0.844979
protein_co	mitochond	596	503	381	1255	805	909	15.76066	15.67484	13.27663	28.7101	23.91514	23.8892
lincRNA	long_interg	0	0	0	0	3	0	0	0	0	0	0.209422	0
pseudogen	aquaporin_	2	1	0	0	0	0	0.101712	0.059931	0	0	0	0
pseudogen	-	0	0	2	0	3	0	0	0	0.34622	0	0.442749	0
protein_co	small_nucl	1020	1008	625	2026	1632	2077	55.84262	65.03292	45.09002	95.9551	100.3771	113.0087
protein_co	rhotekin_2	47	32	48	688	484	555	0.374677	0.300618	0.504237	4.744714	4.33464	4.397048
protein_co	paraneopla	93	50	48	110	94	100	1.334647	0.845591	0.907736	1.365649	1.515515	1.426242
lincRNA	-	2	0	0	1	0	2	0.041263	0	0	0.017848	0	0.041009
protein_co	carbohydra	912	928	807	156	134	142	10.03788	12.03655	11.70457	1.48537	1.656917	1.553263
protein_co	adipogenin	0	5	0	0	0	0	0	0.404066	0	0	0	0
protein_co	Usher_synd	0	0	0	10	9	10	0	0	0	0.128612	0.150318	0.147751
pseudogen	transient_r	1	0	0	0	6	4	0.016685	0	0	0	0.112466	0.066327
protein_co	mannosyl_(	0	0	0	1	6	5	0	0	0	0.014344	0.111762	0.08239
protein_co	tripartite_r	0	0	3	2	0	0	0	0	0.145644	0.063742	0	0
protein_co	isocitrate_(	2242	1892	1305	3327	2714	3126	44.05854	43.81499	33.79402	56.56012	59.91746	61.05105
lincRNA	-	9	9	2	15	13	5	0.38363	0.452085	0.11234	0.553127	0.622534	0.211812
protein_co	transmemb	2361	2109	1566	3576	2509	3428	24.51818	25.80928	21.42984	32.12571	29.2713	35.37877
protein_co	tryptophan	446	435	398	638	459	473	14.61119	16.79373	17.1818	18.0815	16.89322	15.40003
protein_co	trinucleoti	8053	6144	5627	2796	3678	3842	40.3267	36.25711	37.13186	12.11254	20.69168	19.12062
protein_co	family_with	1	6	0	4	2	3	0.028555	0.201902	0	0.098811	0.06416	0.085136
protein_co	transmemb	9	1	2	306	251	243	0.106569	0.013954	0.031207	3.134526	3.338952	2.859587
protein_co	Dexi_homo	2	4	1	0	1	9	0.06783	0.159866	0.044691	0	0.038101	0.303348
antisense	-	9	12	4	8	6	25	0.212614	0.334071	0.124522	0.163495	0.159239	0.586948
protein_co	NOP10_rib	1125	824	720	2610	1417	2112	108.0919	93.29853	91.16073	216.9422	152.9535	201.6713
protein_co	family_with	296	272	211	737	520	616	9.943232	10.76743	9.340135	21.41738	19.62403	20.56488
protein_co	Kv_channel	64	46	23	2	3	0	1.682335	1.424943	0.796701	0.045481	0.088594	0
protein_co	tudor_and_	33	26	18	111	120	101	0.564841	0.524436	0.405994	1.643608	2.307504	1.718079

protein_co	zinc_finger_	174	177	140	412	346	305	2.300633	2.757899	2.439276	4.712575	5.139527	4.007814
protein_co	increased_s	1186	1161	926	2424	1412	1715	23.65788	27.29169	24.34092	41.8299	31.6428	33.99891
protein_co	excision_re	265	229	218	244	342	212	3.073918	3.130322	3.332251	2.448495	4.456784	2.443948
protein_co	mitochond	939	775	637	1307	802	1289	39.39112	38.31259	35.21332	47.43199	37.7969	53.73971
protein_co	cAMP_resp	2262	1746	2121	1082	1226	995	16.15657	14.6963	19.96329	6.685701	9.83776	7.063003
processed_	TP53_targe	187	167	146	285	186	325	11.57891	12.18567	11.91279	15.2663	12.93862	19.99949
protein_co	unc-5_hom	3	1	8	1444	1418	1335	0.016083	0.006318	0.056517	6.697075	8.540441	7.112887
protein_co	tRNA_splici	135	163	95	531	346	464	3.676458	5.23107	3.409214	12.50989	10.58573	12.55809
protein_co	RGM_doma	551	414	334	167	168	145	9.070425	8.031256	7.245316	2.378239	3.106951	2.372213
protein_co	ankyrin_rep	0	0	0	3	0	3	0	0	0	0.037882	0	0.043519
protein_co	ubiquitin-li	54	51	36	4	0	4	0.86657	0.964466	0.761285	0.055531	0	0.063794
protein_co	mitochond	1394	1203	880	2785	2131	2839	28.01813	28.49371	23.3074	48.42443	48.11814	56.70892
protein_co	family_with	0	0	0	4	2	5	0	0	0	0.091966	0.059715	0.132063
protein_co	RAD51_hor	55	67	58	91	51	60	1.121631	1.610161	1.558656	1.605432	1.168441	1.216041
protein_co	leucine_zip	1753	1441	1145	836	513	574	67.74129	65.62096	58.30581	27.94736	22.27091	22.04413
protein_co	ADP-ribosy	4	5	4	3	6	14	0.118835	0.17505	0.156595	0.077103	0.200256	0.413354
protein_co	exostosin_g	1152	991	1020	2168	1761	1866	7.37461	7.475966	8.604419	12.00629	12.6647	11.87156
protein_co	serine_hydr	4958	4459	3067	5195	4213	4719	76.83883	81.43644	62.63583	69.65027	73.35247	72.68317
protein_co	MOB_kinas	311	257	225	416	338	515	5.18735	5.051558	4.945412	6.002629	6.333604	8.536936
protein_co	histone_clu	4	0	3	3	1	1	0.124861	0	0.123402	0.081012	0.035068	0.031022
protein_co	HHIP-like_1	51	33	38	37	32	26	0.365357	0.278592	0.358729	0.229304	0.257541	0.18511
protein_co	ATPase_H+_	2627	2262	2230	2310	1625	1700	66.44816	67.42525	74.32973	50.54729	46.17695	42.73478
protein_co	zygote_arre	6	0	1	0	0	0	0.217566	0	0.047783	0	0	0
protein_co	cytochrom	330	321	273	541	368	384	4.978777	5.70717	5.427579	7.061045	6.237429	5.757707
protein_co	family_with	0	1	0	0	0	0	0	0.014408	0	0	0	0
protein_co	beta-site_A	350	266	274	287	234	196	6.190895	5.54465	6.386615	4.391676	4.649971	3.445491
protein_co	ubiquitin-c	692	589	451	694	552	581	13.33157	13.37204	11.44951	11.56639	11.94713	11.124
protein_co	synemin_in	205	174	178	574	473	558	1.467997	1.468344	1.679679	3.555873	3.805236	3.97114
protein_co	potassium_	0	0	0	3	1	0	0	0	0	0.032933	0.014256	0
protein_co	gamma-am	23	27	13	50	45	53	0.607606	0.840553	0.452556	1.142687	1.335537	1.391489
protein_co	chromoson	6	7	9	0	0	0	0.11276	0.155028	0.222886	0	0	0
protein_co	NLR_family	0	0	1	1	0	2	0	0	0.029687	0.019489	0	0.044778
protein_co	fidgetin	92	96	99	668	652	537	0.510756	0.628064	0.724262	3.208229	4.066516	2.962851
protein_co	izumo_sper	2	0	0	0	2	2	0.047738	0	0	0	0.05363	0.047443
protein_co	beta-14-N-a	2161	1847	1201	417	315	433	33.21878	33.45823	24.32802	5.545338	5.43987	6.614949
protein_co	adaptor-rel	735	692	682	2639	1757	1826	11.14308	12.3632	13.62502	34.61149	29.92531	27.51239
protein_co	chromoson	1001	796	711	1278	993	1079	19.79602	18.55085	18.52884	21.8644	22.06185	21.20678
protein_co	DDB1_and_	3	3	4	28	11	28	0.033338	0.039287	0.058575	0.269179	0.137329	0.309235
pseudogen	long_interg	142	137	110	50	53	83	3.835521	4.360775	3.915286	1.168339	1.608277	2.228044
protein_co	zinc_finger_	268	231	173	235	166	229	3.065065	3.113322	2.607269	2.325069	2.132859	2.602855
protein_co	Tyrosine-pr	1138	929	876	6131	4655	4981	12.3179	11.84997	12.49492	57.41016	56.60609	53.58221
protein_co	potassium_	37	26	25	70	40	55	0.627826	0.519898	0.559001	1.02754	0.762512	0.927491
protein_co	F-box_and_	140	92	67	410	199	356	2.384729	1.846741	1.503906	6.041683	3.808143	6.026577
protein_co	complemer	589	562	422	8	5	3	10.13727	11.39854	9.570905	0.119113	0.096677	0.051314

protein_co	glycolipid_	16	27	21	37	22	45	0.828012	1.646597	1.432091	1.656461	1.279052	2.314401
protein_co	uncharacte	0	2	1	0	2	0	0	0.024299	0.013586	0	0.023165	0
protein_co	olfactory_r	0	0	2	0	0	0	0	0	0.149067	0	0	0
pseudogen	-	4	0	3	0	0	0	0.190093	0	0.187872	0	0	0
protein_co	kelch_repe	33	38	23	38	28	40	0.465757	0.632027	0.427767	0.463972	0.443968	0.561067
protein_co	ybeY_metal	436	295	213	334	275	356	16.46382	13.12723	10.59884	10.91072	11.6661	13.35992
lincRNA	family_witl	1	1	1	0	6	0	0.013192	0.015546	0.017384	0	0.088925	0
protein_co	family_witl	6	2	2	6	9	3	0.515659	0.202558	0.226504	0.446093	0.868966	0.256237
protein_co	ceroid-lipo	893	697	728	1438	1305	1493	6.646465	6.113348	7.140119	9.258938	10.91186	11.04355
antisense	-	6	14	10	1	6	15	0.148641	0.408717	0.326454	0.021431	0.166989	0.369308
protein_co	phosphatid	828	759	478	2256	1661	2130	7.959895	8.598563	6.055357	18.762	17.9389	20.35009
protein_co	neurexophi	433	339	247	34	27	49	11.42175	10.53784	8.585715	0.775866	0.800124	1.284548
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.117181
protein_co	calcium_ch	18	22	21	0	2	3	0.118304	0.170395	0.181878	0	0.014767	0.019596
pseudogen	DNM1_pse	15	16	9	0	3	2	0.207287	0.26056	0.163892	0	0.046575	0.027468
protein_co	trafficking_	415	434	370	533	400	418	4.846793	5.973147	5.694334	5.385135	5.248261	4.851682
sense_intrc	-	4	0	0	0	3	2	0.111221	0	0	0	0.093712	0.055267
protein_co	piggyBac_t	33	37	35	37	28	23	0.75369	0.995835	1.053371	0.731044	0.718432	0.522055
protein_co	nuclear_pr	1681	1250	1292	3826	3110	3484	16.06967	14.08174	16.27558	31.64077	33.40016	33.09992
protein_co	otolin_1	0	0	0	0	1	0	0	0	0	0	0.041476	0
protein_co	testis_expr	7	0	1	5	11	2	0.191419	0	0.036035	0.118282	0.337931	0.054353
protein_co	teashirt_zir	122	142	152	5	16	12	0.529975	0.726927	0.870109	0.01879	0.078084	0.051807
protein_co	calpain_12	9	16	6	16	25	20	0.172509	0.361406	0.151549	0.265309	0.538341	0.380985
protein_co	exocyst_co	1290	1024	1053	1029	1306	1215	14.37463	13.44665	15.46216	9.919401	16.3493	13.45529
pseudogen	olfactory_r	0	0	2	0	0	0	0	0	0.148749	0	0	0
protein_co	karyopheri	1786	1312	1391	13935	9149	10536	38.49862	33.32765	39.5117	259.8566	221.5575	225.7091
pseudogen	WAS_prote	24	16	5	20	8	20	0.299384	0.235204	0.08219	0.215829	0.112113	0.247946
pseudogen	neutrophil_	0	0	0	1	4	7	0	0	0	0.03021	0.156929	0.242941
protein_co	XK_Kell_blc	0	2	1	5	2	4	0	0.043766	0.02447	0.080321	0.041723	0.073818
protein_co	biglycan	6663	5444	4437	1348	1223	1154	146.8551	141.3983	128.8675	25.7023	30.2827	25.27752
protein_co	ORAI_calciu	319	253	181	694	461	541	7.895361	7.379194	5.903298	14.85949	12.81833	13.30725
pseudogen	abhydrolas	0	0	0	0	1	1	0	0	0	0	0.066084	0.05846
protein_co	centrosom	253	219	189	473	387	384	1.60197	1.634124	1.576996	2.590944	2.752922	2.416433
protein_co	lipoma_HM	1	0	2	4	4	15	0.031607	0	0.083299	0.109371	0.142032	0.471171
protein_co	feline_sarc	32	11	10	67	61	104	0.598838	0.242582	0.246601	1.084668	1.282443	1.934203
protein_co	glutaredoxi	908	786	692	2189	1722	2156	25.8027	26.32139	25.91315	53.8131	54.97452	60.88883
protein_co	family_witl	175	145	107	252	196	217	7.538384	7.360635	6.073776	9.390825	9.485175	9.289869
protein_co	TATA_box_l	0	0	0	4	0	0	0	0	0	0.089934	0	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.041635	0	0
protein_co	caveolin_3	1	0	0	1	1	1	0.036996	0	0	0.032005	0.041562	0.036767
protein_co	matrix-rem	3816	3259	3001	1594	1100	1148	35.68677	35.9162	36.9828	12.89586	11.55688	10.66966
protein_co	LIM_domai	407	330	331	1349	1168	1297	5.871113	5.609796	6.292002	16.83453	18.92858	18.59412
protein_co	major_facil	566	474	456	861	729	842	14.70295	14.5102	15.60945	19.3488	21.27475	21.7375
protein_co	ribonuclea	0	0	0	1	0	0	0	0	0	0.039078	0	0

protein_co	acireductor	884	735	624	1880	1294	1488	12.09298	11.84883	11.24865	22.24856	19.88678	20.2299
protein_co	RWD_doma	268	211	195	534	305	358	5.372278	4.984404	5.151019	9.260362	6.868669	7.132083
protein_co	spinster_ho	0	0	0	4	9	2	0	0	0	0.085886	0.250953	0.049333
protein_co	SATB_home	402	297	328	724	689	622	2.71978	2.367943	2.924263	4.237496	5.236921	4.182229
protein_co	histone_clu	0	0	0	0	1	0	0	0	0	0	0.124687	0
protein_co	neurexophi	13	19	9	42	50	50	0.132505	0.228218	0.120884	0.370342	0.572544	0.506489
protein_co	colony_stir	14	13	27	6	2	9	0.185804	0.203319	0.472201	0.068888	0.02982	0.118708
protein_co	EPH_recept	190	164	115	838	775	769	2.374596	2.415389	1.893951	9.060312	10.88145	9.551512
protein_co	variable_ch	0	4	1	0	1	0	0	0.258067	0.072144	0	0.061506	0
protein_co	actin-like_1	24	38	16	11	17	19	0.626521	1.169001	0.550401	0.248416	0.498565	0.492932
protein_co	epithelial_r	11	12	15	6	8	8	0.486915	0.625964	0.874958	0.22976	0.397832	0.351933
lincRNA	long_interg	0	2	1	2	0	1	0	0.211843	0.118444	0.155514	0	0.089328
protein_co	chromoson	34	16	9	26	38	38	0.647014	0.358808	0.22569	0.428027	0.812396	0.718668
protein_co	heparan_su	0	0	0	78	78	93	0	0	0	1.115303	1.448368	1.527664
protein_co	trafficking_	639	484	581	1028	919	811	6.110783	5.454419	7.321616	8.504566	9.87326	7.70773
protein_co	histone_clu	1	1	5	4	16	4	0.106736	0.125782	0.703259	0.369346	1.918578	0.424307
polymorph	tetraspanin	56	42	50	45	34	49	1.563658	1.382007	1.839749	1.086999	1.066551	1.359751
protein_co	phospholip	136	110	154	136	161	136	0.986974	0.940733	1.472727	0.853825	1.312628	0.980879
pseudogen	-	6	0	2	0	0	0	1.534522	0	0.674041	0	0	0
protein_co	spindle_an	395	359	319	1406	1002	1218	7.4738	8.004716	7.953712	23.01403	21.2991	22.90347
protein_co	relaxin/insu	0	1	2	0	1	5	0	0.02463	0.055084	0	0.02348	0.103857
protein_co	necdin_me	524	503	387	1552	971	1153	14.70895	16.63893	14.31516	37.68818	30.62095	32.16543
protein_co	family_with	16	16	20	19	20	29	0.287625	0.338949	0.473774	0.295477	0.403911	0.518101
processed_	-	0	0	0	2	1	0	0	0	0	0.119579	0.077645	0
protein_co	neurotrimi	1158	882	952	388	204	311	19.21808	17.24952	20.81964	5.570525	3.803476	5.129458
protein_co	tetratricop	8385	7152	8051	2037	1735	1651	42.83607	43.05674	54.19899	9.002448	9.95761	8.382302
protein_co	potassium_	0	1	0	11	16	9	0	0.017417	0	0.140644	0.265666	0.132196
protein_co	protein_ph	5	0	3	5	2	3	0.183441	0	0.145038	0.158693	0.082434	0.109385
protein_co	BRICHOS_d	38	24	20	138	107	149	1.051625	0.7827	0.72936	3.303842	3.326672	4.09801
protein_co	galanin_rec	2	0	0	15	12	9	0.077626	0	0	0.503654	0.523249	0.34716
protein_co	IgA-inducin	113	96	110	52	29	34	2.08371	2.08611	2.672923	0.829517	0.600767	0.623085
protein_co	tsukushi_sr	1710	1461	1072	955	755	861	25.47245	25.64673	21.04284	12.30668	12.63487	12.7464
protein_co	annexin_A2	41548	34186	28676	60866	38126	46009	623.4672	604.5314	567.0442	790.135	642.7378	686.1451
pseudogen	selenophos	0	0	0	4	11	0	0	0	0	0.191227	0.682918	0
protein_co	regulator_c	2	5	0	15	13	31	0.0341	0.100463	0	0.221251	0.249014	0.525293
protein_co	homeobox_	74	48	61	49	79	84	1.042756	0.797075	1.132702	0.597324	1.250625	1.176359
protein_co	progestin_a	297	257	198	629	651	832	4.769025	4.863102	4.189606	8.737492	11.74365	13.27719
protein_co	pregnancy-	1365	1155	1352	1081	981	882	6.594074	6.575219	8.606621	4.517622	5.324014	4.234473
protein_co	v-maf_musc	5	9	4	13	3	1	0.112784	0.239237	0.118898	0.253679	0.076024	0.022418
protein_co	neugrin_ne	429	368	366	800	650	736	8.157933	8.246654	9.171466	13.1606	13.88626	13.90946
protein_co	glutamate_	2	8	3	50	33	43	0.018149	0.085551	0.035874	0.392517	0.336425	0.387796
protein_co	hydroxycar	0	0	0	3	3	4	0	0	0	0.06699	0.086995	0.102612
protein_co	coiled-coil_	3	14	1	13	10	5	0.054485	0.299632	0.023933	0.204249	0.204034	0.090247
protein_co	chromoson	0	1	2	21	35	26	0	0.011358	0.025401	0.175091	0.378965	0.249038

pseudogen	transmemb	155	123	92	91	95	88	2.944332	2.753387	2.302914	1.495407	2.027346	1.661298
protein_co	melanoma_	1	0	2	0	1	2	0.036918	0	0.097299	0	0.041476	0.073381
protein_co	cysteine-ric	1182	925	659	204	144	208	31.66815	29.20478	23.2662	4.728227	4.334277	5.538321
protein_co	DEAD_(Asp	82	63	65	244	148	218	1.674831	1.516368	1.749465	4.311317	3.396001	4.425101
protein_co	acyl-CoA_b	1085	925	1071	873	755	721	16.0764	16.15132	20.91141	11.19016	12.56768	10.61705
protein_co	chromoson	1369	1118	1138	1400	1010	1033	12.17474	11.71669	13.33624	10.77078	10.09082	9.129903
protein_co	phosphatid	4	2	3	252	300	224	0.027488	0.016196	0.027166	1.498095	2.31604	1.529796
pseudogen	ribosomal_	116	130	73	310	178	369	2.58575	3.414907	2.144303	5.977962	4.457563	8.174562
protein_co	vitelline_m	2	3	1	4	2	1	0.138227	0.244338	0.091075	0.239159	0.15529	0.068687
protein_co	ALG12_alp	685	677	435	1029	667	752	15.36635	17.89682	12.85891	19.9691	16.80951	16.76515
protein_co	lymphocyt	0	0	0	0	1	3	0	0	0	0	0.027459	0.072873
protein_co	UDP-N-acet	89	46	53	3	1	4	1.955082	1.190803	1.534213	0.057011	0.024679	0.087326
protein_co	collagen_ty	17969	14627	11987	7232	7701	9078	143.9832	138.118	126.5707	50.13133	69.32406	72.29156
protein_co	RNA_bindi	1413	1247	1010	2372	1667	2015	19.96414	20.76261	18.80462	28.99253	26.4602	28.29392
antisense	-	39	32	24	96	71	92	0.913584	0.883366	0.740849	1.94544	1.868491	2.141811
protein_co	glutamate_	3	5	5	82	87	78	0.068077	0.133707	0.149514	1.609734	2.217919	1.759064
protein_co	transmemb	1	1	0	0	0	0	0.044451	0.052383	0	0	0	0
protein_co	trichohyali	0	0	0	0	0	1	0	0	0	0	0	0.014603
protein_co	ribosomal_	11072	10665	7458	8431	7099	10787	407.9072	463.0238	362.07	268.706	293.8201	394.9532
protein_co	regulator_c	7	3	2	24	10	13	0.148591	0.075045	0.055945	0.440727	0.238476	0.274251
protein_co	solute_carr	14	16	18	46	31	35	0.302027	0.406766	0.511711	0.858496	0.751326	0.750404
protein_co	zinc_finger_	196	200	214	310	359	319	2.309981	2.777726	3.32354	3.160655	4.753307	3.736394
protein_co	leukocyte_	131	82	72	12	23	5	3.623443	2.672829	2.624324	0.28714	0.714705	0.137445
protein_co	chromoson	45	23	21	28	11	8	0.983627	0.592452	0.604884	0.529467	0.270122	0.173787
protein_co	transcriptic	396	380	309	265	231	307	17.81192	20.14217	18.31508	10.31156	11.67284	13.72346
protein_co	chromoson	200	193	185	318	234	337	2.586272	2.941092	3.152469	3.557414	3.399454	4.330956
protein_co	centrosom	265	237	236	514	367	349	2.428066	2.558998	2.849452	4.074184	3.777719	3.177969
protein_co	signal_reco	2081	1791	1730	2510	1662	1869	35.89775	36.40809	39.32567	37.45691	32.20885	32.0416
protein_co	Ewing_sarc	4025	3430	3371	8820	7329	9025	29.25017	29.37404	32.28168	55.44905	59.83514	65.18076
protein_co	outer_dens	2	0	1	3	0	0	0.08853	0	0.058331	0.11488	0	0
protein_co	high_mobil	656	508	505	669	475	554	28.35044	25.87181	28.75956	25.01181	23.06209	23.79444
protein_co	spermatoge	105	73	115	309	318	262	0.646147	0.529386	0.932556	1.644991	2.198459	1.602334
protein_co	gap_junctic	1409	1271	1086	3655	2777	3172	9.763594	10.3789	9.916613	21.91034	21.61841	21.84447
protein_co	SRY_(sex_d	0	0	0	0	2	2	0	0	0	0	0.028956	0.025615
protein_co	CCR4-NOT_	322	274	269	833	449	527	6.055773	6.072553	6.666545	13.55257	9.486567	9.849948
protein_co	metastasis_	1955	1648	1132	2677	1933	2446	35.98736	35.7493	27.45898	42.62993	39.9746	44.74755
protein_co	zinc_finger_	0	0	0	0	0	1	0	0	0	0	0	0.009347
protein_co	cell_adhesi	134	113	100	686	541	486	1.679871	1.669385	1.651984	7.439746	7.61934	6.055039
protein_co	zinc_finger_	462	460	363	1216	794	1019	3.793229	4.450738	3.92743	8.637014	7.323802	8.314782
protein_co	chromoson	21	13	24	57	31	38	0.387373	0.282593	0.583386	0.909595	0.642423	0.696632
protein_co	pyrroline-5	2068	1681	1269	336	296	345	57.92697	55.48877	46.84106	8.142028	9.314747	9.604152
protein_co	LSM_doma	912	689	503	623	534	797	48.33052	43.02817	35.12606	28.56128	31.79193	41.97537
pseudogen	IQ_motif_c	0	0	0	0	2	0	0	0	0	0	0.048433	0
protein_co	spinster_ho	6	11	5	874	745	991	0.092151	0.199091	0.101194	11.61249	12.85453	15.12635

protein_co	chromoson	0	0	1	0	0	0	0	0	0.040326	0	0	0
protein_co	adaptor-rel	2891	2392	2107	2550	1827	2010	33.45408	32.6189	32.12923	25.52726	23.75137	23.11568
protein_co	solute_carr	82	78	104	448	446	449	0.710385	0.796309	1.187266	3.357537	4.34074	3.865768
protein_co	solute_carr	11	7	15	26	41	32	0.209103	0.156809	0.375745	0.427566	0.875588	0.604542
protein_co	Purkinje_ce	10	10	12	4	2	2	0.749872	0.883679	1.185778	0.259484	0.168487	0.149048
protein_co	4-aminobu	137	106	136	20	36	23	1.29841	1.18387	1.698497	0.163977	0.383303	0.216635
protein_co	solute_carr	12	10	17	179	109	169	0.32646	0.320595	0.609443	4.212746	3.331385	4.569257
protein_co	calcium/ca	789	634	769	42	21	19	5.122694	4.850849	6.579343	0.235903	0.153176	0.122598
protein_co	RANBP2-lik	4	1	1	0	3	0	0.029555	0.008707	0.009737	0	0.024903	0
pseudogen	family_witl	6	0	0	0	1	4	0.451202	0	0	0	0.084483	0.298943
protein_co	LysM_putat	141	106	129	137	113	133	2.453873	2.173931	2.958403	2.062607	2.209329	2.300351
protein_co	WBP2_N-te	1	0	0	0	0	0	0.015557	0	0	0	0	0
protein_co	immunoglo	0	0	3	4	0	0	0	0	0.101302	0.088672	0	0
protein_co	NK2_home	1	0	0	11	2	6	0.030978	0	0	0.294785	0.069603	0.184719
protein_co	arylformam	335	260	185	543	354	444	10.25158	9.376191	7.460235	14.37503	12.17022	13.50326
protein_co	GATS_prote	0	0	2	0	0	0	0	0	0.140936	0	0	0
protein_co	growth_arr	1656	1373	939	519	310	440	33.30938	32.54497	24.88895	9.031015	7.005142	8.795662
protein_co	FRAS1_rela	0	0	2	0	0	0	0	0	0.020735	0	0	0
protein_co	nebulin	22	10	16	30	31	32	0.044451	0.02381	0.0426	0.052437	0.070367	0.064257
protein_co	brain-enric	404	382	214	27	44	22	3.680634	4.101207	2.569152	0.212798	0.450343	0.199193
protein_co	glypican_6	871	900	949	261	201	164	7.130293	8.682381	10.23741	1.848386	1.848563	1.334267
protein_co	Rho_guanir	30	23	23	86	84	53	0.319692	0.288832	0.322978	0.792815	1.005631	0.561301
protein_co	family_witl	54	49	31	1	0	0	1.107638	1.184424	0.837916	0.017745	0	0
protein_co	CUB_and_S	3	0	1	0	2	1	0.013089	0	0.005749	0	0.009803	0.004336
pseudogen	olfactory_r	0	0	0	0	2	0	0	0	0	0	0.124818	0
protein_co	calcium_ho	0	0	0	0	3	2	0	0	0	0	0.108007	0.063697
protein_co	prostaglanc	98	59	54	0	2	5	1.79213	1.27146	1.301284	0	0.041089	0.090871
protein_co	centrosom	182	162	163	378	249	279	2.514421	2.637477	2.967488	4.517742	3.864693	3.83072
protein_co	Down_syno	1	1	1	2	0	3	0.023687	0.027914	0.031214	0.040983	0	0.070623
protein_co	ankyrin_rep	0	0	0	0	4	1	0	0	0	0	0.06776	0.014985
protein_co	G_protein-	2	1	4	64	43	68	0.060469	0.03563	0.159368	1.673975	1.460574	2.043264
protein_co	gap_junctio	1	0	1	6	6	4	0.059418	0	0.078298	0.30841	0.400511	0.236202
protein_co	Uncharacte	0	5	0	3	0	6	0	0.149539	0	0.065866	0	0.151335
protein_co	RAB_intera	164	152	120	519	351	345	3.572972	3.902442	3.4451	9.781742	8.590966	7.469896
protein_co	transmemb	2673	2163	1692	32	33	29	52.27605	49.85026	43.60527	0.541398	0.725048	0.563653
protein_co	Fanconi_an	227	233	175	392	230	265	3.631794	4.392971	3.689506	5.425558	4.134017	4.213576
protein_co	calneuron_	1	0	0	0	0	0	0.005597	0	0	0	0	0
pseudogen	-	3	0	2	1	0	0	0.074112	0	0.065108	0.021371	0	0
protein_co	single-pass_	385	304	281	383	274	447	13.0072	12.1033	12.5102	11.19399	10.39975	15.0086
polymorph	gamma-am	0	0	0	0	3	0	0	0	0	0	0.036972	0
protein_co	C2_calcium	22	14	5	55	77	95	0.376804	0.282571	0.112849	0.814927	1.481606	1.617061
protein_co	carbohydra	59	66	75	62	77	93	1.055956	1.392018	1.768846	0.95995	1.548224	1.654194
pseudogen	heat_shock	3	3	5	15	18	17	0.073089	0.086131	0.160523	0.316145	0.492668	0.411615
protein_co	POTE_anky	0	0	0	0	1	0	0	0	0	0	0.009072	0

protein_co	RuvB-like_2	2331	1966	1449	5444	3669	5047	49.60026	49.29834	40.62982	100.2127	87.70785	106.7295
protein_co	GDP-D-gluc	5	6	5	31	28	24	0.165959	0.234687	0.218694	0.890135	1.044091	0.791685
protein_co	catenin_(ca	7	2	9	2	2	1	0.114662	0.038606	0.194267	0.028341	0.036804	0.016279
pseudogen	-	3	2	0	2	3	0	0.349061	0.274232	0	0.201314	0.392149	0
antisense	WT1_antise	0	0	0	0	0	1	0	0	0	0	0	0.013745
protein_co	RIMS_bindi	0	2	0	0	0	0	0	0.021573	0	0	0	0
protein_co	Protein_FL	12	2	6	82	74	74	0.140614	0.027617	0.092647	0.831233	0.974152	0.861762
protein_co	chromoson	58	37	39	35	38	54	1.333295	1.002321	1.181402	0.696032	0.981366	1.233677
protein_co	pituitary_t	5074	3946	3918	7170	5637	5801	97.32703	89.19637	99.03353	118.9776	121.4731	110.5848
protein_co	DEAD_(Asp	2021	1648	1400	1769	1327	1622	36.28137	34.86435	33.11923	27.47313	26.76315	28.93862
protein_co	abhydrolas	55	43	43	146	115	113	1.639502	1.510514	1.689088	3.765	3.8512	3.347628
protein_co	coiled-coil_	0	0	0	34	26	20	0	0	0	0.635577	0.631173	0.429502
protein_co	plasminoge	14	6	6	1	4	2	0.356162	0.179878	0.201144	0.022008	0.114322	0.050566
protein_co	DAZ_associ	1962	1596	1516	1750	1326	1398	42.39601	40.64115	43.16781	32.7135	32.18982	30.02222
protein_co	collagen_a	56	59	67	226	188	247	0.912214	1.132577	1.438197	3.184785	3.440453	3.998668
protein_co	Homo_sapi	2185	2100	1715	2736	1654	2079	65.09627	73.72776	67.32922	70.51537	55.35913	61.55577
pseudogen	-	14	22	14	13	8	21	0.842243	1.559693	1.10987	0.676575	0.54069	1.255563
protein_co	olfactory_r	0	0	0	1	6	1	0	0	0	0.042843	0.333822	0.049218
protein_co	cat_eye_syr	8	12	3	23	53	32	0.085492	0.151121	0.042247	0.212631	0.636299	0.339857
protein_co	zinc_finger_	327	281	365	280	356	306	4.386041	4.441589	6.45138	3.248972	5.364435	4.079022
protein_co	EPH_recept	0	0	0	0	4	4	0	0	0	0	0.043853	0.038794
protein_co	coiled-coil_	42	20	27	105	118	123	0.529662	0.297226	0.448692	1.145518	1.671786	1.541574
protein_co	chromoson	0	6	1	0	2	1	0	0.403804	0.075257	0	0.128319	0.056757
protein_co	BCL6_corep	329	284	277	430	494	361	2.725757	2.772788	3.024167	3.081929	4.597982	2.972406
protein_co	jerky_homo	375	387	371	287	221	206	5.561029	6.76304	7.24991	3.681873	3.681842	3.035993
protein_co	chromoson	13	7	2	0	1	0	0.408447	0.259178	0.082805	0	0.035297	0
protein_co	guanylate_l	0	0	0	0	1	0	0	0	0	0	0.019912	0
protein_co	KIAA2026	365	237	343	260	206	144	2.765235	2.115898	3.424271	1.704023	1.753297	1.084205
polymorph	ovochymas	3	3	3	36	82	63	0.090036	0.106102	0.118645	0.934672	2.764754	1.879073
protein_co	synapse_di	0	0	0	6	0	1	0	0	0	0.105406	0	0.020182
protein_co	four_and_a	1449	1209	869	1518	1027	1203	46.5765	45.79646	36.80892	42.21174	37.08668	38.4303
protein_co	pro-melani	2	1	0	5	0	0	0.138227	0.081446	0	0.298948	0	0
protein_co	transmemb	0	0	0	0	5	4	0	0	0	0	0.449214	0.31791
protein_co	chromoson	106	65	54	71	64	67	8.326032	6.016621	5.589343	4.824514	5.647565	5.23018
protein_co	coiled-coil_	66	93	33	37	40	39	2.481609	4.12078	1.635077	1.203522	1.689657	1.457349
pseudogen	ribosomal_	38	54	29	69	43	78	3.109363	5.207013	3.126948	4.884273	3.952804	6.342961
protein_co	receptor-in	4	0	0	515	456	427	0.052717	0	0	5.871655	6.75156	5.592781
protein_co	leucine-rich	2	6	8	7	0	1	0.028004	0.099002	0.147608	0.08479	0	0.013915
protein_co	nuclear_po	149	157	84	143	66	84	1.476363	1.833216	1.096784	1.225761	0.734683	0.827172
protein_co	splicing_fac	1578	1392	1065	3685	2627	2940	22.74459	23.64381	20.22812	45.94853	42.53832	42.11416
pseudogen	zinc_finger_	0	0	0	0	0	1	0	0	0	0	0	0.105651
protein_co	tripartite_r	0	0	0	0	1	0	0	0	0	0	0.037595	0
pseudogen	-	71	44	34	114	37	74	4.024422	2.939037	2.539563	5.590016	2.356112	4.168565
protein_co	glutamate_	0	0	1	27	31	22	0	0	0.007473	0.132466	0.19751	0.123997

pseudogen	-	230	231	170	71	125	143	1.782786	2.110039	1.736421	0.476094	1.088505	1.101583
protein_co	parahox_cl	0	0	0	17	12	17	0	0	0	1.491535	1.367262	1.713484
protein_co	general_tra	117	131	94	384	241	240	2.098271	2.768561	2.22146	5.957581	4.855588	4.277565
protein_co	ankyrin_rep	203	174	195	255	185	219	2.155872	2.177626	2.728955	2.342772	2.207231	2.31143
protein_co	SH2_domai	0	0	1	2	2	0	0	0	0.025368	0.033308	0.043255	0
protein_co	three_prim	2	3	4	18	9	22	0.046809	0.082742	0.123366	0.364448	0.236642	0.511719
protein_co	G_protein-	20	10	5	2	1	1	0.289453	0.170551	0.095357	0.02504	0.016259	0.014383
protein_co	myxovirus_	0	0	0	0	1	0	0	0	0	0	0.014635	0
protein_co	E1A_bindin	1438	1248	1129	1667	2185	1756	6.151353	6.2912	6.364152	6.168938	10.50056	7.465277
protein_co	mex-3_hon	264	219	190	346	262	295	3.225576	3.153222	3.059087	3.657148	3.596282	3.582078
pseudogen	-	0	0	0	0	4	5	0	0	0	0	0.695625	0.769211
pseudogen	phosphatid	421	367	240	760	580	811	5.756239	5.9133	4.32417	8.989455	8.909099	11.02014
protein_co	family_with	8	12	9	51	37	52	0.073644	0.130178	0.109176	0.406146	0.382648	0.475731
protein_co	cytochrom	337	276	192	383	316	366	10.17167	9.816997	7.636574	10.00056	10.71516	10.97876
protein_co	UTP11-like_	664	492	475	1338	943	1186	17.41101	15.20295	16.41286	30.35113	27.77899	30.90652
protein_co	proteasom	423	374	333	1373	903	1127	10.39649	10.83241	10.78513	29.19308	24.9335	27.52834
protein_co	proline_ric	1110	959	986	1430	1449	1260	5.42809	5.526495	6.353833	6.049551	7.960521	6.123564
processed_	COL18A1_a	41	45	47	8	39	21	0.633746	0.819693	0.957336	0.106976	0.677244	0.322597
protein_co	acyl-CoA_sy	0	0	0	0	1	0	0	0	0	0	0.021272	0
protein_co	histone_clu	11	5	5	1	3	3	0.597896	0.320266	0.358128	0.047021	0.183191	0.162056
protein_co	folate_rece	0	0	0	1	0	2	0	0	0	0.056893	0	0.130718
protein_co	HCG17829	6	3	12	5	38	13	0.215939	0.127235	0.569109	0.155673	1.536428	0.464978
protein_co	serine_hydr	67	69	38	181	135	158	1.692293	2.053795	1.264792	3.954963	3.830748	3.966135
protein_co	poly(rC)_bi	663	554	420	52	18	26	15.94	15.6961	13.30635	1.081536	0.486179	0.621238
protein_co	pyroglutam	0	0	0	0	1	5	0	0	0	0	0.040105	0.177391
protein_co	SET_domai	657	575	548	1657	1253	1313	12.08556	12.46454	13.28363	26.36858	25.89414	24.00356
protein_co	tumor_nec	3	1	6	31	17	19	0.070214	0.027581	0.185048	0.62766	0.44699	0.441939
protein_co	zinc_and_ri	502	454	435	1076	1198	1077	3.879197	4.134291	4.429576	7.193055	10.40026	8.271104
protein_co	F-box_and_	1485	1252	1223	344	252	239	17.23309	17.12175	18.70243	3.45349	3.285386	2.756413
protein_co	transport_a	156	120	107	191	174	150	2.656415	2.408018	2.400988	2.813635	3.328662	2.538471
protein_co	histone_clu	5	2	12	1	13	6	0.644051	0.30359	2.036884	0.111433	1.881233	0.768088
pseudogen	-	40	44	43	40	27	44	0.384746	0.498739	0.545026	0.332841	0.29176	0.420607
protein_co	sideroflexir	170	144	102	421	266	294	6.603059	6.59122	5.22073	14.14625	11.60719	11.34889
protein_co	gastrokine_	0	0	0	0	0	1	0	0	0	0	0	0.035123
protein_co	family_with	12	5	6	24	10	13	0.678731	0.333268	0.447201	1.174331	0.635426	0.730751
protein_co	mitochond	442	363	295	503	385	587	37.38006	36.17691	32.87567	36.80008	36.57864	49.33618
protein_co	zinc_finger_	55	40	37	56	33	39	0.851888	0.730108	0.755191	0.750362	0.574226	0.600336
protein_co	chromoson	239	188	190	1652	1218	1477	5.030973	4.663576	5.270387	30.08342	28.80384	30.89899
protein_co	chemokine_	0	0	0	46	31	44	0	0	0	1.053375	0.921877	1.157509
protein_co	DiGeorge_s	34	22	22	84	89	79	0.554698	0.422968	0.472971	1.185549	1.631235	1.280897
protein_co	retinitis_pi	0	1	3	3	0	0	0	0.007825	0.02625	0.017233	0	0
protein_co	chromoson	5	11	3	37	7	5	0.085416	0.221447	0.067535	0.546808	0.134344	0.084889
protein_co	zinc_finger_	56	57	59	174	154	190	0.678886	0.814312	0.942531	1.824825	2.097388	2.289139
protein_co	NADH_deh	340	321	300	519	433	678	13.50333	15.0236	15.70066	17.83168	19.31963	26.76093

protein_co	membrane-	2	0	0	3	2	3	0.060817	0	0	0.078918	0.068324	0.090662
protein_co	kelch-like_f	221	171	188	257	228	295	3.113347	2.838824	3.49002	3.13207	3.608438	4.130161
protein_co	-	2	1	1	11	9	0	0.036436	0.021469	0.024007	0.173361	0.184199	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.062409	0
protein_co	tRNA_meth	140	111	84	298	209	264	3.346158	3.126428	2.64565	6.161659	5.611949	6.27093
pseudogen	glucuronid	114	59	87	148	132	122	4.624731	2.820595	4.650885	5.194052	6.015955	4.918708
protein_co	pregnancy_	0	0	0	34	28	24	0	0	0	0.550234	0.588454	0.446197
protein_co	G_protein-	114	103	69	43	14	13	2.629749	2.799972	2.097458	0.858106	0.362816	0.298032
processed_	long_interg	0	0	0	5	15	13	0	0	0	0.147929	0.576317	0.441849
protein_co	bone_morp	3	2	3	3	6	0	0.093867	0.073744	0.123694	0.081204	0.210908	0
protein_co	Aly/REF_ex	875	631	600	3569	2710	3363	42.30445	35.95129	38.22646	149.2752	147.1961	161.59
protein_co	family_witl	503	398	462	419	220	251	7.354134	6.857309	8.901032	5.29957	3.61356	3.647094
protein_co	EF-hand_dc	11	13	5	1	0	1	0.17913	0.249474	0.107295	0.014088	0	0.016184
protein_co	noggin	12	9	7	624	642	686	0.335778	0.29677	0.258109	15.10492	20.18157	19.07676
protein_co	uridine_ph	31	28	13	1748	1048	1222	0.589925	0.627914	0.325997	28.77659	22.40502	23.11084
protein_co	opioid_bin	6	1	5	16	3	4	0.046487	0.00913	0.051049	0.107242	0.026113	0.0308
protein_co	tripartite_r	121	111	137	93	102	98	1.847667	1.997415	2.756726	1.228526	1.749796	1.487216
protein_co	lipoma_HM	1579	1290	1188	919	901	1229	39.61793	38.14226	39.27904	19.94749	25.39706	30.64581
protein_co	CKLF-like_M	264	262	274	978	1142	1097	1.989243	2.326443	2.720629	6.375082	9.667164	8.214861
protein_co	transmemb	1158	989	908	1422	1098	1371	22.84967	22.99719	23.60979	24.27359	24.34013	26.88552
protein_co	neuropepti	0	0	1	122	122	95	0	0	0.025963	2.079444	2.700432	1.860192
protein_co	achaete-scu	6	3	0	2	0	0	0.171515	0.10106	0	0.049459	0	0
protein_co	TANK-bindi	396	377	321	555	436	399	6.43877	7.223641	6.877768	7.806632	7.96422	6.447483
protein_co	chromobo	2403	1829	2046	647	803	756	20.78033	18.63887	23.3152	4.840231	7.801235	6.497259
protein_co	metastasis_	1	1	2	597	627	600	0.00578	0.006812	0.015234	2.985255	4.071558	3.446711
protein_co	cDNA_FLJ5	2	0	0	0	4	0	0.020476	0	0	0	0.046007	0
protein_co	transducin_	682	492	426	1932	1300	1629	5.307329	4.511945	4.368537	13.00654	11.36538	12.5986
protein_co	Iron/zinc_p	0	2	0	3	0	1	0	0.042069	0	0.046324	0	0.017739
protein_co	kringle_cor	588	463	389	328	402	354	5.035475	4.67252	4.389828	2.429965	3.86757	3.012839
protein_co	TRAF_inter	114	71	49	548	291	391	2.978911	2.186342	1.687266	12.38786	8.542691	10.15404
protein_co	checkpoint	188	208	174	524	362	418	3.887854	5.069003	4.741723	9.374463	8.410266	8.590888
protein_co	forkhead_b	133	82	89	267	215	213	2.413833	1.753786	2.128533	4.192084	4.383724	3.84189
protein_co	apoptosis-i	2	5	1	4	5	7	0.037152	0.109452	0.024478	0.064279	0.104344	0.129227
protein_co	potassium_	129	137	184	17	21	15	1.209598	1.513836	2.273547	0.1379	0.221218	0.139782
protein_co	UDP-Gal:be	5	8	7	7	3	4	0.09059	0.170808	0.167126	0.109717	0.061064	0.072025
protein_co	zinc_finger_	1180	802	711	3670	3208	3313	18.66459	14.9492	14.81975	50.2187	57.0059	52.07958
protein_co	solute_carr	2	0	1	7	7	12	0.036625	0	0.024131	0.110893	0.144009	0.218391
protein_co	potassium_	4	1	5	6	4	2	0.081857	0.024116	0.134834	0.106221	0.091961	0.040676
protein_co	chromoson	0	0	0	24	19	17	0	0	0	0.394535	0.405615	0.321048
protein_co	tubulin_alp	6	5	3	0	5	1	0.157406	0.154578	0.103712	0	0.147364	0.026072
protein_co	transcriptic	0	1	0	0	5	0	0	0.033238	0	0	0.158433	0
protein_co	Homo_sapi	52	29	19	72	28	30	2.61437	1.718181	1.258787	3.131549	1.581506	1.498976
protein_co	elastin_mic	9	2	10	31	24	37	0.125519	0.03287	0.183781	0.374016	0.376033	0.512835
protein_co	olfactomed	50	49	32	75	70	56	0.948084	1.094914	0.799579	1.230271	1.491158	1.055296

protein_co	family_witl	0	3	0	10	4	9	0	0.181184	0	0.443358	0.230304	0.458399
protein_co	RNA_bindi	266	230	264	416	490	384	1.93731	1.974024	2.533706	2.621041	4.009245	2.779446
protein_co	chemokine	0	0	0	1	0	2	0	0	0	0.014798	0	0.033999
protein_co	lin-9_homc	72	57	58	358	243	263	1.068616	0.996944	1.134362	4.596582	4.051766	3.879309
protein_co	BTB_(POZ)_	404	377	362	188	223	241	2.508875	2.758965	2.962382	1.009993	1.555792	1.487388
protein_co	nudix_(nuc	59	42	44	178	115	193	2.997619	2.514669	2.945858	7.823613	6.564041	9.745213
protein_co	ankyrin_rep	18	19	20	55	41	44	0.522444	0.649872	0.764948	1.380998	1.336904	1.269199
protein_co	MYCBP-ass	3	3	3	21	11	11	0.035827	0.04222	0.047212	0.216958	0.147583	0.130556
protein_co	paraneopla	2	4	0	0	1	2	0.028228	0.066529	0	0	0.015856	0.028053
protein_co	G_protein-	14	2	7	22	20	19	0.266226	0.044819	0.175411	0.361917	0.42727	0.359076
protein_co	family_witl	0	0	0	0	2	0	0	0	0	0	0.043381	0
protein_co	zinc_finger	14	12	36	117	135	137	0.312205	0.315355	1.05791	2.257149	3.38216	3.036278
protein_co	kin_of_IRR	3189	2573	2627	3555	3927	3764	24.57479	23.36588	26.67659	23.69943	33.99737	28.82668
protein_co	IQ_motif_c	312	254	251	1463	1508	1556	2.758449	2.646373	2.924279	11.18968	14.97824	13.67192
protein_co	transducer	1565	1449	1312	1695	1861	1856	18.16546	19.82018	20.06784	17.0202	24.26763	21.41015
protein_co	sodium_ch	7	6	3	65	84	80	0.043578	0.044018	0.024611	0.350062	0.587486	0.494958
protein_co	arylsulfatas	80	68	73	245	252	292	1.339854	1.342096	1.61111	3.549741	4.741516	4.860267
protein_co	ubiquitous	240	180	162	210	204	169	1.946062	1.719986	1.730993	1.473085	1.858338	1.361889
protein_co	chromoson	0	0	1	0	0	0	0	0	0.022956	0	0	0
protein_co	NPIP-like_p	3	2	2	8	2	13	0.035185	0.027642	0.03091	0.081168	0.026352	0.151525
protein_co	tetratricop	58	41	46	61	63	70	3.735496	3.111797	3.904028	3.398702	4.558373	4.480515
protein_co	leucine_ric	0	0	0	0	4	0	0	0	0	0	0.043975	0
pseudogen	ribosomal_	9	1	2	0	2	2	1.031318	0.135038	0.302006	0	0.257472	0.227766
protein_co	dynein_axc	9	1	0	0	0	2	0.03186	0.004172	0	0	0	0.007036
protein_co	short_chai	5	0	1	0	3	3	0.104709	0	0.027596	0	0.070581	0.062438
pseudogen	dual_specif	42	30	32	15	13	13	0.90277	0.759899	0.906385	0.278921	0.313921	0.277703
pseudogen	5-hydroxyt	84	101	113	255	195	211	1.008171	1.428511	1.78718	2.647636	2.629291	2.516791
protein_co	histone_clu	1	2	0	1	0	4	0.031215	0.07357	0	0.027004	0	0.12409
protein_co	protein_kir	455	402	372	991	852	830	3.994056	4.158492	4.303091	7.52557	8.402169	7.240866
protein_co	SET_domai	649	652	538	1502	1215	1302	10.94226	12.95439	11.95307	21.90763	23.01377	21.8164
protein_co	potassium_	0	0	0	33	25	31	0	0	0	0.294211	0.289449	0.317507
protein_co	smoothelin	1468	1164	999	926	959	1171	15.2987	14.29514	13.7192	8.348383	11.22784	12.12816
protein_co	neuropepti	144	146	82	39	14	31	7.510841	8.973999	5.636048	1.759761	0.820357	1.606932
protein_co	protein_ph	6	0	4	9	4	3	0.147674	0	0.129732	0.191627	0.110601	0.073381
protein_co	cytochrom	440	463	312	886	565	629	16.95345	21.02294	15.84144	29.53263	24.45698	24.08605
protein_co	ST6_(alpha	513	418	423	802	646	597	3.958422	3.800914	4.301103	5.353552	5.599977	4.578136
protein_co	protein_tyr	3903	3290	3190	4519	3388	3563	52.59066	52.24119	56.64161	52.67632	51.28644	47.71287
protein_co	actin_gamr	94789	75807	66296	160176	108134	113532	2224.39	2096.377	2050.1	3251.722	2850.784	2647.774
protein_co	transmemb	0	2	0	13	13	13	0	0.038511	0	0.183761	0.238638	0.211106
protein_co	DENN/MAD	1893	1562	1418	2572	2131	2183	19.91996	19.36983	19.66296	23.41379	25.19244	22.82975
protein_co	olfactory_r	0	0	0	0	2	0	0	0	0	0	0.113395	0
protein_co	-	1	0	0	1	0	3	0.009687	0	0	0.00838	0	0.028882
protein_co	diablo_IAP-	62	79	71	53	49	74	1.277673	1.918502	1.928063	0.944859	1.134418	1.515547
protein_co	vacuolar_p	259	238	190	421	291	388	4.955445	5.366202	4.790395	6.968319	6.254966	7.377756

protein_co	T-box_1	553	416	336	407	175	273	14.06166	12.46556	11.25863	8.953004	4.999177	6.89896
protein_co	ArfGAP_wit	1	1	7	16	7	7	0.018044	0.021264	0.166443	0.249755	0.141899	0.125528
processed_	-	98	45	54	180	96	115	1.73577	0.93926	1.26036	2.758047	1.910234	2.024294
protein_co	ubiquinol-(	1012	804	663	1480	1175	1574	58.4894	54.75954	50.4946	73.99823	76.2928	90.40886
protein_co	family_witl	146	145	166	178	116	142	0.959338	1.122778	1.437347	1.011816	0.8563	0.927292
pseudogen(	-	1	1	2	5	0	2	0.026887	0.031685	0.070862	0.1163	0	0.053442
pseudogen(	triggering_	0	0	1	0	0	2	0	0	0.056996	0	0	0.085971
protein_co	tripartite_r	1	0	0	2	2	3	0.029461	0	0	0.050973	0.066195	0.087836
protein_co	eukaryotic_	490	389	363	412	420	530	6.555746	6.133138	6.399816	4.768549	6.312834	7.047118
pseudogen(	-	2	2	0	0	4	2	0.242849	0.286182	0	0	0.545651	0.241349
protein_co	claudin_5	3	2	6	17	9	12	0.062332	0.04897	0.164278	0.305566	0.21008	0.24779
protein_co	nipsnap_hc	1144	979	750	1130	891	893	27.07398	27.30335	23.38957	23.1349	23.68933	21.00328
protein_co	contactin_	0	0	0	4	2	0	0	0	0	0.022503	0.014611	0
protein_co	leucine_ric	95	110	120	105	96	147	1.315906	1.795565	2.19037	1.258212	1.493901	2.023617
protein_co	potassium_	18	21	20	21	6	4	0.083291	0.114513	0.121953	0.084064	0.031191	0.018395
protein_co	adrenocept	44	41	32	132	100	105	1.095159	1.202584	1.049565	2.842245	2.796235	2.597309
protein_co	nuclear_rec	68	79	57	330	197	267	2.300312	3.149285	2.540899	9.657277	7.486745	8.976327
protein_co	family_witl	14	30	10	22	12	52	0.715419	1.806594	0.673391	0.972564	0.68891	2.64086
protein_co	cysteine-ric	855	661	598	1118	782	1084	17.26337	15.7278	15.91092	19.52829	17.73843	21.75196
protein_co	sec1_family	408	301	318	344	333	332	6.800984	5.912691	6.985115	4.960587	6.235983	5.499957
protein_co	ubiquitin-c	111	95	83	311	157	184	2.925062	2.950142	2.882206	7.089826	4.647944	4.818808
protein_co	potassium_	114	68	74	81	92	105	1.113519	0.782724	0.952488	0.684449	1.009554	1.019276
protein_co	G_protein-(	403	355	248	154	145	186	4.757017	4.938159	3.857591	1.572582	1.922856	2.181987
protein_co	protein_ph	567	483	507	1624	1250	1268	8.695696	8.729222	10.24623	21.54618	21.53676	19.32637
protein_co	TSPY-like_2	921	992	703	500	502	567	11.67033	14.81298	11.73853	5.48096	7.146221	7.140298
protein_co	golgin_A6_	27	25	23	5	8	14	0.31326	0.341813	0.351645	0.050185	0.104275	0.161428
protein_co	phosphogly	390	238	217	1826	1124	1425	7.571319	5.444914	5.551387	30.66696	24.51446	27.49359
protein_co	chromoson	152	194	117	247	250	282	1.617494	2.432808	1.640664	2.273835	2.98874	2.982344
protein_co	small_nucl(	255	282	203	274	237	344	6.247086	8.141296	6.553423	5.806988	6.52281	8.375397
protein_co	interleukin	758	622	488	3607	2914	3589	10.94634	10.58515	9.286547	45.06183	47.27573	51.50895
protein_co	cms1_ribos	194	162	158	910	409	648	4.788137	4.711801	5.138741	19.42984	11.34063	15.89459
protein_co	oligodendr	0	0	0	2	2	0	0	0	0	0.040227	0.052241	0
protein_co	protocadhe	130	76	106	196	261	250	1.105417	0.761559	1.187746	1.44179	2.493289	2.112675
protein_co	acyl-CoA_th	47	33	41	23	24	28	1.452555	1.201865	1.669757	0.61493	0.833288	0.860008
protein_co	OAF_homo	1828	1538	1334	1572	1179	1284	38.32718	38.00092	36.85712	28.51322	27.77113	26.75503
protein_co	aldehyde_d	1	3	12	9	14	10	0.013492	0.047697	0.213343	0.105043	0.212197	0.134083
protein_co	cerebellar_	100	53	58	3	9	12	4.075519	2.545458	3.114912	0.105771	0.412073	0.486042
protein_co	histone_clu	10	4	10	13	31	16	1.211464	0.571055	1.596414	1.362439	4.219115	1.926373
protein_co	potassium_	38	18	18	181	121	157	0.987608	0.551291	0.616465	4.069515	3.532934	4.055182
protein_co	histone_clu	6	0	0	0	2	2	0.709031	0	0	0	0.265517	0.234884
protein_co	POU_class_	174	140	112	59	55	48	1.786258	1.693675	1.515123	0.523974	0.634318	0.489718
lincRNA	long_interg	1	2	3	0	1	6	0.02279	0.053713	0.090095	0	0.025603	0.135895
protein_co	defensin_b(	0	1	0	0	2	0	0	0.102611	0	0	0.195644	0
protein_co	TM2_doma	393	343	282	537	359	450	6.707225	6.89845	6.342117	7.928437	6.883254	7.632599

protein_co	tumor_sup	579	495	430	1318	994	1355	18.1808	18.31668	17.79253	35.80247	35.06469	42.28472
protein_co	tumor-asso	5	0	2	299	244	206	0.128	0	0.067469	6.621795	7.017468	5.241051
protein_co	SIX_homeo	1	1	0	0	0	0	0.018996	0.022385	0	0	0	0
pseudogen	dopamine_	0	0	0	0	1	0	0	0	0	0	0.04136	0
protein_co	protein_kir	25	40	26	102	116	87	0.355213	0.669756	0.486808	1.253754	1.851639	1.228508
protein_co	coiled-coil_	0	0	0	18	54	45	0	0	0	0.140992	0.54929	0.404931
protein_co	zinc_finger_	27	20	27	95	60	77	0.270721	0.236317	0.356744	0.824033	0.675863	0.767288
protein_co	maestro_he	0	1	1	5	0	5	0	0.010484	0.011723	0.03848	0	0.044206
pseudogen	-	582	522	373	874	599	823	10.31525	10.90271	8.711652	13.40082	11.92704	14.49661
protein_co	SRSF_prote	9	6	2	17	18	5	0.106378	0.083574	0.031151	0.173829	0.239019	0.058734
protein_co	slit_homol	122	106	96	495	504	439	0.665444	0.681341	0.690014	2.335716	3.088385	2.379721
protein_co	histone_clu	14	12	6	7	14	3	1.611248	1.627506	0.909956	0.69694	1.810137	0.343135
protein_co	ephrin-A5	628	599	520	1080	923	932	6.231855	7.004733	6.799795	9.271381	10.28984	9.191433
protein_co	keratin_ass	0	0	0	1	0	0	0	0	0	0.070896	0	0
protein_co	histone_clu	0	0	0	0	7	0	0	0	0	0	0.527002	0
protein_co	spermatoge	4	3	6	0	0	2	0.111046	0.098145	0.219496	0	0	0.05518
protein_co	plakophilin	0	0	0	525	368	515	0	0	0	8.559781	7.79179	9.646221
protein_co	MAP7_dom	11	16	17	74	54	73	0.148181	0.253996	0.301775	0.862371	0.817226	0.977309
protein_co	colony_stir	1393	1229	1057	518	415	359	17.51706	18.21247	17.51539	5.635115	5.862828	4.486566
protein_co	collectin_s	0	0	2	5	3	13	0	0	0.110211	0.18088	0.140938	0.540271
protein_co	actin-relate	117	89	103	81	48	59	3.089325	2.769331	3.583849	1.85023	1.423862	1.548244
protein_co	phospholip	175	163	114	105	88	123	2.832367	3.108896	2.431371	1.470157	1.600086	1.978456
protein_co	mastermin	624	518	660	360	440	377	4.648914	4.547825	6.479562	2.320237	3.682719	2.791373
protein_co	poly(A)_bin	0	0	0	5	0	0	0	0	0	0.104088	0	0
pseudogen	alpha_13-g	0	0	1	5	5	0	0	0	0.069763	0.228995	0.29738	0
protein_co	synovial_sa	465	416	355	617	541	648	5.479092	5.776384	5.512122	6.289322	7.161467	7.588227
protein_co	potassium_	1	0	0	0	0	0	0.009931	0	0	0	0	0
pseudogen	-	0	0	3	1	4	21	0	0	0.208042	0.045526	0.236485	1.098305
protein_co	topoisomer	647	621	453	620	531	609	16.88163	19.09452	15.57554	13.99474	15.56516	15.79199
protein_co	coatomer_	4331	3643	3871	3837	3258	3401	65.06454	64.49447	76.63271	49.86674	54.98653	50.77763
protein_co	leucine_ric	1	0	1	0	3	2	0.014669	0	0.01933	0	0.04944	0.029157
protein_co	THAP_dom	232	153	133	492	306	371	6.276091	4.877528	4.741194	11.51408	9.29976	9.974355
processed_	-	5	6	20	14	12	23	0.060796	0.085973	0.320456	0.147263	0.163921	0.277934
protein_co	kinetochor	187	179	205	1021	787	711	1.41935	1.601061	2.05039	6.70404	6.710759	5.363239
protein_co	chemokine_	17	5	13	1	12	4	0.463438	0.160628	0.467004	0.023583	0.367513	0.108371
protein_co	noncompa	0	0	0	5	0	3	0	0	0	0.056361	0	0.038849
protein_co	WD_repeat	543	539	462	591	621	606	8.187684	9.577609	9.179902	7.709243	10.51967	9.081206
protein_co	thioredoxir	4	14	5	400	226	281	0.067656	0.279051	0.111443	5.852895	4.294427	4.723498
protein_co	forkhead_b	109	110	65	423	544	756	1.748127	2.078961	1.373709	5.868809	9.801545	12.04975
protein_co	POU_class_	4	2	10	81	123	97	0.05189	0.030575	0.170947	0.90902	1.792585	1.250567
protein_co	protein_tyr	59	45	35	210	128	190	1.673911	1.504527	1.308529	5.154218	4.079806	5.357272
protein_co	forkhead_b	3	2	3	0	0	7	0.0768	0.060336	0.101204	0	0	0.178094
protein_co	transmemb	54	46	33	21	18	17	2.772855	2.783546	2.232966	0.932858	1.038377	0.867545
protein_co	protein_S_	573	619	581	1066	804	854	8.530706	10.85996	11.39833	13.72937	13.44731	12.63566

protein_co	gastrin	0	0	0	7	0	2	0	0	0	0.682111	0	0.22389
protein_co	NUT_midlir	3	0	1	8	2	4	0.038718	0	0.017007	0.08932	0.028998	0.051306
protein_co	HD_domair	18	21	24	76	61	72	0.781097	1.073887	1.372392	2.853047	2.973796	3.105091
protein_co	brain_expr	0	0	0	3	3	6	0	0	0	0.159764	0.207474	0.367075
protein_co	ZFP1_zinc_	192	163	167	250	149	147	3.127591	3.128985	3.584759	3.522993	2.726742	2.379774
protein_co	cell_cycle_	58	67	38	5	17	17	1.862085	2.534856	1.607644	0.138869	0.613154	0.542413
protein_co	chromoson	4	0	1	7	14	5	0.17647	0	0.058136	0.26716	0.693886	0.219225
protein_co	dual_specif	92	63	50	603	436	550	1.087181	0.877327	0.778608	6.164451	5.788281	6.459314
pseudogen	-	7	10	8	1	12	10	0.134319	0.226124	0.202286	0.0166	0.258685	0.1907
protein_co	suppressor_	3525	3146	2353	619	708	846	68.38293	71.92078	60.15134	10.38825	15.43018	16.31055
protein_co	chromoson	0	1	0	0	0	0	0	0.037788	0	0	0	0
protein_co	SLIT_and_N	10	14	6	184	104	140	0.122605	0.202276	0.096938	1.951598	1.432491	1.705875
protein_co	lysophosph	6	9	7	4	0	0	0.100172	0.17707	0.154003	0.057772	0	0
protein_co	exportin_t	2201	1935	1869	3193	2496	2350	18.167	18.82137	20.32859	22.79949	23.14498	19.27705
protein_co	transmemb	1220	888	726	11	2	5	20.18375	17.31259	15.82754	0.157434	0.037172	0.082209
protein_co	phosphodi	28	5	19	93	97	75	0.326077	0.068618	0.291576	0.936933	1.269064	0.868028
pseudogen	-	3	18	3	12	7	16	0.195354	1.381278	0.257429	0.675999	0.512093	1.035455
protein_co	family_with	1	0	1	2	2	7	0.041296	0	0.054418	0.071449	0.092786	0.287284
protein_co	stannin	835	719	744	980	965	1063	13.34714	13.54371	15.67146	13.55161	17.32918	16.8867
protein_co	chromoson	0	0	0	2	0	0	0	0	0	0.074957	0	0
protein_co	potassium_	0	0	0	36	46	21	0	0	0	0.400866	0.665182	0.268635
pseudogen	ribosomal_	2	2	1	5	6	4	0.140427	0.165485	0.092524	0.303706	0.473283	0.27912
protein_co	NEL-like_2_	15	11	22	627	521	617	0.219855	0.189996	0.424915	7.950142	8.578891	8.987505
pseudogen	-	17	12	7	13	4	22	0.319261	0.265574	0.173233	0.211205	0.084393	0.41061
pseudogen	zinc_finger_	4	0	2	3	3	2	0.106094	0	0.069903	0.068836	0.089393	0.052719
protein_co	KRAB-A_do	5	12	11	4	9	6	0.10332	0.292214	0.29953	0.071505	0.208932	0.123218
protein_co	mediator_c	1500	1353	1150	1126	1220	1254	11.3819	12.09841	11.49889	7.391367	10.39997	9.456503
protein_co	zinc_finger_	81	85	73	813	490	551	1.619419	2.002627	1.923232	14.06137	11.00574	10.94801
protein_co	septin_9	22762	18447	15309	11533	10153	11861	270.6137	258.4474	239.8397	118.6164	135.6072	140.1427
protein_co	protease_se	0	0	0	0	0	2	0	0	0	0	0	0.044325
protein_co	cell_divisio	141	149	140	881	748	716	2.000718	2.491496	2.617759	10.81448	11.92388	10.09693
pseudogen	olfactory_r	2	0	2	80	34	26	0.104626	0	0.137872	3.620467	1.998203	1.351744
protein_co	RALY_RNA_	0	0	0	9	17	10	0	0	0	0.152606	0.374339	0.194795
protein_co	glutathione	2	0	0	1	0	0	0.05125	0	0	0.022168	0	0
protein_co	APC_memb	173	136	144	275	390	336	1.084779	1.004943	1.189851	1.491733	2.747318	2.093844
protein_co	zinc_finger_	722	542	607	729	804	798	4.250823	3.76047	4.709332	3.713012	5.317909	4.669263
protein_co	histone_clu	479	359	333	173	125	151	11.40744	10.07521	10.45037	3.564197	3.34435	3.573874
protein_co	chromoson	25	10	8	0	0	0	0.773991	0.364841	0.326378	0	0	0
protein_co	claudin_6	1	8	12	19814	14326	19222	0.030443	0.287005	0.481403	521.8284	489.9666	581.5683
protein_co	septin_5	825	717	529	49	28	67	10.61909	10.87576	8.972715	0.545623	0.404893	0.857073
protein_co	eukaryotic_	251	216	213	448	413	364	3.596262	3.647023	4.021537	5.552885	6.647782	5.183089
protein_co	leucine_ric	0	0	0	0	5	0	0	0	0	0	0.245972	0
protein_co	renalase_FA	74	69	59	158	85	119	1.157351	1.271714	1.215963	2.137733	1.493487	1.849652
protein_co	apolipopro	0	0	0	7	5	2	0	0	0	0.084544	0.078423	0.02775

protein_co	family_with	0	1	0	80	54	49	0	0.016592	0	0.974445	0.854175	0.685662
protein_co	atlastin_GT	1660	1533	1247	1088	844	856	12.31704	13.4044	12.19269	6.983771	7.035413	6.312211
protein_co	NADH_dehy	535	494	390	946	730	1064	34.83817	37.90841	33.46578	53.29122	53.40396	68.85775
protein_co	Putative_in	0	2	0	2	5	1	0	0.044404	0	0.032597	0.105829	0.018724
protein_co	ribosomal_	0	0	0	2	0	0	0	0	0	0.047658	0	0
protein_co	small_integ	20	46	41	40	56	53	0.690235	1.870818	1.864599	1.194235	2.17122	1.817826
protein_co	t-complex-a	5	7	8	3	10	7	0.34422	0.567899	0.725756	0.178669	0.773419	0.478932
protein_co	ubiquitin-c	1411	1239	1029	2850	2340	2479	17.21192	17.81069	16.54065	30.07532	32.06766	30.05305
protein_co	spermidine	62	57	73	123	98	90	1.475873	1.598966	2.289892	2.532943	2.620791	2.129166
protein_co	oxysterol_b	96	96	80	33	64	64	1.171045	1.380005	1.285959	0.348241	0.877064	0.775875
protein_co	chromoson	5	9	7	2	0	1	0.195066	0.413773	0.35987	0.0675	0	0.038772
protein_co	tumor_sup	0	3	0	0	0	0	0	0.052048	0	0	0	0
protein_co	histone_clu	1	1	2	0	8	4	0.115845	0.136516	0.30531	0	1.041154	0.460517
protein_co	zinc_finger_	0	1	0	23	14	12	0	0.012606	0	0.212846	0.168249	0.127575
protein_co	apolipopro	190	141	116	327	176	279	8.997128	7.86822	7.238409	13.39557	9.362935	13.12998
protein_co	proline_ric	114	122	107	25	16	16	3.305188	4.168293	4.087991	0.627039	0.521147	0.461021
protein_co	transmemb	5984	4876	4209	5146	3817	5714	215.0705	206.5191	199.344	160.0008	154.1206	204.0982
protein_co	dopamine_	53	40	50	0	0	0	0.692124	0.615567	0.860425	0	0	0
lincRNA	long_interg	1	0	2	0	0	0	0.072821	0	0.191921	0	0	0
protein_co	transmemb	78	60	82	177	152	193	2.851794	2.585127	3.950683	5.598347	6.243328	7.012784
protein_co	RNA_bindir	1007	855	993	1025	994	952	5.25289	5.255839	6.82579	4.625468	5.825112	4.935321
protein_co	armadillo_t	1578	1282	1240	1176	1020	957	30.24652	28.95766	31.32023	19.50019	21.96431	18.23014
protein_co	phosphatid	158	103	163	889	503	693	3.585374	2.754366	4.87416	17.45188	12.82314	15.62861
protein_co	BTB_(POZ)_	706	543	443	725	528	586	17.02795	15.4335	14.07979	15.1272	14.30674	14.04639
protein_co	sex_determ	0	0	0	0	3	1	0	0	0	0	0.211157	0.062265
protein_co	H1_histone	1107	839	615	3331	2446	3071	38.91479	34.75651	28.48899	101.2989	96.599	107.2893
protein_co	RNA_bindir	187	209	196	53	46	55	2.361633	3.110457	3.261833	0.579042	0.652646	0.690308
protein_co	SMT3_supp	1895	1611	1428	2764	2040	2465	55.51919	55.62072	55.13114	70.05433	67.14492	71.7729
protein_co	IMP2_inner	127	83	69	211	107	148	4.426271	3.408941	3.168971	6.361797	4.189548	5.12632
protein_co	transcriptic	0	0	0	0	1	5	0	0	0	0	0.054069	0.239155
pseudogen	-	0	0	0	1	0	0	0	0	0	0.047707	0	0
protein_co	chloride_ch	0	1	5	9	1	3	0	0.024304	0.135885	0.160573	0.023169	0.061489
protein_co	jagged_2	14	15	4	92	76	105	0.127022	0.16038	0.047824	0.722108	0.774665	0.946782
protein_co	formin-like	14	9	8	23	30	23	0.150676	0.114147	0.113459	0.214144	0.362732	0.24601
protein_co	NUT_family	36	28	38	24	38	55	0.479586	0.439571	0.667087	0.276591	0.568718	0.728176
protein_co	peptidyl-tR	124	139	81	151	110	98	6.474047	8.552164	5.572807	6.820153	6.452023	5.084987
protein_co	lipocalin_1	0	0	0	2	3	3	0	0	0	0.050775	0.098907	0.087496
protein_co	Wilms_tum	0	0	0	8	1	8	0	0	0	0.117358	0.019051	0.134821
protein_co	ZFP90_zinc	70	51	60	43	42	33	0.794569	0.682199	0.897469	0.422245	0.535589	0.372269
protein_co	family_with	125	108	124	77	59	43	0.641118	0.652768	0.838079	0.34165	0.339961	0.219183
protein_co	mucin_6_o	16	24	21	2	11	13	0.105803	0.187023	0.182991	0.011441	0.081718	0.085434
pseudogen	-	1	0	1	0	0	0	0.09112	0	0.120074	0	0	0
protein_co	nucleolar_c	361	295	251	1126	711	869	11.7106	11.27719	10.72952	31.599	25.91138	28.01569
protein_co	ubiquitin_s	7	1	1	66	32	38	0.174066	0.029304	0.032768	1.419788	0.893955	0.939095

protein_co	NADH_deh	1030	783	604	1310	1062	1398	43.41499	38.89299	33.54858	47.76797	50.28935	58.56245
protein_co	cholinergic	0	0	1	6	4	6	0	0	0.022926	0.090303	0.078181	0.103741
protein_co	sortilin-rel	234	217	168	7	10	11	2.013685	2.200607	1.905109	0.052112	0.096677	0.094076
protein_co	transmemb	84	69	22	66	35	56	2.90277	2.809891	1.001823	1.97306	1.358784	1.923229
protein_co	transmemb	155	137	99	56	55	53	2.51174	2.616198	2.114039	0.785044	1.001278	0.853549
protein_co	SIVA1_apo	633	578	452	2231	1393	2267	8.090693	8.705965	7.61299	24.6686	20.0024	28.79673
protein_co	BRI3_bindi	220	212	175	1241	1178	1130	1.751958	1.9895	1.836428	8.549405	10.5389	8.943122
protein_co	interferon_	32	10	3	10	7	3	1.150891	0.42383	0.142181	0.311134	0.282834	0.10723
protein_co	diacylglyce	502	439	301	517	384	439	13.26167	13.66677	10.47842	11.81539	11.39658	11.52573
protein_co	regulatory_	0	0	0	5	5	3	0	0	0	0.066183	0.085948	0.045619
protein_co	roundabou	109	65	133	58	61	53	0.602985	0.423741	0.969542	0.277569	0.379105	0.291384
protein_co	adaptor-rel	733	659	693	2154	1591	1608	10.74059	11.37933	13.38111	27.30441	26.19047	23.41638
protein_co	coagulatio	30	24	25	43	17	13	0.175321	0.165284	0.192525	0.217392	0.111612	0.075503
protein_co	5'-nucleoti	1	1	1	0	1	0	0.019769	0.023296	0.026051	0	0.022209	0
protein_co	carbonic_a	78	73	61	146	76	92	1.082411	1.193789	1.115481	1.752724	1.184841	1.268805
protein_co	U-box_dom	166	112	82	208	140	152	1.897691	1.508837	1.235282	2.057044	1.79802	1.726913
pseudogen	-	6	5	3	26	10	9	0.08821	0.086626	0.05812	0.330678	0.165165	0.131499
protein_co	v-maf_mus	262	201	147	437	269	399	5.570498	5.036118	4.118555	8.0378	6.42531	8.430926
protein_co	BRF1_hom	729	577	460	873	664	973	2.113697	1.971506	1.75755	2.189739	2.162879	2.803739
protein_co	leucine_ric	0	0	0	0	4	0	0	0	0	0	0.151242	0
protein_co	sema_dom	386	380	296	345	223	310	5.367802	6.227302	5.424201	4.150413	3.48388	4.284307
protein_co	maestro_he	1	0	0	8	1	1	0.009875	0	0	0.068344	0.011094	0.009814
pseudogen	-	4	0	4	1	4	2	0.240095	0	0.316387	0.051926	0.269732	0.119306
protein_co	calcium_an	506	418	322	555	294	382	21.48207	20.91265	18.01426	20.38363	14.02239	16.11754
lincRNA	-	3	6	1	5	1	1	0.088778	0.209238	0.038996	0.128001	0.033245	0.02941
protein_co	ankyrin_re	117	161	141	4	13	3	1.594362	2.585437	2.531949	0.047155	0.199019	0.040629
protein_co	negative_el	605	499	346	1042	761	970	9.581005	9.312437	7.220489	14.27534	13.53909	15.26642
protein_co	solute_carr	9	4	21	38	36	11	0.12127	0.063515	0.372876	0.442952	0.544956	0.147303
protein_co	sarcoglycar	0	9	0	0	0	0	0	0.251338	0	0	0	0
protein_co	EF-hand_ca	12	12	10	40	12	6	0.409866	0.483002	0.450086	1.181907	0.460459	0.203667
protein_co	chromoson	0	0	2	0	2	2	0	0	0.055324	0	0.047166	0.041724
processed_	-	3	3	1	16	13	13	0.075738	0.089253	0.033268	0.349443	0.368711	0.326172
protein_co	general_tra	468	399	300	948	680	949	11.65948	11.71421	9.848934	20.4317	19.03229	23.49682
protein_co	fibronectin	816	738	682	345	300	253	5.438732	5.796569	5.989999	1.989251	2.246352	1.67586
protein_co	integrator_	636	540	405	865	810	869	10.24976	10.25552	8.600953	12.05968	14.66529	13.9183
protein_co	ribosomal_	1850	1596	1318	2047	1487	2289	33.26795	33.82161	31.23234	31.84455	30.04099	40.90814
protein_co	mannosida	4	12	9	31	34	20	0.078869	0.278828	0.233843	0.528777	0.75314	0.391911
protein_co	adenylosuc	24	13	13	4	18	10	0.488686	0.311939	0.348816	0.07046	0.411756	0.202362
protein_co	anoctamin_	3	0	1	30	22	41	0.028945	0	0.012714	0.250404	0.238467	0.393143
protein_co	Fas_(TNFRS	380	339	264	1388	1017	922	4.606727	4.843014	4.217428	14.55665	13.85093	11.10835
protein_co	myeloid-as	5	4	2	0	3	0	0.107955	0.101774	0.056903	0	0.072768	0
protein_co	family_wit	2462	1949	2078	231	153	218	41.49657	38.71177	46.15349	3.36821	2.897108	3.65166
protein_co	necdin-like	481	455	337	545	381	460	15.14849	16.88663	13.98586	14.84854	13.48026	14.39766
protein_co	heat_shock	1950	1577	1121	3546	2490	3015	29.9145	28.50926	22.66144	47.05967	42.91366	45.96678

protein_co	chromoson	649	538	572	828	652	510	8.289193	8.097611	9.627165	9.148732	9.35544	6.473623
protein_co	TBC1_dom	77	91	50	58	49	110	1.202849	1.675209	1.029261	0.783811	0.859935	1.707744
protein_co	purine-rich	207	194	186	438	338	341	4.192343	4.630153	4.964028	7.674032	7.690459	6.863577
protein_co	histone_clu	6	5	8	15	21	13	0.701205	0.688606	1.232023	1.51652	2.757162	1.509895
protein_co	inositol_pc	6	7	7	48	76	53	0.094905	0.130479	0.145905	0.656811	1.350514	0.833147
protein_co	neuropepti	0	0	0	4	2	13	0	0	0	0.050523	0.032805	0.188633
protein_co	Mix_paired	1	0	4	7	6	7	0.026404	0	0.139179	0.159896	0.177983	0.18369
protein_co	major_facil	0	0	0	7	5	7	0	0	0	0.143635	0.133235	0.165008
protein_co	leucine_ric	106	89	60	139	120	105	1.774746	1.756011	1.323781	2.013298	2.257151	1.747146
protein_co	DEAD_(Asp	282	280	182	627	542	786	3.164341	3.702536	2.691165	6.086459	6.832545	8.765291
protein_co	NODAL_mo	1057	932	1069	703	822	737	12.85814	13.36061	17.13625	7.398123	11.23373	8.910054
lincRNA	long_interg	0	0	0	0	1	0	0	0	0	0	0.0294	0
pseudogen	golgin_A8_	0	0	0	0	1	0	0	0	0	0	0.021348	0
lincRNA	long_interg	3	1	0	0	1	4	0.164243	0.064517	0	0	0.061506	0.217638
protein_co	single_imm	104	49	54	262	151	191	2.949043	1.637386	2.017792	6.427056	4.810318	5.382584
protein_co	nuclear_rec	635	546	412	259	267	282	8.671017	8.786098	7.413586	3.059561	4.095969	3.82697
protein_co	protease_se	0	0	0	0	0	1	0	0	0	0	0	0.048852
protein_co	interferon_	853	773	526	80	34	74	68.52605	73.18014	55.68359	5.559806	3.06856	5.908103
protein_co	tumor_nec	209	126	132	97	59	99	2.362731	1.678594	1.966422	0.948643	0.749323	1.112277
protein_co	zinc_finger_	952	790	833	824	1053	1019	4.920417	4.811706	5.673417	3.684301	6.114238	5.234181
protein_co	piggyBac_t	104	100	65	254	170	193	1.912422	2.166993	1.575065	4.040612	3.511951	3.527097
protein_co	WW_doma	2084	1665	1629	2191	1860	2505	100.6652	94.77698	103.6901	91.55602	100.9354	120.2538
protein_co	RAB11B_m	2211	1818	1346	3242	1919	2470	66.84896	64.77492	53.62729	84.79729	65.18234	74.21856
protein_co	protein_arg	155	165	133	496	382	370	1.973035	2.475108	2.230949	5.461952	5.462804	4.68074
protein_co	glycoprotei	17	47	38	51	50	58	0.359855	1.17242	1.059978	0.933924	1.189043	1.220158
protein_co	PRP39_pre	518	460	453	622	578	610	7.819628	8.183164	9.011339	8.122874	9.802418	9.151574
protein_co	melanoma_	0	0	0	1	3	2	0	0	0	0.01359	0.052946	0.031225
protein_co	peptidylpro	17	20	15	19	12	17	0.223269	0.30954	0.2596	0.215872	0.177056	0.22189
protein_co	zinc_finger_	469	394	298	718	587	703	6.400961	6.336882	5.359489	8.477343	9.000351	9.535364
protein_co	KIAA0825	21	23	43	45	15	18	0.193316	0.249508	0.521617	0.358364	0.155128	0.164676
protein_co	UBA-like_d	102	72	53	501	470	491	3.400492	2.828663	2.328372	14.44915	17.60307	16.26795
protein_co	cerebral_d	6	24	14	25	10	19	0.212899	1.003556	0.654615	0.767408	0.398632	0.670018
protein_co	notum_pec	3	5	4	142	104	130	0.06834	0.134225	0.120074	2.798384	2.661573	2.943127
protein_co	kelch-like_f	1	0	1	0	2	0	0.028417	0	0.037447	0	0.06385	0
protein_co	RNA_bindi	0	0	0	10	15	10	0	0	0	0.229914	0.447861	0.264127
protein_co	Williams-B	1	0	0	451	410	366	0.013631	0	0	5.31805	6.278354	4.957967
pseudogen	CD24_mole	241	143	203	2436	2585	2317	52.50527	36.71377	58.27961	459.1199	632.6965	501.6739
protein_co	zinc_finger_	27	22	38	23	40	20	0.486193	0.466847	0.901702	0.358291	0.809196	0.357919
protein_co	interleukin	80	63	66	84	77	120	2.482579	2.303884	2.698931	2.255046	2.684435	3.700871
protein_co	coiled-coil_	841	617	526	2014	1493	2138	18.04027	15.59693	14.86851	37.37399	35.97956	45.57895
protein_co	surfactant_	0	3	0	0	0	1	0	0.085502	0	0	0	0.024036
protein_co	RANBP2-lik	10	3	1	0	0	0	0.076383	0.027004	0.010065	0	0	0
protein_co	ADP-ribosy	192	184	202	432	414	462	3.129517	3.53428	4.338726	6.09148	7.580982	7.483895
protein_co	chromoson	1	0	0	1	1	3	0.01633	0	0	0.014127	0.018345	0.048687

protein_co	cyclin-depe	766	732	512	1240	817	1097	12.12703	13.65664	10.68146	16.98285	14.53105	17.26005
protein_co	transmemb	0	0	0	2	6	11	0	0	0	0.027615	0.107584	0.174481
protein_co	suppressor_	63	40	39	397	277	261	2.72268	2.03715	2.221035	14.84258	13.44884	11.21001
protein_co	transcobala	1010	960	800	670	451	471	21.09286	23.62612	22.01603	12.10464	10.58132	9.775628
protein_co	growth_arr	679	532	416	893	602	650	10.63204	9.816703	8.583711	12.09655	10.58991	10.11509
protein_co	ATPase_H+_	239	248	219	744	566	603	2.185679	2.672682	2.639171	5.886057	5.815058	5.480441
protein_co	parkinson_	37	23	33	7	1	5	0.468616	0.343282	0.550763	0.076697	0.014229	0.062935
protein_co	chromoson	74	56	48	520	437	658	0.882946	0.787404	0.754708	5.367462	5.857781	7.802579
protein_co	heparan_su	0	0	0	4	3	7	0	0	0	0.110425	0.107551	0.222
protein_co	hepatocyte	2516	2175	1551	2475	2025	2758	44.84833	45.68798	36.43194	38.16575	40.55176	48.85843
protein_co	tumor_nec	201	130	112	252	191	247	2.767527	2.109338	2.032116	3.001645	2.95446	3.379888
protein_co	RAD51_hor	93	71	89	109	112	134	2.04805	1.842566	2.58275	2.076573	2.770925	2.93273
protein_co	mitogen-ac	571	530	321	100	69	132	12.43493	13.6016	9.211853	1.883953	1.688128	2.856872
protein_co	SP140_nuc	155	126	115	86	47	43	2.285117	2.189043	2.234135	1.096827	0.778437	0.630021
protein_co	mitochond	1	0	0	0	0	0	0.020323	0	0	0	0	0
protein_co	threonyl-tR	318	329	220	323	227	238	4.6635	5.685752	4.251502	4.097797	3.739898	3.468738
protein_co	SET_and_M	802	742	536	211	106	174	22.79049	24.84793	20.07145	5.187101	3.38403	4.914034
protein_co	methyltran	1521	1442	1198	916	893	991	19.75546	22.07142	20.50452	10.29239	13.03042	12.79208
lincRNA	long_interg	0	3	0	0	0	0	0	0.126804	0	0	0	0
protein_co	interferon_	0	0	0	160	169	177	0	0	0	1.610865	2.209591	2.047194
protein_co	SH3_domai	53	22	24	43	33	54	2.242904	1.097146	1.338384	1.574223	1.568909	2.27111
protein_co	family_witl	29	27	20	51	33	55	0.549889	0.60332	0.499737	0.836585	0.702975	1.036452
protein_co	family_witl	0	0	0	0	1	1	0	0	0	0	0.023062	0.020401
protein_co	chromoson	114	95	94	115	119	196	2.650537	2.602914	2.879995	2.313076	3.108315	4.528921
protein_co	transmemb	187	168	119	242	134	128	9.677386	10.24549	8.115181	10.83415	7.790589	6.583185
protein_co	GPRIN_fam	0	0	0	30	93	55	0	0	0	0.216305	0.87079	0.455569
protein_co	PARP1_bin	66	60	71	189	220	218	1.095674	1.173805	1.553212	2.714328	4.103074	3.596696
protein_co	SH3_and_c	26	25	6	13	15	15	0.831199	0.941844	0.252766	0.359532	0.538731	0.476577
protein_co	receptor_ty	738	648	753	1611	1547	1206	6.699323	6.93197	9.007502	12.65124	15.77662	10.88007
pseudogen	succinate_d	261	286	218	400	314	367	5.547009	7.162943	6.105337	7.3543	7.497165	7.751648
processed_	-	0	2	0	0	0	4	0	0.066335	0	0	0	0.111885
protein_co	mucin_1_c	146	118	86	16	9	25	4.26802	4.06502	3.312889	0.404629	0.295573	0.726312
protein_co	chromoson	933	947	608	1320	944	1191	12.92359	15.45818	11.09787	15.81752	14.69002	16.39543
protein_co	interferon_	96	78	67	203	129	171	2.477979	2.37262	2.278957	4.532997	3.740806	4.386642
protein_co	l(3)mbt-like	132	113	67	116	117	119	1.616893	1.631146	1.081476	1.229216	1.610061	1.448652
protein_co	BRCA1/BRC	349	300	348	886	758	788	6.492061	6.576359	8.530436	14.25785	15.84074	14.56777
protein_co	synaptic_ve	0	0	0	1	1	0	0	0	0	0.004061	0.005273	0
protein_co	family_witl	3	4	8	1	0	0	0.093701	0.147228	0.329266	0.02702	0	0
protein_co	chromoson	14	5	3	24	10	19	0.35565	0.149683	0.100427	0.527435	0.285393	0.479687
protein_co	chromoson	0	0	0	0	0	2	0	0	0	0	0	0.207961
protein_co	phosphodi	2	0	2	5	8	0	0.070353	0	0.092709	0.152156	0.316151	0
protein_co	protein_kir	64	67	84	50	40	53	0.489062	0.603346	0.84586	0.330535	0.343394	0.402504
protein_co	nuclear_rec	8765	6985	6961	4511	4159	3671	87.96736	82.612	92.06108	39.16566	46.89296	36.61539
protein_co	delta-like_1	376	312	177	2	6	6	11.7093	11.44998	7.263589	0.053881	0.209915	0.185697

protein_co	TLC_domai	27	16	24	17	5	6	1.442388	1.007269	1.689524	0.785652	0.30008	0.318551
protein_co	limbic_syst	566	470	468	123	120	84	17.22104	16.85186	18.76392	3.237509	4.101787	2.539989
protein_co	AHNAK_nu	4612	3944	4636	25	32	35	13.31682	13.42008	17.63963	0.062447	0.103803	0.100436
protein_co	olfactomed	998	833	780	560	577	515	8.223364	8.088557	8.469317	3.991811	5.341261	4.217313
protein_co	Sp1_transc	1336	1157	1282	1743	1543	1562	9.302797	9.493963	11.76332	10.49947	12.07041	10.80931
protein_co	spermatoge	0	0	0	3	1	0	0	0	0	0.099132	0.042912	0
pseudogen	WAS_prote	346	305	157	388	310	473	10.64357	11.05651	6.364227	10.32538	10.71327	14.46046
pseudogen	actin_beta_	0	0	3	3	2	7	0	0	0.186201	0.122239	0.105829	0.327668
protein_co	mitochond	464	365	286	986	636	758	17.71061	16.41782	14.38522	32.55784	27.2723	28.75375
protein_co	developing	0	0	0	3	0	2	0	0	0	0.048965	0	0.037501
protein_co	family_witl	21	28	17	26	32	28	1.069001	1.67967	1.140361	1.144973	1.830028	1.416532
protein_co	protein_dis	2	0	2	1	0	0	0.054132	0	0.071333	0.023415	0	0
protein_co	polycomb_	1455	1141	1190	1563	1257	1340	13.54954	12.52144	14.60304	12.59168	13.15061	12.40155
protein_co	leishmanol	212	194	218	131	95	116	1.593567	1.718475	2.159363	0.851861	0.802245	0.866567
protein_co	prolyl_4-hy	24541	20493	16419	14792	11781	11683	499.126	491.1686	440.0474	260.2602	269.1839	236.1467
protein_co	proteasom	1649	1307	1110	3655	2457	3025	39.68168	37.06398	35.19875	76.08864	66.42379	72.34432
protein_co	pre-B-cell_l	438	381	372	1388	1385	1220	2.048243	2.099614	2.292372	5.615129	7.276225	5.669918
pseudogen	-	4	0	0	0	0	0	0.510275	0	0	0	0	0
protein_co	NADH_deh	643	636	318	7	17	12	28.36755	33.0655	18.48727	0.26716	0.842575	0.526141
protein_co	SHC_(Src_h	37	30	39	52	33	24	0.429754	0.410626	0.596921	0.522497	0.430607	0.277038
pseudogen	ferritin_hea	0	0	0	0	1	0	0	0	0	0	0.107942	0
pseudogen	-	92	125	55	139	80	135	12.98819	20.79591	10.23195	16.97613	12.6882	18.94106
protein_co	ZFP36_ring	8268	7065	6371	5562	5512	4719	137.2151	138.1722	139.3297	79.85377	102.7684	77.83251
protein_co	ubiquitin-c	2406	2052	1687	4668	3214	3655	36.90989	37.09638	34.10335	61.94995	55.39136	55.72424
protein_co	neurotroph	14	5	9	279	205	240	0.63511	0.2673	0.53802	10.94935	10.44778	10.82037
protein_co	bromodom	468	335	512	566	485	483	1.916342	1.616512	2.762689	2.004964	2.231094	1.965549
protein_co	premelanos	15	6	10	140	83	166	0.288036	0.135773	0.253041	2.325661	1.790534	3.167912
protein_co	synapsin_II	0	1	0	2	0	0	0	0.019958	0	0.029302	0	0
protein_co	POU_class_	10	6	4	33	9	13	0.180809	0.127844	0.095305	0.516176	0.182815	0.233601
protein_co	snail_homo	59	73	56	31	15	23	1.803417	2.629506	2.255626	0.819726	0.515092	0.698685
protein_co	zinc_finger_	115	104	82	196	121	189	2.044397	2.178752	1.92095	3.0143	2.416584	3.339172
protein_co	lysozyme_C	8	5	9	12	10	9	0.482378	0.355283	0.715113	0.625953	0.677402	0.539324
protein_co	MORN_rep	0	0	0	2	0	0	0	0	0	0.059363	0	0
protein_co	EP400_N-te	281	259	207	254	264	291	3.780539	4.106333	3.669885	2.95627	3.990252	3.890899
protein_co	chromoson	9	8	3	3	9	2	0.190893	0.199961	0.08385	0.055047	0.214456	0.042159
protein_co	v-myb_mye	84	73	96	382	362	342	0.856518	0.877177	1.289922	3.369642	4.146819	3.465717
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.028795	0
protein_co	chromoson	239	179	223	161	130	145	2.902041	2.561331	3.568168	1.691198	1.773365	1.749779
protein_co	developme	1110	834	736	2512	1503	1777	33.65665	29.80032	29.40766	65.89167	51.19834	53.54821
protein_co	ankyrin_rep	1051	833	1209	1128	1209	825	7.500807	7.005794	11.37015	6.964298	9.6935	5.851522
protein_co	YTH_domai	1362	1224	1527	1922	1816	1591	13.96855	14.79322	20.63707	17.0526	20.92372	16.21638
protein_co	zinc_finger_	199	162	135	429	322	321	3.769323	3.616033	3.369604	7.029599	6.851966	6.042615
protein_co	adenosine_	0	0	0	0	2	1	0	0	0	0	0.032987	0.014591
protein_co	neuregulin_	1	6	4	0	1	0	0.014997	0.106041	0.079052	0	0.016849	0

protein_co	sarcalumen	0	2	2	0	0	0	0	0.022333	0.024973	0	0	0
protein_co	chromoson	1245	894	1273	42	32	34	11.20182	9.479033	15.09325	0.326913	0.323458	0.304024
protein_co	interferon-i	213	189	154	21	17	15	4.072384	4.258317	3.879937	0.347337	0.365146	0.285017
protein_co	chromoson	92	83	51	128	111	88	1.750116	1.860647	1.27845	2.106453	2.372198	1.663685
protein_co	claudin_24	0	0	0	2	0	0	0	0	0	0.138157	0	0
protein_co	potassium_	67	35	51	49	22	17	0.53036	0.326491	0.531987	0.335548	0.195644	0.133738
protein_co	ADAMTS-lik	60	41	26	99	51	63	1.114156	0.897193	0.636214	1.590351	1.063933	1.162639
protein_co	Kv_channel	30	24	26	46	53	66	0.640157	0.603509	0.731094	0.849153	1.270546	1.399648
protein_co	mortality_f	6653	5613	5149	7160	5845	6877	149.3075	148.4452	152.2726	139.0081	147.3661	153.3814
protein_co	NLR_family	1	0	0	0	3	0	0.015195	0	0	0	0.051213	0
protein_co	WD_repeat	73	63	67	217	188	236	2.312802	2.352141	2.797211	5.947554	6.691486	7.430829
protein_co	dystrophia_	1207	892	789	903	897	1238	19.33428	16.83808	16.65453	12.51329	16.14218	19.70838
protein_co	solute_carr	627	537	443	1683	998	1470	15.46064	15.6042	14.39457	35.90105	27.64647	36.02359
protein_co	phosphatid	171	121	93	173	140	174	2.633957	2.196368	1.887688	2.305269	2.422644	2.663615
protein_co	IKAROS_fan	0	0	0	9	20	11	0	0	0	0.0666	0.192199	0.093513
protein_co	phosphate_	937	872	725	1528	1207	1544	9.637791	10.56967	9.826769	13.59641	13.94743	15.78319
protein_co	N-acetyltra	4	10	13	70	49	57	0.036076	0.106282	0.154501	0.546154	0.496477	0.510903
protein_co	nuclear_po	0	0	0	2	0	0	0	0	0	0.011374	0	0
protein_co	B-cell_rece	3657	2867	2462	4704	3111	3978	106.9642	98.82078	94.89348	119.0265	102.2263	115.6346
protein_co	ADP-ribosy	39	40	32	48	52	57	0.523371	0.632575	0.565887	0.557249	0.783966	0.760203
pseudogen	ribosomal_	67	59	33	64	42	102	6.705192	6.958178	4.351963	5.540888	4.722096	10.14486
antisense	CECR5_anti	3	9	1	3	1	0	0.25783	0.911509	0.113252	0.223047	0.096552	0
protein_co	guanine_nu	111	90	79	500	291	426	0.876297	0.837294	0.821846	3.414771	2.580896	3.342318
pseudogen	-	1	0	1	5	4	5	0.076726	0	0.101106	0.331876	0.344788	0.381261
protein_co	dynein_axo	98	95	88	203	164	217	0.376285	0.429855	0.445254	0.674295	0.70743	0.828057
lincRNA	-	0	0	0	111	117	154	0	0	0	7.210891	9.870471	11.493
protein_co	chromoson	1	5	3	3	5	2	0.020307	0.119654	0.08028	0.052703	0.11407	0.040364
protein_co	ecotropic_	6	0	2	0	3	9	0.158902	0	0.069798	0	0.089259	0.236882
protein_co	transmemb	0	0	1	0	0	0	0	0	0.079912	0	0	0
protein_co	Nuclear_po	79	71	65	175	142	140	1.098592	1.163522	1.191125	2.105282	2.218435	1.934848
protein_co	zinc_finger_	44	28	22	113	104	109	0.468034	0.350986	0.308377	1.039839	1.242816	1.152287
protein_co	threonine_	165	179	129	169	144	120	2.306036	2.9481	2.375782	2.043299	2.260964	1.66676
protein_co	tripartite_r	728	674	561	360	226	237	6.77228	7.388742	6.877034	2.897137	2.361897	2.191096
protein_co	ATPase_H+_	9	15	3	12	9	13	0.405505	0.796439	0.178119	0.467734	0.45556	0.582113
protein_co	interferon_	397	387	324	11	24	25	24.58196	28.23866	26.43661	0.589226	1.669499	1.538423
protein_co	lysosomal-a	9365	8096	7166	10487	9384	11495	94.58077	96.35465	95.36888	91.62402	106.4712	115.3755
protein_co	Probable_i	123	116	185	123	203	142	3.491551	3.880416	6.920218	3.020518	6.473786	4.006003
pseudogen	olfactory_r	0	1	1	3	1	0	0	0.073139	0.081786	0.161075	0.069726	0
protein_co	kelch_dom	352	291	203	504	447	524	9.522345	9.276867	7.236559	11.79491	13.58494	14.08777
protein_co	kelch-like_f	0	0	1	7	11	10	0	0	0.024565	0.112885	0.230364	0.185261
protein_co	SET_domai	264	174	163	511	367	512	3.271634	2.541073	2.661848	5.478287	5.109471	6.305804
protein_co	patched_1	469	418	366	386	580	531	2.335559	2.453021	2.401784	1.662908	3.244853	2.62798
protein_co	reticulon_4	28	26	11	28	37	26	0.807379	0.883486	0.417972	0.698458	1.198589	0.745079
protein_co	PAXIP1_ass	224	239	166	305	312	450	5.896958	7.414554	5.75868	6.946129	9.227492	11.77341

protein_co	calcium_ho	0	0	0	0	1	0	0	0	0	0	0.019481	0
protein_co	Na+/K+_tra	3	0	0	5	4	7	0.079891	0	0	0.115188	0.11967	0.185261
protein_co	RNA-bindin	113	113	103	158	127	120	1.635411	1.927232	1.964357	1.978192	2.06491	1.725994
protein_co	zinc_finger_	22	27	41	57	44	33	0.352193	0.509365	0.864921	0.789398	0.791334	0.525027
protein_co	insulin_rec	359	331	380	1229	1134	915	2.715505	2.95047	3.787691	8.042128	9.636475	6.878391
protein_co	chromoson	6	6	1	6	6	7	0.31638	0.372835	0.069485	0.273699	0.355434	0.366831
protein_co	family_with	1	11	1	5	2	2	0.006456	0.083691	0.008508	0.027926	0.014506	0.012833
protein_co	short_statu	42	19	40	4	3	10	0.591834	0.315509	0.742755	0.048761	0.047492	0.140043
protein_co	bicaudal_D	1070	907	1010	1472	1452	1404	8.813889	8.804368	10.96327	10.4895	13.43691	11.49372
protein_co	calicin	13	13	4	0	0	0	0.354576	0.417847	0.143768	0	0	0
protein_co	trimethylly	115	87	90	135	112	75	2.149793	1.916572	2.217053	2.183211	2.352155	1.393381
protein_co	G_protein-r	0	0	0	0	0	1	0	0	0	0	0	0.025042
protein_co	H2A_histor	1	0	0	0	0	0	0.1024	0	0	0	0	0
protein_co	SLIT_and_N	0	0	0	2	2	1	0	0	0	0.011939	0.015505	0.006858
pseudogen	succinate_d	4	4	6	147	93	116	0.206398	0.243227	0.407972	6.561831	5.391092	5.948567
protein_co	polo-like_k	10	7	7	3	2	4	0.251382	0.207367	0.231882	0.065241	0.056482	0.099932
protein_co	RAS_p21_p	2337	1967	1741	574	673	718	29.52114	29.281	28.98064	6.272625	9.550774	9.013812
protein_co	coagulation	5	3	4	7	3	6	0.155617	0.110031	0.164052	0.188473	0.104896	0.185587
protein_co	leucine-rich	1133	1049	955	1341	928	993	8.112273	8.851059	9.01054	8.306239	7.464654	7.065966
protein_co	LEM_doma	1	0	0	5	2	18	0.056987	0	0	0.246496	0.128043	1.019433
protein_co	ATPase_H+/	2	0	1	1	0	4	0.071157	0	0.046884	0.030779	0	0.141436
protein_co	NADH_dehy	2	25	10	9	17	35	0.090808	1.337644	0.598313	0.353508	0.867145	1.579324
protein_co	zinc_finger_	161	217	146	308	172	212	1.622597	2.57722	1.938976	2.685335	1.947432	2.123392
antisense	-	9	5	8	3	2	0	0.148943	0.097511	0.174463	0.04295	0.037184	0
protein_co	zinc_finger_	219	197	198	293	206	229	2.213455	2.346388	2.6371	2.561871	2.339068	2.300232
protein_co	zinc_finger_	93	109	79	61	50	61	1.131582	1.562919	1.266674	0.64209	0.683474	0.737637
protein_co	5-hydroxyt	0	0	0	1	0	0	0	0	0	0.021411	0	0
protein_co	deleted_in_	4	0	4	6	1	1	0.092433	0	0.121804	0.119945	0.025961	0.022966
protein_co	T-cell_acut	5	0	0	0	0	1	0.420167	0	0	0	0	0.083514
antisense	MATN1_ant	6	7	6	13	3	3	0.080929	0.111265	0.106645	0.151691	0.045459	0.040215
protein_co	axin_intera	818	749	777	1618	1206	1242	10.69277	11.53788	13.38421	18.29695	17.71061	16.13498
protein_co	chromoson	132	106	95	817	582	753	1.195997	1.131799	1.134265	6.403852	5.92418	6.780486
pseudogen	-	37	36	36	57	36	66	2.560545	2.935893	3.282978	3.412467	2.798867	4.539251
protein_co	gamma-sec	2	1	1	13	9	20	0.030619	0.018042	0.020174	0.172176	0.154796	0.304303
protein_co	ATP/GTP_b	0	2	0	5	2	6	0	0.031685	0	0.05815	0.030206	0.080164
protein_co	cytochrom	118	138	155	206	164	145	2.686898	3.703014	4.650885	4.057882	4.195291	3.281306
protein_co	leucine_ric	1	0	0	0	2	0	0.02354	0	0	0	0.052891	0
protein_co	ankyrin_rep	131	108	117	427	281	325	2.120878	2.060512	2.496117	5.980469	5.110927	5.229225
protein_co	phosphatid	2647	2154	1810	1215	1276	1395	27.58559	26.45338	24.8566	10.95387	14.93923	14.44815
protein_co	cytochrom	0	0	0	0	1	0	0	0	0	0	0.02472	0
protein_co	testis_expr	1	2	2	1	1	1	0.052783	0.124402	0.139109	0.045662	0.059298	0.052457
protein_co	zinc_finger_	193	142	172	243	265	306	2.488459	2.157588	2.922378	2.710456	3.838558	3.921067
protein_co	chromoson	70	74	76	87	72	113	3.222495	4.014515	4.610443	3.464787	3.72371	5.169902
protein_co	taste_recep	2	0	1	0	0	0	0.112044	0	0.073824	0	0	0

protein_co	polymerase	564	485	372	781	504	499	16.13113	16.34687	14.0205	19.32412	16.19442	14.18391
protein_co	chromoson	0	0	1	0	0	0	0	0	0.034864	0	0	0
protein_co	WW_doma	93	106	78	135	98	157	1.983688	2.664424	2.1924	2.491077	2.348364	3.328125
protein_co	cytochrom	0	0	0	0	3	0	0	0	0	0	0.093614	0
pseudogen	cell_death-	120	96	92	245	146	169	3.561053	3.357187	3.597658	6.289648	4.867424	4.984179
protein_co	coiled-coil_	174	215	136	866	535	731	5.172225	7.531365	5.327235	22.26943	17.86615	21.5951
protein_co	B-cell_CLL/	2968	2582	2135	2559	2971	3107	15.70503	16.10046	14.88702	11.71408	17.66146	16.33902
protein_co	polymerase	2218	1915	1539	2409	1482	2017	60.37179	61.42545	55.20087	56.72471	45.3179	54.56172
protein_co	kinesin_fan	356	338	248	1646	1536	1851	4.46929	5.000487	4.102749	17.87645	21.66351	23.09429
protein_co	zinc_and_ri	603	515	426	466	484	474	5.988261	6.026952	5.574781	4.003431	5.399802	4.67812
protein_co	free_fatty_a	0	0	0	2	0	0	0	0	0	0.025075	0	0
protein_co	suppressor_	87	60	49	549	472	623	1.198508	0.974047	0.889514	6.542701	7.304875	8.529418
protein_co	EDAR-assoc	0	0	0	33	39	27	0	0	0	0.488009	0.74897	0.458695
protein_co	solute_carr	0	2	0	0	0	1	0	0.13274	0	0	0	0.055972
protein_co	cytochrom	1	0	0	0	0	1	0.01626	0	0	0	0	0.016159
protein_co	mitochond	2	1	4	513	288	361	0.039114	0.023047	0.103086	8.67929	6.327693	7.016502
protein_co	sosondowa	1	0	0	130	113	96	0.018124	0	0	2.038294	2.300849	1.729185
protein_co	biogenesis_	303	291	223	372	249	415	10.37589	11.7431	10.06288	11.02018	9.579239	14.12344
protein_co	zinc_finger_	72	105	71	103	144	125	1.473425	2.532165	1.914647	1.823459	3.310604	2.542233
protein_co	kelch-like_f	0	1	3	6	5	3	0	0.016871	0.056595	0.074309	0.080416	0.042683
protein_co	Protein_LO	9	14	20	9	10	19	0.252367	0.462621	0.739018	0.218321	0.315021	0.529485
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.159881	0
protein_co	MKL/myoc	219	166	314	254	467	261	1.317659	1.176993	2.489564	1.322073	3.156637	1.560662
protein_co	B_and_T_ly	0	4	1	0	2	0	0	0.077669	0.021713	0	0.037022	0
protein_co	zinc_finger_	58	54	69	64	57	55	1.116574	1.225068	1.750424	1.065865	1.232774	1.052281
protein_co	neuroblast	76	92	72	85	102	79	0.323044	0.460833	0.403288	0.312558	0.487077	0.333722
protein_co	lysine_(K)-s	13	11	15	67	49	62	0.231106	0.230445	0.351393	1.030398	0.978617	1.09539
protein_co	glycerol-3-p	0	0	1	0	0	2	0	0	0.01583	0	0	0.023877
protein_co	torsin_fami	456	328	299	832	570	798	8.862369	7.512179	7.65757	13.98851	12.4454	15.41337
protein_co	poly(A)_bin	0	0	0	1	0	0	0	0	0	0.020473	0	0
protein_co	gamma-am	20	23	13	41	25	36	0.325691	0.441377	0.278967	0.577593	0.457366	0.582623
protein_co	protein_ph	2949	2456	2340	5479	3985	4140	55.81802	54.78165	58.36471	89.71477	84.73777	77.87707
protein_co	zinc_finger_	87	84	95	69	68	73	0.538257	0.612431	0.774513	0.369303	0.472638	0.448852
pseudogen	macrophag	24	11	6	26	23	38	0.536564	0.289808	0.176765	0.50286	0.57768	0.844313
protein_co	nucleosom	81	97	64	206	103	130	1.624941	2.293145	1.691872	3.575057	2.321341	2.591825
pseudogen	carbonic_a	199	176	165	498	262	298	8.334856	8.686899	9.106758	18.04419	12.32808	12.40426
protein_co	PRELI_dom	251	213	168	151	125	134	6.209434	6.20962	5.476744	3.231605	3.474061	3.294525
protein_co	beta-site_A	1185	899	945	402	321	292	6.321552	5.651609	6.643118	1.855216	1.923798	1.548096
pseudogen	-	0	0	0	1	0	3	0	0	0	0.025788	0	0.088875
protein_co	regulator_c	2	10	6	2	0	6	0.036587	0.215576	0.144637	0.031651	0	0.109082
protein_co	solute_carr	0	0	0	0	1	0	0	0	0	0	0.016716	0
protein_co	solute_carr	0	0	0	1	0	0	0	0	0	0.013388	0	0
protein_co	thrombosp	2926	2312	2679	23	11	13	26.65726	24.82196	32.16242	0.181273	0.112586	0.117705
protein_co	retinoid_X_	1448	1302	1127	606	753	881	13.28571	14.07779	13.62621	4.810076	7.761762	8.033445

protein_co	ankyrin_rep	72	29	24	23	44	43	2.639717	1.252939	1.159501	0.729484	1.812286	1.566762
protein_co	chromoson	32	24	22	9	46	32	0.35024	0.309553	0.317303	0.085216	0.565618	0.348077
protein_co	nudix_(nuc	37	23	17	42	17	38	0.836386	0.612689	0.506394	0.82133	0.431721	0.853687
protein_co	KIAA1024-l	2	0	2	6	0	4	0.04498	0	0.059272	0.116735	0	0.089404
lincRNA	long_interg	0	0	0	3	3	13	0	0	0	0.070029	0.090942	0.348615
protein_co	zinc_finger_	225	189	231	142	165	117	2.130137	2.108598	2.881852	1.162991	1.754922	1.10083
protein_co	cytochrom	0	0	0	6	6	1	0	0	0	0.116586	0.151402	0.022322
protein_co	keratin_10	653	580	468	402	392	643	16.27612	17.0362	15.37157	8.668154	10.97672	15.92789
protein_co	golgin_A8_	12	9	8	0	0	11	0.207476	0.183373	0.182269	0	0	0.189012
protein_co	coiled-coil_	21	18	21	42	38	54	0.162848	0.164491	0.214593	0.281757	0.331051	0.416165
protein_co	NFKB_repre	200	146	166	473	373	391	2.830312	2.434806	3.095617	5.790666	5.930103	5.499089
protein_co	gliomedin	0	0	0	1	1	2	0	0	0	0.009213	0.011965	0.021168
protein_co	karyopherii	1134	926	1011	3360	2455	2475	6.684677	6.432584	7.853321	17.13443	16.25803	14.49947
protein_co	triadin	0	0	0	9	1	1	0	0	0	0.08685	0.012532	0.011086
protein_co	keratin_3	0	0	0	7	1	3	0	0	0	0.138246	0.025647	0.068065
protein_co	zinc_finger_	92	68	68	92	84	65	1.571659	1.368947	1.530785	1.359632	1.612126	1.103554
protein_co	zinc_finger_	498	415	471	464	422	464	6.132732	6.022542	7.64329	4.943171	5.838297	5.678744
protein_co	spermatoge	7	10	0	12	5	4	0.153579	0.258548	0	0.227761	0.123241	0.087218
protein_co	transmemb	0	0	0	2	2	0	0	0	0	0.027457	0.035657	0
protein_co	family_witl	1	0	3	0	0	0	0.029843	0	0.117976	0	0	0
protein_co	nucleosom	0	0	0	28	15	26	0	0	0	0.50289	0.349858	0.536457
pseudogen	aquaporin_	15	14	6	8	9	30	0.577538	0.635221	0.304422	0.266466	0.389297	1.147943
protein_co	ribosomal_	4252	3898	3227	3095	2019	2253	65.49465	70.75571	65.50076	41.24167	34.93799	34.48922
protein_co	guanine_nu	447	398	385	124	111	86	6.346105	6.658706	7.202699	1.522946	1.770401	1.213411
protein_co	butyrophili	507	430	339	95	70	53	8.896614	8.891854	7.838831	1.442127	1.379952	0.924277
protein_co	A_kinase_(A	0	0	1	9	4	1	0	0	0.071406	0.421894	0.243504	0.053853
protein_co	piccolo_pr	90	68	85	123	132	84	0.277922	0.247455	0.345887	0.328585	0.457934	0.257792
protein_co	regulator_c	0	0	0	0	0	1	0	0	0	0	0	0.012648
protein_co	insulin_ind	1326	1095	1256	495	382	375	23.32218	22.69587	29.11053	7.531714	7.548106	6.554907
pseudogen	ankyrin_rep	0	0	0	36	43	37	0	0	0	0.483508	0.74999	0.570886
protein_co	myelin_tra	1	0	0	0	0	0	0.007496	0	0	0	0	0
protein_co	chromoson	90	79	35	71	65	55	3.306516	3.420285	1.694459	2.256573	2.682814	2.00817
protein_co	zinc_finger_	15	15	5	18	19	18	0.284833	0.335659	0.125113	0.295689	0.405324	0.339689
protein_co	transmemb	1062	827	645	1456	811	1102	19.65164	18.03378	15.72783	23.30766	16.85948	20.26588
protein_co	chloride_ch	0	1	0	0	0	1	0	0.020388	0	0	0	0.017194
protein_co	Rho_GTPas	2	12	13	11	8	29	0.0218	0.154139	0.186725	0.103724	0.097963	0.314146
protein_co	septin_10	1177	996	1108	1666	1281	1204	20.15903	20.10294	25.00735	24.68488	24.64854	20.49412
protein_co	family_witl	14	14	7	67	33	22	0.309596	0.364841	0.203986	1.281757	0.819843	0.483504
protein_co	cytochrom	0	5	0	1	0	0	0	0.06177	0	0.009069	0	0
processed_	XK_Kell_blo	20	8	9	30	40	27	0.216351	0.101982	0.128294	0.280745	0.486113	0.29027
protein_co	SET_and_M	273	254	180	660	476	728	3.296736	3.614618	2.864368	6.894908	6.457695	8.737005
protein_co	forkhead_b	7	3	1	4	4	12	0.07927	0.040035	0.014923	0.039186	0.050888	0.135052
protein_co	G_patch_d	896	928	904	1045	1137	894	5.849689	7.139698	7.777285	5.902066	8.339391	5.800587
protein_co	carcinoemb	129	173	114	217	98	140	2.083401	3.29258	2.426179	3.031837	1.778109	2.247092

protein_co	neurofibro	1132	971	803	1616	1243	1481	9.946756	10.05452	9.297911	12.28399	12.2703	12.93301
protein_co	chromoson	280	285	179	226	183	256	9.968714	11.9573	8.397866	6.960694	7.319498	9.057967
protein_co	spermatoge	0	4	2	0	0	0	0	0.127713	0.071406	0	0	0
protein_co	ubiquitin-c	4239	3410	3533	2102	1995	1962	43.56763	41.30114	47.84967	18.68944	23.03523	20.04053
lincRNA	MIR22_hos	397	391	337	534	263	326	8.003646	9.289262	8.952866	9.313258	5.956651	6.531676
protein_co	4-hydroxyp	31	31	16	182	125	194	0.910244	1.072668	0.619086	4.623073	4.1234	5.66119
antisense	KTN1_antis	69	63	33	95	86	56	1.671821	1.798822	1.053633	1.991257	2.340929	1.348461
protein_co	katanin_p6	285	222	219	347	252	280	7.966306	7.312606	8.06661	8.390824	7.913374	7.778212
protein_co	fibronectin	37	24	22	38	28	57	0.305207	0.233298	0.239139	0.271168	0.259477	0.46728
protein_co	ArfGAP_wit	1136	1076	867	353	383	476	10.42847	11.64023	10.48808	2.803366	3.949935	4.342689
protein_co	kinesin_fan	56	35	52	187	222	231	0.47618	0.350718	0.582668	1.375585	2.120728	1.952111
protein_co	phosphodi	0	2	2	4	1	5	0	0.028917	0.032335	0.042456	0.013784	0.060966
pseudogen	speedy_hor	5	2	4	8	5	4	0.091784	0.043265	0.096759	0.127043	0.103114	0.072974
protein_co	leucine_ric	2	1	3	0	7	0	0.023033	0.013571	0.045527	0	0.090566	0
protein_co	proline_ric	188	144	104	214	153	235	4.367225	3.942007	3.183581	4.300555	3.992898	5.425319
protein_co	ZFP91_zinc	1093	910	976	1761	1227	1253	11.08515	10.87602	13.04386	15.45055	13.98026	12.62939
protein_co	chromoson	173	93	104	359	191	231	5.537359	3.507895	4.386567	9.940633	6.868138	7.348153
protein_co	BCDIN3_dc	29	20	27	28	28	20	1.022163	0.830729	1.254067	0.853775	1.108739	0.700587
protein_co	melanoma_	0	0	0	6	2	1	0	0	0	0.121752	0.052704	0.023311
pseudogen	eukaryotic_	0	2	0	0	0	0	0	0.096055	0	0	0	0
protein_co	cytochrom	87	62	46	139	155	160	1.04655	0.8789	0.729178	1.4465	2.094698	1.912803
protein_co	LYR_motif_	387	351	351	569	441	479	3.225975	3.447976	3.855599	4.103224	4.129882	3.968214
pseudogen	deltex_hon	7	7	8	4	14	5	0.224326	0.264355	0.337837	0.110893	0.504033	0.159243
protein_co	coiled-coil_	4	1	0	0	0	1	0.139871	0.041207	0	0	0	0.034752
protein_co	coiled-coil_	0	0	0	0	1	0	0	0	0	0	0.013576	0
pseudogen	macrophag	3	9	1	10	3	9	0.036286	0.128282	0.015939	0.104635	0.040765	0.108185
protein_co	breakpoint	1016	800	763	2035	2016	1888	7.595037	7.04747	7.516151	13.16023	16.93073	14.02645
protein_co	fascin_hom	38	28	29	18	32	31	1.208263	1.049163	1.215096	0.495123	1.143081	0.979601
protein_co	spindlin_fa	128	135	116	548	531	464	1.645967	2.045748	1.96564	6.096138	7.67105	5.929784
protein_co	zinc_finger_	40	38	19	194	230	235	0.965636	1.081046	0.604424	4.051522	6.237784	5.638077
protein_co	spindlin_fa	103	89	82	85	59	80	4.334596	4.413758	4.547368	3.094521	2.789411	3.345886
protein_co	forkhead_b	1	0	0	91	25	29	0.026738	0	0	2.104899	0.750959	0.77061
protein_co	hyaluronog	135	149	109	118	72	73	3.680244	4.7867	3.915653	2.782838	2.20508	1.977768
protein_co	V-set_and_i	15	24	16	49	53	65	0.233769	0.440773	0.328588	0.660626	0.927943	1.006745
protein_co	chemokine	2	4	1	0	2	0	0.056895	0.134095	0.037487	0	0.063918	0
protein_co	zinc_finger_	291	300	266	178	184	150	5.84218	7.09758	7.037176	3.09147	4.150007	2.992836
protein_co	zinc_finger_	335	362	247	270	241	247	4.102529	5.224233	3.986012	2.860445	3.315683	3.006169
protein_co	two_pore_s	1161	1083	896	859	784	857	11.49944	12.64096	11.69465	7.360385	8.723876	8.435967
protein_co	tumor_nec	3	1	0	0	1	1	0.093042	0.036548	0	0	0.034842	0.030823
pseudogen	keratin_17_	0	0	0	0	0	5	0	0	0	0	0	0.200206
protein_co	keratin_16	5	0	1	6	6	5	0.161013	0	0.042435	0.167149	0.217065	0.160018
protein_co	hexamethy	862	679	685	1068	1353	1444	9.537124	8.85293	9.987011	10.2222	16.81733	15.87768
protein_co	Selenoprot	0	0	0	5	16	11	0	0	0	0.134386	0.558459	0.339645
lincRNA	long_interg	1	0	6	6	4	1	0.029776	0	0.235422	0.154552	0.133804	0.029592

protein_co	keratin_14	6	1	5	3	3	0	0.191123	0.037538	0.209878	0.08267	0.107357	0
protein_co	TraB_doma	69	51	61	74	36	30	0.937851	0.816887	1.09257	0.87012	0.549713	0.405243
protein_co	PDZ_domai	13	25	23	24	14	22	0.159831	0.362214	0.372632	0.255266	0.193373	0.268813
protein_co	protein_O-	2107	1747	1458	895	809	954	23.11848	22.58888	21.0808	8.495341	9.972232	10.40286
protein_co	pyroglutam	30	16	16	170	142	123	0.929877	0.584428	0.65352	4.558439	4.944719	3.788951
protein_co	microtubul	40	45	34	29	42	40	0.310687	0.411891	0.347998	0.19486	0.366489	0.308768
protein_co	excision_re	62	47	46	535	391	377	0.756126	0.675472	0.739256	5.644417	5.35708	4.569338
protein_co	transmemb	54	49	49	85	24	48	1.162119	1.242682	1.389594	1.582483	0.580253	1.026616
protein_co	tumor_nec	1	0	0	1	0	0	0.044903	0	0	0.038846	0	0
protein_co	fibroblast_	0	1	0	0	0	4	0	0.069941	0	0	0	0.235937
protein_co	complemer	18	14	10	0	1	4	0.461471	0.422968	0.337837	0	0.028802	0.101916
protein_co	reticulon_4	34	40	14	13	4	7	0.817065	1.132778	0.443344	0.270261	0.107991	0.16718
protein_co	zinc_finger_	523	506	595	509	456	450	5.264906	6.002698	7.892974	4.432714	5.157068	4.502058
protein_co	pyrimidine	0	0	0	1	0	0	0	0	0	0.027943	0	0
protein_co	zinc_finger_	1483	1486	992	1124	1102	1043	16.32935	19.28206	14.39376	10.70673	13.63196	11.41357
protein_co	zinc_activa	8	12	9	6	9	16	0.159762	0.282404	0.236843	0.103657	0.201917	0.31755
pseudogen	coiled-coil-	0	0	0	0	2	0	0	0	0	0	0.260859	0
protein_co	peroxisome	235	220	215	73	84	105	1.23817	1.365973	1.492745	0.332735	0.497211	0.549808
protein_co	transmemb	3	4	5	8	3	2	0.037663	0.059177	0.082717	0.086884	0.042312	0.024953
protein_co	family_witl	6	1	7	3	7	11	0.599332	0.117713	0.921402	0.259239	0.785531	1.09199
protein_co	EF-hand_ca	11	13	6	8	13	11	0.11374	0.158406	0.081754	0.071561	0.151013	0.113038
protein_co	KN_motif_a	7	12	3	57	35	57	0.13297	0.268623	0.075095	0.936684	0.746917	1.076068
protein_co	EMI_domai	108	108	68	27	22	30	2.631214	3.100725	2.183112	0.569061	0.602149	0.726379
protein_co	actin-like_7	0	0	0	0	0	5	0	0	0	0	0	0.18358
processed_	polycystic_	11	11	12	8	2	4	0.112098	0.132101	0.161147	0.070528	0.022897	0.040511
protein_co	Rh_blood_	20	17	9	6	10	7	0.361372	0.361977	0.21429	0.093786	0.202989	0.125699
protein_co	chromoson	23	20	20	9	9	10	0.795845	0.815526	0.911938	0.269405	0.349858	0.343883
protein_co	espin	3	4	5	4	7	11	0.04498	0.070674	0.098787	0.051882	0.117908	0.163907
protein_co	G_protein-	3	0	5	1	3	4	0.125057	0	0.274659	0.036062	0.140494	0.165714
protein_co	transmemb	10	23	3	0	2	1	0.162396	0.440159	0.064199	0	0.036488	0.016139
protein_co	transmemb	99	114	75	306	158	180	2.680899	3.637955	2.676341	7.168524	4.806749	4.84426
protein_co	ribosomal_	1096	801	661	2556	1736	2303	20.71522	17.84098	16.46324	41.79293	36.8619	43.25961
protein_co	transmemb	0	2	3	1	0	0	0	0.038428	0.064456	0.014105	0	0
pseudogen	-	2	2	3	0	4	0	0.17706	0.208655	0.349983	0	0.397832	0
protein_co	uncharacte	6	11	5	1	6	5	0.07693	0.166206	0.08448	0.011092	0.086427	0.063713
protein_co	chromoson	49	45	49	69	89	85	0.439605	0.475758	0.579292	0.535524	0.897027	0.757871
protein_co	TEA_domai	2847	2242	3139	3284	3286	2903	15.98335	14.8328	23.22237	15.94948	20.72512	16.19709
protein_co	phospholip	473	469	340	371	276	331	7.655485	8.945229	7.251457	5.194556	5.018451	5.324137
protein_co	cholecystol	0	0	0	13	3	5	0	0	0	0.389906	0.116849	0.172279
protein_co	ectonucleo	286	243	301	247	216	198	2.591771	2.595039	3.594445	1.93638	2.199041	1.783222
protein_co	microphth	30	20	35	43	35	43	0.329919	0.259193	0.507211	0.409089	0.432417	0.469963
protein_co	HEAT_repea	16	0	1	16	6	9	0.240436	0	0.019802	0.208	0.101293	0.13441
protein_co	nucleosom	14498	12890	11513	16469	11504	12231	147.5468	154.5901	154.3992	144.9947	131.5284	123.7067
protein_co	COX_assem	197	211	124	275	205	288	1.728721	2.181968	1.433888	2.087635	2.020978	2.51166

protein_co	slit_homol	0	0	0	0	1	0	0	0	0	0	0.007505	0
protein_co	LY6/PLAUR	86	54	61	1469	1325	1247	1.11838	0.827545	1.045335	16.52631	19.3578	16.11636
protein_co	aldo-keto_r	826	665	607	145	99	111	6.521888	6.187597	6.315632	0.990431	0.878168	0.871016
protein_co	V-set_and_t	0	0	0	15	15	9	0	0	0	0.461683	0.599556	0.31823
protein_co	forkhead_b	0	0	1	16	12	17	0	0	0.033735	0.354344	0.345121	0.432514
protein_co	spermatoge	0	5	1	0	0	6	0	0.086195	0.019277	0	0	0.08723
protein_co	mitochond	1347	1084	852	2021	1299	2153	48.74335	46.22577	40.62769	63.26698	52.80876	77.42861
protein_co	ring_finger_	433	350	266	754	483	922	5.977432	5.693795	4.838861	9.004531	7.490709	12.64932
protein_co	angiopoieti	7	2	1	9	0	0	0.156498	0.052692	0.029461	0.174067	0	0
protein_co	KIAA1598	85	105	97	1512	1303	1117	1.141838	1.662195	1.717087	17.57116	19.66433	14.91243
pseudogen	B_melanon	0	2	0	0	0	0	0	0.048028	0	0	0	0
protein_co	Uncharacte	1	0	0	2	3	6	0.040444	0	0	0.069975	0.136308	0.241164
protein_co	HCG20402	1	0	1	0	5	0	0.034715	0	0.045746	0	0.195003	0
protein_co	zinc_finger_	80	60	62	38	55	32	0.930217	0.822153	0.949994	0.382244	0.718466	0.369789
protein_co	TSPY-like_4	622	541	577	748	782	833	8.010046	8.21011	9.791636	8.33315	11.31359	10.66103
protein_co	metallothic	6	8	8	4	4	0	0.183929	0.288999	0.323165	0.106077	0.137755	0
protein_co	glucosamin	287	264	208	257	203	223	2.544217	2.75793	2.4298	1.970917	2.021703	1.964657
processed_	-	18	9	5	0	8	1	0.463942	0.273364	0.169823	0	0.231649	0.025615
protein_co	SEC14_and	1712	1439	1542	579	490	498	8.538387	8.45746	10.13424	2.498122	2.745473	2.468375
protein_co	formin_bin	1202	940	778	995	948	852	11.78864	10.86411	10.0548	8.441999	10.4452	8.304404
protein_co	dynein_cyt	947	755	929	690	568	503	3.665384	3.443686	4.738272	2.31037	2.469829	1.934849
protein_co	keratin_12	1	2	1	0	0	2	0.028356	0.066832	0.037367	0	0	0.056362
protein_co	melanoma_	38	59	32	18	15	23	0.622835	1.13959	0.691153	0.255226	0.276204	0.374651
protein_co	basal_cell_	162	115	87	942	844	1127	3.193016	2.671105	2.259645	16.06201	18.68864	22.07596
protein_co	round_sper	201	135	141	401	242	314	3.44262	2.724796	3.182343	5.94156	4.656478	5.344811
protein_co	neuropepti	0	0	0	1	3	0	0	0	0	0.029227	0.113866	0
protein_co	WD_repeat	215	197	175	435	464	490	5.626453	6.075325	6.034886	9.84801	13.64154	12.74389
protein_co	erythropoi	32	19	21	109	82	98	0.794239	0.555728	0.68684	2.340404	2.286463	2.417336
protein_co	family_with	0	0	1	0	0	0	0	0	0.011909	0	0	0
protein_co	cell_death-	8	10	12	2	2	4	0.331659	0.488549	0.655567	0.071729	0.093149	0.164805
protein_co	deleted_in_	182	203	277	30	56	35	1.684192	2.213723	3.377806	0.240162	0.58218	0.321883
protein_co	TAF9B_RNA	455	372	376	656	448	405	8.878788	8.554455	9.66863	11.07412	9.821309	7.854291
protein_co	protocadhe	63	42	78	43	30	34	0.957039	0.751875	1.561416	0.565094	0.511988	0.513308
protein_co	membrane_	108	93	84	29	32	28	0.833352	0.845658	0.85412	0.193582	0.277398	0.21472
protein_co	leucine_zip	19	17	14	148	99	107	0.200534	0.211442	0.194714	1.351323	1.173867	1.122349
protein_co	lipoma_HM	1	0	0	0	0	0	0.01668	0	0	0	0	0
protein_co	calcineurin	1598	1271	989	2079	1697	1684	25.76118	24.1458	21.00971	28.99389	30.73405	26.97992
protein_co	RAD52_mo	0	0	3	51	22	35	0	0	0.136345	1.521657	0.852424	1.199669
protein_co	formyl_pep	0	0	0	0	0	1	0	0	0	0	0	0.020082
protein_co	histone_clu	5	1	4	1	0	0	0.36511	0.086052	0.384901	0.063171	0	0
protein_co	chromoson	84	43	76	30	12	16	2.424778	1.462744	2.890954	0.749164	0.389155	0.45901
pseudogen	hydroxy-de	0	0	0	0	1	0	0	0	0	0	0.053534	0
protein_co	potassium_	0	0	0	16	19	21	0	0	0	0.261615	0.403442	0.394464
protein_co	cadherin-re	0	0	0	0	1	0	0	0	0	0	0.024021	0

protein_co	collagen_ty	5994	5134	5559	10805	10893	10879	48.64015	49.09543	59.44422	75.8518	99.30582	87.73578
protein_co	pleckstrin_	0	1	2	0	0	0	0	0.017407	0.03893	0	0	0
protein_co	gap_junctic	1	0	0	0	0	1	0.032639	0	0	0	0	0.032438
protein_co	prothymos	17878	15204	12179	28188	21398	26386	578.8863	580.1486	519.6618	789.5899	778.3888	849.0974
protein_co	chromoson	0	0	3	0	0	5	0	0	0.41858	0	0	0.526141
protein_co	heat_shock	244	182	233	909	650	676	6.784455	5.963533	8.537208	21.86513	20.30428	18.6802
protein_co	ATPase_typ	2	0	0	0	0	5	0.026293	0	0	0	0	0.065327
protein_co	sirtuin_7	276	297	244	860	620	796	4.241427	5.378565	4.941144	11.43311	10.70394	12.15698
pseudogen	-	45	33	39	39	34	58	2.440927	2.109421	2.787672	1.830079	2.071907	3.126655
protein_co	intraflagell	754	716	602	326	322	350	7.57448	8.476208	7.969164	2.833101	3.634012	3.494292
pseudogen	tropomyos	2	0	1	0	0	2	0.144648	0	0.095305	0	0	0.143754
protein_co	alkylglycer	98	114	64	1	1	1	2.096249	2.873617	1.80398	0.018505	0.024031	0.021258
protein_co	SH3-bindin	0	0	0	4	1	0	0	0	0	0.168844	0.054817	0
protein_co	cytochrom	0	0	0	0	2	0	0	0	0	0	0.075814	0
protein_co	toll-like_re	9	8	12	5	7	4	0.116553	0.122089	0.204785	0.056016	0.101842	0.051481
protein_co	ubiquitin_s	1626	1287	1411	3121	2314	2175	15.90578	14.83611	18.18847	26.41138	25.43002	21.14478
protein_co	nanos_hom	6	1	1	2	5	1	0.409338	0.080397	0.089901	0.118038	0.383221	0.067802
protein_co	forkhead_b	2	1	1	3	0	0	0.038856	0.022895	0.025601	0.050421	0	0
protein_co	NHL_repeat	13	14	4	1	0	2	0.322508	0.409292	0.130765	0.021462	0	0.04931
protein_co	pleckstrin_	3	14	11	106	70	138	0.064694	0.355775	0.312585	1.977468	1.695851	2.957531
protein_co	zinc_finger_	8	2	3	20	22	10	0.203131	0.059844	0.100379	0.439318	0.627564	0.252346
protein_co	transmemb	2	0	0	3	0	0	0.142891	0	0	0.185421	0	0
protein_co	melanoma_	330	256	205	234	158	258	11.95792	10.93173	9.788825	7.335348	6.432029	9.291188
protein_co	tet_methyl	362	372	344	865	1143	930	1.744937	2.113105	2.185065	3.607034	6.189654	4.455164
protein_co	Zinc_finger_	547	454	352	727	577	630	5.156468	5.043452	4.372627	5.92874	6.110685	5.902217
protein_co	ISG15_ubic	291	234	193	148	69	97	21.66783	20.53267	18.93715	9.533387	5.771924	7.178007
protein_co	exonucleas	206	193	123	119	143	123	3.719592	4.106696	2.926632	1.858823	2.900769	2.207206
processed_	T-cell_leuke	0	0	0	1	0	3	0	0	0	0.010822	0	0.037297
protein_co	chromoson	33	26	27	45	25	27	0.950002	0.882045	1.024257	1.120691	0.808536	0.772474
protein_co	zinc_finger_	111	103	103	116	116	131	2.474295	2.705657	3.025523	2.236915	2.904929	2.90208
protein_co	RANBP2-lik	6	0	1	0	0	0	0.047431	0	0.010417	0	0	0
protein_co	dehydroger	150	135	97	293	132	126	5.796459	6.147696	4.939444	9.794948	5.730526	4.838956
protein_co	sterile_alpl	74	55	33	108	80	98	1.535725	1.34509	0.902465	1.938958	1.86518	2.021238
protein_co	chromoson	4	2	0	31	18	24	0.069114	0.040723	0	0.46337	0.349402	0.41212
protein_co	vimentin-ty	61	86	78	88	77	138	1.432742	2.380366	2.414169	1.788067	2.031786	3.221268
pseudogen	thymosin_b	174	134	125	200	138	214	16.30395	14.79638	15.43435	16.212	14.52686	19.92815
pseudogen	WAS_prote	57	77	52	13	14	7	0.826976	1.316485	0.99416	0.163164	0.228189	0.100931
protein_co	ELKS/RAB6-	1	5	6	46	44	35	0.008625	0.050821	0.068195	0.343231	0.426351	0.300015
protein_co	beta_13-ga	115	66	103	465	306	387	1.431174	0.967934	1.689144	5.006227	4.278239	4.786469
protein_co	sprouty_ho	863	731	787	2186	2019	2022	9.252345	9.235608	11.11861	20.27469	24.31792	21.54427
protein_co	ES_cell_exp	2	0	0	0	0	0	0.083635	0	0	0	0	0
pseudogen	-	6	1	5	0	1	2	0.095161	0.01869	0.104499	0	0.017818	0.031524
protein_co	transient_r	42	38	37	40	14	22	0.791852	0.844278	0.919246	0.652406	0.296532	0.412218
protein_co	chromoson	0	0	0	0	4	0	0	0	0	0	0.123844	0

protein_co	Uncharacte	0	0	2	4	5	2	0	0	0.060902	0.079963	0.129803	0.045931
protein_co	chromoson	26	20	25	21	52	26	0.341132	0.309233	0.432238	0.238359	0.76648	0.339025
protein_co	transmemb	526	427	297	1011	617	788	17.88501	17.10954	13.30745	29.7384	23.56881	26.62805
protein_co	solute_carr	1	0	0	318	133	178	0.021885	0	0	6.020691	3.270069	3.871559
protein_co	thrombosp	492	343	401	362	443	398	2.831192	2.325977	3.040769	1.802087	2.863895	2.27613
protein_co	DnaJ_(Hsp4	0	1	0	12	4	2	0	0.033273	0	0.293113	0.126882	0.056122
protein_co	gamma-am	1	0	0	0	0	0	0.027674	0	0	0	0	0
protein_co	transcriptic	1205	1073	977	2877	1918	2013	21.50839	22.5698	22.98002	44.42463	38.46083	35.70873
protein_co	nonhomolo	5	5	7	3	1	0	0.125274	0.147628	0.231114	0.065024	0.028148	0
protein_co	Fanconi_an	216	182	158	692	716	720	2.097827	2.083025	2.022124	5.814134	7.812283	6.949572
protein_co	SECIS_bind	585	510	438	955	895	834	5.729969	5.886724	5.653343	8.092129	9.848464	8.118431
protein_co	olfactory_r	3	4	2	0	0	0	0.157562	0.24757	0.138419	0	0	0
protein_co	chromoson	5	5	0	6	3	0	0.143472	0.169072	0	0.14894	0.096709	0
protein_co	alcohol_de	1	1	0	0	3	1	0.035318	0.04162	0	0	0.119031	0.035099
pseudogen	-	2	2	2	0	4	6	0.341555	0.402501	0.450086	0	0.767431	1.018336
pseudogen	olfactory_r	0	0	2	2	0	0	0	0	0.149386	0.09807	0	0
protein_co	sema_dom	53	36	31	440	448	410	0.493644	0.395137	0.380482	3.545306	4.687757	3.795173
protein_co	lin-28_hom	13	7	16	2058	1814	1517	0.12502	0.07933	0.202763	17.12155	19.59842	14.49873
protein_co	dynein_axo	48	46	30	90	40	75	0.184249	0.20808	0.151747	0.298862	0.172494	0.286112
protein_co	microspher	829	691	604	1670	1183	1377	17.9135	17.59589	17.19878	31.21803	28.71837	29.57124
protein_co	transmemb	2	2	0	11	21	8	0.035188	0.041467	0	0.167427	0.415086	0.139884
protein_co	scleraxis_h	0	0	0	0	0	1	0	0	0	0	0	0.086822
protein_co	Fanconi_an	54	63	90	253	184	165	0.402027	0.552725	0.882955	1.629465	1.538963	1.220829
pseudogen	family_with	1	0	0	0	0	0	0.012763	0	0	0	0	0
protein_co	zinc_finger_	338	322	234	161	161	175	4.451258	4.997226	4.060848	1.834235	2.381996	2.290413
protein_co	caspase_rec	216	200	162	259	236	355	2.500056	2.727929	2.470846	2.593335	3.068718	4.083513
protein_co	platelet_en	81	51	57	191	185	130	0.862821	0.640196	0.800102	1.760079	2.213892	1.376223
protein_co	ZFP69_zinc	49	20	33	33	42	27	1.089046	0.523826	0.966494	0.634494	1.048694	0.596381
protein_co	sosondowa	10	14	7	17	9	13	0.333172	0.549672	0.307327	0.489982	0.336868	0.430448
protein_co	ZFP69_zinc	61	55	46	76	64	63	1.124835	1.195167	1.117768	1.212371	1.32583	1.15454
protein_co	transmemb	59	41	48	66	57	46	1.00564	0.823534	1.078119	0.97319	1.091477	0.779216
protein_co	histone_clu	698	604	519	760	712	783	50.48199	51.4784	49.46331	47.55078	57.85089	56.27978
protein_co	phospholip	1	1	1	1	0	1	0.020704	0.024399	0.027283	0.017911	0	0.020576
protein_co	eukaryotic_	2334	1983	1276	1916	1373	1741	121.1415	121.2891	87.2725	86.0301	80.05925	89.80496
protein_co	purinergic_	0	0	1	11	2	10	0	0	0.037367	0.269838	0.063713	0.281811
protein_co	coiled-coil_	166	143	120	157	115	139	1.835081	1.862904	1.748088	1.501447	1.428217	1.527115
protein_co	tetratricop	0	0	2	0	1	1	0	0	0.069589	0	0.029664	0.026241
protein_co	family_with	257	197	253	461	299	305	3.731716	3.370922	4.840952	5.790811	4.877482	4.40134
protein_co	paralemmi	138	109	85	30	49	91	3.229822	3.006305	2.62152	0.607413	1.288382	2.116657
protein_co	chromoson	0	0	0	7	4	8	0	0	0	0.102262	0.075886	0.134262
protein_co	shisa_homo	3	8	1	1	1	0	0.026326	0.082729	0.011564	0.007591	0.009858	0
processed_	-	0	2	0	0	4	1	0	0.211126	0	0	0.402544	0.089025
protein_co	Leucine-ric	1	5	0	1	4	1	0.011022	0.064947	0	0.009535	0.049532	0.010954
protein_co	deleted_in_	4	2	3	0	0	1	0.027552	0.016234	0.02723	0	0	0.006845

protein_co	C-type_lect	0	1	0	0	0	2	0	0.030212	0	0	0	0.050958
protein_co	low_densit	1	2	2	3	7	1	0.013196	0.031101	0.034777	0.034246	0.103772	0.013114
protein_co	chromoson	31	11	12	0	6	11	0.983326	0.411183	0.501593	0	0.213814	0.346767
protein_co	ovochymas	22	5	13	0	4	12	0.342056	0.091612	0.26635	0	0.069869	0.185424
protein_co	Rho_GTPas	88	62	70	179	305	283	2.280376	1.893313	2.390323	4.012728	8.879175	7.288192
pseudogen	heparan_su	1	0	1	1	0	3	0.042902	0	0.056534	0.037114	0	0.127911
pseudogen	PMS2_C-te	145	208	142	179	146	157	2.307317	3.900405	2.977573	2.464083	2.610004	2.482839
protein_co	cysteine/hi	688	555	443	1020	756	933	5.914811	5.622798	5.018697	7.586048	7.301688	7.971567
protein_co	collagen_ty	532	395	416	44	45	41	4.355801	3.81119	4.488327	0.311654	0.413921	0.333618
protein_co	delta/notch	165	117	120	17	21	25	2.679529	2.239069	2.567974	0.238829	0.383127	0.403482
protein_co	cleavage_ar	0	0	1	1	3	1	0	0	0.054716	0.035921	0.139943	0.041266
protein_co	kelch-like_f	299	337	248	389	242	332	6.183343	8.21276	6.758318	6.959287	5.622333	6.823385
pseudogen	ankyrin_rep	20	37	12	63	32	76	0.446759	0.973986	0.353232	1.217439	0.80305	1.687202
protein_co	zinc_finger_	32	35	39	1	14	13	0.541942	0.698519	0.870367	0.014651	0.266367	0.218804
protein_co	histone_clu	40	15	17	30	17	27	4.758741	2.102957	2.665114	3.087567	2.272114	3.192313
protein_co	Ras_and_Ra	11	8	6	53	21	56	0.192768	0.165211	0.138557	0.80349	0.413437	0.975302
pseudogen	-	0	1	0	0	0	0	0	0.067519	0	0	0	0
protein_co	olfactory_r	1	3	3	0	0	1	0.016467	0.058216	0.065098	0	0	0.016365
protein_co	tumor_pro	18	19	8	3	9	8	0.173926	0.216347	0.101863	0.025077	0.097697	0.076823
pseudogen	-	0	0	0	62	44	76	0	0	0	1.214513	1.119307	1.710294
protein_co	chromoson	4	4	3	5	3	9	0.084672	0.09978	0.083682	0.091561	0.071343	0.189335
protein_co	MORN_rep	251	261	196	193	155	181	14.4594	17.71839	14.87878	9.618268	10.0313	10.36251
protein_co	CXXC_finge	5	2	0	0	0	0	0.101731	0.047954	0	0	0	0
pseudogen	Meis_home	0	0	0	4	1	9	0	0	0	0.111501	0.0362	0.288208
protein_co	S100_calci	110	94	64	300	162	243	6.803165	6.850989	5.215946	16.05102	11.25596	14.936
protein_co	ubiquilin_2	1326	1027	1115	1156	1061	980	20.53826	18.74552	22.75777	15.48962	18.46224	15.08536
protein_co	Rab_intera	328	292	222	221	194	255	6.658223	6.985129	5.938439	3.880966	4.424206	5.144395
protein_co	chromoson	5	1	0	0	0	1	0.185498	0.04372	0	0	0	0.03687
protein_co	zinc_finger_	31	6	35	17	24	21	0.387343	0.088347	0.576284	0.183758	0.336895	0.260773
protein_co	chloride_ch	0	3	0	6	2	1	0	0.059005	0	0.086631	0.037501	0.016587
protein_co	NACHT_and	0	0	0	1	1	9	0	0	0	0.005457	0.007086	0.056419
protein_co	ADP-ribosy	2851	2309	2420	3606	3087	3420	37.61146	35.89665	42.07006	41.15396	45.75185	44.83929
protein_co	transmemb	1	3	1	11	0	4	0.027431	0.096976	0.036147	0.26103	0	0.109045
protein_co	RAB42_mer	70	79	27	8	10	10	1.900446	2.527503	0.965953	0.187893	0.305005	0.269816
protein_co	wingless-ty	130	106	86	40	33	51	1.756144	1.687446	1.530912	0.467455	0.500818	0.684694
processed_	chromoson	1469	1316	1395	981	979	1123	13.93234	14.70839	17.43457	8.048858	10.43119	10.58502
protein_co	protease_se	0	0	0	0	1	1	0	0	0	0	0.019014	0.01682
protein_co	phospholip	0	0	0	2	0	0	0	0	0	0.017394	0	0
protein_co	G_protein-	21	28	34	20	25	25	0.411611	0.646744	0.878175	0.339126	0.550499	0.486987
protein_co	mesoderm_	0	2	1	1	3	0	0	0.080397	0.044951	0.02951	0.114966	0
protein_co	eyes_shut_l	17	6	18	16	15	15	0.084994	0.03535	0.118589	0.069202	0.084251	0.074531
protein_co	chromoson	234	183	163	1238	1010	1294	1.994878	1.838479	1.831146	9.130281	9.673217	10.96338
protein_co	mitogen-ac	666	555	459	201	120	157	5.643198	5.541804	5.125055	1.473364	1.142303	1.322088
protein_co	transmemb	0	0	0	11	19	26	0	0	0	0.140684	0.315566	0.382007

protein_co	NUT_family	21	29	18	55	70	53	0.389955	0.6346	0.440456	0.883529	1.4603	0.978094
protein_co	collagen_ty	963	778	980	1610	1585	1409	7.863979	7.486912	10.54574	11.37378	14.541	11.43501
protein_co	agrin	9435	7365	6849	7754	9154	10049	68.20951	62.74555	65.24767	48.49443	74.34693	72.19973
protein_co	Nance-Hora	85	60	102	39	51	55	0.513638	0.427264	0.812219	0.203876	0.346224	0.330302
protein_co	otogelin	0	0	0	0	3	0	0	0	0	0	0.017927	0
protein_co	family_with	2	4	0	1	1	0	0.061559	0.145088	0	0.026627	0.034579	0
protein_co	transmemb	31	28	44	32	137	93	0.414228	0.440903	0.774756	0.369905	2.056588	1.235009
protein_co	zinc_finger_	65	60	71	358	258	301	0.577086	0.627748	0.830655	2.749624	2.573333	2.655849
protein_co	smoothelin	57	36	31	543	392	439	1.323525	0.985069	0.948536	10.90737	10.22568	10.13051
protein_co	zinc_finger_	154	130	162	55	86	69	0.706492	0.702808	0.979346	0.218279	0.443235	0.31459
processed_	long_interg	110	103	86	148	134	143	1.909974	2.107555	1.967741	2.223102	2.613897	2.467632
protein_co	late_endos	1085	885	691	1005	807	1474	78.68627	75.63444	66.0362	63.05192	65.7494	106.2371
protein_co	protein_kir	337	268	223	1165	967	1184	6.988294	6.549123	6.093698	20.89923	22.5277	24.40072
protein_co	NUT_family	25	11	15	13	16	21	0.333382	0.172863	0.263589	0.149971	0.239701	0.278311
processed_	HNRNPU_a	84	56	97	108	82	72	0.888165	0.697766	1.351516	0.987873	0.974041	0.756583
protein_co	natural_kill	270	217	309	145	126	124	2.220265	2.102848	3.348377	1.031507	1.164021	1.01338
protein_co	DCN1_defe	476	434	431	190	217	202	8.363728	8.986483	9.979414	2.888082	4.283529	3.527394
protein_co	zinc_finger_	141	114	111	356	302	322	1.112139	1.059625	1.153713	2.429143	2.676062	2.524095
protein_co	tubulin_be	3537	2885	2401	22958	14056	17298	92.01587	88.44649	82.31039	516.6837	410.8076	447.2324
protein_co	ArfGAP_wit	70	29	30	95	55	49	1.519422	0.741798	0.858097	1.783885	1.341195	1.057027
protein_co	Uncharacte	146	132	129	139	99	112	4.120141	4.389755	4.797155	3.393416	3.138654	3.141137
protein_co	COMM_dor	1026	888	743	1215	691	1003	30.29418	30.89811	28.90916	31.03495	22.92128	29.43218
protein_co	phospholip	0	1	0	26	23	18	0	0.04777	0	0.91177	1.047432	0.725155
protein_co	aminoglyco	15	2	11	10	3	9	0.364273	0.057236	0.352017	0.210087	0.081848	0.217214
protein_co	olfactory_r	1	0	0	2	0	2	0.050516	0	0	0.087402	0	0.100408
protein_co	chromoson	26	25	15	22	26	29	0.55391	0.627643	0.421106	0.405463	0.622283	0.614007
protein_co	family_with	0	0	0	0	0	1	0	0	0	0	0	0.005942
protein_co	RUN_and_F	0	0	0	0	3	0	0	0	0	0	0.050008	0
protein_co	zinc_finger_	130	90	64	112	58	85	3.034537	2.475704	1.968629	2.261674	1.520989	1.971867
protein_co	hairy_and_	24	13	17	306	185	294	1.221715	0.779847	1.140361	13.47545	10.57985	14.87359
protein_co	zinc_finger_	114	86	87	290	222	215	3.093426	2.750049	3.11092	6.807628	6.767634	5.798063
protein_co	chromoson	16	11	4	1	0	7	0.330365	0.267654	0.108835	0.017862	0	0.143642
protein_co	leucine-rich	1	0	3	0	4	0	0.028977	0	0.114554	0	0.130215	0
protein_co	centromere	57	71	57	146	96	105	0.344243	0.505308	0.453628	0.762793	0.651345	0.630216
protein_co	phospholip	205	193	163	2021	1759	1914	4.860235	5.392222	5.092438	41.45078	46.85094	45.09776
protein_co	chromoson	163	152	122	206	176	214	2.037634	2.239182	2.00971	2.227763	2.471726	2.658656
protein_co	enolase_far	2	11	2	40	16	36	0.038101	0.246947	0.050207	0.659214	0.342431	0.681578
protein_co	zinc_finger_	122	133	99	131	90	139	2.123209	2.727669	2.270403	1.972274	1.759643	2.404127
protein_co	SH3-bindin	29	37	47	482	601	566	0.30755	0.462409	0.656826	4.42209	7.160462	5.965455
processed_	solute_carr	3	0	0	10	2	4	0.064301	0	0	0.185421	0.048159	0.085205
protein_co	general_tra	549	526	492	847	633	753	20.29651	22.91616	23.96895	27.08916	26.29068	27.66647
protein_co	family_with	475	465	405	694	471	517	5.929491	6.840437	6.662138	7.494563	6.605319	6.413927
protein_co	focadhesin	842	697	800	991	966	719	7.312388	7.133243	9.155286	7.445327	9.424825	6.205627
antisense	-	16	12	6	7	8	13	1.124908	0.994227	0.555883	0.425753	0.631882	0.908343

protein_co	proline_ric	71	38	31	64	40	31	1.921682	1.212032	1.105655	1.498533	1.216276	0.833863
protein_co	zona_pellu	12	9	6	25	8	20	0.344145	0.304166	0.22675	0.620245	0.25775	0.570033
protein_co	H3_histone	0	0	0	1	1	0	0	0	0	0.043494	0.056482	0
protein_co	interferon_	0	0	0	0	6	9	0	0	0	0	0.31221	0.414284
pseudogen	-	0	0	0	0	1	3	0	0	0	0	0.056322	0.149472
pseudogen	-	4	7	4	3	11	13	0.044035	0.090812	0.058027	0.028571	0.136044	0.14223
protein_co	Janus_kina	5	3	5	0	1	6	0.039949	0.028247	0.052644	0	0.008976	0.047643
protein_co	protein_ph	0	0	0	0	1	0	0	0	0	0	0.01756	0
pseudogen	golgin_A6_	2	4	1	0	0	0	0.063063	0.148631	0.04155	0	0	0
protein_co	programme	2	0	0	0	0	0	0.050086	0	0	0	0	0
protein_co	C-type_lect	2	0	2	0	2	0	0.115592	0	0.152322	0	0.12986	0
protein_co	G_protein-	5	5	4	2	0	0	0.226244	0.266614	0.238507	0.078289	0	0
protein_co	Tctex1_dor	13	20	4	4	4	2	0.545351	0.988712	0.22112	0.145163	0.188513	0.083382
pseudogen	ankyrin_rep	0	0	0	8	15	11	0	0	0	0.555981	1.353777	0.878231
protein_co	selectin_L	0	0	0	21	19	16	0	0	0	0.394818	0.463893	0.345577
protein_co	choroidere	334	353	367	470	317	329	3.249227	4.046834	4.704727	3.955437	3.46451	3.18082
protein_co	biogenesis_	136	120	84	384	197	236	2.682554	2.789317	2.183352	6.552451	4.365408	4.626273
pseudogen	signal_reco	3	2	7	2	8	22	0.080254	0.06305	0.246762	0.046285	0.240428	0.584896
protein_co	ceramide_k	142	129	133	87	58	63	2.343398	2.508734	2.892306	1.242053	1.075313	1.033256
pseudogen	WAS_prote	0	1	1	1	0	0	0	0.03322	0.037148	0.024387	0	0
protein_co	solute_carr	0	2	0	15	17	13	0	0.041815	0	0.230222	0.338837	0.229217
protein_co	immediate_	1272	1004	724	1880	1058	995	24.88579	23.14755	18.66542	31.8189	23.25407	19.34626
protein_co	H2A_histor	1139	728	683	10678	6802	7419	37.36047	28.14019	29.52188	302.9992	250.6538	241.8486
protein_co	inscuteable	0	0	0	5	2	4	0	0	0	0.07752	0.040268	0.071244
protein_co	serpin_pep	4	1	0	1	0	2	0.091593	0.026984	0	0.019809	0	0.045514
protein_co	chromoson	288	202	211	430	340	381	5.538324	4.577668	5.346913	7.15348	7.345373	7.281494
protein_co	lactase-like	20	26	16	89	41	65	0.336454	0.515437	0.354691	1.295234	0.774869	1.086722
protein_co	non-specifi	0	0	0	0	8	1	0	0	0	0	0.24055	0.0266
protein_co	keratinocyt	0	0	0	12	1	6	0	0	0	1.119322	0.121132	0.642942
pseudogen	-	0	0	1	1	0	0	0	0	0.219381	0.144022	0	0
protein_co	collagen_ty	44	49	64	101	85	79	0.503111	0.660259	0.96433	0.999069	1.09189	0.897734
protein_co	family_witl	125	129	115	756	651	756	1.25667	1.528298	1.523505	6.575004	7.352606	7.553403
protein_co	chromoson	2	4	3	3	1	1	0.058241	0.137267	0.115121	0.075576	0.032715	0.028941
antisense	-	0	0	0	0	1	0	0	0	0	0	0.024658	0
protein_co	serine/argi	1455	1254	1367	3227	2285	2476	19.46655	19.77109	24.10068	37.34978	34.34482	32.92201
protein_co	hemoglobi	0	0	0	0	0	4	0	0	0	0	0	0.328838
protein_co	dual_specif	40	36	34	64	30	70	0.611858	0.648933	0.685337	0.846903	0.515538	1.064139
protein_co	chromoson	94	28	52	15	15	29	0.991128	0.34791	0.722504	0.136822	0.177681	0.303885
protein_co	neighbor_c	909	819	863	699	638	608	9.676928	10.27459	12.10652	6.437449	7.630331	6.432605
protein_co	olfactory_r	0	0	0	3	0	0	0	0	0	0.130979	0	0
protein_co	Ral_GTPase	268	258	208	259	370	345	1.617994	1.835561	1.65478	1.35271	2.509532	2.070002
protein_co	NADPH_de	256	229	193	703	667	818	5.427671	5.721582	5.392196	12.89413	15.88724	17.236
protein_co	fibrillarin-li	55	43	26	37	16	18	1.916889	1.766078	1.194105	1.115576	0.626474	0.623471
protein_co	Na+/K+_tra	1	1	3	0	5	0	0.016996	0.020028	0.067188	0	0.095467	0

protein_co	progestin_a	6	11	2	9	8	10	0.151044	0.326327	0.066346	0.196001	0.226252	0.250186
protein_co	chromoson	35	21	20	1	3	1	0.672328	0.475378	0.506265	0.016618	0.064742	0.019091
pseudogen	nuclear_po	16	9	14	32	12	12	0.291887	0.193484	0.336556	0.505019	0.245938	0.217563
protein_co	ceroid-lipo	5	1	6	6	12	12	0.085915	0.020249	0.135858	0.08919	0.231649	0.204923
protein_co	family_witl	28	22	26	183	168	184	0.624409	0.578151	0.764046	3.530413	4.208911	4.077921
protein_co	N-acylsphir	14	1	8	31	9	12	0.154508	0.013006	0.116345	0.29597	0.111587	0.131617
protein_co	SMT3_supp	2461	2185	1790	3870	3186	4113	89.05522	93.17648	85.35631	121.1495	129.5217	147.9163
protein_co	nanos_hom	105	136	96	378	286	313	1.201384	1.833744	1.447434	3.741514	3.676272	3.559152
protein_co	IGF-like_far	0	0	0	4	4	1	0	0	0	0.276731	0.359371	0.079477
protein_co	golgin_A8_	1	1	1	0	4	1	0.027878	0.032853	0.036737	0	0.125278	0.027706
protein_co	zinc_finger_	0	1	0	0	0	0	0	0.025685	0	0	0	0
protein_co	leucine_zip	1100	887	943	718	854	761	10.59783	10.07059	11.97212	5.984279	9.243391	7.286495
protein_co	dihydropyr	78	53	68	78	30	63	0.935947	0.749445	1.075227	0.809681	0.404415	0.751289
protein_co	S100_calci	624	557	393	1034	663	847	28.82651	30.32283	23.92406	41.32292	34.40884	38.88665
protein_co	protein_pr	890	779	1054	752	675	596	4.770908	4.921025	7.445373	3.48732	4.065031	3.175169
protein_co	family_witl	38	21	38	85	70	76	0.641914	0.418042	0.845885	1.242153	1.328435	1.275899
lincRNA	long_interg	1	3	4	10	9	9	0.015096	0.053368	0.07957	0.130593	0.152633	0.135023
pseudogen	histone_lin	4	4	2	0	0	0	0.173719	0.204718	0.11446	0	0	0
protein_co	Rh_blood_	10	4	2	0	0	3	0.292492	0.137873	0.077086	0	0	0.087206
protein_co	indoleamin	1	0	0	0	0	0	0.012416	0	0	0	0	0
protein_co	parvin_beta	165	135	99	138	105	119	5.120319	4.936895	4.048397	3.704718	3.660593	3.67003
pseudogen	tektin_4_ps	72	73	38	67	45	65	1.74851	2.08913	1.216057	1.407581	1.227714	1.568768
protein_co	solute_carr	2	6	1	27	18	7	0.016101	0.056923	0.010609	0.188043	0.162799	0.056006
protein_co	uroporphyr	1216	973	747	1230	709	853	41.37291	39.01238	33.49176	36.2035	27.10053	28.84305
processed_	-	4	7	3	4	0	3	0.071614	0.147688	0.070778	0.061953	0	0.053379
protein_co	zinc_finger_	1890	1694	1524	1430	1032	990	21.89943	23.13084	23.2697	14.33409	13.43383	11.40029
protein_co	chromoson	0	0	0	8	9	6	0	0	0	0.127618	0.186445	0.109956
protein_co	pyroglutam	8	2	1	5	3	4	1.030482	0.30359	0.16974	0.557164	0.434131	0.512059
protein_co	dual_specif	0	0	0	0	0	1	0	0	0	0	0	0.079358
protein_co	small_integ	623	429	481	1081	734	718	11.41649	9.264221	11.61514	17.13694	15.11088	13.07611
protein_co	osteocrin	1	2	1	5	0	0	0.016892	0.039813	0.02226	0.073068	0	0
protein_co	von_Willeb	1	0	0	7	1	4	0.027996	0	0	0.169536	0.031452	0.111294
protein_co	family_witl	31	34	9	111	146	119	0.395082	0.510636	0.151148	1.223803	2.090391	1.507239
protein_co	transmemb	826	700	540	889	652	820	5.861046	5.853292	5.049212	5.457074	5.197467	5.782539
protein_co	fibrous_she	28	51	42	26	24	30	0.070407	0.151124	0.139169	0.056558	0.067798	0.07497
protein_co	RNA_bindir	21	10	4	8	12	15	0.541266	0.303738	0.135858	0.178379	0.347474	0.384231
protein_co	NADPH_oxi	0	8	2	71	45	134	0	0.297439	0.083151	1.937856	1.595004	4.201599
protein_co	transmemb	136	114	83	239	140	217	3.008765	2.972086	2.419704	4.574149	3.479577	4.771103
protein_co	BCL2-like_1	6	1	2	5	2	4	0.078606	0.015439	0.034528	0.056668	0.029436	0.05208
protein_co	frizzled_fan	62	50	70	41	25	14	1.401512	1.331933	2.085154	0.801774	0.634884	0.314516
protein_co	sprouty-rel	61	42	65	11	10	16	2.098376	1.702589	2.946467	0.327348	0.386458	0.546995
protein_co	opticin	2	0	1	0	2	0	0.077912	0	0.051334	0	0.087529	0
protein_co	chromoson	0	0	0	4	0	0	0	0	0	0.118881	0	0
protein_co	SKI_family_	8	7	3	4	0	1	0.115246	0.118834	0.05695	0.049849	0	0.014317

protein_co	proline/arg	9	10	3	81	69	51	0.082907	0.108557	0.036417	0.645504	0.714084	0.466907
protein_co	zinc_finger_	175	139	103	192	136	176	2.740217	2.56489	2.125294	2.600825	2.392406	2.738856
protein_co	metal-regul	397	369	382	332	413	460	2.636424	2.887741	3.342897	1.90733	3.081229	3.035934
protein_co	transmemb	2	0	0	0	0	0	0.143277	0	0	0	0	0
pseudogen	zinc_finger_	7	1	4	3	3	28	0.156102	0.02628	0.117546	0.057876	0.075159	0.620553
protein_co	shisa_homo	0	0	0	13	12	24	0	0	0	0.078599	0.094219	0.166698
protein_co	transmemb	332	276	210	740	643	755	4.564116	4.47131	3.804282	8.800621	9.930671	10.31514
protein_co	NHL_repeat	153	144	136	246	242	229	2.282325	2.53137	2.673375	3.174565	4.055557	3.394933
protein_co	H6_family_	0	0	0	0	0	1	0	0	0	0	0	0.032318
protein_co	zinc_finger_	27	17	13	174	157	249	0.364366	0.270352	0.231181	2.031356	2.38025	3.33951
protein_co	family_with	9	12	10	30	8	14	0.429638	0.67507	0.629065	1.238924	0.429042	0.664199
protein_co	cannabinoi	0	0	0	0	1	2	0	0	0	0	0.011117	0.019669
lincRNA	-	17	19	17	13	9	3	0.311418	0.410162	0.410372	0.206016	0.185219	0.054617
protein_co	SLX4_struc	404	316	297	398	542	448	2.927078	2.698032	2.835595	2.494589	4.411653	3.225824
protein_co	glycine_rec	1	3	1	0	0	1	0.028819	0.101885	0.037977	0	0	0.028641
protein_co	ectonucleo	2	0	0	1	5	12	0.037335	0	0	0.016149	0.104859	0.222626
protein_co	ribosomal_	23248	20348	14133	20825	15736	19989	1274.091	1314.146	1020.667	987.3315	968.8541	1088.719
protein_co	BEN_domai	0	0	1	8	13	12	0	0	0.007959	0.041802	0.088213	0.072033
pseudogen	-	0	0	0	2	0	3	0	0	0	0.212032	0	0.365375
pseudogen	ribosomal_	218	196	194	256	215	168	12.99678	13.77026	15.24108	13.20329	14.40014	9.954009
protein_co	family_with	11	2	1	9	11	6	0.132383	0.028365	0.015859	0.093701	0.148724	0.071763
protein_co	zinc_finger_	12	22	3	29	18	45	0.23068	0.498377	0.075995	0.482269	0.388731	0.859707
protein_co	transmemb	4	0	8	0	0	2	0.045599	0	0.120178	0	0	0.022659
protein_co	Fas_(TNFRS	14	33	28	48	31	61	0.153611	0.426693	0.404844	0.455616	0.382125	0.665172
protein_co	killer_cell_l	1	0	0	115	91	119	0.024097	0	0	2.397303	2.4635	2.849828
protein_co	G_protein-r	2	2	0	0	1	9	0.013268	0.015636	0	0	0.007453	0.059339
protein_co	male-specif	1478	1323	1355	1737	1632	1619	22.85245	24.10601	27.60784	23.23385	28.34833	24.87796
protein_co	Protein_LO	1	3	1	3	7	0	0.006941	0.02454	0.009147	0.018015	0.054587	0
protein_co	leucine-rich	0	1	1	0	0	1	0	0.006812	0.007618	0	0	0.005745
protein_co	gap_junctio	0	0	0	37	15	26	0	0	0	0.764348	0.402408	0.617034
protein_co	family_with	43	38	20	13	21	7	0.517025	0.538436	0.31689	0.135223	0.283669	0.083647
protein_co	tRNA_meth	168	121	122	476	311	388	2.59985	2.20664	2.487904	6.372487	5.406902	5.967335
protein_co	protein_tyr	174	124	142	180	162	192	2.213827	1.859187	2.38077	1.981207	2.315573	2.427757
protein_co	chromoson	148	124	149	84	118	124	10.12308	9.994933	13.42988	4.970424	9.067388	8.429124
pseudogen	ubiquitin_s	0	0	0	0	1	0	0	0	0	0	0.015464	0
protein_co	nyctalopin	0	6	1	1	12	3	0	0.137975	0.025714	0.016881	0.263071	0.05818
protein_co	family_with	317	278	230	799	529	685	6.056404	6.259036	5.790529	13.20582	11.3543	13.00636
protein_co	urotensin_2	5	7	5	4	3	1	0.110524	0.182344	0.145644	0.076491	0.0745	0.021968
protein_co	chromoson	1	2	0	2	1	0	0.019485	0.045924	0	0.033713	0.02189	0
protein_co	Uncharacte	423	317	404	323	375	298	6.12361	5.40796	7.706964	4.045132	6.098843	4.28739
protein_co	nucleolar_c	2120	1712	1494	4880	4124	4847	26.71624	25.42437	24.80989	53.2013	58.38578	60.70467
protein_co	Myb/SANT-	12	12	11	8	17	20	0.200788	0.236616	0.24254	0.1158	0.319561	0.332579
protein_co	arylacetam	0	0	0	4	4	3	0	0	0	0.047807	0.062083	0.041191
pseudogen	dihydrofola	3	7	1	22	26	23	0.10775	0.296278	0.047329	0.683566	1.0491	0.820979

protein_co	negative_el	1638	1211	956	3598	2248	3266	32.14134	28.00279	24.71968	61.07652	49.55592	63.69069
protein_co	histone_clu	12	12	13	3	15	11	1.731041	2.039926	2.471179	0.374378	2.430896	1.576988
protein_co	lipase_mem	15	4	12	11	13	5	0.480699	0.15106	0.506755	0.304956	0.468031	0.159243
protein_co	leucine_ric	34	39	33	20	4	5	0.541026	0.731326	0.691971	0.275317	0.071507	0.079071
protein_co	zinc_finger_	557	562	701	452	418	321	2.779277	3.304609	4.609242	1.951094	2.343161	1.591811
protein_co	HUS1_chec	3	0	0	14	5	1	0.154949	0	0	0.625546	0.290126	0.051331
protein_co	potassium_	292	250	218	333	209	255	4.31207	4.350609	4.24223	4.254124	3.467355	3.742422
protein_co	suprabasin	2	1	4	1	0	4	0.054438	0.032076	0.143472	0.023547	0	0.108204
protein_co	adenosine_	158	142	123	185	110	179	4.050691	4.290101	4.155392	4.10305	3.168209	4.560734
pseudogen	-	0	0	1	1	5	4	0	0	0.077086	0.050607	0.328596	0.232548
pseudogen	family_witl	0	2	3	9	6	7	0	0.046009	0.077172	0.151988	0.131584	0.135803
protein_co	von_Hippel	0	2	0	0	0	0	0	0.123053	0	0	0	0
protein_co	zinc_finger_	78	71	65	198	132	131	1.105891	1.186269	1.214412	2.428544	2.102523	1.84586
protein_co	NADH_deh	1560	1337	1032	2392	1547	2207	38.77369	39.16075	33.8008	51.43239	43.19683	54.51606
protein_co	ankyrin_rep	13	5	4	10	8	20	0.267899	0.121424	0.108623	0.178275	0.185211	0.409607
protein_co	alkB_alkyla	159	164	90	173	101	214	7.262828	8.827944	5.417339	6.836247	5.182975	9.71476
protein_co	ring_finger_	99	126	99	180	105	133	2.494602	3.741482	3.287275	3.923752	2.97238	3.330637
protein_co	ring_finger_	0	0	0	0	3	0	0	0	0	0	0.058272	0
protein_co	chorionic_	0	0	0	2	0	0	0	0	0	0.108915	0	0
protein_co	reelin	1	5	0	692	639	525	0.004575	0.026959	0	2.738989	3.284514	2.387207
protein_co	family_witl	35	29	33	1019	689	765	0.531231	0.518705	0.660031	13.3799	11.74854	11.53949
protein_co	apolipopro	127	131	103	0	2	1	5.556617	6.754374	5.938527	0	0.098307	0.043483
protein_co	H1_histone	3802	3166	2806	3940	4207	4899	86.42407	84.80874	84.05143	77.47861	107.4346	110.6725
protein_co	lipopolysac	246	200	157	1704	1259	1407	5.52545	5.293825	4.646939	33.11045	31.76927	31.40771
protein_co	V-set_and_	0	0	0	6	0	0	0	0	0	0.263971	0	0
polymorph	transmemb	787	737	480	471	273	389	28.61577	31.5795	22.99888	14.81544	11.15173	14.05691
protein_co	AT_rich_int	283	235	303	565	512	410	1.733661	1.696496	2.445993	2.994258	3.523683	2.496154
pseudogen	ribosomal_	7	5	1	1	0	1	0.318374	0.267989	0.059934	0.039346	0	0.045201
protein_co	splicing_fac	2911	2427	2329	5275	4202	3950	22.11382	21.72694	23.31449	34.66627	35.86136	29.82142
protein_co	protease_se	0	0	1	1	3	3	0	0	0.070539	0.046308	0.180412	0.159598
protein_co	interleukin	1	0	1	2	5	8	0.017736	0	0.023371	0.030686	0.099625	0.141009
protein_co	biogenesis_	291	259	177	257	169	230	5.923041	6.212388	4.747444	4.525305	3.864448	4.65253
protein_co	Sp6_transc	4	2	2	996	1244	1663	0.055032	0.032426	0.03626	11.85439	19.22766	22.73835
protein_co	ankyrin_rep	0	0	0	48	50	63	0	0	0	0.55824	0.755154	0.841718
protein_co	placenta-sp	384	318	189	39	54	60	25.89725	25.27299	16.79651	2.27536	4.091337	4.021456
protein_co	NFKB_activ	3	0	0	8	0	1	0.096902	0	0	0.223546	0	0.032101
pseudogen	ubiquitin-c	53	82	72	8	10	10	1.305057	2.379439	2.336259	0.170415	0.276632	0.244717
protein_co	claudin_4	15	7	13	4940	3642	4804	0.190755	0.104904	0.217853	54.34701	52.0325	60.71532
protein_co	zinc_finger_	94	80	68	42	66	64	1.977923	1.983712	1.885494	0.764529	1.560179	1.338354
lincRNA	CRYM_anti	7	10	15	9	14	19	0.182735	0.307632	0.516001	0.20325	0.410583	0.492932
protein_co	GRB2-relat	1	0	0	0	0	0	0.040475	0	0	0	0	0
protein_co	family_witl	0	2	0	4	4	2	0	0.019967	0	0.029316	0.038071	0.016839
protein_co	hematologi	2743	2402	1932	6419	4374	6010	63.4413	65.4676	58.88277	128.433	113.6512	138.1435
protein_co	zinc_finger_	139	105	99	94	62	91	1.379861	1.228335	1.295062	0.807256	0.691451	0.897783

protein_co	zygote_arre	0	0	0	4	5	3	0	0	0	0.117133	0.19014	0.100922
protein_co	S100_calci	788	719	428	1228	857	1025	19.10142	20.53882	13.67156	25.7514	23.33831	24.69295
protein_co	zinc_finger_	290	298	255	471	374	429	2.509872	3.039324	2.908229	3.526448	3.636422	3.689951
protein_co	olfactory_r	0	0	0	0	1	0	0	0	0	0	0.059357	0
protein_co	protocadhe	875	685	790	1431	1089	1057	7.843442	7.235963	9.331695	11.09689	10.96669	9.416365
protein_co	zinc_finger_	45	21	28	161	93	126	0.622185	0.342163	0.510152	1.925731	1.44457	1.731358
protein_co	BTB_(POZ)_	5	3	8	1	3	5	0.163803	0.115819	0.345363	0.028341	0.110413	0.162791
lincRNA	-	2	0	2	1	3	3	0.049733	0	0.065536	0.021512	0.083808	0.074139
pseudogen	dpy-19-like	0	0	4	17	19	8	0	0	0.071296	0.198922	0.288718	0.10754
protein_co	monoamin	195	122	162	64	62	37	2.571231	1.895717	2.814857	0.730045	0.918433	0.484862
processed_	-	1642	1512	1348	671	454	544	32.35174	35.10616	34.99848	11.43694	10.04915	10.65204
protein_co	chromoson	41	23	32	62	34	37	1.550415	1.024941	1.594589	2.028237	1.444415	1.390514
lincRNA	-	40	26	25	76	70	81	1.955346	1.497766	1.610417	3.213958	3.844242	3.935123
protein_co	nuclear_GT	0	0	0	3	1	0	0	0	0	0.035348	0.015301	0
lincRNA	-	0	0	0	2	0	1	0	0	0	0.032539	0	0.018691
protein_co	TSPY-like_1	2027	1807	1387	1389	1589	1638	32.2644	33.89496	29.09251	19.12648	28.41468	25.91155
protein_co	tripartite_r	0	0	0	0	1	1	0	0	0	0	0.022118	0.019566
protein_co	proline-rich	1150	1084	1004	2605	2126	2038	25.19956	27.99185	28.99103	49.38168	52.33684	44.38222
protein_co	chromoson	0	0	0	0	4	0	0	0	0	0	0.183003	0
protein_co	Uncharacte	0	0	0	4	2	0	0	0	0	0.054136	0.035151	0
protein_co	gap_junctio	2	0	0	5	0	8	0.078142	0	0	0.169	0	0.310636
protein_co	fragile_hist	18	26	18	83	76	97	0.311113	0.529573	0.40997	1.241041	1.475733	1.666197
protein_co	family_with	7	9	2	5	4	7	0.266801	0.40424	0.100451	0.164863	0.171277	0.265154
protein_co	zinc_finger_	106	82	89	112	114	107	2.398182	2.186237	2.65339	2.192084	2.897545	2.405856
protein_co	ribosomal_	724	616	459	2095	1553	2177	10.084	10.11072	8.424453	25.24302	24.30047	30.13438
protein_co	lin-54_hom	201	204	188	712	493	444	1.736762	2.077215	2.140607	5.322151	4.785642	3.812737
protein_co	family_with	1429	1119	1025	663	524	629	13.92979	12.85433	13.16652	5.590991	5.738424	6.093581
protein_co	family_with	23	10	11	0	0	0	0.676468	0.346598	0.426331	0	0	0
protein_co	chromoson	0	0	0	0	2	0	0	0	0	0	0.031839	0
protein_co	S100_calci	0	1	1	16	14	37	0	0.051221	0.057277	0.601628	0.683631	1.598292
protein_co	kazrin_peri	192	182	216	344	270	315	1.685683	1.883013	2.498983	2.61274	2.663101	2.748495
protein_co	solute_carr	1954	1617	1605	1114	1193	1054	16.52239	16.1126	17.88374	8.148855	11.33282	8.857245
pseudogen	ribosomal_	15997	13478	9565	12409	9589	12773	917.5483	911.0096	722.9532	615.7298	617.8923	728.1032
pseudogen	family_with	0	0	0	3	0	2	0	0	0	0.099347	0	0.076087
protein_co	family_with	2	2	2	2	5	3	0.008343	0.009832	0.010994	0.007218	0.023432	0.012437
protein_co	transmemb	38	39	35	107	149	99	0.32616	0.394475	0.395868	0.794501	1.436756	0.844486
protein_co	ALG1_chitc	1	0	0	5	1	1	0.065765	0	0	0.284465	0.073883	0.065359
protein_co	KIAA0408	6	2	4	0	6	0	0.048274	0.018963	0.042409	0	0.054233	0
protein_co	G1_to_S_ph	271	231	236	468	478	458	5.044659	5.067358	5.789077	7.536529	9.996304	8.473008
protein_co	chromoson	22	7	4	41	18	32	0.867885	0.32542	0.207938	1.399221	0.79774	1.254582
protein_co	chemokine_	0	0	5	0	0	0	0	0	0.297625	0	0	0
pseudogen	olfactory_r	2	1	0	23	51	35	0.10882	0.064119	0	1.082605	3.117443	1.892592
protein_co	high_mobil	4469	3887	3470	15188	12457	14832	56.34515	57.75211	57.65149	165.657	176.4447	185.847
protein_co	matrix_met	24	28	24	4	14	11	0.829905	1.14099	1.093611	0.119657	0.543869	0.378024

protein_co	SH2_domai	32	23	33	134	94	109	0.45725	0.387292	0.621373	1.656425	1.508971	1.54789
lincRNA	-	0	1	1	3	2	5	0	0.03011	0.03367	0.066311	0.057409	0.126964
pseudogen	ubiquitin_	11	2	5	58	45	48	0.49604	0.106282	0.297118	2.262638	2.279741	2.151171
protein_co	natural_cyt	0	0	0	0	1	0	0	0	0	0	0.036896	0
pseudogen	Ras_associa	0	0	0	6	7	27	0	0	0	0.148698	0.225288	0.768712
protein_co	olfactory_r	0	0	0	2	0	0	0	0	0	0.048645	0	0
protein_co	biogenesis_	658	557	505	1439	955	1379	17.21105	17.16896	17.40635	32.56157	28.06299	35.84722
protein_co	synaptoner	54	42	35	13	22	12	0.513529	0.470682	0.438605	0.106949	0.23504	0.113413
protein_co	zinc_finger_	41	38	28	323	306	316	0.785304	0.857718	0.706719	5.352043	6.584526	6.01521
protein_co	interleukin	94	84	127	38	25	18	1.041535	1.096812	1.854319	0.364244	0.311197	0.198211
protein_co	protein_tyr	0	0	0	10	2	8	0	0	0	0.035907	0.009326	0.033
protein_co	paired_box	0	0	0	5	1	1	0	0	0	0.026827	0.006968	0.006164
processed_	-	0	2	3	2	3	0	0	0.07225	0.121187	0.053039	0.103317	0
protein_co	sparc/ostec	22	29	18	15	5	7	0.390054	0.605909	0.420542	0.230068	0.099591	0.123342
protein_co	zinc_finger_	33	29	48	19	27	18	0.520266	0.538786	0.997212	0.259136	0.478216	0.282029
pseudogen	-	2	1	0	9	0	0	0.265368	0.15636	0	1.033058	0	0
pseudogen	ADAM_met	2	0	0	0	0	0	0.052994	0	0	0	0	0
protein_co	tudor_dom	37	11	12	90	84	61	0.510907	0.178995	0.218351	1.075092	1.303072	0.837104
protein_co	chromoson	3	1	2	8	1	11	0.075129	0.029512	0.066001	0.173317	0.028134	0.273772
protein_co	olfactory_r	0	0	0	1	0	1	0	0	0	0.039999	0	0.045951
protein_co	KIAA0895-l	997	901	624	243	319	427	14.86822	15.83418	12.26262	3.134967	5.344456	6.328507
protein_co	major_hist	0	0	0	2	0	0	0	0	0	0.07453	0	0
protein_co	myelin_tra	0	0	0	0	0	1	0	0	0	0	0	0.009372
protein_co	serpin_pep	7	15	6	5	3	4	0.12083	0.305124	0.136479	0.074664	0.058177	0.06862
protein_co	aldo-keto_r	212	127	133	9	10	7	6.211118	4.384749	5.134763	0.228107	0.329142	0.203818
protein_co	spermatoge	1699	1213	1168	3810	2572	2665	33.33831	28.04904	30.20145	64.67525	56.69832	51.97051
protein_co	zinc_finger_	282	204	188	233	180	178	2.345908	1.999858	2.060889	1.676798	1.682223	1.471606
protein_co	WD_repeat	84	66	67	262	153	215	2.316168	2.144578	2.434448	6.249642	4.739487	5.891677
protein_co	zinc_finger_	129	136	116	156	139	185	3.28652	4.083124	3.894389	3.438224	3.978418	4.684119
protein_co	S100_calci	1006	841	664	302	228	341	70.54124	69.49415	61.35473	18.31956	17.96094	23.76343
protein_co	pleckstrin_	190	200	110	12	5	7	1.447516	1.795589	1.104326	0.079089	0.042795	0.053
protein_co	FAT_tumor_	1499	1285	1613	94	70	71	4.922071	4.97229	6.979357	0.267016	0.258222	0.231694
protein_co	chromoson	2	0	0	0	0	2	0.019265	0	0	0	0	0.019146
protein_co	zinc_finger_	20	21	26	225	141	174	0.162971	0.201653	0.279182	1.586079	1.290766	1.409088
protein_co	histone_clu	2	5	4	3	31	25	0.284629	0.838545	0.750143	0.369346	4.956326	3.53589
protein_co	acyl-CoA_d	158	152	153	235	131	162	1.427663	1.618524	1.821775	1.836959	1.329808	1.454766
protein_co	serine/thre	1305	1085	917	2197	2387	2614	14.28323	13.99435	13.22575	20.80219	29.35063	28.43356
pseudogen	ribosomal_	2	2	0	0	0	6	0.118835	0.14004	0	0	0	0.354303
protein_co	transmemb	412	375	255	749	844	928	4.033973	4.326872	3.290112	6.344254	9.283831	9.030116
protein_co	cathepsin_l	0	1	0	0	0	0	0	0.027814	0	0	0	0
protein_co	sema_dom	20	2	9	1	7	4	0.320855	0.037811	0.190263	0.013878	0.126161	0.063775
pseudogen	-	1	1	0	1	0	0	0.157095	0.185127	0	0.135902	0	0
protein_co	histidine_ri	28	39	45	0	0	2	1.560366	2.56118	3.304577	0	0	0.110766
protein_co	M-phase_pl	832	704	628	1259	959	919	10.40069	10.37095	10.34506	13.61531	13.4681	11.41731

pseudogen	ring_finger	283	249	245	646	426	458	4.125083	4.277132	4.705948	8.145951	6.975975	6.634701
pseudogen	eukaryotic_	2847	2747	2295	2259	1740	2581	89.9302	102.2548	95.52908	61.73015	61.74707	81.02438
protein_co	growth_reg	27	22	13	227	278	218	0.168483	0.161779	0.106898	1.225407	1.948881	1.35194
protein_co	signal-regul	0	0	0	3	1	1	0	0	0	0.052005	0.022512	0.019914
protein_co	zinc_finger_	326	270	284	392	277	360	5.801265	5.66208	6.659755	6.034679	5.537758	6.366742
protein_co	ryanodine_	1	0	0	22	21	30	0.003443	0	0	0.065525	0.081225	0.102648
protein_co	SLIT-ROBO_	486	414	425	84	122	93	2.972426	2.983886	3.4253	0.444444	0.83827	0.565285
protein_co	histone_clu	0	1	0	0	0	5	0	0.144751	0	0	0	0.610372
protein_co	family_with	445	334	380	720	647	612	4.572737	4.044546	5.145584	6.400468	7.469122	6.249961
protein_co	sulfotransfe	0	1	2	0	1	0	0	0.068183	0.152488	0	0.065001	0
protein_co	tubulin_be	34334	28674	24577	88553	56586	67460	626.1371	616.2266	590.6208	1397.048	1159.319	1222.647
protein_co	ligand_dep	358	265	379	458	559	403	2.437042	2.125852	3.399805	2.697171	4.275047	2.726432
protein_co	suppressor_	3855	3321	2688	4164	3572	4344	52.30331	53.09832	48.05836	48.87408	54.44592	58.57392
protein_co	X-prolyl_an	871	785	581	1274	911	1096	5.77261	6.130992	5.07417	7.304432	6.782995	7.218953
protein_co	zinc_finger_	121	126	126	424	405	390	1.051175	1.289933	1.442431	3.186534	3.952699	3.367161
protein_co	olfactory_r	0	0	0	1	0	0	0	0	0	0.040855	0	0
protein_co	peptidylpro	27522	24133	18825	36476	27970	34020	651.0465	672.7449	586.8158	746.4526	743.3161	799.79
protein_co	zinc_finger_	11	14	15	1	6	1	0.092628	0.138926	0.166447	0.007285	0.056761	0.008369
protein_co	zinc_finger_	81	56	55	87	69	83	1.286595	1.048219	1.151209	1.195471	1.231275	1.310221
protein_co	zinc_finger_	83	96	93	206	208	147	0.874796	1.19236	1.291655	1.878275	2.462869	1.53977
lincRNA	long_interg	4	1	1	0	0	0	0.102252	0.030124	0.033686	0	0	0
pseudogen	-	3	1	0	0	0	0	0.897305	0.352473	0	0	0	0
protein_co	GTF2I_repe	96	74	64	56	48	41	1.428425	1.297553	1.254876	0.720837	0.802373	0.606289
protein_co	glutamate_	11	5	2	0	0	0	0.137477	0.07364	0.032938	0	0	0
protein_co	suppressor_	142	147	92	382	171	194	3.146765	3.838843	2.686573	7.323224	4.257171	4.272552
protein_co	NIF3_NGG1	251	173	146	880	554	617	7.909637	6.424451	6.062761	23.9899	19.61289	19.32314
processed_	-	270	208	221	160	145	169	3.543398	3.216819	3.821935	1.816516	2.13783	2.204208
protein_co	ATPase_Ca+	43	59	30	52	17	43	0.643796	1.040972	0.591883	0.673513	0.285942	0.63982
protein_co	isoleucyl-tF	2919	2477	2390	5126	3973	3777	33.19046	33.19038	35.81062	50.42208	50.75125	42.68111
protein_co	hippocamp	72	55	89	101	129	163	4.849557	4.365554	7.899405	5.885101	9.761315	10.91106
protein_co	POM121_tr	1667	1340	1171	1330	2210	1746	12.58774	11.92406	11.65209	8.688139	18.74794	13.10286
protein_co	zinc_finger_	243	177	207	352	333	300	1.381069	1.185467	1.550295	1.730673	2.126192	1.694494
protein_co	histone_clu	20	17	3	11	77	40	2.26728	2.271074	0.448158	1.078775	9.806522	4.506557
protein_co	serine/thre	0	0	0	17	10	8	0	0	0	0.208623	0.159367	0.112785
protein_co	chorionic_p	3	0	4	4	2	1	0.046906	0	0.082414	0.054104	0.03513	0.015539
protein_co	neuroligin_	14	35	20	31	6	22	0.189413	0.55803	0.356572	0.362833	0.091197	0.295811
protein_co	alcohol_de	2	3	3	0	0	0	0.042083	0.074389	0.083184	0	0	0
protein_co	zinc_finger_	157	104	152	77	86	77	2.390491	1.86607	3.049761	1.014241	1.471075	1.165166
protein_co	CD55_mole	273	251	184	548	296	359	5.236555	5.673667	4.650885	9.093406	6.378577	6.843639
protein_co	copine_IV	6	1	2	8	0	6	0.058488	0.011487	0.025691	0.067463	0	0.058126
protein_co	Uncharacte	9	9	4	4	0	0	0.251302	0.296144	0.14718	0.096622	0	0
protein_co	zinc_finger_	91	82	51	69	41	46	1.912517	2.030883	1.412436	1.254515	0.968048	0.960796
protein_co	netrin_G2	4	3	3	1	6	5	0.044191	0.039057	0.043675	0.009557	0.074469	0.054898
protein_co	ELAV_(emb	6	0	1	0	1	4	0.06717	0	0.014752	0	0.012577	0.044503

protein_co	WD_repeat	1091	913	745	2412	1909	2354	18.33025	18.0768	16.49433	35.05775	36.03285	39.30609
protein_co	lon_peptid	2761	2511	1764	4646	3444	4180	45.16999	48.41026	38.02918	65.75455	63.29884	67.96252
protein_co	chromoson	3	3	11	22	12	17	0.061751	0.07277	0.298366	0.391748	0.277493	0.34776
protein_co	transforma	1293	1102	1331	1788	1657	1523	5.399756	5.423308	7.324677	6.459607	7.774047	6.320991
protein_co	nudix_(nuc	497	475	376	596	397	402	11.03215	12.42523	10.99832	11.44493	9.900184	8.86828
pseudogen	SLIT-ROBO_	109	75	161	115	243	133	4.325763	3.507556	8.419706	3.948181	10.83407	5.245629
protein_co	fucosyltran	88	71	81	386	326	399	0.770433	0.732517	0.934484	2.923496	3.206408	3.47164
protein_co	ankyrin_rep	131	109	112	296	270	294	2.494702	2.446138	2.810607	4.87643	5.776438	5.56422
protein_co	histone_clu	2	3	3	6	13	14	0.237404	0.419648	0.46926	0.616129	1.733603	1.651562
protein_co	solute_carr	0	0	1	132	98	113	0	0	0.014378	1.245972	1.201286	1.225348
protein_co	zinc_finger_	54	34	42	54	60	51	1.390474	1.031704	1.425125	1.20289	1.735679	1.305115
protein_co	zinc_finger_	15	17	11	31	29	19	0.25234	0.337017	0.24385	0.451149	0.548078	0.317657
protein_co	zinc_finger_	321	213	235	375	262	286	4.787059	3.743264	4.618133	4.837913	4.38949	4.238766
protein_co	inhibitor_c	29	36	27	27	20	57	0.989232	1.447138	1.213665	0.796759	0.766442	1.932346
pseudogen	-	2	0	0	0	0	0	0.154122	0	0	0	0	0
protein_co	zinc_finger_	6	3	12	34	35	50	0.099202	0.058452	0.261449	0.486309	0.650112	0.821581
protein_co	protein_tyr	1439	1216	1134	2264	2059	2469	21.58744	21.49716	22.41756	29.3819	34.70131	36.81045
protein_co	HDCMB45P	0	0	0	0	2	1	0	0	0	0	0.100128	0.044288
protein_co	Enah/Vasp-	1621	1443	996	598	522	578	23.16883	24.30494	18.75924	7.3941	8.381865	8.210292
protein_co	SPANX_fam	3	0	1	3	4	0	0.232878	0	0.102292	0.201461	0.348832	0
protein_co	thioesteras	1	8	9	23	20	24	0.021151	0.199401	0.250847	0.420845	0.475237	0.504489
protein_co	NADPH_oxi	1	0	0	1	0	0	0.03272	0	0	0.028306	0	0
protein_co	zinc_finger_	48	26	45	48	36	43	0.611593	0.390393	0.755559	0.529085	0.515315	0.544502
protein_co	EPH_recept	3193	2455	2216	4209	4007	4053	33.42044	30.28111	30.56454	38.11143	47.11744	42.15989
protein_co	proteinase_	0	1	0	0	0	0	0	0.059931	0	0	0	0
protein_co	zinc_finger_	192	167	126	328	302	307	2.224704	2.280313	1.923873	3.287818	3.931216	3.53524
protein_co	zinc_finger_	135	106	119	508	374	404	3.186373	2.948328	3.701217	10.37265	9.917072	9.476628
protein_co	X-ray_repai	5669	4503	4045	14385	10737	11455	110.7872	103.7032	104.1685	243.1957	235.7301	222.4784
protein_co	S100_calci	1	4	2	3	0	1	0.074565	0.35148	0.196516	0.193517	0	0.074104
lincRNA	long_interg	4	13	4	13	7	10	0.049213	0.188483	0.064851	0.138365	0.096754	0.122273
protein_co	protein_ph	215	138	179	647	849	961	2.307849	1.745642	2.53196	6.008088	10.23825	10.25185
protein_co	TSC22_dom	861	776	828	1485	1360	1177	9.419755	10.00473	11.93718	14.05484	16.71569	12.79742
protein_co	crystallin_b	0	1	0	0	0	0	0	0.076927	0	0	0	0
protein_co	acetylserot	4	3	0	0	0	1	0.152568	0.134844	0	0	0	0.037906
protein_co	nuclear_po	27	23	13	51	28	24	1.000985	1.004844	0.6351	1.635675	1.166194	0.88427
protein_co	zinc_finger_	129	110	82	141	111	135	1.681701	1.689892	1.408665	1.590161	1.625665	1.749051
protein_co	armadillo_t	168	170	195	105	276	212	1.198664	1.429368	1.833402	0.648098	2.212312	1.503259
protein_co	yrdC_doma	127	165	137	568	339	527	3.682095	5.637445	5.234156	14.24632	11.04181	15.18489
protein_co	zinc_finger_	469	412	260	1008	658	670	7.679965	7.950431	5.610409	14.2794	12.1049	10.90362
protein_co	phosphoin	234	159	277	736	584	539	2.470228	1.977996	3.853326	6.721435	6.926009	5.65483
protein_co	zinc_finger_	435	292	265	544	420	444	8.919184	7.055467	7.160058	9.649343	9.674626	9.047497
protein_co	zinc_finger_	516	508	418	290	344	272	4.395423	5.099431	4.692044	2.137037	3.29199	2.302658
protein_co	trafficking_	282	278	222	410	406	376	4.803526	5.58037	4.983092	6.041683	7.769377	6.365149
protein_co	RFX_family	240	260	143	0	0	0	6.522504	8.326904	5.121227	0	0	0

protein_co	myosin_ligl	1660	1448	1127	900	810	1162	67.34257	69.22409	60.24768	31.58545	36.91609	46.84868
protein_co	zinc_finger_	45	8	22	98	50	66	0.584481	0.122449	0.376544	1.101151	0.729587	0.851945
protein_co	fibroblast_	0	0	0	0	1	0	0	0	0	0	0.053776	0
protein_co	siah_E3_ub	82	81	68	189	136	175	1.295096	1.507579	1.415246	2.582337	2.413104	2.746855
protein_co	chromoson	172	167	166	203	120	153	5.781493	6.61508	7.352828	5.90297	4.531498	5.111079
protein_co	estrogen-re	0	0	0	6	10	12	0	0	0	0.049673	0.107513	0.11413
protein_co	importin_4	0	0	2	4	0	5	0	0	0.038268	0.050246	0	0.072153
protein_co	nuclear_rec	10668	8426	6915	4213	5824	6161	64.85697	60.36736	55.39884	22.15788	39.77811	37.22498
protein_co	sulfotransfe	2	5	0	0	7	9	0.013322	0.039247	0	0	0.052382	0.059578
protein_co	ADP-ribosy	51	38	54	12	5	21	2.146257	1.884526	2.994608	0.436874	0.236391	0.878295
protein_co	PRP40_pre	1479	1168	1295	3681	2638	2615	9.729092	9.054283	11.22558	20.94754	19.49521	17.09564
protein_co	ganglioside	134	73	118	266	247	205	2.447927	1.571534	2.840603	4.203764	5.069203	3.721836
protein_co	transcriptic	992	765	719	79	115	135	43.01185	39.08814	41.08092	2.963238	5.601745	5.817278
protein_co	anaphase_p	457	420	402	1583	996	1310	7.945496	8.605204	9.210128	23.80941	19.45419	22.63527
protein_co	thiamin_py	47	21	45	54	33	44	0.561803	0.29581	0.708816	0.558397	0.443149	0.522695
protein_co	solute_carr	234	230	152	447	348	527	3.957889	4.584402	3.387865	6.54061	6.612658	8.85866
protein_co	actin_filam	1131	1014	1085	1346	1450	1422	7.708067	8.143815	9.744228	7.935804	11.10197	9.63146
protein_co	nascent_pc	14704	13352	9770	14766	9893	12322	117.4301	125.6601	102.819	102.0164	88.76079	97.79911
protein_co	chromoson	0	0	0	0	1	0	0	0	0	0	0.035721	0
protein_co	myosin_XV	385	327	337	293	712	508	2.682938	2.685374	3.094672	1.766366	5.574155	3.518223
protein_co	serine_paln	1	2	3	3	7	8	0.017061	0.040211	0.067448	0.044279	0.134171	0.135647
protein_co	chromoson	174	138	131	175	158	159	4.815333	4.500526	4.777308	4.189654	4.912282	4.373044
protein_co	mannosida	177	164	160	444	383	383	1.494983	1.632353	1.780811	3.244211	3.634218	3.21493
protein_co	membrane_	9080	8626	8941	9325	8536	7745	85.50413	95.72333	110.9487	75.96492	90.30353	72.48236
protein_co	family_with	15	35	19	157	147	181	0.331157	0.91058	0.552753	2.99851	3.645938	3.971286
processed_	long_interg	3	1	0	0	3	2	0.139074	0.05463	0	0	0.156241	0.092144
protein_co	calcium_ch	234	199	200	7	27	36	1.532434	1.535769	1.725959	0.039658	0.198645	0.234303
processed_	long_interg	28	26	18	26	33	28	0.541398	0.592433	0.458634	0.434906	0.716839	0.538055
protein_co	sulfatase_2	2463	2236	1826	2453	2037	2134	26.52974	28.38229	25.91816	22.85752	24.64953	22.84403
protein_co	hemoglobi	0	0	1	6	0	0	0	0	0.03937	0.155075	0	0
protein_co	laminin_alp	3622	2977	3823	183	202	159	19.89132	19.26642	27.6665	0.869419	1.24628	0.867804
protein_co	plexin_B2	11846	10153	8808	4165	3889	4578	98.25145	99.23588	96.26743	29.88445	36.23717	37.73572
protein_co	adherens_j	0	0	0	71	117	88	0	0	0	1.112841	2.381479	1.584544
protein_co	X-ray_repai	95	84	106	1220	946	1086	1.063747	1.108411	1.564067	11.81782	11.90022	12.08521
protein_co	myosin_VI	320	286	372	1116	1068	1035	1.95512	2.059191	2.995031	5.898624	7.330673	6.28454
protein_co	megakaryol	873	647	624	1217	1088	1216	10.25915	8.960014	9.663105	12.37231	14.364	14.20171
protein_co	histone_de	2677	2283	2067	7527	5485	6092	14.35315	14.42487	14.60408	34.91274	33.03883	32.46149
pseudogen	ankyrin_rep	0	0	0	0	0	5	0	0	0	0	0	0.094088
protein_co	zinc_finger_	27	34	45	56	50	69	0.339285	0.503485	0.745157	0.608768	0.705862	0.861706
protein_co	POTE_anky	0	0	0	0	3	0	0	0	0	0	0.044264	0
protein_co	zinc_finger_	154	171	126	82	82	104	4.044104	5.291816	4.360205	1.862852	2.419159	2.714217
protein_co	matrix_met	12	0	5	65	40	62	0.322483	0	0.177064	1.511131	1.207633	1.655874
protein_co	alcohol_de	22	7	13	1	0	1	0.286027	0.107248	0.222722	0.011247	0	0.012921
protein_co	UDP_glucu	0	1	1	0	0	0	0	0.030037	0.033588	0	0	0

protein_co	RIMS_bindi	9	1	2	6	13	8	0.082377	0.010786	0.024123	0.047509	0.133677	0.072772
protein_co	transcriptic	2943	2452	3015	1026	1151	1058	18.69963	18.3599	25.24439	5.639664	8.216128	6.680949
protein_co	WNK_lysin	144	119	174	204	177	153	0.672207	0.654628	1.070348	0.823823	0.928246	0.70981
lincRNA	-	0	0	1	0	0	0	0	0	0.154003	0	0	0
protein_co	ACN9_hom	102	87	76	386	246	316	2.62135	2.634822	2.573791	8.581737	7.102464	8.070893
protein_co	histamine_	840	737	614	2	2	4	9.439702	9.760084	9.092476	0.019443	0.02525	0.044673
protein_co	RAB_membr	2647	2168	1771	5578	4425	5985	35.48615	34.25085	31.2866	64.69139	66.64496	79.74046
protein_co	zinc_finger_	131	110	93	108	107	131	1.937768	1.917477	1.812793	1.382029	1.778129	1.925801
protein_co	Golgin_sub	16	20	10	56	20	31	0.12942	0.190642	0.10659	0.391862	0.181745	0.249203
protein_co	zinc_finger_	412	371	310	565	532	532	3.876944	4.114086	3.844049	4.599428	5.6241	4.975235
protein_co	zinc_finger_	0	0	0	11	6	8	0	0	0	0.154064	0.10913	0.128719
protein_co	trafficking_	531	431	321	1263	767	869	14.61105	13.97563	11.6393	30.06446	23.70999	23.76383
pseudogen	-	51	46	33	197	104	185	6.108576	6.492841	5.208571	20.41263	13.99433	22.02172
protein_co	tetratricop	36	37	44	96	104	72	0.688042	0.833338	1.108153	1.587254	2.233031	1.367585
protein_co	solute_carr	206	221	179	0	2	1	2.987903	3.777449	3.421268	0	0.03259	0.014415
protein_co	tectonin_b	641	510	539	567	576	565	3.906882	3.663106	4.329082	2.989636	3.944063	3.422397
protein_co	toll-like_re	0	0	0	11	1	1	0	0	0	0.100536	0.011869	0.0105
protein_co	family_with	0	1	4	0	0	2	0	0.043476	0.194462	0	0	0.07333
processed_	long_interg	10	4	3	12	8	0	0.331503	0.156262	0.131052	0.344137	0.297938	0
protein_co	ZFP62_zinc	293	200	227	397	390	412	3.858635	3.103867	3.939369	4.522927	5.770052	5.392286
pseudogen	-	6	5	7	0	1	6	0.912776	0.896375	1.403284	0	0.170908	0.907139
protein_co	ERI1_exorib	78	80	99	227	232	183	1.073686	1.297717	1.795779	2.70316	3.587731	2.503477
protein_co	translocase	1584	1500	1014	948	739	1578	107.7873	120.2848	90.92541	55.80638	56.49448	106.7159
protein_co	hematopoi	0	0	0	0	0	6	0	0	0	0	0	0.127601
protein_co	transient_r	12	7	5	2	19	19	0.152348	0.104728	0.083649	0.021966	0.270993	0.239728
protein_co	zinc_finger_	205	212	213	473	441	513	1.825552	2.22476	2.499509	3.643883	4.411923	4.540119
processed_	pyridoxal-d	21	38	13	36	23	34	0.265717	0.566619	0.21676	0.394063	0.326947	0.427552
protein_co	zinc_finger_	1282	1215	914	1130	1204	1626	11.45298	12.79127	10.75998	8.73317	12.08387	14.43646
protein_co	archaelysin	678	568	461	1412	796	1052	14.94338	14.7528	13.38921	26.92259	19.70975	23.04329
protein_co	zinc_finger_	172	226	158	715	546	560	2.369464	3.668911	2.868228	8.521004	8.45013	7.666893
protein_co	family_with	0	0	0	4	11	6	0	0	0	0.150531	0.53758	0.259395
protein_co	neurofibro	1047	874	1048	1277	1351	1140	4.461104	4.388481	5.884259	4.707059	6.466959	4.827366
protein_co	vitamin_K_	701	602	633	1661	1329	1453	6.291174	6.366742	7.486041	12.89574	13.39947	12.95952
protein_co	zinc_finger_	130	102	101	118	136	133	1.86311	1.722671	1.907442	1.462986	2.189693	1.894334
protein_co	death-assoc	635	537	547	1369	1211	1161	5.591738	5.572557	6.347391	10.42893	11.98026	10.1605
protein_co	collagen_ty	3251	3026	2635	697	771	986	22.09386	24.23431	23.59772	4.097797	5.886512	6.659493
protein_co	chromosom	46	35	32	53	31	23	1.967113	1.763789	1.803251	1.960696	1.4893	0.977482
protein_co	GM2_gangl	1425	1191	988	4372	3213	3564	19.36368	19.07181	17.69151	51.39446	49.04931	48.13051
protein_co	histone_clu	32	27	29	6	28	26	3.190418	3.172257	3.810047	0.517502	3.136207	2.576206
protein_co	colipase-lik	0	0	0	2	0	4	0	0	0	0.172176	0	0.395594
protein_co	S100_calci	76	43	60	22	6	29	4.031579	2.688048	4.194185	1.009595	0.357571	1.528865
processed_	-	316	294	223	914	588	705	7.824768	8.579042	7.276526	19.57914	16.35727	17.34935
protein_co	zinc_finger_	125	144	126	194	170	176	2.125803	2.885908	2.823699	2.854156	3.247962	2.974646
protein_co	POU_class_	0	0	0	1	0	0	0	0	0	0.030391	0	0

protein_co	ankyrin_rep	1	0	0	0	0	0	0.015079	0	0	0	0	0
protein_co	CD47_mole	1576	1442	1280	1095	962	970	12.27708	13.23766	13.13964	7.379312	8.419045	7.509657
protein_co	transducin-	1359	1176	1036	1853	1599	1503	18.48107	18.84613	18.56531	21.79948	24.42897	20.3131
protein_co	mastermin	185	118	131	72	109	85	1.431047	1.075651	1.335329	0.481812	0.947235	0.653447
protein_co	histone_clu	126	80	77	132	113	123	2.979261	2.229128	2.399184	2.700069	3.001688	2.890365
protein_co	striatin_cal	364	309	351	699	546	467	4.854036	4.855871	6.167988	8.063837	8.179811	6.189109
protein_co	zinc_finger_	87	65	48	137	119	95	1.927947	1.697448	1.40169	2.626392	2.962593	2.092229
protein_co	Uncharacte	0	0	0	1	0	0	0	0	0	0.033925	0	0
antisense	CTBP1_anti	303	219	227	355	264	361	2.838132	2.417359	2.801887	2.876612	2.778068	3.360522
protein_co	cholinergic	13	14	10	3	5	11	0.304259	0.386131	0.308414	0.060741	0.131468	0.25586
protein_co	zinc_finger_	30	24	11	106	38	65	1.195956	1.127489	0.577859	3.655636	1.701871	2.575236
protein_co	multivesicu	299	322	269	85	80	80	3.28478	4.168676	3.894236	0.807825	0.987357	0.873443
protein_co	chromoson	1542	1384	1272	2190	2639	2766	18.47782	19.54382	20.08576	22.70249	35.5267	32.94035
protein_co	adenosine_	150	114	69	113	87	95	4.486525	4.018193	2.719586	2.923885	2.923393	2.823918
protein_co	AT_rich_int	709	626	417	229	130	156	12.1907	12.68422	9.448291	3.406284	2.511162	2.665733
protein_co	prostate_ar	0	0	0	0	2	0	0	0	0	0	0.071787	0
protein_co	PTC7_prote	347	268	325	502	514	408	2.6524	2.414079	3.273616	3.319528	4.413893	3.099413
protein_co	keratin_39	1	0	0	0	0	0	0.031215	0	0	0	0	0
protein_co	translocase	3	6	0	22	10	9	0.256166	0.603752	0	1.625122	0.959289	0.763752
protein_co	RANBP2-lik	0	1	0	0	0	0	0	0.011418	0	0	0	0
protein_co	NHL_repeat	264	248	309	508	461	428	1.26472	1.400068	1.95067	2.105316	2.481078	2.037717
protein_co	ZFP28_zinc	125	131	121	69	57	76	1.619585	2.000194	2.065922	0.773403	0.829693	0.978626
protein_co	KIAA1211-l	21	16	15	18	11	5	0.284556	0.255491	0.26784	0.211001	0.167452	0.067333
protein_co	COBW_dom	18	16	20	61	42	56	0.43414	0.454762	0.635656	1.272771	1.138036	1.342317
protein_co	sodium_ch	245	189	309	30	38	25	1.532075	1.392781	2.546286	0.162292	0.26696	0.155369
protein_co	laminin_be	75	33	39	74	75	102	0.922317	0.478233	0.632002	0.787252	1.036166	1.246605
protein_co	histone_clu	0	0	1	1	2	2	0	0	0.154344	0.101325	0.263168	0.232806
protein_co	karyopherin	153	141	144	276	208	128	1.591663	1.728566	1.974045	2.483886	2.430928	1.323364
pseudogen	ankyrin_rep	41	18	30	53	37	37	0.36261	0.187601	0.349632	0.405503	0.367626	0.325212
protein_co	Rho_guanir	1809	1546	2034	1782	1798	1411	9.914105	9.98462	14.68929	8.448618	11.07016	7.685137
protein_co	hydroxycar	0	0	0	0	10	4	0	0	0	0	0.164662	0.058266
pseudogen	zinc_finger_	309	292	276	418	331	347	3.139879	3.496587	3.695713	3.674461	3.778604	3.504237
protein_co	PDZ_and_L	4786	4173	2848	8181	5732	7536	133.0754	136.7353	104.3518	196.7862	179.0525	208.2455
protein_co	filamin_A_a	56189	47375	42297	66532	66825	83676	350.5422	348.2935	347.723	359.0729	468.3571	518.7996
protein_co	transmemb	57	51	50	3	2	3	0.585835	0.6177	0.677182	0.026674	0.023093	0.030643
pseudogen	ribosomal_	1	1	0	0	0	0	0.152129	0.179275	0	0	0	0
protein_co	RIMS_bindi	1	0	0	0	0	1	0.009153	0	0	0	0	0.009096
protein_co	SLIT-ROBO_	389	284	337	154	212	180	2.302812	1.981227	2.628897	0.788665	1.409918	1.058988
protein_co	olfactory_r	0	0	0	2	0	0	0	0	0	0.097548	0	0
protein_co	family_with	1571	1432	1449	2744	2268	2673	33.162	35.6217	40.30582	50.10853	53.78444	56.0755
protein_co	NOP9_nucl	270	214	269	499	598	489	2.369314	2.212991	3.110612	3.788108	5.895342	4.26459
protein_co	zinc_finger_	0	0	1	0	0	0	0	0	0.020192	0	0	0
protein_co	solute_carr	378	334	414	1152	955	1011	3.684038	3.836064	5.31701	9.712875	10.45646	9.79249
processed_	-	6	7	2	18	10	11	0.160023	0.220007	0.07029	0.415305	0.299627	0.291564

protein_co	caspase_4_	338	342	190	30	12	35	3.771139	4.49665	2.793472	0.289561	0.150413	0.388091
protein_co	Putative_U	110	85	121	5	8	0	2.255426	2.053818	3.269309	0.088689	0.184279	0
protein_co	adaptor-rel	6075	4802	3820	5306	3540	4071	94.92814	88.42558	78.65872	71.72638	62.14426	63.22072
protein_co	protocadhe	230	171	220	107	48	47	2.529379	2.216099	3.188185	1.017965	0.59303	0.513681
protein_co	histone_clu	51	33	29	12	20	7	5.844136	4.456266	4.37908	1.189582	2.574715	0.797183
protein_co	zinc_finger_	91	101	135	59	61	48	0.735853	0.96245	1.438528	0.412729	0.554152	0.385745
protein_co	fucosyltran	501	424	391	455	393	425	11.01472	10.98521	11.32784	8.653863	9.706825	9.286118
lincRNA	long_interg	56	49	42	28	23	24	1.099665	1.133902	1.086817	0.475656	0.507398	0.468374
protein_co	annexin_A4	663	654	493	1303	811	921	7.944744	9.235304	7.784812	13.50746	10.91783	10.96821
protein_co	L_antigen_f	228	172	128	325	242	342	12.71923	11.30737	9.409589	15.68456	15.16667	18.96102
protein_co	Uncharacte	3	1	1	0	0	0	0.048749	0.019149	0.021413	0	0	0
protein_co	WD_repeat	116	100	115	136	102	152	1.473406	1.496827	1.924851	1.494398	1.455505	1.918747
protein_co	Putative_lu	0	0	0	1	2	10	0	0	0	0.032925	0.085515	0.378246
protein_co	family_witl	0	0	0	2	0	0	0	0	0	0.112944	0	0
protein_co	Uncharacte	4	3	8	6	1	5	0.099748	0.08816	0.262886	0.129436	0.028015	0.123914
protein_co	WD_repeat	126	106	101	135	105	119	2.166471	2.147808	2.288435	2.008072	2.028247	2.033476
protein_co	methyltran	2420	2080	1869	2368	1668	1740	22.86582	23.16018	23.27103	19.35602	17.70584	16.33918
protein_co	zinc_finger_	71	48	62	231	199	153	1.455775	1.159803	1.675183	4.097423	4.58393	3.117719
protein_co	zinc_finger_	67	43	53	187	151	157	1.588467	1.201376	1.655824	3.835376	4.021882	3.699241
protein_co	zinc_finger_	275	244	213	135	151	163	2.035907	2.128738	2.077972	0.864614	1.255889	1.199285
protein_co	SERTA_dom	252	183	166	568	354	482	6.310847	5.400641	5.478101	12.30548	9.959543	11.9962
protein_co	zinc_finger_	98	95	104	523	375	391	0.903084	1.031651	1.262904	4.169335	3.88224	3.580869
protein_co	chromosom	537	437	382	510	459	500	17.19862	16.49331	16.12194	14.13033	16.51509	15.91472
protein_co	zinc_finger_	304	239	290	442	299	308	2.965554	2.747497	3.727907	3.730075	3.276819	2.986019
protein_co	zinc_finger_	243	234	238	687	711	713	2.248281	2.551333	2.901723	5.49875	7.390314	6.556067
protein_co	annexin_A6	10519	8798	7946	3068	2541	2630	214.7653	211.6804	213.7829	54.1886	58.28319	53.36481
protein_co	zinc_finger_	74	68	51	19	46	30	0.899365	0.973913	0.816788	0.199766	0.628074	0.362356
protein_co	glia_matur	909	813	1026	1631	1328	1324	7.160149	7.546678	10.64977	11.11412	11.75183	10.36468
protein_co	sialic_acid_	20	25	14	6	0	4	0.410395	0.604532	0.37856	0.106509	0	0.081572
pseudogen	-	9	6	4	82	26	57	1.430838	1.124103	0.837997	11.27781	4.643765	9.006009
protein_co	zinc_finger_	55	45	49	104	78	90	0.823693	0.794186	0.967016	1.347408	1.31234	1.339537
protein_co	zinc_finger_	4	4	2	4	12	10	0.080795	0.095212	0.053234	0.069895	0.272305	0.20074
protein_co	zinc_finger_	283	269	248	726	550	500	3.564668	3.992933	4.116415	7.911017	7.782954	6.259107
protein_co	death_dom	0	0	0	1	0	0	0	0	0	0.010565	0	0
protein_co	histone_clu	7	13	4	4	45	27	0.892981	1.954314	0.672417	0.441435	6.449196	3.423083
pseudogen	-	327	240	231	179	169	127	6.165137	5.332285	5.739073	2.919517	3.579569	2.379624
protein_co	v-maf_mus	715	598	537	1204	1030	1357	7.510478	7.402354	7.433112	10.94085	12.1548	14.16612
protein_co	arrestin_do	234	163	156	936	777	1119	3.889542	3.192841	3.416977	13.45927	14.50951	18.48512
pseudogen	-	0	1	0	0	0	1	0	0.169072	0	0	0	0.142586
protein_co	KIAA1671	41	34	47	332	391	301	0.206919	0.20221	0.312571	1.449498	2.216881	1.509707
protein_co	insulin-like	6918	5531	6582	4003	5252	4503	40.28663	37.95694	50.50951	20.16643	34.36008	26.06106
processed_	NPSR1_ant	0	0	0	3	1	6	0	0	0	0.028987	0.012548	0.0666
protein_co	galactose-3	269	252	160	113	114	182	4.503835	4.972077	3.530084	1.63671	2.144293	3.028386
protein_co	dynein_cyt	7274	5733	7227	5709	6700	5255	26.86756	24.95422	35.17611	18.24223	27.80218	19.29023

protein_co	solute_carr	13	26	6	27	9	6	0.107085	0.252385	0.065128	0.192402	0.083287	0.049118
protein_co	poly(rC)_bi	4367	4054	3063	5969	3866	5248	73.00073	79.86102	67.47235	86.31944	72.60306	87.18615
protein_co	zinc_finger_	406	309	259	629	597	936	5.078933	4.555248	4.269539	6.807068	8.390152	11.63676
protein_co	solute_carr	1020	813	643	1468	1217	1702	10.44686	9.81258	8.678234	13.00692	14.00313	17.32426
protein_co	post-GPI_at	622	607	675	251	308	218	3.682543	4.234998	5.266184	1.285565	2.0486	1.282695
protein_co	v-src_sarco	636	563	427	926	1042	1116	7.27067	7.584602	6.432503	9.157803	13.3824	12.67918
protein_co	zinc_finger_	43	44	21	312	203	233	0.603996	0.728326	0.388705	3.79126	3.203399	3.252606
protein_co	olfactory_r	0	0	0	0	2	0	0	0	0	0	0.115152	0
protein_co	zinc_finger_	141	111	153	194	147	188	1.377501	1.277918	1.969696	1.639599	1.61339	1.825326
protein_co	pecanex-lik	1264	1047	995	2360	2052	1994	9.418356	9.193519	9.769805	15.21259	17.17728	14.766
protein_co	ADAM_met	21	19	25	15	13	11	0.161805	0.172517	0.253832	0.099983	0.112529	0.084231
protein_co	acyl-CoA_sy	10	8	10	14	18	16	0.15663	0.147663	0.2064	0.1897	0.316736	0.249061
pseudogen	-	2	12	12	6	12	11	0.046076	0.325784	0.364299	0.119579	0.310579	0.251851
protein_co	leucine_ric	121	99	123	298	226	223	0.843653	0.813431	1.130105	1.797455	1.770256	1.54523
pseudogen	-	0	0	0	8	0	4	0	0	0	0.41541	0	0.238612
protein_co	ATP-bindin	810	615	543	1398	1079	1309	9.156994	8.193136	8.089144	13.67219	13.70372	14.70677
protein_co	histone_clu	7	1	0	0	16	0	0.709937	0.119517	0	0	1.823017	0
protein_co	staphyloco	10679	8410	7169	6357	5684	5775	162.6458	150.9438	143.8818	83.75824	97.25579	87.41258
protein_co	zinc_finger_	154	125	105	126	97	137	2.48413	2.376132	2.231915	1.758276	1.75782	2.19626
protein_co	sulfotransfe	1	0	0	1	0	0	0.02659	0	0	0.023003	0	0
protein_co	NIMA-relat	4	12	6	0	4	4	0.072572	0.256564	0.143447	0	0.08153	0.072123
protein_co	proteasom	922	758	763	2889	1962	2294	11.07844	10.73307	12.08111	30.03019	26.48474	27.3937
pseudogen	-	26	42	22	31	27	34	5.397905	10.27563	6.018793	5.56771	6.29745	7.015207
protein_co	piwi-like_R	2	0	0	12	10	6	0.020648	0	0	0.107174	0.115983	0.061561
protein_co	hsa-mir-47	82	85	101	0	0	0	0.952009	1.162929	1.545196	0	0	0
protein_co	chromoson	971	803	766	169	179	175	8.580488	8.362101	8.919825	1.29194	1.77703	1.536882
protein_co	chromoson	39	16	22	29	44	50	1.591903	0.769625	1.18334	1.024031	2.017687	2.028298
protein_co	solute_carr	24	31	22	25	20	32	0.577276	0.8787	0.697316	0.520206	0.540445	0.764948
protein_co	zinc_finger_	0	0	0	2	0	2	0	0	0	0.044487	0	0.051106
pseudogen	transcriptic	0	0	0	2	0	2	0	0	0	0.104088	0	0.119577
protein_co	ectonucleo	890	829	813	2228	2291	2034	8.039155	8.824335	9.677111	17.40999	23.24848	18.25917
protein_co	C1D_nucle	210	170	164	421	258	402	4.978777	4.749626	5.12368	8.634724	6.871826	9.471943
protein_co	TBC1_dom	4512	3762	3221	2513	2579	2776	46.17625	45.3707	43.43853	22.24872	29.65173	28.23441
protein_co	histone_clu	9	13	1	9	1	10	1.273981	2.168557	0.186533	1.102113	0.159027	1.406793
protein_co	solute_carr	5	3	0	0	0	0	0.171998	0.121614	0	0	0	0
protein_co	family_with	0	0	2	42	22	23	0	0	0.091553	1.262175	0.858576	0.794044
protein_co	serpin_pep	59	28	0	1	11	35	0.884348	0.49458	0	0.012967	0.185231	0.521374
protein_co	KN_motif_a	2261	1815	1761	869	810	769	22.88274	21.64667	23.48559	7.608344	9.209614	7.734698
pseudogen	eukaryotic_	24	35	30	4	16	17	0.695068	1.194513	1.144912	0.100216	0.520577	0.489299
protein_co	chromoson	78	81	75	310	272	306	2.2689	2.776597	2.874861	7.800912	8.888709	8.846099
protein_co	general_tra	675	553	491	893	683	762	20.28103	19.58026	19.44028	23.21136	23.05451	22.75364
protein_co	interleukin	0	0	0	1	0	0	0	0	0	0.043869	0	0
protein_co	RAD54_hor	34	9	29	171	95	141	0.586699	0.183015	0.659431	2.552677	1.84166	2.418051
protein_co	zinc_finger_	10	10	5	173	87	119	0.251262	0.296097	0.165551	3.760423	2.455816	2.971558

protein_co	synaptic_R	1564	1469	1132	925	925	1279	13.99589	15.49148	13.34889	7.160917	9.299395	11.37481
pseudogen	-	9	6	3	1	3	6	0.130254	0.102331	0.057214	0.01252	0.048777	0.0863
lincRNA	RAMP2_ant	3	6	1	14	4	7	0.050937	0.120053	0.022374	0.20564	0.0763	0.11812
protein_co	fat_storage	284	247	266	176	94	146	3.270664	3.352136	4.03677	1.753449	1.216171	1.671014
protein_co	Bloom_syn	76	52	71	763	598	548	0.883318	0.71222	1.087419	7.671694	7.808254	6.329857
protein_co	Uncharacte	209	185	224	89	109	115	2.396506	2.499833	3.38466	0.882847	1.404131	1.310508
protein_co	zinc_finger	214	188	196	340	339	296	1.890119	1.956772	2.281215	2.597869	3.363753	2.598225
lincRNA	GATA3_ant	3	0	0	68	61	83	0.071736	0	0	1.406651	1.638677	1.972433
protein_co	DNA-damag	424	383	392	1056	1280	1153	2.112657	2.248894	2.573855	4.551872	7.165099	5.709553
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.025893
protein_co	supervillin	2525	1996	2388	1882	2406	1839	16.72204	15.57742	20.83997	10.78228	17.90081	12.10373
protein_co	chromoson	0	0	0	2	0	0	0	0	0	0.022917	0	0
protein_co	tripartite_r	558	492	596	1238	992	932	3.54252	3.680869	4.986079	6.799262	7.075202	5.880357
protein_co	low_densit	4591	3856	3429	2589	2266	2576	35.29656	34.93568	34.7398	17.21948	19.57195	19.68251
protein_co	pellino_E3_	244	241	195	880	855	799	3.444694	4.009451	3.627691	10.74748	13.56051	11.2103
lincRNA	zinc_finger_	3	2	2	15	4	20	0.046975	0.036905	0.041268	0.203189	0.070365	0.311234
pseudogen	-	3	0	0	0	4	0	0.696592	0	0	0	1.043437	0
protein_co	zinc_finger_	1295	1214	979	1585	1209	1222	14.03164	15.50117	13.97836	14.85699	14.71682	13.1589
protein_co	mitochond	708	652	473	1179	773	1179	16.41797	17.81726	14.4538	23.65173	20.13793	27.17125
protein_co	UDP-N-acte	899	780	607	171	97	123	10.78739	11.02956	9.597986	1.775071	1.307607	1.466801
pseudogen	BCL2/adeno	3	7	6	0	1	3	0.100204	0.275529	0.264088	0	0.037524	0.099585
protein_co	F-box_and_	1	3	2	3	1	3	0.034693	0.12265	0.091433	0.090037	0.038975	0.103435
protein_co	zinc_finger_	97	76	74	393	282	352	1.633358	1.5081	1.642011	5.724863	5.334672	5.890632
protein_co	zinc_finger_	243	200	133	216	137	201	4.031545	3.910231	2.907714	3.100145	2.553494	3.314141
protein_co	zinc_finger_	99	124	82	293	220	229	1.239924	1.830158	1.353345	3.174611	3.095506	2.850394
protein_co	solute_carr	161	80	134	371	278	349	0.816818	0.478296	0.895858	1.628308	1.584505	1.759684
protein_co	olfactory_r	0	0	0	0	1	0	0	0	0	0	0.026924	0
protein_co	dapper_ant	298	294	270	269	311	273	5.113911	5.94554	6.105701	3.993486	5.995789	4.65596
protein_co	adenosine_	479	376	455	345	388	387	3.608757	3.338236	4.51719	2.248559	3.283998	2.897629
protein_co	zinc_finger_	3	3	5	59	41	34	0.051266	0.060414	0.112594	0.872219	0.787125	0.57743
protein_co	huntingtin	2036	1720	1710	2651	3267	3084	7.465568	7.432255	8.262586	8.40926	13.45808	11.23852
protein_co	complemer	37	18	15	17	17	23	0.847606	0.485928	0.452812	0.336902	0.437512	0.523636
protein_co	deiodinase_	4	9	11	8	4	25	0.100744	0.267122	0.365079	0.174306	0.11318	0.625762
protein_co	histone_clu	67	54	58	13	17	12	4.100632	3.894725	4.677769	0.688307	1.168891	0.729906
protein_co	dachsous_2	17	8	20	1	5	3	0.100987	0.056003	0.15656	0.005139	0.033368	0.017711
protein_co	ventricular	96	95	73	47	24	19	1.209504	1.410479	1.211975	0.512268	0.339701	0.237903
protein_co	sedoheptul	60	29	37	147	97	98	0.827634	0.471403	0.672549	1.754153	1.503169	1.343454
pseudogen	gamma-glu	0	0	0	2	2	2	0	0	0	0.039144	0.050834	0.044969
protein_co	intracisterr	317	261	311	339	217	275	5.391036	5.230709	6.969605	4.987417	4.145928	4.647884
protein_co	olfactory_r	0	0	0	0	1	0	0	0	0	0	0.05686	0
protein_co	mitogen-ac	11	6	14	263	246	199	0.112055	0.072027	0.187933	2.317705	2.815293	2.014662
protein_co	oxoglutarat	23	12	19	49	72	59	0.328737	0.20212	0.357857	0.605871	1.156119	0.838075
protein_co	chromoson	5	4	2	0	0	0	0.202374	0.190788	0.106672	0	0	0
protein_co	cytochrom	1	0	0	0	0	4	0.025452	0	0	0	0	0.101181

protein_co	glutathione	1429	1152	951	1704	1019	1303	28.10278	26.69787	24.6452	28.99009	22.51336	25.46661
protein_co	heterogene	2759	2132	2115	8227	8523	11016	81.32751	74.05938	82.15442	209.7926	282.2457	322.7151
protein_co	stathmin-li	2025	1625	1295	2252	1739	2221	47.54125	44.9579	40.06361	45.73798	45.86635	51.82076
protein_co	histone_clu	15	11	12	27	53	44	1.868506	1.614741	1.969787	2.909578	7.416997	5.447102
protein_co	platelet-de	44	48	28	344	206	250	1.010587	1.29918	0.84745	6.835064	5.315418	5.706513
protein_co	glycophorii	3	9	5	0	3	0	0.094313	0.333426	0.207136	0	0.105955	0
protein_co	collagen_ty	564	470	554	230	161	153	9.521276	9.350202	12.32425	3.358976	3.053451	2.566948
protein_co	sialophorin	0	0	0	2	0	0	0	0	0	0.013364	0	0
protein_co	zinc_finger_	10	8	4	130	79	110	0.158506	0.149432	0.083549	1.782592	1.406766	1.732798
protein_co	protocadhe	35	18	25	8	7	8	0.566473	0.343314	0.533195	0.112012	0.12728	0.12868
protein_co	zinc_finger_	310	197	165	420	308	328	4.266106	3.194797	2.992187	5.00014	4.761784	4.485939
protein_co	solute_carr	762	667	573	41	41	39	9.235585	9.526698	9.151639	0.429889	0.558268	0.469768
protein_co	zinc_finger_	4	3	2	58	51	73	0.090036	0.079576	0.059323	1.129395	1.289656	1.633004
protein_co	ribosome_p	371	293	276	1162	694	832	12.82894	11.93965	12.57653	34.7605	26.96034	28.59235
protein_co	Uncharacte	2	0	6	4	0	2	1.7647	0	6.976328	3.05326	0	1.753802
protein_co	solute_carr	3	0	0	3	3	6	0.032499	0	0	0.028115	0.036511	0.064597
protein_co	family_with	0	0	1	0	0	1	0	0	0.034987	0	0	0.026386
protein_co	mindbomb	1455	1282	852	1447	934	1359	18.13731	18.83237	13.99537	15.60419	13.07994	16.836
protein_co	myosin_VA	1493	1104	1510	1146	1120	881	6.465514	5.634033	8.616978	4.293296	5.448918	3.791655
protein_co	chromoson	13	10	21	6	5	9	0.339868	0.308088	0.723471	0.1357	0.146854	0.23384
protein_co	granzyme_I	0	1	4	0	0	2	0	0.068408	0.305979	0	0	0.115382
protein_co	autophagy_	546	407	415	441	345	365	5.828954	5.120348	5.838226	4.072861	4.137768	3.872581
pseudogen	-	3	4	7	7	21	22	0.048496	0.076199	0.149112	0.097891	0.381372	0.353438
protein_co	signal-indu	329	286	367	1275	1088	1042	2.224184	2.278495	3.269458	7.456724	8.263287	7.000873
protein_co	tetratricop	97	68	110	95	107	70	1.099866	0.908624	1.643598	0.931869	1.363016	0.788816
processed_	SCO-spondi	49	45	25	12	7	19	0.16647	0.180161	0.111922	0.035268	0.026717	0.064151
protein_co	elastase_ne	11	3	4	0	0	0	0.569258	0.182955	0.272779	0	0	0
protein_co	RAB40C_m	575	498	391	610	528	598	11.20393	11.43507	10.03954	10.28242	11.55807	11.58013
protein_co	phosphatid	424	389	386	537	413	460	4.080527	4.411712	4.895224	4.470826	4.465289	4.399648
protein_co	collagen_ty	37	31	46	943	1055	1168	0.292361	0.28866	0.478972	6.446025	9.365238	9.172121
protein_co	zinc_finger_	85	39	56	59	69	56	1.061067	0.573714	0.921185	0.637146	0.967658	0.694739
protein_co	HERV-H_LTI	220	209	177	287	144	201	12.96995	14.52008	13.75067	14.63729	9.537341	11.77664
pseudogen	ribosomal_	0	1	1	0	10	4	0	0.135921	0.15199	0	1.295772	0.45851
protein_co	homeobox_	19	10	8	3	0	4	0.575775	0.357114	0.319466	0.078647	0	0.120467
protein_co	topoisomer	255	236	284	432	390	372	3.294279	3.592851	4.834742	4.827996	5.660226	4.776092
protein_co	beta-carote	6	9	14	1	7	2	0.108412	0.191635	0.33334	0.015631	0.142093	0.035914
pseudogen	glutathione	12	22	12	17	12	16	1.048337	2.264901	1.381451	1.284788	1.177741	1.38915
protein_co	potassium_	6	3	6	3	2	5	0.124469	0.07334	0.16402	0.053839	0.046611	0.103084
protein_co	ectonucleo	1748	1592	1222	2203	1832	1988	33.45656	35.9079	30.82094	36.47686	39.39258	37.81516
protein_co	ectonucleo	259	261	199	422	372	376	1.842477	2.188014	1.865479	2.597035	2.972997	2.658275
protein_co	coiled-coil_	4	12	1	8	5	11	0.082591	0.291986	0.027209	0.142898	0.115983	0.225723
protein_co	fatty_acyl_(	978	906	1219	1947	1627	1493	8.89627	9.711904	14.61193	15.32139	16.62669	13.49704
protein_co	chromoson	398	326	451	272	254	249	1.872935	1.807858	2.796732	1.107316	1.342834	1.164524
protein_co	Uncharacte	2	0	1	6	1	9	0.061203	0	0.040326	0.15884	0.034379	0.273715

protein_co	zinc_finger_	369	348	265	219	207	287	5.040048	5.601375	4.769677	2.587709	3.176345	3.895829
protein_co	microfibrill	378	383	315	2960	1741	2116	7.033988	8.39877	7.72423	47.65018	36.39633	39.13228
protein_co	myosin_hea	1	0	0	1	0	0	0.008911	0	0	0.007709	0	0
protein_co	zinc_finger_	137	123	119	111	73	76	1.759562	1.861643	2.01403	1.233304	1.05331	0.97008
protein_co	chromoson	191	177	114	116	130	169	4.193998	4.580103	3.298637	2.203514	3.206914	3.688003
protein_co	CDC42_sma	743	573	647	1442	1537	1654	12.36566	11.23803	14.18951	20.7614	28.73766	27.35732
protein_co	serpin_pep	68	73	49	8	7	6	1.670528	2.113366	1.586265	0.170019	0.193193	0.146489
protein_co	dipeptidyl-	151	142	121	1247	1025	1134	2.047667	2.269226	2.162233	14.6289	15.61548	15.28287
protein_co	serpin_pep	0	0	0	5	5	0	0	0	0	0.073537	0.095498	0
antisense	-	0	0	4	0	0	1	0	0	1.395266	0	0	0.26307
protein_co	programme	30	36	22	18	11	4	0.672124	0.950469	0.64951	0.34887	0.276866	0.089063
protein_co	zinc_finger_	20	29	9	72	64	91	0.455995	0.779175	0.2704	1.420121	1.639302	2.061963
protein_co	dynein_axo	64	62	60	11	28	5	0.23918	0.273051	0.295482	0.035563	0.117558	0.018571
antisense	-	25	5	13	17	40	22	0.679777	0.160215	0.465805	0.399888	1.221899	0.594509
protein_co	TBC1_dom	19	4	14	10	10	12	0.296807	0.073636	0.288193	0.13514	0.175497	0.186299
protein_co	spectrin_al	6750	5394	5515	7188	6569	6633	45.39529	42.74891	48.87506	41.81943	49.63126	44.33295
protein_co	neuromedi	139	115	82	109	62	71	7.23579	7.05466	5.624965	4.908634	3.625867	3.673154
protein_co	histone_clu	15	13	5	1	10	5	1.597817	1.631872	0.701844	0.092151	1.196699	0.529316
protein_co	zinc_finger_	29	13	31	25	38	34	0.527954	0.2789	0.743694	0.393732	0.777196	0.615157
protein_co	parvin_alph	2811	2527	2442	3114	2293	2525	33.38204	35.36424	38.21488	31.99143	30.59181	29.80047
pseudogen	FERM_and_	0	0	0	0	1	0	0	0	0	0	0.030547	0
protein_co	kelch-like_f	3	12	9	39	32	10	0.036833	0.173621	0.14561	0.414229	0.44138	0.122018
protein_co	family_with	2984	2619	2123	660	635	506	39.0064	40.34407	36.56974	7.463525	9.325236	6.573508
protein_co	ribulose-5-p	629	632	626	1076	879	1041	12.9622	15.34801	16.99954	19.18241	20.35007	21.32006
protein_co	zinc_finger_	158	129	176	34	111	75	2.496919	2.402393	3.665175	0.464825	1.970695	1.177926
protein_co	heat_shock	1	1	8	8	0	0	0.085943	0.101279	0.906017	0.594791	0	0
protein_co	PHD_finger	574	453	447	459	472	424	5.460581	5.078462	5.603628	3.777484	5.044498	4.00869
protein_co	ribosomal_	3702	2950	1925	9751	5919	7666	162.7804	152.8603	111.5401	370.9179	292.3903	334.9994
protein_co	chromoson	0	0	1	2	0	0	0	0	0.108666	0.142676	0	0
pseudogen	prothymos	30	25	23	37	24	44	4.856972	4.769704	4.906898	5.182139	4.365205	7.079566
protein_co	prosaposin	22736	19518	17763	24038	18392	21372	419.9813	424.8722	432.3814	384.1291	381.6752	392.3473
protein_co	S100_calci	7274	6288	4873	11060	8133	10886	320.3767	326.3678	282.8257	421.4109	402.4273	476.503
protein_co	WD_repeat	5	4	7	6	10	11	0.049339	0.046515	0.091024	0.05122	0.110859	0.107876
protein_co	lipoma_HM	0	0	0	0	1	0	0	0	0	0	0.027702	0
protein_co	ribosomal_	23884	20921	15322	16202	14565	18398	406.3119	419.4131	343.481	238.4428	278.3633	311.0518
protein_co	homeobox_	421	306	222	116	85	65	7.573278	6.486798	5.26247	1.80519	1.717789	1.16205
protein_co	thioredoxin	93	59	64	111	70	75	1.668987	1.247755	1.513508	1.723281	1.411293	1.337645
protein_co	complemer	103	105	55	30	15	16	4.099942	4.925347	2.884948	1.033058	0.670781	0.632951
protein_co	chromoson	4	11	1	1	2	4	0.175592	0.569042	0.057847	0.037976	0.098633	0.174508
protein_co	microtubul	9	12	8	59	32	33	0.403104	0.633378	0.472171	2.286071	1.610177	1.46892
protein_co	minichrom	633	529	555	2765	1940	2037	8.147739	8.024096	9.413718	30.78871	28.05331	26.05758
protein_co	essential_m	354	273	196	173	143	308	3.338876	3.034358	2.43606	1.411582	1.515243	2.887071
protein_co	kelch_dom	26	62	53	11	15	12	0.511507	1.437398	1.374007	0.187212	0.331527	0.234622
protein_co	zinc_finger_	63	34	75	40	67	42	0.420431	0.267387	0.659555	0.230929	0.502318	0.278557

protein_co	TAF13_RNA	643	471	521	658	474	599	31.63667	27.30913	33.77943	28.00714	26.20036	29.28979
protein_co	zinc_finger_	178	184	212	271	209	158	1.256466	1.530579	1.971975	1.654867	1.657396	1.108403
protein_co	ATPase_fam	1150	897	682	2966	2129	2752	23.30863	21.42488	18.21537	52.00595	48.47788	55.4341
protein_co	family_with	292	302	271	689	488	492	6.435791	7.843919	7.870878	13.13715	12.08337	10.7769
protein_co	zinc_finger_	95	106	73	91	65	65	1.512145	1.988304	1.531184	1.253067	1.162338	1.028236
lincRNA	-	70	64	52	11	14	19	6.467486	6.968263	6.331048	0.879211	1.453164	1.744619
pseudogen	-	24	10	19	12	23	20	1.789555	0.8787	1.866905	0.774066	1.926685	1.482086
protein_co	coiled-coil_	29	45	21	28	23	22	0.194735	0.356094	0.185823	0.162655	0.173509	0.146817
protein_co	solute_carr	480	414	311	342	386	405	4.03168	4.097814	3.442231	2.485043	3.642346	3.380722
protein_co	occludin	1	6	1	515	449	375	0.008223	0.058143	0.010836	3.663628	4.147979	3.064658
pseudogen	-	1	5	0	0	0	0	0.35294	2.079591	0	0	0	0
protein_co	chromoson	5	4	4	0	0	0	0.07904	0.074515	0.083324	0	0	0
pseudogen	-	8	2	4	13	18	4	0.310732	0.091545	0.204735	0.43682	0.785449	0.154407
protein_co	histone_clu	101	75	68	20	96	76	2.787821	2.439562	2.473359	0.477569	2.976897	2.084811
protein_co	zinc_finger_	98	111	71	100	74	73	1.445589	1.929517	1.380104	1.276091	1.226308	1.070166
pseudogen	-	0	0	0	3	0	0	0	0	0	0.282709	0	0
protein_co	histone_clu	9	8	6	1	27	19	0.398719	0.417658	0.350276	0.038325	1.343807	0.836541
pseudogen	solute_carr	14	8	10	51	38	59	0.231907	0.156165	0.218283	0.730834	0.70716	0.971286
pseudogen	POM121_tr	1	0	2	0	1	5	0.032801	0	0.086448	0	0.03685	0.162993
pseudogen	olfactory_r	0	0	0	0	1	2	0	0	0	0	0.063543	0.112423
protein_co	family_with	587	472	486	431	515	497	5.196716	4.924249	5.669725	3.300891	5.12209	4.372773
protein_co	zinc_finger_	103	83	49	265	223	233	1.685081	1.60018	1.056366	3.750528	4.098619	3.788342
protein_co	glycosylph	2870	2506	1816	3209	2119	2670	73.1187	75.23756	60.96733	70.72603	60.64941	67.60323
protein_co	ADAMTS-lik	0	0	0	3	15	16	0	0	0	0.032177	0.208932	0.197149
protein_co	small_gluta	223	218	293	454	301	328	2.158684	2.486839	3.737546	3.80192	3.273405	3.155496
protein_co	zinc_finger_	47	86	75	95	61	98	0.819304	1.766659	1.722834	1.43263	1.19461	1.697786
polymorph	proline-rich	0	0	3	1	7	7	0	0	0.181518	0.039722	0.361085	0.319426
protein_co	family_with	232	203	240	98	69	76	2.630045	2.711929	3.585265	0.961091	0.878766	0.856246
protein_co	myosin_IC	2700	2093	2060	3549	2996	3543	27.78245	25.3795	27.93243	31.5919	34.6336	36.2316
pseudogen	olfactory_r	0	0	0	4	1	9	0	0	0	0.201314	0.065358	0.520359
protein_co	NFKB_inhib	134	123	110	258	126	140	2.966998	3.209406	3.209519	4.941915	3.134239	3.080706
protein_co	UDP_glucu	0	0	0	4	1	0	0	0	0	0.088202	0.028635	0
protein_co	meiosis_exp	2	3	0	15	0	3	0.169411	0.299461	0	1.099174	0	0.252547
protein_co	kinesin_fam	432	337	338	132	155	173	2.615267	2.404193	2.696397	0.691304	1.054176	1.04085
protein_co	nebulin-rel	0	0	0	2	0	0	0	0	0	0.016357	0	0
protein_co	alcohol_de	2900	2482	2287	5794	4161	4828	58.77829	59.28267	61.08293	101.5922	94.74705	97.25139
protein_co	histone_clu	2537	1996	1547	3158	1933	2324	163.7943	151.8609	131.6144	176.3816	140.2036	149.1159
protein_co	TEA_domai	286	237	188	1188	887	1033	8.959245	8.749048	7.760649	32.19473	31.21606	32.15995
protein_co	spastic_par	1676	1541	1263	1961	1522	2034	28.84561	31.25471	28.64468	29.19755	29.42859	34.79096
protein_co	histone_clu	7	13	0	13	4	14	1.046856	2.291075	0	1.681881	0.672044	2.080782
protein_co	hornerin	0	3	0	15	33	21	0	0.01945	0	0.07139	0.20396	0.114818
protein_co	interferon_	0	0	1	1	0	0	0	0	0.079638	0.052282	0	0
protein_co	chromoson	50	58	39	37	26	23	1.988768	2.718624	2.044153	1.273148	1.161814	0.909183
protein_co	zinc_finger_	58	40	55	286	257	249	0.351687	0.285822	0.439466	1.500228	1.750694	1.500504

protein_co	ERO1-like_(	1775	1666	1500	1504	1125	1157	17.78056	19.6666	19.80036	13.03341	12.66044	11.51835
protein_co	coagulatior	127	115	90	335	149	184	3.952679	4.217865	3.691179	9.019773	5.209825	5.691349
protein_co	zinc_finger_	30	18	22	193	120	160	0.655481	0.463466	0.633426	3.648035	2.945568	3.474308
antisense	-	2	4	6	1	2	1	0.031032	0.073139	0.122679	0.013423	0.034863	0.01542
protein_co	zinc_finger_	6	3	0	67	83	76	0.104938	0.061831	0	1.013719	1.630823	1.321
protein_co	zinc_finger_	59	51	63	219	191	179	0.686035	0.69883	0.965317	2.202934	2.495036	2.068508
protein_co	phospholip	15	29	24	50	40	42	0.184335	0.419973	0.388653	0.531556	0.552237	0.51295
protein_co	FCH_and_d	399	430	342	155	189	225	4.889689	6.20989	5.522926	1.643248	2.602071	2.740315
protein_co	zinc_finger_	356	333	327	544	425	459	3.47218	3.827398	4.202762	4.590016	4.656828	4.449125
protein_co	arylacetam	0	0	0	0	1	0	0	0	0	0	0.012268	0
protein_co	S100_calci	6020	5387	4025	846	642	1128	473.5584	499.3799	417.2321	57.57188	56.73631	88.18521
protein_co	ribosomal_	28913	25570	17385	24252	16985	23124	672.8277	701.2107	533.1141	488.2264	444.0433	534.79
protein_co	dynamin_3	28	20	16	50	41	37	0.193948	0.163255	0.146044	0.299613	0.319052	0.254706
protein_co	zinc_finger_	324	297	207	1400	1052	1222	7.126249	7.698029	5.999584	26.63833	25.99446	26.71141
protein_co	myelin_prc	2052	1623	1719	6418	5111	5502	21.68362	20.21064	23.93674	58.67013	60.67493	57.78094
protein_co	vacuolar_p	342	224	365	516	501	443	1.181842	0.912197	1.662115	1.542574	1.945002	1.521412
protein_co	myelin_bas	50	46	41	560	379	427	0.27019	0.29293	0.291956	2.617882	2.300844	2.293171
protein_co	A_kinase_(F	1451	1204	1054	1500	1179	1565	23.76775	23.24097	22.75077	21.25568	21.6962	25.47679
protein_co	ELOVL_fatt	28	28	25	206	160	145	0.370865	0.437042	0.436348	2.360414	2.380822	1.908691
protein_co	golgin_A6_	0	0	0	0	0	1	0	0	0	0	0	0.012877
protein_co	leucine_glu	10	10	4	10	11	6	0.183759	0.216549	0.09686	0.158969	0.227086	0.109575
protein_co	chromosor	987	889	638	1325	811	1198	23.44224	24.88232	19.96814	27.22456	21.63973	28.27799
processed_	small_nucl	291	285	177	1032	659	1155	8.095549	9.343407	6.488755	24.83682	20.59623	31.93338
protein_co	protocadhe	2	5	6	10	14	12	0.016682	0.049147	0.065949	0.072158	0.13119	0.099475
protein_co	C-type_lect	0	0	4	1	3	1	0	0	0.166798	0.027375	0.106651	0.031449
protein_co	Kell_blood_	1	1	3	3	3	1	0.018827	0.022186	0.074427	0.048861	0.063452	0.018711
protein_co	nucleolar_p	538	457	430	930	772	709	6.194488	6.200781	6.524187	9.263371	9.985952	8.112954
protein_co	interleukin	175	121	125	287	253	277	2.234067	1.820332	2.102824	3.169589	3.628504	3.51437
protein_co	coiled-coil_	13	12	2	12	1	15	0.281141	0.305822	0.056996	0.224504	0.024296	0.32239
protein_co	discs_large_	0	0	0	0	1	1	0	0	0	0	0.00587	0.005193
protein_co	mitochond	611	606	562	1531	1027	1059	10.30814	12.04811	12.49425	22.34485	19.46519	17.75598
protein_co	ectonucleo	280	161	292	335	369	290	4.175628	2.829415	5.738276	4.321869	6.182145	4.298049
protein_co	Fc_fragmen	2	0	0	1	0	0	0.10142	0	0	0.043869	0	0
protein_co	zinc_finger_	663	487	392	923	577	739	7.923223	6.858425	6.173184	9.5423	7.746638	8.776926
protein_co	zinc_finger_	0	0	1	0	0	1	0	0	0.026286	0	0	0.019824
protein_co	ribosomal_	21986	19396	13981	20323	12794	15738	639.5388	664.8749	535.9123	511.4127	418.0961	454.967
protein_co	ArfGAP_wit	35	25	20	43	26	42	0.768853	0.647176	0.578948	0.817159	0.641649	0.916925
protein_co	zinc_finger_	75	44	51	324	247	244	1.056847	0.730652	0.947013	3.949653	3.910181	3.417042
protein_co	zinc_finger_	906	791	765	667	542	608	6.697087	6.890351	7.451677	4.265271	4.50097	4.466538
protein_co	MAK16_ho	297	261	257	1067	726	792	3.939733	4.079979	4.492399	12.24441	10.81922	10.44107
protein_co	signal-regul	410	317	322	510	315	395	5.431884	4.949177	5.621566	5.845206	4.688417	5.200838
protein_co	G_protein-r	487	319	308	2161	1411	1834	8.772461	6.771584	7.311021	33.67521	28.55411	32.83231
protein_co	primase_DI	34	34	22	509	251	321	1.292171	1.522744	1.101789	16.73485	10.71677	12.12427
protein_co	membrane-	639	629	584	1360	1035	1055	8.616733	9.995385	10.37742	15.86513	15.67946	14.13852

protein_co	aldo-keto_r	9	9	8	0	1	5	0.299666	0.353138	0.35101	0	0.037406	0.165453
protein_co	sulfotransfe	25	39	30	50	29	36	0.711572	1.30813	1.125214	1.231153	0.927313	1.018336
protein_co	cytochrom	13	1	5	0	4	0	0.301724	0.027351	0.152923	0	0.104298	0
protein_co	zinc_finger_	101	89	79	240	227	193	1.515601	1.57384	1.56216	3.115572	3.826823	2.878263
protein_co	keratin_ass	1	0	0	0	0	0	0.053966	0	0	0	0	0
protein_co	CD2-associa	212	191	255	1301	1291	1213	2.073816	2.201784	3.287073	11.00968	14.18762	11.79247
protein_co	nucleopori	0	0	1	58	36	39	0	0	0.039751	1.513582	1.220019	1.169201
protein_co	Sfi1_homol	246	245	140	430	382	432	2.480664	2.911427	1.860354	3.751148	4.327581	4.329385
protein_co	transmemb	3	0	1	1	0	2	0.076065	0	0.033412	0.021934	0	0.050397
protein_co	zinc_finger_	46	52	26	121	117	141	0.761741	1.014752	0.567359	1.733396	2.176629	2.320482
protein_co	alcohol_de	0	2	3	1	0	4	0	0.058008	0.097299	0.021292	0	0.097841
pseudogen	-	1	0	1	0	2	3	0.2521	0	0.332206	0	0.566437	0.751629
protein_co	zinc_finger_	290	257	315	192	115	188	2.986362	3.11878	4.274545	1.710443	1.330428	1.924031
lincRNA	sorting_nex	15	13	13	13	18	9	0.131346	0.134145	0.150004	0.098476	0.17707	0.078321
protein_co	chondroitii	358	280	302	86	86	82	4.922825	4.537289	5.472341	1.02304	1.328553	1.120611
protein_co	torsin_fami	57	42	30	65	48	95	0.727492	0.631698	0.504556	0.717678	0.688246	1.204999
protein_co	lysophosph	1799	1512	1647	513	396	374	26.18665	25.93628	31.59201	6.45995	6.475794	5.410408
protein_co	3-hydroxyis	303	301	269	460	353	382	4.741685	5.550904	5.547243	6.22746	6.20603	5.941049
protein_co	zinc_finger_	225	248	155	909	550	697	2.898935	3.765431	2.631616	10.13171	7.961001	8.924798
protein_co	transmemb	4	0	0	6	10	4	0.052056	0	0	0.06755	0.146204	0.051735
pseudogen	-	0	0	3	0	0	0	0	0	0.64003	0	0	0
protein_co	sosondowa	295	274	249	499	335	488	3.356457	3.67381	3.733303	4.911595	4.282062	5.518086
protein_co	zinc_finger_	422	312	402	499	627	507	4.107575	3.578778	5.156249	4.201812	6.856297	4.904454
protein_co	HCG19853	21	41	18	29	23	27	0.614912	1.414766	0.694546	0.734606	0.756607	0.785719
pseudogen	zinc_finger_	20	17	10	142	109	117	0.407552	0.408234	0.268527	2.50325	2.495333	2.369455
protein_co	Protein_LO	12	4	5	7	3	13	0.315125	0.123785	0.173024	0.159024	0.088506	0.339277
protein_co	high_mobil	131	104	78	211	143	143	3.262121	3.051893	2.559518	4.545423	4.000497	3.538951
protein_co	mesoderm_	406	400	401	632	561	433	4.317807	5.013076	5.619742	5.814566	6.70269	4.576513
protein_co	peptidylpro	0	0	0	0	4	1	0	0	0	0	0.303062	0.067024
protein_co	mannosida	602	515	678	802	837	767	3.71624	3.746465	5.515334	4.282967	5.804727	4.705571
protein_co	small_VCP/	46	44	29	592	417	586	0.536288	0.604506	0.445526	5.970701	5.461673	6.789657
protein_co	zinc_finger_	300	334	295	152	172	184	5.658104	7.423406	7.331731	2.480026	3.64441	3.448873
protein_co	DDRGK_do	1006	812	631	943	972	1255	40.77997	38.78931	33.70646	33.06919	44.26538	50.55944
protein_co	transcriptio	1509	1321	1195	4652	3472	3880	30.16917	31.12318	31.48305	80.45941	77.98353	77.09309
protein_co	zinc_finger_	89	64	73	185	185	200	1.079686	0.914944	1.166984	1.941521	2.521321	2.411276
protein_co	zinc_finger_	107	85	79	135	108	127	1.624516	1.520779	1.580527	1.773115	1.842099	1.916256
protein_co	hydroxyste	433	402	349	197	176	169	12.16098	13.30497	12.91638	4.786411	5.553189	4.717122
protein_co	seizure_thr	799	778	604	453	609	579	3.444333	3.952256	3.431074	1.68935	2.949339	2.480542
protein_co	sulfotransfe	18	8	10	4	8	1	0.149692	0.078401	0.109587	0.028777	0.074742	0.008265
protein_co	zinc_finger_	49	51	46	71	66	64	0.498484	0.611409	0.616662	0.624851	0.754306	0.64706
protein_co	ribosomal_	7	4	2	100	72	93	0.067923	0.045739	0.025573	0.839423	0.784873	0.89683
protein_co	calcium_ch	4	0	0	0	3	0	0.013096	0	0	0	0.011034	0
protein_co	glutamine-r	947	885	841	2365	1855	1910	14.12655	15.55738	16.53168	30.5197	31.08702	28.31582
processed_	MLLT4_ant	16	21	8	49	52	53	0.378488	0.585408	0.249377	1.002746	1.381925	1.245999

protein_co	colony_stir	1	3	0	33	9	27	0.023108	0.081695	0	0.659696	0.233646	0.62007
protein_co	FK506_bin	10	7	8	18	7	10	0.335282	0.276576	0.353456	0.52209	0.263668	0.333211
protein_co	DEAD_(Asp	2421	2168	2073	2888	3277	3231	29.55272	31.18667	33.34547	30.4974	44.93949	39.19668
pseudogen	-	4	2	5	6	5	0	0.33454	0.197118	0.551053	0.434113	0.469794	0
protein_co	ribosomal_	1098	874	839	1349	923	1095	37.2146	34.90837	37.47208	39.5536	35.14486	36.88373
protein_co	solute_carr	99	126	85	77	61	61	2.322179	3.482877	2.627328	1.562479	1.607457	1.422001
pseudogen	-	0	0	1	0	0	0	0	0	0.105702	0	0	0
protein_co	serine/thre	448	297	381	684	527	480	4.883172	3.814938	5.472475	6.449753	6.453327	5.199659
protein_co	ubiquitin-li	976	784	609	1345	1036	1752	35.63477	33.7324	29.30058	42.48243	42.49452	63.57229
protein_co	helicase_wi	1171	947	1116	727	918	778	4.489059	4.278145	5.637641	2.410992	3.953577	2.964065
protein_co	transmemb	75	63	49	139	121	128	1.090817	1.079788	0.939121	1.748914	1.977084	1.850164
protein_co	uridine-cyt	473	476	348	978	602	781	12.8153	15.19783	12.42458	22.92289	18.3237	21.02946
protein_co	caspase_rec	1	0	0	450	351	423	0.012126	0	0	4.720455	4.781504	5.097513
protein_co	zinc_finger_	59	36	47	77	50	47	1.5207	1.093456	1.596336	1.716902	1.447807	1.203924
protein_co	paternally_	2	1	0	0	1	1	0.012138	0.007152	0	0	0.006818	0.006032
protein_co	SDA1_dom	352	337	379	843	588	536	6.050399	6.82619	8.584508	12.53522	11.35449	9.156211
pseudogen	speedy_hor	0	0	0	1	0	1	0	0	0	0.016252	0	0.018671
pseudogen	-	10	10	17	17	7	13	0.598203	0.704946	1.340086	0.879753	0.470431	0.772862
protein_co	zinc_finger_	156	164	292	45	137	37	1.959382	2.427423	4.832949	0.488956	1.933144	0.461855
protein_co	family_with	712	534	399	371	336	436	11.57678	10.23189	8.549002	5.218487	6.137564	7.04537
protein_co	transmemb	9	0	3	0	0	0	0.122423	0	0.053774	0	0	0
protein_co	hydroletha	108	65	63	320	246	248	2.774201	1.96759	2.132502	7.110941	7.099018	6.331045
protein_co	myosin_ligl	0	2	1	115	108	129	0	0.135625	0.07583	5.724863	6.981956	7.377405
protein_co	histone_clu	43	39	25	18	100	113	1.695058	1.811706	1.298646	0.613835	4.428587	4.426945
protein_co	zinc_finger_	2	2	5	25	19	20	0.037856	0.04461	0.124711	0.409357	0.404019	0.376218
protein_co	zinc_finger_	100	70	74	340	289	292	0.860689	0.709989	0.839292	2.53156	2.79443	2.497692
protein_co	homeobox_	117	84	76	24	15	26	3.717945	3.1456	3.182479	0.659768	0.535497	0.821108
protein_co	DDB1_and_	12	8	7	6	8	10	0.384559	0.30212	0.295607	0.16634	0.288019	0.318487
protein_co	pim-3_onc	539	436	299	1061	773	792	12.04525	11.48208	8.805074	20.51188	19.40687	17.58984
protein_co	arsA_arseni	1929	1591	1237	2075	1549	2344	74.65145	72.55766	63.08273	69.46837	67.34517	90.15156
processed_	-	0	0	0	0	5	0	0	0	0	0	0.139223	0
protein_co	aspartate_k	3759	3461	3756	1665	1513	1337	38.61929	41.90257	50.85016	14.79821	17.46304	13.65127
protein_co	histone_clu	1	0	4	0	2	4	0.112881	0	0.594996	0	0.253629	0.448734
protein_co	sprouty-rel	574	448	502	783	770	697	7.417166	6.821992	8.548003	8.752878	11.17805	8.950938
protein_co	WW_doma	469	427	359	743	711	810	5.499297	5.900235	5.547069	7.536786	9.365975	9.439065
protein_co	histone_clu	0	0	0	1	3	0	0	0	0	0.079928	0.311392	0
protein_co	glutamine--	1477	1312	1465	2270	2059	2075	8.992967	9.413767	11.75425	11.9567	14.08406	12.55597
protein_co	UV_radiatic	222	166	210	371	307	256	2.85057	2.511851	3.553308	4.121124	4.428597	3.266844
pseudogen	transmemb	0	0	3	1	3	0	0	0	0.080188	0.017547	0.068363	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.584601
protein_co	zinc_finger_	153	133	138	202	137	224	1.669065	1.709781	1.98379	1.906322	1.679003	2.428508
protein_co	intersectin_	197	173	194	250	226	239	1.655456	1.713187	2.148266	1.817417	2.133581	1.995993
protein_co	neurotroph	5	5	2	2	6	0	0.086732	0.102208	0.045716	0.030012	0.116925	0
pseudogen	basic_leuci	14	8	18	46	28	76	0.897305	0.60424	1.520265	2.550544	2.016133	4.841002

protein_co	meningiom	1809	1707	1796	2234	2019	2026	18.61062	20.69488	24.34801	19.88239	23.33499	20.71435
pseudogen	-	10	1	2	0	0	3	0.131139	0.015454	0.034562	0	0	0.039099
protein_co	metallothic	105	89	48	199	166	280	3.533887	3.529884	2.128822	5.794013	6.276543	9.365502
protein_co	family_witl	674	564	573	584	556	609	6.224007	6.137568	6.972678	4.665369	5.768116	5.589038
protein_co	zinc_finger_	46	26	54	173	131	186	1.211585	0.807005	1.874237	3.941896	3.876291	4.868763
protein_co	thioredoxir	1162	1046	1190	4542	3658	3405	15.47998	16.42113	20.89036	52.3449	54.74658	45.08073
protein_co	NOTCH-regu	5	7	18	90	41	74	0.100994	0.166621	0.479107	1.572645	0.930375	1.485479
protein_co	zinc_finger_	143	117	110	83	67	47	1.539984	1.484818	1.561017	0.773252	0.810595	0.503023
protein_co	keratin_ass	1	0	0	0	0	0	0.04266	0	0	0	0	0
protein_co	coagulatior	0	1	0	0	0	1	0	0.036677	0	0	0	0.030931
protein_co	zinc_finger_	69	33	56	83	63	95	0.96792	0.545521	1.035173	1.007236	0.992841	1.324413
protein_co	zinc_finger_	129	120	150	129	136	121	1.211314	1.327869	1.856065	1.0479	1.43468	1.129177
protein_co	zinc_finger_	239	221	236	487	405	426	2.670514	2.910023	3.474912	4.707486	5.083948	4.730601
protein_co	zinc_finger_	1129	1010	644	1490	1015	1504	8.685031	9.156002	6.52827	9.915776	8.771877	11.49833
protein_co	tropomyos	12791	10754	7867	10620	8748	12577	315.4021	312.4908	255.6254	226.5414	242.336	308.21
lincRNA	FLVCR1_an	30	32	38	55	62	81	0.629002	0.790656	1.049903	0.9976	1.460399	1.687817
protein_co	zinc_finger_	37	28	47	56	55	31	0.342092	0.305074	0.572629	0.447911	0.571285	0.284847
protein_co	SH3_domai	179	135	116	1523	1168	1145	2.038382	1.811646	1.740706	15.0036	14.94254	12.95829
protein_co	zinc_finger_	131	103	109	224	275	255	1.638382	1.518057	1.796409	2.423566	3.863897	3.169521
protein_co	ankyrin_rep	215	154	170	0	4	0	3.405839	2.874839	3.548701	0	0.071186	0
protein_co	YTH_domai	1763	1571	1476	2795	2533	2457	31.90939	33.50808	35.20363	43.7634	51.50513	44.1958
pseudogen	neighbor_c	93	88	62	166	156	153	3.663328	4.084911	3.218247	5.65671	6.903455	5.989546
protein_co	translation_	332	273	270	717	598	661	8.88595	8.610642	9.522794	16.60152	17.98109	17.58235
protein_co	atlastin_GT	196	177	177	207	156	159	3.637026	3.870532	4.328111	3.322949	3.252101	2.932224
protein_co	cyclic_nucl	0	0	1	5	9	9	0	0	0.024333	0.079873	0.186705	0.165164
protein_co	v-maf_musc	142	150	89	320	245	397	2.232073	2.778551	1.843507	4.35144	4.326484	6.201834
protein_co	histone_clu	49	16	30	16	32	22	1.841099	0.708448	1.485379	0.520073	1.350766	0.821511
protein_co	chromosor	31	46	20	16	8	14	0.776702	1.358181	0.660324	0.346797	0.225181	0.348602
protein_co	zinc_finger_	233	243	216	1123	718	797	2.209035	2.714939	2.69858	9.210632	7.647512	7.509563
protein_co	GPN-loop_(	355	336	284	1027	533	615	7.529669	8.398348	7.937809	18.84434	12.70059	12.9638
protein_co	phospholar	0	2	1	3	0	3	0	0.062357	0.034864	0.068664	0	0.078882
protein_co	C2_calcium	4	2	0	15	16	25	0.06147	0.036219	0	0.199415	0.276231	0.381815
protein_co	zinc_finger_	140	128	121	368	394	429	1.433328	1.54431	1.632442	3.25933	4.531718	4.365002
protein_co	integrin_be	231	133	200	0	7	7	4.903516	3.327012	5.594489	0	0.166933	0.147674
protein_co	zinc_finger_	116	96	80	252	177	240	3.064449	2.988634	2.784961	5.759144	5.253112	6.301084
processed_	chromosor	0	0	0	1	0	0	0	0	0	0.013252	0	0
protein_co	zinc_finger_	301	267	233	343	259	247	5.611	5.865325	5.723537	5.531347	5.424036	4.57594
protein_co	potassium_	12	11	21	9	6	18	0.391431	0.422837	0.902667	0.253968	0.219874	0.58352
protein_co	WD_repeat	131	153	164	1013	772	739	1.156649	1.591948	1.908135	7.73754	7.657673	6.48462
protein_co	zinc_finger_	183	167	165	372	331	390	2.277969	2.449742	2.706546	4.005924	4.628857	4.824707
protein_co	catenin_(ca	3259	2820	2794	7831	6574	6291	26.32912	26.84776	29.74494	54.73085	59.66652	50.51045
protein_co	DEAD_(Asp	1757	1569	1183	1485	1267	1494	18.0336	18.97758	16.00038	13.18561	14.60954	15.23951
protein_co	solute_carr	34	20	13	9	25	25	0.83256	0.57713	0.419483	0.190652	0.687742	0.608396
protein_co	retinal_deg	0	0	0	7	7	7	0	0	0	0.075151	0.097593	0.086333

protein_co	SPANX_fam	2	0	0	1	0	1	0.273597	0	0	0.118343	0	0.135954
protein_co	SH2_domai	1	0	0	0	0	0	0.020983	0	0	0	0	0
protein_co	activity-reg	25	20	15	1	2	0	0.335239	0.316047	0.265058	0.011601	0.03013	0
protein_co	Uncharacte	12	15	10	0	3	4	0.542985	0.799843	0.596267	0	0.152502	0.179877
protein_co	nudix_(nuc	2459	2002	1933	869	848	983	21.28199	20.41854	22.04552	6.506335	8.245149	8.455062
protein_co	tousled-like	329	247	330	888	836	768	3.039719	2.689314	4.017781	7.097631	8.677464	7.051936
protein_co	LPS-respon	378	287	396	913	959	917	1.940434	1.736185	2.67878	4.054533	5.530632	4.678278
protein_co	chromoson	17	13	9	8	22	13	0.48413	0.436278	0.337746	0.197091	0.703857	0.36793
protein_co	zinc_finger_	2	3	0	2	2	0	0.021412	0.037849	0	0.018523	0.024055	0
protein_co	matrix_met	184	112	121	260	195	217	4.040292	2.898144	3.501185	4.938911	4.810371	4.735483
protein_co	bromodom	560	421	548	1304	963	890	4.932938	4.370255	6.361111	9.937067	9.530001	7.791432
protein_co	COP9_signa	2789	2325	2327	1944	1152	1483	36.84862	36.19952	40.51389	22.21938	17.09914	19.47258
pseudogen	peptidylpro	1573	1330	1230	1509	1483	1847	167.2213	166.6178	172.3069	138.7762	177.114	195.1368
protein_co	coiled-coil_	7	7	12	133	118	108	0.107385	0.126547	0.242585	1.765069	2.033659	1.646571
protein_co	Mdm4_p53	1059	920	691	1467	991	1348	5.565821	5.698075	4.785707	6.670008	5.851349	7.040975
protein_co	ryanodine_	0	1	2	96	98	63	0	0.003767	0.008424	0.265469	0.351929	0.200138
protein_co	kelch-like_f	1036	920	985	972	963	862	9.605406	10.05196	12.03447	7.796241	10.0307	7.942787
protein_co	family_with	1	0	2	0	0	0	0.040137	0	0.105782	0	0	0
protein_co	nuclear_rec	866	713	862	1022	1103	911	4.92395	4.777409	6.458592	5.027009	7.045638	5.147825
protein_co	serine_thre	365	305	338	330	287	263	5.058498	4.981219	6.172772	3.95645	4.468479	3.622381
protein_co	tyrosine_ar	5	3	0	1	5	4	0.066459	0.046991	0	0.011499	0.074662	0.052839
protein_co	chromoson	1005	917	743	437	605	425	20.74296	22.30392	20.20823	7.802776	14.02843	8.717728
protein_co	calmodulin	3029	2556	2580	9537	7277	7758	37.80252	37.59147	42.43028	102.9666	102.0288	96.22343
protein_co	lipoprotein	0	0	0	2	0	0	0	0	0	0.014114	0	0
protein_co	family_with	8	6	7	29	25	27	0.102599	0.09068	0.1183	0.321746	0.360198	0.344133
protein_co	tetratricop	1838	1473	1693	1474	1400	1181	17.0532	16.10535	20.69913	11.83098	14.59276	10.8898
protein_co	tumor_sup	380	239	275	509	338	422	8.174554	6.058784	7.795572	9.472427	8.168574	9.021995
protein_co	3'-phospho	1568	1294	1361	249	162	191	21.02089	20.44308	24.04351	2.887801	2.439883	2.544767
protein_co	chromoson	0	0	0	0	0	2	0	0	0	0	0	0.039017
protein_co	solute_carr	327	246	333	317	279	230	3.698292	3.278654	4.962865	3.101528	3.544922	2.585181
protein_co	FANCD2/FA	190	211	214	268	243	204	2.01216	2.633289	2.986466	2.455312	2.891108	2.147083
protein_co	ATP-bindin	135	124	132	115	120	104	0.97784	1.058432	1.25992	0.720601	0.976482	0.748647
protein_co	eukaryotic_	437	410	332	758	562	662	7.349179	8.125467	7.3575	11.02782	10.618	11.06433
protein_co	mitochond	10450	9422	8042	19597	10398	17147	1053.778	1119.652	1068.641	1709.564	1177.963	1718.425
protein_co	importin_9	1823	1476	1399	3470	2646	2475	8.440003	8.052846	8.535097	13.89788	13.76242	11.38782
protein_co	glutathione	0	0	0	0	1	0	0	0	0	0	0.034741	0
protein_co	centrosoma	441	394	385	319	286	239	2.937466	3.092698	3.379324	1.83818	2.140175	1.582129
protein_co	chromoson	13	5	7	1	3	8	0.670139	0.303738	0.475504	0.044595	0.173737	0.409847
protein_co	mitochond	70328	61325	47526	154256	72134	91515	5443.325	5593.461	4847.324	10328.59	6272.275	7039.437
protein_co	chromoson	1277	1073	797	770	608	714	42.14816	41.73443	34.66417	21.98576	22.54449	23.42047
protein_co	family_with	246	189	272	195	197	180	2.0429	1.849613	2.976567	1.400908	1.837922	1.485573
protein_co	delta-like_1	15	18	11	10	34	40	0.250194	0.353806	0.241776	0.144294	0.637108	0.663063
protein_co	ankyrin_rep	505	419	293	371	332	357	8.318358	8.13331	6.359876	5.286681	6.143748	5.844187
protein_co	enoyl-CoA_	250	256	191	412	251	369	3.419961	4.12694	3.443097	4.875749	3.857482	5.016689

protein_co	unc-13_hor	249	218	217	675	619	622	2.091434	2.157786	2.401814	4.90469	5.840963	5.192121
protein_co	chromoson	5	0	0	0	0	1	0.157656	0	0	0	0	0.031337
protein_co	mitochond	54876	45499	36388	100279	56963	67337	2546.179	2487.8	2224.843	4025.126	2969.261	3105.059
protein_co	LIM_domai	2005	1674	1462	1861	1798	1942	46.45369	45.7055	44.63629	37.30055	46.79987	44.71619
protein_co	protein_ph	1	6	1	10	7	5	0.024601	0.173943	0.032418	0.21282	0.193463	0.122245
protein_co	Ctr9_Paf1/l	1023	1050	952	1426	1318	1156	11.80956	14.28415	14.48204	14.241	17.09317	13.2625
protein_co	SPARC_rela	0	1	2	21	0	7	0	0.017018	0.03806	0.262351	0	0.100463
protein_co	coagulatior	1	1	0	15	20	12	0.007521	0.008863	0	0.097597	0.16899	0.089696
protein_co	methionine	769	651	561	681	460	568	28.60971	28.5414	27.5033	21.91782	19.22623	21.00125
protein_co	small_integ	0	0	0	2	0	1	0	0	0	0.106262	0	0.061037
protein_co	leucine_ric	41	29	42	4	1	0	0.498068	0.415155	0.67234	0.042037	0.013648	0
protein_co	zinc_finger_	375	305	282	535	400	444	3.315443	3.177732	3.285445	4.09192	3.973007	3.901242
protein_co	SMAD_spec	414	310	296	874	757	734	3.820389	3.371134	3.59943	6.977208	7.847877	6.731517
protein_co	solute_carr	1254	1017	1567	604	598	567	5.73596	5.48197	9.445227	2.390059	3.072974	2.577516
pseudogen	-	21	25	12	64	17	33	2.03247	2.851359	1.530456	5.358556	1.848429	3.174157
protein_co	G_patch_d	244	173	157	354	309	375	6.084598	5.08388	5.159131	7.636746	8.656646	9.293579
protein_co	GATS_prote	29	12	15	6	11	2	1.214627	0.592289	0.827887	0.2174	0.517591	0.08325
protein_co	CDC42_bin	2350	1937	1917	2095	2697	2581	18.40949	17.88177	19.78932	14.1978	23.7358	20.09424
protein_co	plexin_B3	476	439	327	6	4	26	3.951688	4.294843	3.577324	0.043091	0.037307	0.214515
protein_co	ribosomal_	21543	18052	12955	19481	14641	17246	1066.892	1053.53	845.4474	834.6197	814.5808	848.8138
protein_co	collagen_b	31	25	33	127	132	113	0.317012	0.301274	0.444695	1.12352	1.516481	1.148423
protein_co	EPS8-like_3	0	0	0	0	0	1	0	0	0	0	0	0.02263
protein_co	EGF-like-do	5	0	5	21	15	15	0.110386	0	0.145461	0.401075	0.372035	0.329112
protein_co	mitochond	27796	24812	19430	69287	35433	48681	1412.234	1485.57	1300.864	3045.363	2022.467	2458.066
protein_co	adenomatc	20	19	21	8	6	14	0.309054	0.345991	0.427621	0.106944	0.104161	0.215002
protein_co	RCSD_dom	0	0	0	3	9	7	0	0	0	0.043827	0.170744	0.11748
protein_co	Ras_associa	10	11	19	24	7	3	0.289929	0.37583	0.725905	0.601957	0.228002	0.086441
protein_co	family_with	28	18	40	1404	1539	1275	0.24747	0.187476	0.465865	10.73484	15.28104	11.19915
protein_co	zinc_finger_	301	191	183	323	259	329	9.616922	7.191344	7.704696	8.927608	9.296477	10.4466
protein_co	glutamate_	4	8	8	4	22	18	0.027254	0.064234	0.071828	0.023577	0.1684	0.121886
protein_co	mitochond	34666	29246	27720	49363	33334	39512	1012.833	1006.949	1067.24	1247.666	1094.134	1147.288
protein_co	CCR4-NOT_	899	805	796	3009	2075	2179	17.96676	18.9589	20.96322	52.02299	46.58835	43.27898
protein_co	transmemb	1349	936	897	1140	1010	1090	19.4757	15.92444	17.06508	14.238	16.38142	15.6393
protein_co	mechanisti	537	538	665	1534	1346	1385	3.276399	3.868226	5.346615	8.096752	9.226067	8.398117
protein_co	secretory_c	136	71	90	149	123	174	2.100956	1.292538	1.832126	1.991257	2.134677	2.671387
protein_co	zinc_finger_	1577	1342	1279	400	307	259	17.1398	17.18833	18.31805	3.760945	3.748533	2.797586
protein_co	alpha-kinas	165	141	190	1200	945	771	1.19612	1.204528	1.815011	7.525495	7.696117	5.554626
protein_co	melanoma_	0	0	0	3	11	4	0	0	0	0.05966	0.28408	0.091384
protein_co	leucine-rich	302	250	235	362	353	293	3.14976	3.072682	3.229782	3.266195	4.136131	3.037021
protein_co	mitochond	241659	211168	174721	426380	231934	265126	8296.801	8543.639	7904.741	12663.9	8945.841	9046.273
protein_co	purine_nuc	232	166	151	1396	708	891	4.773537	4.025015	4.094153	24.84853	16.3657	18.21963
protein_co	paired_box	1	3	1	17	13	5	0.011728	0.041463	0.015455	0.172481	0.171286	0.058279
protein_co	glycerol_ki	60	19	43	148	126	160	0.856881	0.319764	0.809231	1.828497	2.021572	2.270906
protein_co	forkhead_b	719	513	599	832	806	706	7.112215	5.97999	7.807961	7.11971	8.956949	6.940493

protein_co	zinc_finger_	564	401	260	396	285	265	15.28082	12.80321	9.282729	9.281661	8.67484	7.135478
protein_co	SFT2_doma	699	571	497	840	653	897	14.36559	13.82896	13.45976	14.93443	15.07678	18.32096
protein_co	CD247_mo	0	0	0	6	3	13	0	0	0	0.094043	0.061064	0.23408
protein_co	glutamate_	0	2	1	3	7	6	0	0.029235	0.016346	0.032192	0.097547	0.073965
protein_co	chromoson	488	356	408	1294	1093	989	6.820276	5.863261	7.514102	15.64514	17.16135	13.73688
protein_co	inositol_pc	197	165	183	892	695	630	2.11764	2.090147	2.592219	8.294949	8.393048	6.730325
protein_co	Rho_GTPas	464	342	443	2112	2098	2260	4.164907	3.6176	5.239935	16.40001	21.1564	20.16069
protein_co	high_mobil	3116	2646	2393	7561	6016	7398	110.2701	110.3462	111.5933	231.4743	239.1759	260.1863
protein_co	Selenoprot	2178	1764	1286	120	95	73	55.70313	53.1652	43.34086	2.655009	2.729571	1.855471
protein_co	ubiquitin-c	979	807	817	8353	5903	6338	12.08141	11.73587	13.28592	89.17442	81.83831	77.73143
protein_co	gap_junctic	75	65	38	25	24	36	1.770207	1.807937	1.181901	0.510465	0.63639	0.844452
protein_co	optic_atrop	955	813	852	1878	1350	1378	7.787839	7.812881	9.155625	13.24867	12.36791	11.16792
protein_co	DENN/MAD	750	633	536	1109	999	1028	6.958595	6.921036	6.553298	8.901329	10.41298	9.479012
protein_co	ryanodine_	28	24	23	110	150	127	0.095273	0.096234	0.103127	0.323792	0.573391	0.429461
protein_co	zinc_finger_	394	302	305	326	236	202	9.404306	8.494632	9.593238	6.731489	6.328366	4.791721
protein_co	mitochond	10692	9840	8944	14818	12450	20873	1635.969	1774.264	1803.361	1961.411	2140.102	3174.026
protein_co	KTI12_hom	209	147	113	280	176	199	6.455465	5.35064	4.59933	7.481735	6.107212	6.108632
protein_co	dual_specif	0	0	0	41	58	52	0	0	0	0.45095	0.828435	0.657044
protein_co	Selenoprot	864	691	791	2302	1651	1833	13.18565	12.42719	15.9074	30.39178	28.30635	27.80097
protein_co	Rho_guanir	0	0	0	1	0	0	0	0	0	0.011025	0	0
protein_co	thymocyte_	210	210	187	161	147	136	2.691263	3.17149	3.158009	1.784949	2.116427	1.73215
protein_co	carboxylest	2	0	0	0	4	4	0.048614	0	0	0	0.10923	0.096628
protein_co	RUN_and_S	743	635	595	566	479	469	6.979269	7.029136	7.365002	4.599393	5.05482	4.378281
protein_co	FIC_domair	58	51	41	48	77	48	0.917412	0.950635	0.854585	0.656811	1.368284	0.754549
protein_co	oligosaccha	4860	4335	3397	3362	2581	2978	238.8981	251.115	220.0426	142.9674	142.5324	145.4825
pseudogen	hydroxy-de	22	8	14	7	10	9	1.028889	0.440903	0.862797	0.283209	0.525406	0.41831
protein_co	R3H_doma	1243	1068	827	1273	894	1086	36.25656	36.7108	31.78746	32.12232	29.29558	31.48146
protein_co	tRNA_splici	204	179	201	1185	787	962	5.510185	5.697655	7.154296	27.68964	23.8814	25.82383
protein_co	listerin_E3_	427	394	492	820	676	502	2.914622	3.169258	4.425417	4.842071	5.183822	3.405396
protein_co	RUN_doma	305	221	241	514	373	434	4.21813	3.601799	4.392098	6.149592	5.795328	5.965125
protein_co	coiled-coil_	0	1	1	0	1	2	0	0.018184	0.020333	0	0.017335	0.03067
protein_co	chromoson	70	44	38	25	19	19	1.311812	0.971703	0.938409	0.4053	0.400015	0.353864
protein_co	G_protein-r	300	251	217	189	176	195	5.984287	5.900271	5.704081	3.261489	3.944145	3.865765
protein_co	tRNA-yW_s	261	219	195	515	339	399	4.12712	4.080918	4.063274	7.044933	6.022203	6.270312
protein_co	DDB1_and_	508	459	438	1274	1027	1093	7.334067	7.809099	8.332784	15.91159	16.65715	15.68234
protein_co	Scm-like_w	104	78	79	245	315	244	0.695009	0.614269	0.695695	1.416401	2.364922	1.620529
protein_co	inositol_14	11	25	22	58	58	67	0.270107	0.72342	0.71187	1.232067	1.600001	1.635038
protein_co	mitochond	82914	73038	61020	215917	102027	134976	3185.45	3306.731	3089.227	7176.17	4403.592	5153.581
protein_co	structural_	1063	952	1062	941	878	742	9.504522	10.03093	12.51285	7.27863	8.819432	6.593418
protein_co	mitochond	44890	38366	29685	104310	56534	73732	2485.901	2503.732	2166.237	4997.159	3517.167	4057.886
protein_co	DDB1_and_	1	0	1	29	19	21	0.015668	0	0.020646	0.393065	0.334431	0.326989
protein_co	protein_arg	391	326	356	804	654	663	7.843853	7.706859	9.411038	13.95313	14.73939	13.21831
protein_co	shisa_homo	466	357	314	66	53	96	18.39709	16.60881	16.33532	2.254085	2.350651	3.766554
protein_co	KIAA1737	143	159	176	355	322	251	1.687597	2.211246	2.737035	3.6243	4.269114	2.943853

protein_co	capping_pr	1426	1329	1239	2137	1492	1599	31.53461	34.63379	36.10556	40.88231	37.06686	35.14197
protein_co	mitochond	32456	27973	24500	83293	38569	59787	2523.132	2562.661	2509.839	5601.657	3368.468	4619.143
protein_co	topoisomer	1633	1363	1528	2770	2641	2528	23.12805	22.74866	28.51747	33.93873	42.02137	35.58275
protein_co	protein_reg	470	403	452	1871	1604	1625	6.08815	6.151763	7.71544	20.96642	23.34215	20.91946
protein_co	basic_helix	168	131	110	126	90	88	1.73374	1.593137	1.495899	1.124885	1.043437	0.902541
protein_co	mitogen-ac	612	534	574	529	591	641	6.724759	6.914705	8.311358	5.028564	7.295614	6.999918
protein_co	L1_cell_adh	38	22	29	2263	1878	2246	0.393459	0.268439	0.395685	20.27047	21.84545	23.1119
protein_co	sterol_regu	5367	4366	4112	4429	3804	4189	49.85687	47.7952	50.33631	35.5928	39.69931	38.6735
protein_co	chromoson	331	249	187	972	600	797	5.008136	4.43971	3.728418	12.72265	10.19879	11.98439
protein_co	POU_class_	42	18	41	0	0	0	0.4482	0.226361	0.576556	0	0	0
protein_co	RasGEF_do	4	2	5	60	52	45	0.051599	0.030403	0.084994	0.669575	0.753593	0.576908
protein_co	chromoson	354	323	282	693	693	852	4.372635	4.701642	4.590118	7.405189	9.616615	10.45898
protein_co	ribosomal_	6685	6604	5299	4760	4006	6437	184.8097	215.1481	193.0421	113.8396	124.418	176.8546
protein_co	DAZ_intera	289	280	256	713	571	489	2.859803	3.265152	3.338206	6.103667	6.347804	4.809023
protein_co	KIAA0753	393	398	345	605	547	510	4.281912	5.11017	4.953351	5.702477	6.695478	5.522364
pseudogen	-	0	0	2	0	0	0	0	0	0.70468	0	0	0
protein_co	DNA_cross-	44	49	46	349	314	263	0.52182	0.684812	0.718887	3.580604	4.183566	3.099797
protein_co	autophagy_	1749	1392	1324	1342	899	909	17.65373	16.55743	17.61041	11.71823	10.19425	9.118431
protein_co	nitric_oxid	19	8	19	14	29	43	0.180946	0.089783	0.238443	0.115342	0.310272	0.40698
protein_co	adenine_ph	1802	1580	1121	2244	1474	2034	100.7388	104.0893	82.58146	108.5245	92.57392	113.0063
protein_co	G_protein-r	107	125	126	43	50	68	0.947272	1.304091	1.469929	0.329323	0.49729	0.598287
protein_co	TBK1_bindi	496	440	303	512	311	587	6.371932	6.66115	5.129404	5.690133	4.488476	7.494406
protein_co	melanoma_	30	18	21	83	90	71	0.429367	0.30359	0.396061	1.027659	1.447103	1.009894
protein_co	coiled-coil_	237	229	145	491	370	453	20.26982	23.08044	16.34196	36.32837	35.55103	38.5043
protein_co	mitochond	115123	96098	72870	197485	140099	153568	7773.885	7647.112	6484.248	11536.48	10628.21	10305.91
protein_co	ZFP2_zinc_	16	19	21	18	8	11	0.348726	0.488006	0.603141	0.339391	0.195886	0.238269
protein_co	sosondowa	1	2	0	41	54	53	0.015319	0.036104	0	0.543332	0.929311	0.806871
protein_co	l(3)mbt-like	439	366	386	448	450	436	5.144112	5.053986	5.960298	4.54137	5.923896	5.077407
protein_co	dystrophin	35	48	59	168	192	204	0.13277	0.214575	0.294929	0.55132	0.818241	0.769079
protein_co	microfibrill	25	36	51	67	82	78	0.209485	0.355486	0.563141	0.48568	0.771925	0.649556
protein_co	N-acetylgal	568	534	492	341	277	275	8.140359	9.018692	9.291699	4.227782	4.459889	3.916855
protein_co	smg-5_hom	1875	1561	1331	4699	3866	4490	21.77328	21.36154	20.36739	47.20532	50.43516	51.81774
protein_co	KIAA1279	458	382	417	1023	797	718	9.568656	9.404938	11.48038	18.48946	18.70651	14.90801
protein_co	transglutan	53	9	20	2367	1402	1715	0.70217	0.140513	0.349166	27.12863	20.86718	22.58085
protein_co	armadillo_r	11	5	6	396	384	442	0.302049	0.161794	0.217106	9.406829	11.84583	12.06193
protein_co	praja_ring_	2547	2322	2592	1555	1491	1214	27.58043	29.63066	36.98638	14.56684	18.13839	13.06473
protein_co	RAR-relatec	0	0	2	4	7	6	0	0	0.039116	0.051358	0.116718	0.088501
protein_co	sphingomy	216	197	169	367	256	284	3.054288	3.282688	3.149037	4.489369	4.066729	3.991023
antisense	-	1	2	0	0	1	5	0.093535	0.220451	0	0	0.105081	0.464788
pseudogen	-	1	0	0	0	7	16	0.067014	0	0	0	0.527002	1.065601
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.13666
pseudogen	-	7	18	6	19	3	2	0.213349	0.646505	0.240979	0.500967	0.102722	0.06058
lincRNA	-	2	5	4	12	10	12	0.183187	0.539686	0.482791	0.950842	1.028995	1.092333
antisense	-	2	3	1	1	7	9	0.111455	0.197014	0.073435	0.048209	0.438244	0.498449

pseudogen	-	0	0	0	0	2	3	0	0	0	0	0.489514	0.649556
pseudogen	-	0	0	2	0	2	0	0	0	0.547163	0	0.466478	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.224846
protein_co	Uncharacte	4	1	4	2	0	0	0.678731	0.199961	0.894401	0.293583	0	0
antisense	-	0	0	1	1	1	0	0	0	0.070326	0.046168	0.059956	0
protein_co	Uncharacte	3	1	7	3	1	0	0.070245	0.027593	0.215985	0.060768	0.026305	0
pseudogen	-	7	9	3	18	3	1	0.182286	0.276188	0.102946	0.405499	0.087766	0.02588
pseudogen	-	9	5	2	6	5	10	3.873731	2.536087	1.134362	2.234093	2.41772	4.277565
processed_	-	3	1	4	6	4	5	0.220894	0.08677	0.388113	0.382188	0.330881	0.365884
antisense	-	4	7	1	11	3	3	0.339365	0.699862	0.1118	0.807352	0.285942	0.252952
protein_co	zinc_finger_	39	22	35	234	186	219	0.338087	0.224747	0.399822	1.754862	1.811449	1.886766
antisense	-	14	9	11	7	15	2	0.809142	0.61298	0.837769	0.349992	0.973951	0.114878
antisense	-	0	0	0	1	0	0	0	0	0	0.018542	0	0
lincRNA	-	0	1	1	0	0	1	0	0.026368	0.029486	0	0	0.022238
antisense	-	58	41	42	206	187	228	3.101594	2.583734	2.959654	9.529873	11.23434	12.11718
pseudogen	-	1	0	1	0	3	2	0.215207	0	0.283591	0	0.725316	0.427757
protein_co	Uncharacte	52	46	20	17	17	21	1.136636	1.184903	0.57608	0.321462	0.417461	0.456191
pseudogen	-	0	0	1	2	0	0	0	0	0.15199	0.19956	0	0
pseudogen	-	1	1	0	0	0	0	0.022683	0.02673	0	0	0	0
pseudogen	BTB_(POZ)_	3	0	0	0	0	0	0.109307	0	0	0	0	0
pseudogen	-	0	3	0	1	3	1	0	0.115462	0	0.028253	0.110073	0.032458
pseudogen	-	0	0	1	1	0	1	0	0	0.750143	0.492461	0	0.565742
pseudogen	-	1	1	0	0	0	0	0.569258	0.670836	0	0	0	0
pseudogen	-	0	3	1	2	0	9	0	2.012507	0.750143	0.984923	0	5.091682
pseudogen	-	0	1	0	0	0	3	0	0.611644	0	0	0	1.547472
pseudogen	-	3	0	0	0	0	0	1.654406	0	0	0	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.565742
pseudogen	-	0	1	0	5	0	0	0	0.670836	0	2.462307	0	0
lincRNA	-	3	2	0	6	0	0	0.276214	0.217001	0	0.477902	0	0
pseudogen	-	11	2	3	2	0	0	0.409529	0.087746	0.14718	0.064415	0	0
pseudogen	-	0	1	0	0	1	1	0	0.079882	0	0	0.076154	0.067368
antisense	long_interg	1	1	5	15	18	15	0.060712	0.071546	0.400019	0.787825	1.227714	0.905058
protein_co	Uncharacte	2	1	0	1	0	5	0.534758	0.31509	0	0.231308	0	1.328638
antisense	-	2	3	2	0	1	0	0.059787	0.105682	0.078784	0	0.033583	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.240247
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.36046	0
processed_	-	4	6	9	10	5	6	0.369571	0.653275	1.095758	0.799283	0.518987	0.550932
pseudogen	-	0	1	0	0	0	0	0	0.340917	0	0	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.35076
pseudogen	-	0	0	2	0	0	0	0	0	0.930177	0	0	0
protein_co	inverted_fc	2621	2009	1490	3836	2806	3596	29.69999	26.82726	22.24899	37.60372	35.7212	40.4966
antisense	PDCD4_ant	6	21	12	9	14	25	0.408285	1.683988	1.07604	0.529807	1.070261	1.690683
processed_	-	2	1	0	494	424	399	0.02021	0.011908	0	4.318507	4.813474	4.007064
pseudogen	-	1	0	1	1	3	2	0.028757	0	0.037894	0.024877	0.096919	0.057158

antisense	RBMS3_ant	1	2	0	3	14	3	0.061203	0.144249	0	0.15884	0.962616	0.182476
pseudogen	-	3	0	0	0	0	0	0.069416	0	0	0	0	0
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.666001
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.219225
pseudogen	-	0	0	0	2	4	1	0	0	0	0.372349	0.967088	0.213878
pseudogen	-	0	0	1	0	0	0	0	0	0.310059	0	0	0
pseudogen	taste_recep	18	9	10	0	0	0	1.047184	0.617021	0.766629	0	0	0
pseudogen	-	0	0	1	4	1	0	0	0	0.264255	0.693923	0.225288	0
protein_co	Uncharacte	0	4	0	4	0	1	0	0.06465	0	0.04746	0	0.013631
pseudogen	-	0	3	1	0	1	2	0	0.8787	0.327527	0	0.27923	0.494029
pseudogen	-	9	1	0	1	2	2	1.291244	0.169072	0	0.124116	0.322363	0.285171
lincRNA	-	1	0	0	0	0	0	0.117126	0	0	0	0	0
pseudogen	-	0	2	0	0	0	0	0	0.7171	0	0	0	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.288043	0	0
pseudogen	olfactory_r	0	0	0	0	1	0	0	0	0	0	0.060504	0
antisense	IGBP1_anti	7	8	2	4	15	20	0.68374	0.920852	0.257429	0.337999	1.646012	1.941478
pseudogen	-	7	21	9	6	5	5	0.326796	1.155328	0.553677	0.242322	0.262239	0.231984
antisense	-	1	0	0	3	3	0	0.084167	0	0	0.218437	0.283669	0
pseudogen	-	3	1	1	6	3	2	0.341555	0.134167	0.150029	0.590954	0.383716	0.226297
pseudogen	-	1	0	0	4	2	3	0.075738	0	0	0.262082	0.170174	0.225811
pseudogen	-	8	19	5	2	0	11	0.247099	0.691579	0.20351	0.053441	0	0.337663
pseudogen	-	1	0	1	1	3	8	0.430415	0	0.567181	0.372349	1.450632	3.422052
protein_co	HCG20436	13	9	18	5	7	15	0.518248	0.422808	0.945587	0.172436	0.313503	0.594285
pseudogen	-	1	17	0	1	0	6	0.028694	0.574846	0	0.024823	0	0.171103
lincRNA	-	0	0	0	5	13	9	0	0	0	0.139546	0.471168	0.28856
pseudogen	-	6	10	7	153	88	83	0.350603	0.688606	0.53901	7.734252	5.77691	4.820051
lincRNA	long_interg	0	0	0	1	0	0	0	0	0	0.022385	0	0
pseudogen	-	5	2	0	0	11	0	0.617028	0.290852	0	0	1.525024	0
pseudogen	-	0	0	2	0	1	2	0	0	0.19061	0	0.081251	0.143754
processed_	-	0	0	0	8	0	0	0	0	0	0.159996	0	0
pseudogen	-	3	1	3	0	0	1	0.099513	0.03909	0.131134	0	0	0.032966
protein_co	olfactory_r	0	0	0	4	0	0	0	0	0	0.161548	0	0
pseudogen	olfactory_r	0	0	0	0	3	2	0	0	0	0	0.133056	0.07847
protein_co	EF-hand_ca	57	46	63	302	201	239	0.48932	0.465354	0.712678	2.242787	1.938489	2.03904
protein_co	COX20_Co	38	25	36	21	40	52	0.764636	0.592814	0.954572	0.365556	0.904233	1.039882
protein_co	choroidere	355	308	400	871	770	674	2.655277	2.714809	3.942542	5.635892	6.470254	5.010154
protein_co	chromoson	0	0	3	0	2	7	0	0	0.35234	0	0.200256	0.620031
protein_co	chromoson	26	22	20	0	2	0	0.178646	0.178135	0.181086	0	0.015438	0
lincRNA	-	0	0	0	0	0	5	0	0	0	0	0	0.102882
protein_co	-	9	3	9	9	17	8	0.291062	0.114333	0.383549	0.251796	0.617648	0.257124
protein_co	calpain_8	0	0	1	9	8	4	0	0	0.026873	0.158779	0.183285	0.081069
protein_co	TatD_DNas	196	125	93	209	127	114	4.343422	3.264322	2.715774	4.006685	3.161759	2.510675
antisense	SERTAD4_a	33	19	19	79	84	88	2.406409	1.632737	1.825761	4.983627	6.881511	6.377461
protein_co	chromoson	0	0	1	0	1	0	0	0	0.021821	0	0.018604	0

protein_co	complemer	1	0	0	0	0	0	0.007087	0	0	0	0	0
protein_co	chromoson	2	5	0	12	8	14	0.10401	0.306423	0	0.539869	0.467394	0.723572
protein_co	long_interg	1	5	10	2	0	8	0.037361	0.22014	0.492331	0.064642	0	0.297045
protein_co	retinoic_ac	3	6	8	0	0	4	0.143472	0.338145	0.504161	0	0	0.190114
protein_co	chromoson	105	95	84	36	23	28	9.453749	10.07965	9.966183	2.804015	2.326439	2.505431
protein_co	sterile_alpl	672	549	561	1581	1355	1215	5.842724	5.625039	6.427525	11.89162	13.23532	10.49862
protein_co	transmemb	0	0	1	3	2	2	0	0	0.027905	0.054959	0.047581	0.042091
protein_co	epithelial_(	5	3	5	17	10	13	0.061288	0.043335	0.080763	0.180269	0.137708	0.158366
protein_co	G_protein-(	0	1	1	2	1	0	0	0.042383	0.047394	0.062227	0.040405	0
antisense	-	33	12	17	38	26	39	0.962564	0.412481	0.65343	0.958875	0.851997	1.13055
protein_co	methyltran	0	0	0	7	1	2	0	0	0	0.323178	0.059956	0.106077
protein_co	transmemb	0	1	0	0	0	0	0	0.109838	0	0	0	0
protein_co	centromere	120	81	70	780	608	684	8.470559	6.737875	6.51124	47.63086	48.21514	47.98401
pseudogen	misato_hor	14	43	24	29	31	26	0.362432	1.31182	0.818738	0.649471	0.901591	0.668932
protein_co	shadow_of_	94	72	67	157	108	113	1.568869	1.416115	1.473562	2.266844	2.025031	1.874334
protein_co	family_witl	184	193	118	66	26	56	3.830571	4.734893	3.237148	1.188646	0.60809	1.158626
protein_co	fibronectin	104	70	66	89	77	123	3.47812	2.758775	2.90864	2.574923	2.893017	4.088142
protein_co	loricrin	0	0	0	2	0	0	0	0	0	0.07447	0	0
protein_co	proline_ric	0	0	0	6	13	9	0	0	0	0.223591	0.629119	0.385294
protein_co	small_proli	0	0	0	15	3	21	0	0	0	0.992751	0.257844	1.596669
protein_co	methyltran	69	79	49	140	96	154	1.01838	1.374026	0.952997	1.787523	1.591773	2.258869
protein_co	family_witl	0	1	0	0	0	0	0	0.104677	0	0	0	0
protein_co	D-aspartate	1	2	0	0	0	0	0.024855	0.05858	0	0	0	0
pseudogen	coiled-coil_	4	19	3	4	6	2	0.071955	0.402775	0.071114	0.062248	0.121256	0.035755
lincRNA	long_interg	2	0	2	1	2	0	0.059318	0	0.078166	0.025658	0.06664	0
protein_co	chromoson	3	4	1	0	0	2	0.324129	0.509288	0.142374	0	0	0.214751
protein_co	phosphatid	500	452	402	590	381	372	17.40335	18.53994	18.43842	17.76552	14.89831	12.86813
antisense	BVES_antis	2	1	0	1	1	4	0.061703	0.036356	0	0.026689	0.03466	0.122643
lincRNA	long_interg	0	0	0	4	4	2	0	0	0	0.318601	0.413746	0.183005
protein_co	histone_clu	2	0	0	0	1	1	0.063938	0	0	0	0.035915	0.031772
protein_co	histone_clu	9	5	4	2	2	7	0.867885	0.568194	0.508293	0.166845	0.21667	0.670853
protein_co	histone_clu	88	61	53	53	46	54	9.849487	8.045775	7.817027	5.131801	5.784127	6.006678
protein_co	histone_clu	27	8	28	13	60	52	1.365241	0.476697	1.865685	0.568659	3.408362	2.613114
protein_co	Protein_LO	1	2	1	9	0	0	0.083767	0.19743	0.110385	0.6522	0	0
protein_co	family_witl	0	0	0	6	8	7	0	0	0	0.221073	0.382789	0.296298
pseudogen	histone_clu	9	4	12	4	5	12	0.821498	0.43026	1.443378	0.315855	0.512723	1.088567
protein_co	neuroblast	29	26	37	25	13	11	0.400859	0.42352	0.673953	0.298948	0.201876	0.151111
protein_co	neuroblast	184	165	168	132	75	88	0.62085	0.656085	0.746987	0.385306	0.284302	0.295095
protein_co	neuroblast	13	13	7	1	11	3	0.133586	0.157422	0.094787	0.00889	0.126987	0.030637
pseudogen	profilin_1_	5	3	2	0	0	0	0.633265	0.447759	0.333796	0	0	0
processed_	-	13	7	6	7	3	0	0.118948	0.075478	0.072344	0.055408	0.030838	0
protein_co	histone_clu	1	2	0	1	1	0	0.031969	0.075347	0	0.027656	0.035915	0
pseudogen	hydroxy-de	0	0	0	3	0	0	0	0	0	0.122676	0	0
protein_co	hydroxy-de	0	0	0	5	0	1	0	0	0	0.136306	0	0.031318

pseudogen	hydroxy-de	0	0	0	1	0	0	0	0	0	0.040965	0	0
protein_co	Uncharacte	0	3	0	8	8	2	0	0.076706	0	0.15016	0.195003	0.043126
processed_	ATP1A1_op	10	13	6	9	27	10	0.52365	0.802216	0.414025	0.407705	1.588378	0.520416
protein_co	RNA_bindi	22	14	11	49	72	44	0.161026	0.120756	0.106097	0.310265	0.592046	0.320063
protein_co	small_integ	0	0	0	0	5	0	0	0	0	0	0.32896	0
protein_co	chromoson	15	7	8	7	7	7	0.509048	0.279945	0.35776	0.205508	0.266879	0.236089
protein_co	chromoson	10	2	9	21	20	8	0.408495	0.096277	0.484467	0.742112	0.917838	0.324778
processed_	small_nucl	7189	6284	4557	4962	3721	5815	369.8667	380.9956	308.9517	220.8495	215.0728	297.3282
protein_co	Uncharacte	12	14	6	0	2	7	0.597641	0.821663	0.393772	0	0.111902	0.346471
protein_co	ripply2_ho	1	1	1	0	0	0	0.07973	0.093957	0.105065	0	0	0
pseudogen	chitinase_a	0	0	0	0	0	1	0	0	0	0	0	0.018598
protein_co	GDP_disso	3312	2636	2177	3149	2345	2963	43.09181	40.41633	37.32481	35.44378	34.27649	38.31296
protein_co	protein-L-is	488	427	416	389	279	388	6.722666	6.93197	7.551789	4.635903	4.317924	5.312061
protein_co	SRY_(sex_d	39	8	20	4	9	2	1.198316	0.28967	0.809789	0.106324	0.310669	0.061073
protein_co	chromoson	0	0	1	1	2	2	0	0	0.080096	0.052582	0.136569	0.120813
protein_co	Uncharacte	19	6	7	1	3	2	0.72837	0.271055	0.353615	0.033164	0.129202	0.076197
protein_co	sterile_alph	4	3	5	9	6	7	0.135312	0.119593	0.222886	0.26338	0.228023	0.235334
protein_co	family_with	1377	991	820	2035	1109	1286	58.60108	49.69955	45.98544	74.92024	53.02154	54.39041
protein_co	coiled-coil_	10	5	7	75	50	29	0.29576	0.174267	0.272817	1.918949	1.661338	0.852406
protein_co	EF-hand_ca	116	103	109	102	79	80	1.618223	1.693264	2.003741	1.230959	1.238102	1.109124
antisense	-	0	5	0	0	0	0	0	0.096815	0	0	0	0
protein_co	Rhox_hom	0	0	0	0	1	0	0	0	0	0	0.035193	0
protein_co	chromoson	203	187	135	303	277	355	7.547066	8.192771	6.613794	9.745132	11.5694	13.11656
protein_co	zyg-11_fam	7	4	2	175	134	155	0.082924	0.05584	0.031221	1.793423	1.783346	1.824833
processed_	-	2	0	2	0	0	0	0.046419	0	0.061169	0	0	0
antisense	COL5A1_an	14	21	11	15	9	11	2.205875	3.899233	2.283917	2.044594	1.593105	1.722484
protein_co	TraB_doma	26	22	11	48	31	30	0.714676	0.712632	0.39844	1.141406	0.957297	0.819533
protein_co	lipase_fami	0	0	1	0	0	0	0	0	0.056718	0	0	0
protein_co	lipase_fami	2	0	0	2	1	0	0.029617	0	0	0.025622	0.016637	0
protein_co	leucine-rich	0	0	0	0	0	1	0	0	0	0	0	0.017077
protein_co	Uncharacte	1	0	0	17	2	4	0.013471	0	0	0.198112	0.030268	0.053551
antisense	-	0	0	0	0	2	0	0	0	0	0	0.060845	0
protein_co	Uncharacte	4	2	5	6	6	5	0.110179	0.06492	0.181486	0.142973	0.185669	0.136873
protein_co	leucine_ric	37	37	17	5	5	13	0.923535	1.088329	0.559159	0.107965	0.140207	0.322481
lincRNA	-	175	126	74	82	84	124	4.625399	3.92454	2.577375	1.874943	2.494247	3.257185
antisense	-	5	7	6	9	16	15	0.129314	0.213343	0.204484	0.201363	0.464883	0.385545
protein_co	forkhead_b	0	6	0	36	22	21	0	0.156099	0	0.687557	0.545651	0.460757
protein_co	transcriptic	0	4	0	1	2	8	0	0.213657	0	0.039211	0.101842	0.36037
protein_co	SYS1_Golgi	472	382	356	812	485	502	8.572264	8.175682	8.519975	12.75771	9.89565	9.060807
protein_co	transcriptic	1	0	1	0	0	0	0.047867	0	0.063077	0	0	0
pseudogen	-	0	0	0	4	5	6	0	0	0	0.279688	0.454015	0.481961
protein_co	inositol_pc	359	347	281	646	493	639	4.04896	4.61196	4.176285	6.30296	6.246618	7.162415
protein_co	replication	1	1	0	3	6	11	0.034377	0.040512	0	0.089219	0.231724	0.375815
antisense	testis_deve	2	1	4	0	0	0	0.090886	0.053552	0.239531	0	0	0

lincRNA	-	3	1	0	0	0	0	0.286684	0.112613	0	0	0	0
protein_co	sialidase_4	1	1	0	0	0	3	0.016849	0.019856	0	0	0	0.050236
protein_co	v-maf_musc	10129	8077	7945	1283	1365	1267	158.0428	148.5133	163.3567	17.31801	23.92709	19.64692
protein_co	TNF_recept	346	261	237	369	344	384	4.28081	3.805374	3.863963	3.949473	4.781425	4.721616
pseudogen	BMP2_indu	0	0	0	0	2	0	0	0	0	0	0.097104	0
protein_co	cysteine-ric	155	166	163	115	92	106	1.207276	1.523667	1.673005	0.774882	0.805029	0.820522
protein_co	nucleosom	0	0	0	22	9	13	0	0	0	0.492943	0.26188	0.334629
protein_co	GRB10_int	959	742	905	976	1102	971	6.444582	5.876072	8.014188	5.673995	8.319683	6.484925
pseudogen	-	1	0	1	1	4	4	0.030391	0	0.040048	0.026291	0.136569	0.120813
protein_co	chromoson	18	13	9	209	273	301	0.260579	0.221778	0.17169	2.617438	4.439958	4.330552
protein_co	RUN_and_F	370	319	318	361	292	266	4.341349	4.410835	4.916827	3.664318	3.849062	3.101803
protein_co	NHS-like_2	97	86	132	33	61	38	1.290919	1.348754	2.31492	0.379931	0.912024	0.502598
pseudogen	glycoprotei	5	4	1	16	6	5	0.076108	0.071751	0.020058	0.210691	0.102604	0.075638
protein_co	phosphatas	791	784	685	1747	1467	1447	6.765158	7.901774	7.720169	12.9258	14.0955	12.29928
protein_co	N-acylsphir	30	35	22	83	62	80	0.427518	0.587771	0.413134	1.023233	0.992599	1.133008
protein_co	ArfGAP_wit	199	181	136	512	301	371	3.897617	4.177647	3.510102	8.67519	6.623104	7.221536
pseudogen	centaurin_	0	0	0	5	0	4	0	0	0	0.094665	0	0.087001
protein_co	translocase	6	9	11	12	14	16	0.405161	0.716186	0.978822	0.701004	1.06207	1.073756
protein_co	zinc_finger_	641	524	430	1699	1259	1510	10.82462	10.42781	9.568807	24.82052	23.88522	25.34201
pseudogen	BMS1_pseu	48	86	19	70	67	107	0.623753	1.316972	0.325356	0.786923	0.978126	1.381861
protein_co	chromoson	0	0	0	17	3	3	0	0	0	1.016425	0.232934	0.20606
protein_co	ArfGAP_wit	47	55	22	92	54	101	1.028193	1.417903	0.634212	1.741115	1.327149	2.195876
protein_co	ArfGAP_wit	4	6	6	12	7	2	0.04231	0.07479	0.083632	0.109808	0.083183	0.021025
pseudogen	leucine_ric	22	22	15	9	3	6	1.05594	1.244361	0.94873	0.373699	0.161766	0.286205
protein_co	neuropepti	2	2	0	0	0	1	0.054132	0.063791	0	0	0	0.026899
protein_co	G_protein_	0	1	0	8	10	18	0	0.008083	0	0.047472	0.077061	0.122707
protein_co	synaptotag	36	25	21	75	53	108	0.53884	0.440965	0.414201	0.971139	0.891214	1.606536
pseudogen	BMS1_pseu	9	12	7	3	1	4	0.116982	0.183809	0.119898	0.033734	0.014602	0.051671
protein_co	transmemb	818	741	627	706	563	584	11.05584	11.80222	11.16711	8.254794	8.548619	7.844423
protein_co	growth_dif	1	1	5	0	0	0	0.030531	0.035979	0.201163	0	0	0
protein_co	zinc_finger_	192	177	198	150	136	97	0.988589	1.073977	1.343428	0.668142	0.786688	0.496359
protein_co	thioredoxir	0	2	0	0	2	0	0	0.069824	0	0	0.066565	0
pseudogen	ribosomal_	1	1	0	2	0	1	0.106307	0.125277	0	0.183931	0	0.105651
protein_co	acyl-CoA_w	0	0	1	0	0	1	0	0	0.051109	0	0	0.038545
protein_co	death-dom	955	802	681	2196	1508	1709	19.34889	19.14847	18.1817	38.49001	34.32441	34.41156
protein_co	bone_morp	949	895	1116	788	787	638	4.383649	4.871915	6.793109	3.1489	4.084072	2.928869
protein_co	transcriptic	94	120	74	15	36	25	3.19208	4.802134	3.311407	0.440657	1.373402	0.843715
protein_co	prefoldin_s	693	616	449	556	821	1628	19.15828	20.06832	16.35703	13.29723	25.49855	44.72881
protein_co	ring_finger_	654	602	512	643	534	792	19.76222	21.43688	20.38744	16.80862	18.12793	23.78443
protein_co	hydroxyste	29	16	19	101	58	68	1.550797	1.008287	1.338891	4.672414	3.484448	3.613894
protein_co	retinoid_X_	1135	862	808	396	362	490	20.66301	18.4932	19.38402	6.236715	7.403811	8.865504
protein_co	oxidoreduc	185	156	132	280	209	240	6.121302	6.082804	5.755471	8.014808	7.769042	7.892108
processed_	-	0	2	0	3	0	6	0	0.056562	0	0.062283	0	0.143103
protein_co	collagen_ty	92	66	56	19	20	26	0.758066	0.64087	0.608054	0.135436	0.185139	0.212913

protein_co	major_hist	1	0	0	3	2	0	0.015174	0	0	0.03938	0.034093	0
pseudogen	-	55	41	38	69	88	80	3.305056	2.903402	3.009086	3.586974	5.940841	4.777666
protein_co	bromodom	3951	3228	2785	4221	3592	4029	42.70516	41.11629	39.66736	39.4686	43.61729	43.2793
protein_co	major_hist	30	42	19	35	31	14	0.915406	1.510251	0.763978	0.923897	1.062682	0.424551
processed_	-	5	1	0	0	0	0	0.208923	0.049241	0	0	0	0
protein_co	collagen_ty	30744	26958	26684	8678	9429	8378	234.2233	242.0274	267.8894	57.19426	80.70203	63.43366
protein_co	proteasom	121	92	87	33	16	29	4.741569	4.248461	4.492528	1.1187	0.704378	1.129391
protein_co	transporter	68	84	82	76	60	65	0.633355	0.921986	1.006437	0.612371	0.627825	0.601674
protein_co	spindlin_fa	92	77	81	68	78	60	2.91651	2.87656	3.383728	1.864866	2.777917	1.890325
processed_	-	739	672	472	687	461	555	25.58757	27.41959	21.53582	20.57806	17.93224	19.09797
lincRNA	-	6	11	6	1	0	0	0.108264	0.233901	0.142665	0.01561	0	0
processed_	-	0	1	1	123	97	111	0	0.019545	0.021856	1.764807	1.807382	1.829624
protein_co	collagen_ty	267	205	180	34	35	31	2.574257	2.329172	2.286904	0.283585	0.379103	0.297038
protein_co	chromoson	0	0	0	0	2	0	0	0	0	0	0.054741	0
protein_co	notch_4	7	6	4	9	19	26	0.054942	0.055497	0.041372	0.06111	0.167538	0.202812
protein_co	pre-B-cell_l	1502	1447	1063	1865	2259	3276	21.16512	24.02849	19.73872	22.73488	35.76154	45.878
protein_co	advanced_g	42	28	17	72	58	75	1.392312	1.093836	0.742627	2.064822	2.160052	2.470917
protein_co	ring_finger_	701	637	479	1165	877	1176	28.00878	29.9932	25.22008	40.26847	39.36632	46.69745
protein_co	1-acylglyce	912	689	552	1517	1147	1162	19.34382	17.22161	15.42842	27.83531	27.33128	24.4942
protein_co	deafness_au	21	18	16	26	30	26	0.572482	0.578259	0.574775	0.613168	0.918783	0.704411
protein_co	proline-rich	32	30	16	26	13	17	0.608955	0.672765	0.401227	0.428027	0.277925	0.321509
protein_co	FK506_bin	121	92	49	246	209	256	4.762721	4.267413	2.541562	8.376603	9.241983	10.01427
protein_co	mitochond	12	19	18	29	21	32	0.336489	0.627843	0.665116	0.703479	0.661544	0.891764
protein_co	small_integ	57	40	45	5	11	21	0.694668	0.574473	0.722686	0.052715	0.150607	0.25435
protein_co	glutamate-r	3	0	4	13	8	2	0.264265	0	0.464315	0.990659	0.791693	0.175088
protein_co	Sp5_transc	6	2	0	12	9	3	0.156245	0.061375	0	0.270333	0.263297	0.07764
pseudogen	cytochrom	1	1	1	0	1	1	0.02686	0.031653	0.035395	0	0.030176	0.026694
protein_co	serine/thre	328	266	222	237	246	286	9.16824	8.761951	8.177111	5.730908	7.724961	7.944888
protein_co	dom-3_hor	160	162	155	326	194	288	4.04709	4.828864	5.166416	7.133513	5.512818	7.239774
protein_co	superkiller_	1062	989	795	1304	1165	1493	12.47467	13.69014	12.3057	13.25089	15.37374	17.42906
protein_co	chromoson	1	0	0	0	0	0	0.045876	0	0	0	0	0
protein_co	negative_el	1228	972	778	1760	1273	1577	35.04665	32.6905	29.25921	43.45341	40.81555	44.72903
protein_co	neurexophi	3	4	1	0	3	0	0.069874	0.109789	0.030692	0	0.078499	0
lincRNA	-	0	0	0	1	0	2	0	0	0	0.009794	0	0.022504
protein_co	chromoson	0	0	0	3	3	3	0	0	0	0.063935	0.083028	0.073449
protein_co	zinc_finger_	152	119	127	131	155	223	4.29175	3.959541	4.7253	3.199817	4.916676	6.257564
protein_co	succinate_d	286	265	255	615	432	535	10.52198	11.48905	12.3625	19.57354	17.85517	19.56117
protein_co	euchromat	1480	1242	984	2143	1694	2291	18.97619	18.76618	16.62559	23.77018	24.40111	29.19322
protein_co	chromoson	28	27	11	14	14	29	5.882333	6.6844	3.045223	2.544384	3.304218	6.054791
antisense	-	5	0	4	10	15	5	0.065086	0	0.068614	0.112611	0.21936	0.064684
protein_co	layilin	1016	891	818	1250	720	805	24.7643	25.59276	26.27365	26.35757	19.71577	19.50014
protein_co	solute_carr	6	3	3	1	0	3	0.120595	0.071057	0.079457	0.017388	0	0.059925
protein_co	sialidase_1_	1210	1007	916	1858	1126	1298	13.87751	13.61015	13.84384	18.43465	14.50821	14.79485
protein_co	chromoson	3641	3153	2598	2123	1632	2766	183.0562	186.8077	172.1225	92.3372	92.1792	138.2056

protein_co	heat_shock	625	454	438	997	1118	1139	13.13021	11.23969	12.12552	18.11965	26.38654	23.78072
protein_co	heat_shock	303	256	247	334	338	390	6.609444	6.580659	7.09993	6.302775	8.283008	8.454668
protein_co	heat_shock	26	36	24	32	39	16	0.541064	0.882845	0.658144	0.576087	0.911777	0.330906
protein_co	LSM2_hom	607	511	406	1944	1126	1559	36.684	36.39284	32.33321	101.6359	76.44964	93.63619
protein_co	valyl-tRNA_	2860	2237	2167	5922	4132	4617	35.11392	32.3658	35.05961	62.89915	56.99316	56.33559
protein_co	von_Willeb	6	6	9	17	10	22	0.107969	0.127235	0.213416	0.264644	0.202162	0.393443
protein_co	methyl-CpG	378	299	335	163	186	134	2.357368	2.197424	2.753057	0.879399	1.303159	0.83052
protein_co	mutS_hom	61	66	42	95	89	91	0.810186	1.033013	0.735087	1.091544	1.327987	1.201174
protein_co	chromoson	6	2	7	15	5	15	0.132573	0.052077	0.203816	0.286721	0.124115	0.329387
protein_co	lymphocyt	1	0	0	3	3	12	0.053368	0	0	0.138505	0.179867	0.63646
protein_co	abhydrolas	5	12	5	2	4	14	0.117126	0.331262	0.154344	0.04053	0.105267	0.325928
protein_co	lymphocyt	12	7	9	53	21	59	0.444882	0.305822	0.439685	1.699819	0.874646	2.17383
protein_co	casein_kina	33	38	30	55	35	64	0.974918	1.322954	1.167912	1.405658	1.161639	1.879073
protein_co	G_patch_d	274	229	210	397	371	439	5.193639	5.115213	5.24536	6.509905	7.90031	8.269806
protein_co	chromoson	307	281	189	346	347	399	6.566822	7.083213	5.327378	6.402594	8.338644	8.482023
protein_co	family_with	93	75	86	45	44	45	2.409942	2.290298	2.936682	1.008786	1.28093	1.1589
protein_co	apolipopro	33	48	20	41	23	37	1.475551	2.529232	1.178434	1.585942	1.15536	1.644189
protein_co	chromoson	4	8	6	7	0	4	0.065379	0.154091	0.129231	0.098979	0	0.064976
protein_co	tripartite_r	0	0	0	2	3	0	0	0	0	0.042348	0.082491	0
protein_co	BCL2-assoc	4808	4007	3484	6608	5258	6424	65.58627	64.4132	62.62697	77.97969	80.5783	87.08906
protein_co	chromoson	1	0	0	0	0	3	0.120048	0	0	0	0	0.357919
processed_	diacylglyce	0	0	0	6	6	3	0	0	0	0.037104	0.048185	0.021313
protein_co	proline-rich	10237	8661	7601	9173	12235	13306	78.62425	78.38969	76.92887	60.94783	105.5691	101.5643
protein_co	allograft_in	0	0	0	0	0	2	0	0	0	0	0	0.089176
protein_co	natural_cyt	0	0	0	0	0	1	0	0	0	0	0	0.047962
protein_co	PRAME_fam	0	0	0	0	0	1	0	0	0	0	0	0.025054
protein_co	leukocyte_	0	9	0	1	0	0	0	0.30649	0	0.024999	0	0
protein_co	nuclear_fac	478	340	245	289	211	353	17.12165	14.35171	11.56428	8.955266	8.490811	12.56614
protein_co	mitochond	3	3	3	2	2	1	0.166307	0.195982	0.219152	0.095914	0.124557	0.055093
protein_co	zinc_finger_	383	409	272	488	338	479	6.445137	8.110801	6.031663	7.104217	6.389975	8.010849
protein_co	MHC_class_	177	154	197	377	246	278	3.830971	3.927927	5.618711	7.058948	5.981634	5.979847
protein_co	arylacetam	0	0	2	0	0	0	0	0	0.088588	0	0	0
protein_co	zinc_finger_	157	141	109	307	243	251	1.821152	1.927404	1.666126	3.080689	3.166663	2.893542
protein_co	MHC_class_	515	420	301	445	356	369	19.67144	18.90537	15.15061	14.70455	15.27664	14.00764
protein_co	zinc_finger_	38	12	32	26	24	30	0.833716	0.310258	0.925166	0.493482	0.591555	0.654132
protein_co	major_hist	310	256	207	359	284	385	8.729632	8.49535	7.681383	8.745642	8.98466	10.77469
sense_intro	psoriasis_su	4	0	0	0	1	0	0.357106	0	0	0	0.100297	0
protein_co	POU_class_	0	0	2	0	4	9	0	0	0.042773	0	0.072932	0.145164
protein_co	zinc_finger_	0	0	0	4	1	0	0	0	0	0.096826	0.031435	0
protein_co	Uncharacte	24	10	20	5	22	23	1.772083	0.870122	1.945977	0.319379	1.824924	1.687759
protein_co	coiled-coil_	303	257	184	465	418	537	5.422962	5.420435	4.339569	7.199625	8.404643	9.551638
protein_co	psoriasis_su	5	1	3	5	2	2	0.230178	0.05425	0.181991	0.199126	0.103436	0.091503
protein_co	corneodesr	5	2	1	0	0	0	0.103725	0.048893	0.027337	0	0	0
protein_co	psoriasis_su	52	60	34	7	5	8	0.719345	0.97812	0.619794	0.083771	0.077706	0.109985

protein_co	chromoson	0	0	0	0	0	1	0	0	0	0	0	0.046153
pseudogen	-	6	1	5	11	7	6	0.899847	0.176736	0.988148	1.427161	1.179409	0.89429
protein_co	DEAH_(Asp	678	509	467	1349	1025	1197	10.41916	9.21781	9.457025	17.93403	17.69603	18.28128
protein_co	chromoson	89	67	66	280	155	236	2.382077	2.113235	2.327794	6.483162	4.660651	6.277511
protein_co	mitochond	1041	962	702	1776	1292	1524	34.23079	37.27764	30.41852	50.52103	47.7285	49.80361
protein_co	protein_ph	1385	1056	1140	1646	1426	1457	16.20404	14.55943	17.57572	16.65967	18.74313	16.94114
protein_co	ATP-bindin	1723	1438	1265	3804	2687	3003	26.20435	25.77235	25.35207	50.04856	45.90974	45.38925
protein_co	proline_ric	419	407	375	546	365	417	6.469022	7.405018	7.629405	7.292564	6.330916	6.398384
protein_co	leukocyte_i	11	11	6	16	16	19	0.204477	0.240964	0.146973	0.257297	0.334134	0.351007
protein_co	discoidin_c	930	688	592	3251	3073	3973	11.86961	10.34782	9.956573	35.89495	44.06208	50.39432
antisense	-	5	4	2	25	13	16	0.12605	0.118834	0.066441	0.545225	0.368184	0.400869
processed_	-	3	7	6	2	1	10	0.065198	0.179275	0.171831	0.037602	0.024415	0.215985
protein_co	guanine_nu	2009	1849	1473	1734	1556	1781	14.20006	15.40119	13.7198	10.60284	12.35574	12.51076
protein_co	major_hist	4669	3993	3238	1207	977	1220	95.03326	95.77632	86.84871	21.25309	22.34063	24.67864
protein_co	tripartite_r	164	122	99	193	183	241	2.456103	2.153127	1.953767	2.500478	3.078951	3.586983
protein_co	zinc_finger_	153	144	112	460	365	360	1.837979	2.038537	1.772972	4.780462	4.925961	4.297948
protein_co	zinc_finger_	214	180	200	245	212	240	2.613465	2.590494	3.218606	2.588404	2.908626	2.912889
protein_co	tripartite_r	0	0	3	0	0	0	0	0	0.102442	0	0	0
protein_co	ring_finger_	52	53	45	12	14	6	1.247929	1.498889	1.423095	0.249133	0.377454	0.143103
protein_co	protein_ph	863	783	647	1074	712	866	26.39404	28.22045	26.07559	28.41596	24.46381	26.32222
protein_co	Uncharacte	5	7	4	0	8	8	0.14755	0.24343	0.155548	0	0.265221	0.234622
pseudogen	major_hist	2	0	1	0	0	5	0.081073	0	0.053418	0	0	0.201432
antisense	ZNRD1_ant	144	119	102	123	76	101	0.780217	0.759814	0.728263	0.576529	0.462611	0.543856
protein_co	patched_d	19	13	5	5	7	8	0.192882	0.155521	0.066887	0.043911	0.079833	0.080712
lincRNA	HLA_compl	2	3	0	0	0	1	0.160671	0.284011	0	0	0	0.079839
protein_co	guanine_nu	41419	35791	25885	37338	22983	27173	1328.142	1352.465	1093.775	1035.76	827.9437	865.9489
protein_co	major_hist	0	0	0	0	1	2	0	0	0	0	0.037691	0.066684
protein_co	TBC1_dom	197	169	168	397	382	415	2.742408	2.772423	3.081838	4.781006	5.974178	5.741475
protein_co	major_hist	2	0	2	0	0	1	0.065279	0	0.086021	0	0	0.032438
protein_co	ZFP57_zinc	0	0	0	8	1	6	0	0	0	0.185046	0.030038	0.159437
pseudogen	CRHR1_int	53	76	42	383	273	378	1.075459	1.81735	1.123058	6.723258	6.223429	7.622887
pseudogen	ribosomal_	1	0	0	3	1	2	0.120048	0	0	0.311557	0.134866	0.238612
protein_co	aspartate_c	12	10	2	0	4	9	0.610858	0.599882	0.13416	0	0.228754	0.455314
protein_co	myelin_olig	0	0	0	1	0	0	0	0	0	0.018327	0	0
protein_co	olfactory_r	2	4	1	0	0	1	0.099607	0.234761	0.065629	0	0	0.049496
protein_co	chibby_hor	2	5	0	0	0	1	0.134882	0.397374	0	0	0	0.067024
protein_co	chromoson	3	0	0	2	0	5	0.048944	0	0	0.028227	0	0.081069
sense_over	-	0	6	0	0	1	0	0	0.24546	0	0	0.039001	0
protein_co	chromoson	1	0	0	0	0	0	0.035247	0	0	0	0	0
protein_co	AKT1_subst	3285	2616	2036	3005	2285	2736	47.77779	44.8369	39.02144	37.80926	37.33584	39.54726
protein_co	family_with	0	0	0	0	1	0	0	0	0	0	0.039388	0
protein_co	gamma-am	973	873	809	741	569	787	11.37875	12.03103	12.46709	7.496574	7.475546	9.146732
protein_co	chromoson	530	385	334	1142	828	974	7.381933	6.319199	6.130212	13.76016	12.95608	13.48226
protein_co	chromoson	1	4	0	3	1	0	0.086223	0.406435	0	0.223773	0.096866	0

processed_	-	85	50	54	90	68	83	2.61475	1.812543	2.18897	2.395062	2.350007	2.537459
antisense	-	39	30	37	19	21	22	0.984596	0.892528	1.230921	0.414964	0.59561	0.551983
protein_co	chromoson	0	0	0	0	0	1	0	0	0	0	0	0.112906
protein_co	speedy_hor	2	3	1	0	0	0	0.106844	0.188863	0.070397	0	0	0
protein_co	chromoson	5	0	1	5	5	14	0.303213	0	0.079912	0.262308	0.340641	0.843753
protein_co	tripartite_r	1043	924	860	2477	1832	1968	7.881453	8.228128	8.563577	16.19239	15.55237	14.7794
pseudogen	-	0	0	0	4	0	0	0	0	0	0.343063	0	0
protein_co	chromoson	0	0	0	2	0	3	0	0	0	0.019652	0	0.033864
pseudogen	-	51	21	25	123	72	63	0.706989	0.343059	0.456686	1.475063	1.121306	0.867946
processed_	-	4	7	9	9	16	15	0.10245	0.211279	0.303759	0.199415	0.460384	0.381815
protein_co	RAN_bindir	58	48	48	287	314	299	0.647938	0.631908	0.706613	2.773641	3.940797	3.319604
protein_co	family_witl	57	18	74	5	1	3	1.006214	0.374451	1.721401	0.076357	0.019832	0.052632
pseudogen	-	0	0	0	4	1	3	0	0	0	0.04849	0.015743	0.041779
protein_co	KM-PA-2_p	1	1	0	0	8	3	0.026887	0.031685	0	0	0.241649	0.080164
pseudogen	-	7	5	4	15	2	15	0.565782	0.476242	0.426035	1.04883	0.181606	1.204902
protein_co	forkhead_b	0	0	0	0	0	1	0	0	0	0	0	0.016923
pseudogen	zinc_finger_	2	2	0	41	28	24	0.026431	0.031147	0	0.468736	0.415708	0.315211
protein_co	COBW_dor	68	72	43	227	138	171	1.07978	1.347305	0.899766	3.118282	2.461811	2.698561
antisense	-	2	4	0	0	5	7	0.076174	0.179533	0	0	0.213942	0.264963
lincRNA	-	0	0	1	8	5	6	0	0	0.019051	0.100052	0.081207	0.086205
protein_co	forkhead_b	0	1	0	0	1	0	0	0.022895	0	0	0.021826	0
pseudogen	phosphogl	1	3	5	0	3	6	0.023436	0.082852	0.154412	0	0.078985	0.139745
processed_	-	1	10	5	3	0	1	0.020835	0.245524	0.137275	0.054072	0	0.020706
protein_co	Uncharacte	1	0	0	0	0	0	0.138953	0	0	0	0	0
pseudogen	family_witl	8	5	7	10	11	8	0.302304	0.222654	0.348567	0.326902	0.466977	0.300437
protein_co	family_witl	0	0	0	3	0	2	0	0	0	0.102688	0	0.078646
processed_	tetratricop	18	20	15	15	14	11	0.543914	0.712189	0.597288	0.392114	0.475264	0.330339
protein_co	mitochond	38	29	33	53	51	51	1.731289	1.557009	1.981229	2.088935	2.610389	2.309223
antisense	ST8SIA6_an	0	0	1	0	0	0	0	0	0.038522	0	0	0
lincRNA	-	17	7	25	76	48	36	0.476189	0.231066	0.922795	1.841649	1.510499	1.002172
protein_co	maestro_he	63	72	28	132	78	132	0.961454	1.294874	0.563094	1.742708	1.337308	2.002034
protein_co	ataxin_2	681	572	553	1326	1025	1055	7.667549	7.58949	8.204827	12.91564	12.96529	11.80515
protein_co	dynactin_1	3911	3195	3308	2790	2826	3067	38.24385	36.81729	42.62596	23.60158	31.04524	29.80556
protein_co	paraneopla	16	33	17	5	18	9	0.159581	0.387866	0.223432	0.043141	0.201689	0.08921
protein_co	tectonic_fa	638	554	415	358	270	364	8.024793	8.211642	6.878537	3.895464	3.815276	4.550134
protein_co	family_witl	211	189	158	247	143	188	6.653097	7.0228	6.564978	6.73754	5.065549	5.891269
protein_co	zinc_finger_	401	308	222	415	361	481	8.546433	7.735677	6.234883	7.651588	8.643642	10.18815
antisense	family_witl	0	0	0	24	26	11	0	0	0	0.319806	0.44992	0.168389
protein_co	IGF-like_far	6	8	1	25	11	13	0.165441	0.259949	0.036335	0.59634	0.340747	0.356241
protein_co	IGF-like_far	10	11	1	18	18	36	0.194708	0.252396	0.025658	0.303192	0.393735	0.696619
protein_co	G_protein-r	5	2	5	0	0	0	0.174723	0.08236	0.230242	0	0	0
protein_co	keratin_40	0	2	0	0	3	2	0	0.05936	0	0	0.084885	0.050061
protein_co	mitotic_spi	324	295	260	1183	983	1057	7.461019	8.005385	7.889714	23.56681	25.43055	24.1901
protein_co	chromoson	1	0	0	14	12	10	0.101614	0	0	1.230681	1.369887	1.009867

protein_co	serine_pept	5	0	2	8	1	2	0.438253	0	0.231004	0.606608	0.09847	0.174219
protein_co	zinc_finger_	72	71	49	38	21	20	1.468317	1.70629	1.316795	0.6704	0.481123	0.405347
protein_co	chromoson	50	39	24	76	48	40	1.156927	1.063427	0.731783	1.521292	1.247747	0.919826
protein_co	F-box_prot	13	23	10	24	28	22	0.252008	0.525418	0.25545	0.40248	0.609786	0.423841
processed_	-	6	4	2	0	0	0	0.250905	0.197118	0.110211	0	0	0
protein_co	family_with	0	0	0	2	2	1	0	0	0	0.024342	0.031611	0.013982
processed_	ATP6V0E2_	8	2	8	51	32	42	0.14241	0.041955	0.187662	0.785388	0.639956	0.743036
protein_co	CD177_mo	0	0	0	38	43	25	0	0	0	0.70091	1.02999	0.529743
protein_co	pregnancy_	5	0	0	46	42	55	0.123406	0	0	0.982168	1.164563	1.349078
protein_co	zinc_finger_	330	310	259	292	217	296	3.924198	4.344159	4.058556	3.003881	2.898983	3.498149
protein_co	zinc_finger_	128	104	101	95	89	125	2.104487	2.015007	2.188227	1.35121	1.6439	2.042471
protein_co	leucine_ric	2	3	0	38	41	34	0.047889	0.084651	0	0.787136	1.1029	0.809081
protein_co	F-box_prot	0	0	0	0	1	0	0	0	0	0	0.025837	0
protein_co	chromoson	104	119	106	192	123	195	3.167931	4.271657	4.254838	5.059488	4.20917	5.903187
protein_co	protocadhe	11	8	1	12	1	1	0.126543	0.108453	0.015159	0.119423	0.012924	0.011433
protein_co	-	13	3	8	36	24	25	0.312975	0.085113	0.2538	0.749777	0.649123	0.598159
pseudogen	-	28	29	17	45	105	136	0.293825	0.358621	0.235079	0.408514	1.237854	1.418337
protein_co	protocadhe	18	31	8	6	16	10	0.149176	0.302758	0.087368	0.043017	0.148969	0.082364
protein_co	protocadhe	9	15	13	36	11	9	0.090583	0.177912	0.172419	0.313453	0.124379	0.090024
protein_co	protocadhe	13	4	5	21	14	38	0.13182	0.047798	0.06681	0.184213	0.159483	0.382941
protein_co	protocadhe	8	3	8	6	8	13	0.081167	0.035869	0.106958	0.052663	0.091186	0.131081
protein_co	protocadhe	94	85	98	138	137	107	0.947715	1.009895	1.302	1.203628	1.551743	1.07212
protein_co	protocadhe	124	70	155	34	26	19	1.249464	0.831203	2.05811	0.296377	0.294323	0.190268
protein_co	protocadhe	5	7	3	5	10	4	0.050324	0.083025	0.039789	0.043535	0.113072	0.040011
protein_co	tripartite_r	398	364	266	693	394	482	2.906679	3.132726	2.559944	4.378348	3.232654	3.49841
protein_co	chromoson	1	0	0	0	0	1	0.055963	0	0	0	0	0.055617
pseudogen	protease_se	0	0	0	2	4	0	0	0	0	0.565419	1.468541	0
protein_co	spire_homo	129	91	81	258	266	332	2.111094	1.754956	1.746778	3.652587	4.890446	5.399649
pseudogen	-	0	1	2	1	3	3	0	0.033273	0.074414	0.024426	0.095161	0.084182
protein_co	alanine_an	32	29	12	46	54	40	0.736891	0.78697	0.364141	0.916377	1.396998	0.915425
protein_co	Uncharacte	0	0	0	0	2	0	0	0	0	0	0.065647	0
protein_co	poly(A)_bin	1	0	0	0	0	1	0.04162	0	0	0	0	0.041363
processed_	-	1	3	6	0	1	2	0.015266	0.053969	0.120698	0	0.01715	0.030343
protein_co	polycystic_	0	0	0	4	0	0	0	0	0	0.01401	0	0
sense_intrc	-	110	66	44	7	48	17	3.983249	2.816409	2.099579	0.219283	1.952698	0.611791
protein_co	schlafen_fa	0	0	0	0	0	2	0	0	0	0	0	0.033738
protein_co	HCG19806	41	42	44	42	88	83	0.312854	0.377671	0.442431	0.277249	0.754379	0.629427
processed_	-	18	16	10	0	0	0	0.428094	0.448429	0.313402	0	0	0
lincRNA	-	1	1	0	0	0	0	0.004982	0.005871	0	0	0	0
protein_co	solute_carr	458	440	509	794	652	620	3.567305	4.038635	5.224292	5.350056	5.705208	4.799281
protein_co	synaptoner	48	17	12	28	51	57	2.961734	1.236121	0.97571	1.494603	3.535282	3.495339
protein_co	chromoson	0	0	0	0	4	0	0	0	0	0	0.083183	0
protein_co	transmemb	203	177	145	190	115	146	3.59312	3.691952	3.382038	2.909325	2.28677	2.568255
protein_co	family_with	28	22	18	50	20	32	0.690427	0.639278	0.584881	1.066579	0.554037	0.784187

protein_co	chromoson	2	0	0	0	0	1	0.028455	0	0	0	0	0.01414
protein_co	cyclin_l_far	0	0	0	8	7	10	0	0	0	0.15558	0.176786	0.223414
protein_co	transmemb	122	89	75	49	30	52	8.995545	7.733298	7.287251	3.125552	2.485066	3.810488
protein_co	FSHD_regic	2	6	4	0	0	0	0.05042	0.178251	0.132882	0	0	0
pseudogen	cytochrom	1	0	0	0	0	0	0.132022	0	0	0	0	0
protein_co	Uncharacte	3	1	0	0	0	0	0.24472	0.096129	0	0	0	0
protein_co	family_witl	2	13	13	0	2	3	0.025061	0.191962	0.214656	0	0.028154	0.037359
protein_co	cyclin-depe	2	0	3	4	0	2	0.06757	0	0.133561	0.116909	0	0.067153
protein_co	transmemb	3	4	1	14	13	17	0.322811	0.507217	0.141795	1.303221	1.571518	1.817965
protein_co	chromoson	45	71	28	15	9	21	2.100833	3.90611	1.72255	0.605806	0.472031	0.974334
protein_co	triple_QxxI	183	163	173	206	174	119	2.638399	2.76939	3.286778	2.569329	2.818303	1.705085
protein_co	succinate_(	237	184	110	295	300	303	11.09374	10.14973	6.785111	11.94578	15.77611	14.09554
protein_co	AT_rich_int	3	4	1	0	1	0	0.112561	0.176861	0.049442	0	0.042152	0
protein_co	-	7	13	8	4	2	9	0.182735	0.399921	0.2752	0.090333	0.058655	0.233494
protein_co	-	2	0	3	0	0	0	0.277905	0	0.549317	0	0	0
protein_co	presenilin_	29	34	33	23	22	62	1.332716	1.841305	1.998427	0.914388	1.135825	2.831659
protein_co	chromoson	0	0	6	0	0	2	0	0	0.516128	0	0	0.129751
lincRNA	long_interg	3	0	0	0	0	1	0.025981	0	0	0	0	0.008607
protein_co	zinc_finger_	485	430	454	832	787	721	2.534187	2.647722	3.12599	3.760826	4.619774	3.744052
protein_co	chromoson	350	377	309	1021	647	719	5.262524	6.67997	6.122367	13.28051	10.92897	10.74397
protein_co	secretoglot	14	6	8	7	17	11	0.295878	0.149432	0.222797	0.127981	0.403629	0.23104
protein_co	coiled-coil_	0	0	0	7	10	12	0	0	0	0.114252	0.21196	0.225007
protein_co	leucine-rich	480	423	442	602	615	466	4.881229	5.069153	5.923045	5.295993	7.026064	4.709594
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.025482	0
pseudogen	family_witl	2	1	0	16	8	13	0.065238	0.03844	0	0.451499	0.293165	0.421431
protein_co	proteasom	50	51	37	37	33	34	2.173276	2.612294	2.119246	1.391264	1.611416	1.468701
protein_co	vitrin	7	0	0	72	68	73	0.131881	0	0	1.173495	1.439275	1.366842
protein_co	speedy_hor	121	99	88	89	91	139	3.677302	3.545571	3.524207	2.339898	3.106951	4.198251
pseudogen	olfactory_r	1	2	1	0	0	0	0.051801	0.122089	0.068262	0	0	0
protein_co	ribosomal_	268	294	188	533	310	479	10.15618	13.12956	9.38833	17.47374	13.19795	18.04018
protein_co	E2F_transcr	926	886	605	2397	1617	1951	18.74698	21.13787	16.14026	41.98087	36.77727	39.25431
processed_	-	0	0	0	0	0	4	0	0	0	0	0	0.082467
pseudogen	diacylglyce	0	0	0	0	1	0	0	0	0	0	0.079941	0
protein_co	phosphodi	257	281	263	1017	858	787	3.704284	4.772925	4.995302	12.68105	13.89337	11.27342
protein_co	transmemb	14	16	31	90	93	78	0.088636	0.119374	0.25863	0.492932	0.661476	0.490779
pseudogen	-	0	2	4	0	5	5	0	0.025501	0.057031	0	0.060777	0.053765
TR_V_gene	T_cell_rece	0	0	0	0	2	0	0	0	0	0	0.285942	0
pseudogen	-	1	2	6	1	1	3	0.010747	0.02533	0.084974	0.009297	0.012074	0.032043
protein_co	mucin_12_	0	6	2	6	7	5	0	0.022365	0.008336	0.016418	0.024875	0.015718
lincRNA	-	1	0	1	3	1	0	0.025102	0	0.033079	0.065148	0.028201	0
protein_co	sorting_nex	1079	943	795	2486	1793	1903	26.84367	27.64644	26.06288	53.5038	50.11293	47.051
protein_co	5'3'-nucleo	45	23	14	59	53	47	1.473312	0.887395	0.604011	1.671079	1.949427	1.529289
protein_co	glucosamin	0	0	0	1	1	1	0	0	0	0.038945	0.050575	0.04474
protein_co	SAP_domai	81	69	88	71	36	66	1.912676	1.920051	2.738255	1.450367	0.95501	1.548853

lincRNA	-	1	0	1	0	0	0	0.017659	0	0.02327	0	0	0
protein_co	Uncharacte	2	18	5	3	4	3	0.037022	0.39265	0.121964	0.048041	0.083183	0.05519
protein_co	G_protein-	23	22	24	715	662	747	0.301248	0.339567	0.41423	8.101489	9.740984	9.723576
protein_co	importin_7	3685	3240	3568	6857	6102	5876	31.51148	32.65002	40.20601	50.72575	58.62091	49.93703
protein_co	proline_ric	530	473	394	889	592	870	20.40635	21.46138	19.99035	29.61107	25.60709	33.29034
protein_co	tectonin_b	449	438	371	397	305	404	3.621345	4.162984	3.94305	2.769983	2.763582	3.238281
protein_co	metallothic	0	0	0	33	18	16	0	0	0	2.168384	1.535963	1.207783
protein_co	solute_carr	10	5	2	10	6	2	0.19688	0.116005	0.051888	0.170319	0.132709	0.039133
protein_co	metallothic	9	9	14	1	4	0	1.203204	1.417903	2.466379	0.115654	0.600767	0
protein_co	chromoson	41	16	26	43	41	15	0.984837	0.452905	0.822979	0.893536	1.106403	0.358081
protein_co	metallothic	5	0	0	13	7	11	0.319306	0	0	0.718198	0.502209	0.698136
protein_co	complemer	270	257	246	0	1	2	6.041449	6.776689	7.253494	0	0.025138	0.044475
protein_co	sterile_alpl	86	91	81	7	3	4	0.664467	0.828559	0.824697	0.046788	0.02604	0.030715
antisense	-	35	20	15	1	8	4	0.75048	0.505368	0.423835	0.01855	0.192713	0.085239
protein_co	keratin_6A	0	0	0	12	3	6	0	0	0	0.237916	0.077241	0.13666
protein_co	CTD_nuclea	301	280	181	452	304	381	5.374448	5.89159	4.258737	6.981823	6.098037	6.760861
antisense	-	7	15	4	0	2	0	0.106921	0.269999	0.080512	0	0.03432	0
protein_co	keratin_81	17	9	11	7	5	3	0.466561	0.291078	0.397821	0.166196	0.154163	0.081826
protein_co	exocyst_co	0	0	0	1	1	0	0	0	0	0.019564	0.025406	0
protein_co	keratin_ass	0	0	0	0	2	0	0	0	0	0	0.074578	0
protein_co	ATPase_H+_	51	34	35	62	41	42	0.766172	0.601925	0.692882	0.80577	0.691973	0.627069
protein_co	coiled-coil_	56	44	50	752	920	1004	0.558639	0.517253	0.657276	6.489688	10.3105	9.953742
pseudogen	-	6	8	9	7	10	25	0.338281	0.531525	0.668658	0.341419	0.633396	1.4008
pseudogen	-	105	85	55	104	88	94	2.084291	1.98836	1.438688	1.785934	1.96246	1.854413
processed_	-	8	8	8	1	3	0	0.215426	0.253867	0.283879	0.023295	0.090757	0
protein_co	C2_calcium	2	0	1	3	3	4	0.067056	0	0.044182	0.087015	0.113	0.133284
pseudogen	-	0	0	1	0	0	0	0	0	0.034299	0	0	0
pseudogen	-	2	0	0	0	0	0	0.077343	0	0	0	0	0
pseudogen	-	0	0	0	0	0	6	0	0	0	0	0	0.17064
pseudogen	-	1	0	1	0	1	0	0.028617	0	0.03771	0	0.032149	0
protein_co	ral_guanine	0	0	0	355	227	407	0	0	0	6.395992	5.311185	8.424043
protein_co	nucleosom	2474	1972	1868	5152	3591	4324	52.1609	48.99586	51.89877	93.96892	85.05696	90.60261
pseudogen	-	52	34	30	53	73	62	0.652199	0.502531	0.49583	0.575063	1.028605	0.77282
antisense	-	2	0	0	0	0	0	0.08227	0	0	0	0	0
protein_co	thymosin_b	52748	43473	31521	62651	41828	57074	1640.735	1593.526	1292.014	1685.868	1461.668	1764.333
protein_co	transmemb	21	33	20	25	16	19	2.175657	4.028953	2.730461	2.240651	1.86226	1.956295
protein_co	chromoson	0	2	1	0	0	0	0	0.329223	0.184072	0	0	0
antisense	-	6	12	15	6	13	23	0.54956	1.295247	1.810466	0.475421	1.337694	2.093639
protein_co	carnitine_p	0	0	2	5	3	14	0	0	0.047571	0.078075	0.060835	0.251141
lincRNA	-	1	3	2	4	6	1	0.030304	0.107134	0.079866	0.104863	0.204268	0.030117
pseudogen	-	4	2	1	0	3	0	0.04885	0.028783	0.016093	0	0.04116	0
protein_co	survival_of	56	71	55	206	146	183	1.88474	2.815975	2.439276	5.997822	5.520333	6.121024
protein_co	small_EDRI	27	17	27	30	28	45	0.7567	0.561457	0.997146	0.727352	0.881591	1.253379
pseudogen	POM121_tr	35	38	26	27	47	48	0.604152	0.772981	0.591407	0.403186	0.911434	0.823435

pseudogen	dynein_ligh	1	3	6	5	3	10	0.196078	0.693197	1.550295	0.848128	0.660844	1.948669
protein_co	high_mobil	4950	4316	3896	9454	8642	10464	60.95788	62.63444	63.22348	100.7171	119.5606	128.0655
pseudogen	stromal_an	83	53	53	140	130	216	2.416998	1.818784	2.033803	3.526868	4.252953	6.251174
pseudogen	-	0	0	2	3	0	0	0	0	0.298134	0.293583	0	0
protein_co	mucin_19_	0	6	4	63	60	70	0	0.019129	0.01426	0.147444	0.182358	0.188205
protein_co	DENN/MAD	229	146	125	27	42	81	4.948362	3.717799	3.559351	0.504723	1.019587	1.739485
protein_co	amphiregul	0	0	0	2	0	0	0	0	0	0.073929	0	0
protein_co	eukaryotic_	97	97	106	239	87	159	1.658681	1.954654	2.388536	3.53551	1.671319	2.702078
lincRNA	-	6	4	5	0	1	0	0.095447	0.074985	0.104813	0	0.017871	0
protein_co	leucine_ca	499	419	378	1148	764	915	17.27767	17.09644	17.24691	34.38662	29.71851	31.48584
protein_co	major_facil	11	6	9	7	4	3	0.205487	0.132084	0.221549	0.113124	0.083946	0.055696
protein_co	variable_ch	0	0	1	0	0	2	0	0	0.059576	0	0	0.089862
protein_co	cysteine-ric	217	197	137	232	155	142	6.127038	6.554871	5.09737	5.666851	4.916676	3.984637
pseudogen	-	0	0	0	5	2	5	0	0	0	0.263212	0.136726	0.30238
protein_co	lin-52_hom	62	57	77	323	201	252	1.183252	1.28194	1.936472	5.332749	4.309538	4.779647
processed_	-	1	0	0	0	0	0	0.02413	0	0	0	0	0
protein_co	HCG19813	204	183	163	494	333	377	11.71363	12.38281	12.33342	24.53868	21.481	21.51355
protein_co	arylsulfatas	1	0	0	0	0	0	0.028235	0	0	0	0	0
protein_co	acyl-CoA_th	0	0	0	0	1	0	0	0	0	0	0.059239	0
protein_co	small_integ	186	181	152	210	195	249	5.302652	6.080872	5.710296	5.179198	6.245452	7.054873
protein_co	trans-23-en	0	1	0	0	0	0	0	0.017461	0	0	0	0
lincRNA	-	0	0	1	0	0	0	0	0	0.033556	0	0	0
protein_co	D4_zinc_an	424	312	344	17	7	27	5.977891	5.183747	6.391097	0.207345	0.110874	0.378317
protein_co	MANSC_do	0	3	0	0	4	2	0	0.182955	0	0	0.232555	0.102862
polymorph	cytochrom	20	12	15	27	17	30	0.609217	0.430755	0.6021	0.71149	0.581755	0.908183
pseudogen	long_interg	3	9	4	5	10	12	0.105181	0.371847	0.184803	0.151652	0.39388	0.418125
protein_co	LYR_motif_	102	113	90	153	89	95	4.745151	6.194915	5.517307	6.157498	4.651456	4.39221
protein_co	chromoson	15	4	4	1	1	0	0.248238	0.078009	0.087231	0.014317	0.018592	0
pseudogen	-	0	3	2	0	0	0	0	0.469081	0.349691	0	0	0
protein_co	intersectin_	2481	2259	2344	1965	1640	1727	7.71946	8.28292	9.610645	5.289148	5.732619	5.340257
protein_co	inositol_14	1001	862	904	747	681	704	6.888592	6.99054	8.197843	4.447131	5.264929	4.814805
protein_co	Uncharacte	7	1	0	5	7	0	0.197646	0.033273	0	0.12213	0.222043	0
protein_co	DENN/MAD	6	0	0	197	208	387	0.108301	0	0	3.076162	4.217863	6.942256
pseudogen	-	176	181	150	59	98	111	1.454741	1.763026	1.633801	0.421879	0.910014	0.911813
protein_co	cytokine_re	1	2	0	0	0	0	0.051151	0.120556	0	0	0	0
protein_co	crystallin_z	410	337	312	552	419	472	8.48546	8.219181	8.509048	9.88311	9.742146	9.7083
pseudogen	retinitis_pi	210	182	133	196	147	158	8.532317	8.714172	7.120888	6.889168	6.709869	6.379908
protein_co	chromoson	634	525	663	1190	965	908	6.404234	6.249486	8.825235	10.39891	10.95101	9.115352
pseudogen	cation_cha	10	12	7	9	4	5	0.320272	0.452905	0.295428	0.249359	0.143922	0.159147
processed_	-	10	6	5	0	11	10	0.17239	0.121891	0.113584	0	0.213036	0.171325
protein_co	loss_of_het	12	13	14	9	1	9	0.413064	0.527335	0.635036	0.268004	0.038671	0.307885
pseudogen	-	0	2	0	0	1	0	0	0.077356	0	0	0.036873	0
protein_co	cystin_1	75	61	44	7	2	4	1.450173	1.389938	1.121105	0.11709	0.043445	0.076865
protein_co	phosphatid	87	61	63	198	145	135	1.556562	1.286128	1.485328	3.064611	2.914501	2.400438

protein_co	killer_cell_l	0	0	0	2	2	0	0	0	0	0.089103	0.115712	0
processed_	-	7	16	13	32	16	48	0.140161	0.377535	0.343012	0.554298	0.359915	0.955172
processed_	transmemb	0	0	0	3	6	0	0	0	0	0.080349	0.208687	0
lincRNA	-	0	0	3	0	0	0	0	0	0.083416	0	0	0
protein_co	chromoson	3	4	1	3	2	0	0.041544	0.065276	0.018248	0.03594	0.031115	0
protein_co	geminin_co	0	0	4	6	10	10	0	0	0.081547	0.080302	0.173805	0.153752
protein_co	tetratricop	12	10	7	17	13	8	0.186303	0.182955	0.143209	0.228323	0.226741	0.123435
protein_co	C-type_lect	0	0	0	0	0	2	0	0	0	0	0	0.062561
pseudogen	olfactory_r	0	0	0	6	4	3	0	0	0	0.4746	0.410887	0.272612
protein_co	RFPL3_anti	6	0	2	5	2	3	0.245286	0	0.107743	0.17683	0.091855	0.121886
antisense	C1QTNF9B_	0	0	2	5	3	3	0	0	0.173325	0.284465	0.221649	0.196077
protein_co	C1q_and_t	0	0	3	3	0	3	0	0	0.18838	0.123669	0	0.142072
protein_co	keratin_ass	2	0	0	0	0	0	0.188738	0	0	0	0	0
protein_co	keratin_ass	0	0	0	20	5	17	0	0	0	0.972376	0.31569	0.94951
pseudogen	ribosomal_	0	0	2	0	0	1	0	0	0.17617	0	0	0.066432
protein_co	Uncharacte	86	107	84	253	190	218	1.820442	2.669127	2.343109	4.632996	4.518362	4.586111
pseudogen	family_with	0	0	1	3	4	7	0	0	0.028792	0.056705	0.098186	0.152001
antisense	C1RL_antis	108	95	71	64	131	179	1.084527	1.12421	0.939528	0.555981	1.477873	1.786403
antisense	-	0	0	2	8	11	19	0	0	0.045582	0.119697	0.213732	0.326582
pseudogen	olfactory_r	0	0	0	0	1	0	0	0	0	0	0.058597	0
pseudogen	-	0	0	4	1	2	1	0	0	0.486155	0.079789	0.207233	0.091662
protein_co	basic_helix	0	0	0	0	0	1	0	0	0	0	0	0.05833
pseudogen	zinc_finger_	746	614	526	559	753	773	13.09916	12.70516	12.17097	8.491406	14.85418	13.48944
antisense	SRRM2_ant	17	12	13	19	27	17	0.255463	0.212504	0.257429	0.246999	0.455819	0.253886
pseudogen	-	78	83	53	60	70	77	1.729953	2.169326	1.548996	1.151208	1.744162	1.697227
protein_co	one_cut_ho	0	0	0	2	0	2	0	0	0	0.011012	0	0.012651
protein_co	chromoson	10	1	2	0	1	3	0.13613	0.016042	0.035877	0	0.015293	0.040587
protein_co	chromoson	13	8	9	11	12	12	0.280568	0.203466	0.25596	0.205376	0.290954	0.257386
protein_co	RNA_bindi	1815	1558	1330	3638	2669	3536	28.7947	29.12798	27.80496	49.93	47.57004	55.75166
pseudogen	heat_shock	0	7	1	2	3	1	0	0.200696	0.03206	0.042095	0.081998	0.024179
pseudogen	heat_shock	0	1	1	3	0	4	0	0.028462	0.031826	0.062681	0	0.096011
processed_	-	10	9	6	12	1	15	0.165234	0.175246	0.130643	0.171531	0.018563	0.24632
protein_co	LOC40129(	0	1	4	0	6	2	0	0.043842	0.196102	0	0.250777	0.073948
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.024128	0
protein_co	NYN_doma	2324	2024	1840	290	372	319	15.65927	16.07137	16.33759	1.690427	2.815966	2.136169
protein_co	DnaJ_(Hsp4	300	245	162	662	431	607	9.743741	9.377297	6.933529	18.60054	15.72645	19.59308
protein_co	interferon_	0	7	4	0	1	2	0	0.593362	0.379148	0	0.08081	0.142973
protein_co	small_integ	4	5	5	0	0	0	0.082915	0.122137	0.136577	0	0	0
protein_co	Uncharacte	5	12	16	6	7	16	0.281901	0.797287	1.188725	0.292645	0.443377	0.896512
protein_co	docking_pr	69	50	60	41	26	30	0.410903	0.350887	0.470843	0.211221	0.173945	0.17755
protein_co	hematologi	1225	1154	1036	6593	4728	5433	17.4429	19.36402	19.43915	81.2136	75.63263	76.88331
pseudogen	immunoglo	0	5	0	0	0	2	0	0.718753	0	0	0	0.242461
polymorph	serpin_pep	2	0	0	0	0	2	0.055204	0	0	0	0	0.054863
protein_co	serpin_pep	9	9	9	0	0	0	0.272424	0.321035	0.358988	0	0	0

protein_co	serpin_pep	0	0	1	2	0	10	0	0	0.025068	0.032913	0	0.189055
protein_co	zinc_finger_	1	2	1	0	0	4	0.019371	0.045655	0.025526	0	0	0.077006
pseudogen	-	0	0	0	3	2	2	0	0	0	0.092961	0.080482	0.071196
antisense	-	1	1	2	0	0	0	0.018975	0.022361	0.05001	0	0	0
pseudogen	EGF-like_an	8	3	2	8	15	6	0.182006	0.080431	0.05996	0.157452	0.383386	0.135661
protein_co	golgin_A8_	2	1	5	0	0	2	0.053021	0.031241	0.17467	0	0	0.052693
lincRNA	-	14	3	6	10	6	8	0.289747	0.073168	0.163636	0.179042	0.139506	0.164547
processed_	transmemb	6	8	8	41	27	42	0.122501	0.19248	0.215236	0.724163	0.619302	0.852214
pseudogen	purinergic_	2	3	0	0	0	0	0.226244	0.399921	0	0	0	0
pseudogen	-	0	0	0	5	0	0	0	0	0	0.491405	0	0
pseudogen	hect_doma	262	195	238	239	173	227	2.674097	2.345403	3.201014	2.110264	1.983677	2.302562
protein_co	ribonuclea	0	0	0	0	0	1	0	0	0	0	0	0.032741
pseudogen	glycogenin_	2	6	0	47	43	41	0.112163	0.396532	0	2.280242	2.709178	2.285144
pseudogen	-	5	4	3	4	0	2	0.780841	0.736138	0.617374	0.5404	0	0.310407
protein_co	hemoglobi	0	0	2	0	0	0	0	0	0.207013	0	0	0
lincRNA	-	4	2	0	20	16	31	0.268736	0.158344	0	1.162409	1.207633	2.069842
protein_co	transcriptic	0	2	1	2	2	0	0	0.040964	0.022903	0.030072	0.039052	0
protein_co	ATPase_cla	22	18	13	27	7	18	0.17214	0.165974	0.134041	0.182762	0.061533	0.139972
processed_	-	25	33	23	12	14	3	0.320001	0.497774	0.387949	0.132879	0.201321	0.038163
protein_co	ankyrin_rep	0	5	0	0	0	0	0	0.12624	0	0	0	0
pseudogen	heterogene	2	2	3	2	3	8	0.140056	0.165047	0.276838	0.121161	0.236016	0.556762
protein_co	Protein_LO	2	1	5	0	1	0	0.16727	0.098559	0.551053	0	0.093959	0
protein_co	chromoson	71	57	66	98	108	104	1.062411	1.005116	1.301407	1.268596	1.815545	1.546597
processed_	HLA_compl	8	6	6	9	5	4	0.159341	0.14083	0.157479	0.155075	0.111881	0.079178
pseudogen	major_hist	1	1	1	1	0	5	0.038756	0.045672	0.051071	0.033528	0	0.192584
protein_co	HLA_compl	6	0	1	7	3	6	0.184678	0	0.04056	0.186391	0.103737	0.183537
pseudogen	-	0	1	0	0	0	0	0	0.019793	0	0	0	0
protein_co	collagen_ty	1	2	3	215	223	222	0.005526	0.013023	0.021844	1.027739	1.384316	1.219113
antisense	H1FX_antis	18	15	17	32	26	49	0.366515	0.359929	0.456145	0.563679	0.594759	0.991572
protein_co	RAB12_mer	379	279	293	508	493	559	9.389161	8.145146	9.565111	10.88715	13.72093	13.76287
protein_co	leucine_ric	0	0	0	0	0	1	0	0	0	0	0	0.057003
protein_co	transmemb	272	182	197	153	166	95	4.376885	3.451236	4.177315	2.129858	3.000913	1.519251
pseudogen	peptidylpro	2	5	1	0	5	0	0.204012	0.601038	0.134419	0	0.572986	0
protein_co	major_hist	748	723	497	45	40	70	21.19907	24.14686	18.56122	1.103293	1.273574	1.971619
protein_co	protein_tyr	1136	862	1076	1718	1454	1311	14.12755	12.63289	17.63338	18.48309	20.3143	16.2032
protein_co	WD_repeat	210	161	187	87	65	56	1.083693	0.979084	1.271638	0.388391	0.376833	0.2872
protein_co	CD200_rec	0	0	0	2	0	0	0	0	0	0.057356	0	0
protein_co	Uncharacte	122	106	121	102	62	93	7.545329	7.725583	9.861399	5.457346	4.307835	5.716246
protein_co	leukemia_N	37	31	34	57	35	46	0.886342	0.875122	1.073281	1.181239	0.941926	1.095134
protein_co	vestigial_lik	535	480	512	612	724	651	2.723407	2.879434	3.4345	2.695089	4.140439	3.293437
protein_co	protease_se	0	0	0	2	2	0	0	0	0	0.030966	0.040214	0
protein_co	tripartite_r	0	1	0	1669	2465	1666	0	0.008113	0	9.93997	19.06478	11.39857
protein_co	zinc_finger_	30	9	9	9	7	4	0.925542	0.327208	0.365891	0.240204	0.242617	0.122643
protein_co	ankyrin_rep	678	605	647	892	927	830	5.468311	5.75024	6.876423	6.223739	8.399478	6.652904

protein_co	collagen-lik	46	19	28	8	16	15	0.773844	0.376666	0.620709	0.116426	0.302388	0.250782
protein_co	methyltran	296	281	164	354	214	310	3.898143	4.360933	2.846064	4.033038	3.166131	4.057302
lincRNA	-	22	32	16	80	62	72	0.61397	1.052402	0.588409	1.931425	1.943862	1.996949
antisense	SETD5_anti	261	187	160	590	394	450	4.247648	3.586383	3.431333	8.306595	7.203662	7.278304
protein_co	XK_Kell_blc	0	0	0	46	103	47	0	0	0	0.529201	1.538814	0.621166
protein_co	glutathione	77	51	41	138	112	162	2.491722	1.94485	1.748346	3.863233	4.071701	5.209949
protein_co	deiodinase_	11	12	12	23	23	18	0.091464	0.117583	0.131484	0.165443	0.214849	0.148744
protein_co	chromosor	339	355	302	623	439	681	12.34319	15.23222	14.49004	19.6236	17.95731	24.64248
pseudogen	gonadotrop	27	10	8	9	19	25	0.893938	0.390167	0.349035	0.25778	0.706718	0.822609
protein_co	deiodinase_	9	7	7	6	3	5	0.256028	0.234666	0.262409	0.147659	0.095877	0.14136
polymorph	aldo-keto_r	38	8	10	15	12	8	0.951186	0.235982	0.32985	0.324815	0.337452	0.199013
protein_co	serine/thre	475	398	463	843	711	663	4.961912	4.899431	6.373402	7.618089	8.343997	6.883014
protein_co	SAC1_supp	472	336	440	956	834	774	5.361113	4.497378	6.585678	9.393639	10.64212	8.737025
protein_co	translin	1203	1021	1000	2731	2178	2407	18.62223	18.62511	20.39862	36.57217	37.87677	37.02983
protein_co	solute_carr	98	109	102	277	226	313	1.72366	2.259223	2.364071	4.214717	4.465634	5.471162
IG_V_gene	immunoglc	4	0	1	5	0	0	0.558744	0	0.184072	0.604207	0	0
IG_V_gene	immunoglc	0	0	3	2	6	3	0	0	0.523225	0.228995	0.892139	0.394605
IG_V_gene	immunoglc	1	0	0	6	2	0	0.130719	0	0	0.678502	0.293708	0
TR_V_gene	T_cell_rece	0	0	0	0	2	0	0	0	0	0	0.06856	0
TR_V_gene	T_cell_rece	0	2	2	0	0	0	0	0.319937	0.35776	0	0	0
TR_V_gene	T_cell_rece	0	0	0	4	2	0	0	0	0	0.443573	0.288019	0
TR_J_gene	T_cell_rece	0	0	0	0	2	0	0	0	0	0	2.379037	0
TR_J_gene	T_cell_rece	0	0	0	0	0	1	0	0	0	0	0	0.992718
TR_J_gene	T_cell_rece	0	1	0	0	1	0	0	1.327398	0	0	1.265445	0
TR_C_gene	T_cell_rece	209	225	175	629	372	448	14.59719	18.51879	16.1063	38.00463	29.18871	31.09643
TR_V_gene	T_cell_rece	0	0	0	8	2	1	0	0	0	0.774612	0.251484	0.111235
TR_V_gene	T_cell_rece	0	0	0	0	2	2	0	0	0	0	0.210162	0.185915
TR_V_gene	T_cell_rece	0	0	0	0	1	0	0	0	0	0	0.174416	0
TR_V_gene	T_cell_rece	2	3	2	6	2	6	0.294117	0.519898	0.387574	0.763315	0.330422	0.876901
TR_J_gene	T_cell_rece	0	0	0	0	1	0	0	0	0	0	0.90115	0
protein_co	testis-speci	0	1	0	0	0	0	0	0.025177	0	0	0	0
protein_co	proline_ric	5	22	9	71	41	80	0.161405	0.836909	0.382847	1.982757	1.486898	2.566539
protein_co	taste_recep	6	2	5	6	3	6	0.317012	0.124526	0.34812	0.274245	0.178072	0.315054
pseudogen	taste_recep	9	1	6	6	8	4	0.513436	0.067228	0.451056	0.296114	0.512723	0.226785
protein_co	taste_recep	0	0	4	0	0	0	0	0	0.279053	0	0	0
protein_co	taste_recep	22	31	20	25	29	19	0.626858	1.040915	0.75095	0.616239	0.928311	0.538034
protein_co	taste_recep	0	2	2	0	0	3	0	0.076222	0.085233	0	0	0.096422
lincRNA	-	1	0	0	0	0	1	0.097318	0	0	0	0	0.096717
pseudogen	-	9	13	15	18	7	25	0.821498	1.398346	1.804223	1.421345	0.717813	2.267847
protein_co	Uncharacte	24	16	15	44	39	26	0.71261	0.559845	0.586904	1.130203	1.300931	0.767227
protein_co	HCG20323	3	9	7	7	5	8	0.101032	0.357182	0.310651	0.203939	0.189173	0.267756
lincRNA	-	108	112	50	224	154	264	3.566829	4.358968	2.176023	6.399847	5.713844	8.665071
pseudogen	-	2	1	0	0	1	0	0.199401	0.117491	0	0	0.112007	0
protein_co	cutaneous_	0	0	0	6	2	0	0	0	0	0.063816	0.027625	0

protein_co	chromoson	538	482	494	465	450	478	3.598971	3.799708	4.354696	2.69099	3.381876	3.177851
protein_co	keratin_ass	2	3	5	3	4	2	0.091514	0.161766	0.301484	0.118753	0.205621	0.090949
protein_co	keratin_ass	11	8	11	109	29	49	0.685119	0.587179	0.902819	5.873036	2.029178	3.033045
protein_co	-	0	8	0	0	1	1	0	0.204048	0	0	0.024316	0.02151
protein_co	family_with	708	547	567	777	458	491	18.58316	16.91923	19.6112	17.64291	13.50519	12.80788
processed_	long_interg	0	0	1	15	10	2	0	0	0.027928	0.275013	0.238094	0.042125
pseudogen	suppressio	0	0	2	2	1	4	0	0	0.1257	0.082521	0.053582	0.1896
pseudogen	ribosomal_	167	153	126	152	97	196	14.37585	15.52085	14.29297	11.3194	9.380754	16.76806
protein_co	olfactory_r	1	0	1	0	2	2	0.056743	0	0.074773	0	0.127494	0.112785
pseudogen	ribosomal_	1	1	0	2	2	3	0.121424	0.143091	0	0.210087	0.272825	0.362023
protein_co	ring_finger_	39	31	9	104	52	63	1.832031	1.716078	0.557116	4.226341	2.74423	2.941158
protein_co	keratin_ass	2	0	1	71	23	29	0.161405	0	0.106346	4.956894	2.085284	2.325926
protein_co	mitochond	6210	5659	7487	6827	7610	7035	1106.948	1188.728	1758.645	1052.758	1523.945	1246.262
protein_co	microtubul	53	43	34	122	54	44	0.514839	0.492233	0.43522	1.025223	0.589303	0.424774
pseudogen	ribosomal_	0	1	0	1	0	0	0	0.134747	0	0.098918	0	0
pseudogen	-	1	0	0	0	0	5	0.030942	0	0	0	0	0.153752
processed_	-	104	91	67	301	161	237	2.346915	2.419984	1.992387	5.87616	4.081681	5.31523
protein_co	POU_class_	0	1	0	33	13	34	0	0.011646	0	0.282129	0.144332	0.333933
pseudogen	ribosomal_	6	6	1	13	9	14	0.767261	0.90417	0.16851	1.43813	1.292955	1.779219
protein_co	HCG20091	10	6	3	2	2	5	0.284629	0.201251	0.112521	0.049246	0.063953	0.141436
protein_co	RBM12B_a	7	7	9	1	12	5	0.567514	0.668781	0.961515	0.070136	1.092972	0.402864
pseudogen	basic_trans	1	1	0	1	0	0	0.112881	0.133023	0	0.097652	0	0
pseudogen	vomeronas	0	2	0	1	1	0	0	0.149971	0	0.055047	0.071485	0
protein_co	zinc_finger_	595	514	345	856	418	575	22.21431	22.61445	16.97344	27.64729	17.53239	21.33503
pseudogen	-	2	6	0	4	8	6	0.245097	0.866496	0	0.424064	1.101406	0.730751
protein_co	zinc_finger_	232	182	146	891	804	887	2.560949	2.367508	2.123736	8.508512	9.970525	9.730747
protein_co	synaptotag	0	1	0	0	0	0	0	0.021402	0	0	0	0
protein_co	nucleopori	1084	939	713	3429	2145	2572	15.98553	16.31813	13.85549	43.74497	35.53645	37.69452
pseudogen	COX20_Cox	1	0	2	0	5	3	0.148294	0	0.390831	0	0.832996	0.442135
pseudogen	-	0	0	0	4	1	0	0	0	0	0.202203	0.065647	0
pseudogen	aurora_kin	1	0	1	0	1	0	0.043681	0	0.05756	0	0.049073	0
pseudogen	-	1	2	0	0	2	4	0.092071	0.217001	0	0	0.206873	0.366011
pseudogen	-	2	0	0	0	0	0	0.191815	0	0	0	0	0
pseudogen	eukaryotic_	3	0	3	3	0	0	0.117909	0	0.155375	0.102002	0	0
protein_co	DENN/MAD	55	49	40	89	93	55	0.418356	0.439224	0.400938	0.585647	0.794721	0.415772
pseudogen	olfactory_r	0	0	3	0	0	0	0	0	0.220073	0	0	0
pseudogen	-	1	0	0	0	0	0	0.055727	0	0	0	0	0
pseudogen	tropomyos	0	0	0	1	2	1	0	0	0	0.06131	0.159239	0.070434
pseudogen	-	0	0	2	0	0	0	0	0	0.156245	0	0	0
pseudogen	-	1	2	0	0	0	2	0.078315	0.184579	0	0	0	0.155663
protein_co	chromoson	4	3	11	10	3	6	0.081605	0.072125	0.295721	0.176489	0.068758	0.121651
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.166599	0
pseudogen	-	4	0	0	0	0	2	0.500624	0	0	0	0	0.248766
pseudogen	profilin_1_	1	0	0	0	4	2	0.136095	0	0	0	0.611578	0.270509

pseudogen	-	0	1	2	12	3	7	0	0.042644	0.09537	0.375657	0.12196	0.251742
pseudogen	-	0	0	1	0	0	0	0	0	0.152655	0	0	0
protein_co	SFT2_doma	170	178	213	205	280	204	7.792181	9.614732	12.86544	8.12881	14.4184	9.292871
protein_co	FGFR1_onc	329	292	287	1054	626	800	4.499506	4.706075	5.172323	12.47017	9.618167	10.87348
pseudogen	-	0	0	0	5	0	6	0	0	0	0.551794	0	0.760685
pseudogen	keratin_8_p	0	1	1	1	0	0	0	0.110813	0.123913	0.081348	0	0
pseudogen	high_mobil	0	0	0	1	0	3	0	0	0	0.076587	0	0.26395
pseudogen	lipoprotein	9	1	9	21	6	20	0.201212	0.026346	0.265148	0.406156	0.150699	0.444375
pseudogen	-	79	74	59	23	48	76	1.335784	1.47451	1.314607	0.336434	0.911799	1.277122
pseudogen	-	0	2	0	0	0	0	0	0.21513	0	0	0	0
protein_co	family_with	0	0	1	0	1	1	0	0	0.030585	0	0.026074	0.023066
protein_co	SR-related_	522	399	496	566	675	544	5.466904	4.924373	6.84522	5.128028	7.941888	5.662125
pseudogen	-	1	0	1	14	5	18	0.04826	0	0.063595	0.584489	0.271084	0.863312
pseudogen	protein_ph	0	0	0	0	0	1	0	0	0	0	0	0.1185
protein_co	coiled-coil_	25	3	11	37	29	28	0.6698	0.094718	0.388358	0.857571	0.872875	0.745543
protein_co	Duffy_bloo	0	1	0	25	10	36	0	0.032801	0	0.601984	0.312702	0.99585
pseudogen	phosducin-	12	13	21	11	8	14	0.879906	1.123325	2.029126	0.697767	0.659013	1.020217
pseudogen	-	8	4	3	1	1	3	0.153175	0.090253	0.075693	0.016564	0.02151	0.057086
protein_co	zinc_finger_	173	225	223	389	348	332	2.308745	3.538502	3.921657	4.490994	5.217449	4.403293
pseudogen	nucleophos	1	6	1	7	1	6	0.061203	0.432747	0.080651	0.370627	0.068758	0.364953
pseudogen	-	0	2	3	0	1	2	0	0.096203	0.161365	0	0.045857	0.081132
pseudogen	-	2	0	0	0	0	0	0.240641	0	0	0	0	0
pseudogen	cytochrom	4	3	1	0	0	0	0.188235	0.166367	0.062012	0	0	0
pseudogen	-	0	0	0	4	0	1	0	0	0	0.15343	0	0.044065
protein_co	Tctex1_dor	44	27	22	60	54	50	2.911755	2.105586	1.91849	3.434918	4.014624	3.288378
pseudogen	tyrosine_3-	8	10	11	3	9	8	0.598203	0.881183	1.083893	0.194063	0.75605	0.594509
protein_co	Uncharacte	5	15	5	7	22	16	0.116713	0.412617	0.153799	0.141355	0.576927	0.371175
pseudogen	protein_ph	3	0	0	0	2	0	0.36511	0	0	0	0.273452	0
pseudogen	-	11	14	4	10	7	14	4.73456	7.101042	2.268725	3.723488	3.384808	5.988591
pseudogen	ADP-ribosy	0	1	0	0	1	0	0	0.115962	0	0	0.11055	0
protein_co	crystallin_g	549	378	345	22	31	28	18.92227	15.35323	15.66949	0.655974	1.20036	0.95911
pseudogen	-	1	0	1	2	13	3	0.097139	0	0.128006	0.168069	1.418692	0.289619
protein_co	cysteine-ric	6	3	0	0	0	4	0.141743	0.083518	0	0	0	0.093912
pseudogen	ribosomal_	0	0	0	0	1	0	0	0	0	0	0.131004	0
pseudogen	calponin_2	7	10	7	13	7	4	0.407686	0.686334	0.537231	0.65499	0.45801	0.231525
pseudogen	-	1	0	1	0	0	0	0.061559	0	0.08112	0	0	0
pseudogen	ribosomal_	0	4	1	0	1	0	0	0.314296	0.087863	0	0.074907	0
protein_co	kelch-like_f	118	116	121	609	579	513	1.532263	1.775074	2.070482	6.84119	8.446543	6.620311
pseudogen	-	8	8	17	0	0	0	0.71301	0.840239	1.996592	0	0	0
pseudogen	ribosomal_	0	3	2	0	3	2	0	0.298983	0.222886	0	0.285028	0.168096
pseudogen	-	36	41	25	40	30	73	4.648478	6.238773	4.253859	4.468186	4.351896	9.367867
pseudogen	ribosomal_	0	0	0	0	1	0	0	0	0	0	0.189414	0
protein_co	tripartite_r	170	141	169	684	617	632	1.950156	1.906104	2.554712	6.787963	7.951602	7.205218
pseudogen	Y_box_bind	1	3	6	4	5	4	0.065521	0.231638	0.518044	0.226727	0.368044	0.260466

pseudogen	basic_trans	6	1	5	17	8	13	0.446132	0.087623	0.489911	1.093513	0.668269	0.96065
protein_co	myeloid/ly	893	808	690	1503	1047	1108	11.6101	12.37949	11.82138	16.90465	15.29256	14.3164
pseudogen	-	20	14	15	1	7	4	1.525677	1.258542	1.507852	0.065993	0.599901	0.303251
protein_co	acid-sensin	14	18	27	67	29	36	0.332067	0.503127	0.843911	1.374788	0.772761	0.848614
protein_co	chromoson	23	21	19	31	32	36	0.471955	0.507807	0.513761	0.550297	0.737686	0.73415
pseudogen	STE20-relat	0	0	0	0	0	1	0	0	0	0	0	0.041073
pseudogen	nucleolin_	8	11	4	3	10	22	0.215755	0.3496	0.142156	0.069993	0.302985	0.589663
protein_co	KIAA1984	34	60	36	39	42	68	0.424127	0.882013	0.591771	0.420866	0.588593	0.843015
protein_co	Rho_guanir	10	17	8	141	202	224	0.217775	0.436278	0.229579	2.656374	4.942055	4.848024
pseudogen	-	0	0	1	0	2	1	0	0	0.183106	0	0.31221	0.138095
protein_co	DNL-type_z	7	4	5	5	0	2	0.126308	0.085055	0.118888	0.078049	0	0.035865
pseudogen	-	63	50	41	13	18	16	3.247597	3.037377	2.785097	0.579733	1.042421	0.819693
pseudogen	-	0	0	0	1	0	0	0	0	0	0.020492	0	0
pseudogen	ribosomal_	2	2	4	4	4	4	0.045658	0.053806	0.120333	0.078998	0.102589	0.090753
pseudogen	suppressior	0	0	1	0	0	2	0	0	0.064476	0	0	0.097253
pseudogen	eukaryotic_	0	1	1	0	0	0	0	0.044121	0.049338	0	0	0
pseudogen	tyrosine_3-	0	2	0	1	7	9	0	0.171395	0	0.062911	0.571884	0.650448
pseudogen	nucleophos	0	0	0	5	0	0	0	0	0	0.37913	0	0
protein_co	notch_2_N	478	422	541	75	107	86	5.024979	5.227884	7.494427	0.682073	1.263686	0.898493
pseudogen	histone_clu	0	0	0	1	3	0	0	0	0	0.110094	0.428913	0
protein_co	suppressor_	231	235	223	868	469	674	7.443317	8.923382	9.468784	24.19565	16.97761	21.58361
pseudogen	RNA_bindir	8	5	3	1	4	1	0.345455	0.254436	0.170709	0.037356	0.194049	0.042915
pseudogen	-	1	1	1	0	0	0	0.035318	0.04162	0.04654	0	0	0
pseudogen	-	0	0	0	5	0	0	0	0	0	0.458907	0	0
pseudogen	tyrosine_3-	0	0	0	0	1	0	0	0	0	0	0.081474	0
pseudogen	-	4	4	6	10	8	4	0.314657	0.370804	0.621961	0.680519	0.706995	0.312714
protein_co	testis_speci	0	1	0	1	3	0	0	0.030493	0	0.022385	0.087208	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.14869	0
pseudogen	interferon_	2	0	0	0	2	0	0.267379	0	0	0	0.300383	0
pseudogen	MARCKS-lik	2	2	2	3	2	13	0.195715	0.230639	0.257905	0.253968	0.219874	1.264293
pseudogen	-	1	1	3	4	0	0	0.118172	0.139258	0.467165	0.408919	0	0
protein_co	neuroblast	1706	1412	1418	3357	2647	2552	20.30059	19.80029	22.23518	34.55764	35.3861	30.18005
pseudogen	-	0	1	0	0	1	1	0	0.04372	0	0	0.041679	0.03687
pseudogen	phosphogly	1	0	1	0	2	0	0.043609	0	0.057466	0	0.097983	0
pseudogen	-	17	31	12	21	28	67	0.894629	1.922485	0.832166	0.956041	1.655393	3.504117
pseudogen	-	3	3	2	0	1	3	0.401068	0.472634	0.35234	0	0.150192	0.398591
pseudogen	-	2	3	0	2	1	9	0.199401	0.352473	0	0.172501	0.112007	0.891764
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.1665
pseudogen	-	1	1	0	0	1	0	0.11534	0.135921	0	0	0.129577	0
pseudogen	ribosomal_	17	10	15	38	15	33	1.535831	1.064637	1.78575	2.969895	1.522421	2.962907
protein_co	ankyrin_rep	55	21	27	92	43	47	0.586456	0.263876	0.379377	0.84864	0.515099	0.498058
protein_co	queuine_tR	853	742	472	972	586	915	22.2019	22.75895	16.18892	21.8862	17.13515	23.66856
protein_co	conserved_	268	263	299	627	553	533	2.928418	3.386578	4.305309	5.926917	6.788479	5.788088
pseudogen	PEST_conta	0	0	2	0	0	0	0	0	0.296235	0	0	0

protein_co	MAX_dime	187	179	129	289	276	314	4.343996	4.900133	3.948865	5.807759	7.202875	7.24915
pseudogen	glyceraldeh	0	0	0	2	2	0	0	0	0	0.090961	0.118125	0
pseudogen	-	3	0	0	0	0	0	0.168067	0	0	0	0	0
pseudogen	-	0	0	1	0	10	0	0	0	0.218694	0	1.864449	0
pseudogen	-	0	0	1	0	0	0	0	0	0.097982	0	0	0
protein_co	glutathione	376	312	254	38	25	44	4.606761	4.504738	4.100873	0.402768	0.34411	0.53576
pseudogen	suppressio	2	0	2	0	5	1	0.147058	0	0.193787	0	0.413027	0.073075
pseudogen	glyceraldeh	0	1	0	0	0	0	0	0.062201	0	0	0	0
protein_co	componen	365	347	280	611	486	631	4.549909	5.097373	4.599416	6.588917	6.80605	7.817157
pseudogen	-	1	0	1	2	2	2	0.060852	0	0.080188	0.105285	0.136726	0.120952
pseudogen	-	3	3	4	5	0	9	0.200029	0.235722	0.351452	0.288406	0	0.596381
protein_co	Rho_GTPas	289	203	210	713	575	610	2.769221	2.292255	2.651636	5.910338	6.189801	5.808972
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.159881	0
protein_co	HAUS_augn	11	11	8	6	26	13	0.274177	0.3231	0.262762	0.129375	0.728048	0.322026
protein_co	lecithin-ch	142	125	55	290	178	284	4.988468	5.174828	2.546105	8.813326	7.025025	9.915322
pseudogen	-	0	1	3	1	0	2	0	0.071219	0.238915	0.052282	0	0.120123
protein_co	protein_tyr	7	9	5	11	5	25	0.286832	0.434589	0.269982	0.389929	0.23017	1.018074
pseudogen	CDGSH_iro	1	0	0	0	0	0	0.161899	0	0	0	0	0
pseudogen	annexin_A2	2	2	1	0	0	1	0.114343	0.134747	0.075338	0	0	0.056819
pseudogen	-	0	0	0	2	7	4	0	0	0	0.111028	0.504644	0.255098
pseudogen	-	0	0	1	0	0	0	0	0	0.227985	0	0	0
pseudogen	RNA_bindi	0	3	2	5	1	2	0	0.103177	0.076917	0.126237	0.032787	0.058009
pseudogen	heterogene	0	0	0	53	47	56	0	0	0	4.326813	4.982831	5.252026
protein_co	poliovirus_	12	8	7	3	3	2	0.401321	0.315289	0.308492	0.086795	0.112715	0.066474
protein_co	keratin_ass	0	0	0	7	0	0	0	0	0	0.297672	0	0
protein_co	keratin_ass	0	0	2	0	0	0	0	0	0.182866	0	0	0
protein_co	glypican_2	178	146	154	133	139	168	3.72176	3.597397	4.243106	2.405709	3.265068	3.49098
pseudogen	RNA_bindi	0	0	0	2	0	0	0	0	0	0.096826	0	0
pseudogen	heat_shock	12	8	2	15	5	16	0.368072	0.289167	0.080838	0.398021	0.172294	0.487732
pseudogen	-	0	4	3	2	0	4	0	0.479906	0.40248	0.17615	0	0.404723
pseudogen	vesicle_tra	0	0	1	2	0	1	0	0	0.100235	0.131606	0	0.075595
pseudogen	-	4	1	1	2	0	0	0.278637	0.082089	0.091794	0.120523	0	0
pseudogen	olfactory_r	0	0	0	4	0	0	0	0	0	0.198049	0	0
pseudogen	H2A_histor	1	0	3	2	7	0	0.134028	0	0.529848	0.231893	1.054004	0
pseudogen	ribosomal_	211	192	107	245	128	292	19.84112	21.2761	13.25874	19.93025	13.52206	27.28828
pseudogen	-	11	11	11	20	8	30	0.689989	0.81311	0.909237	1.085282	0.563753	1.870168
protein_co	signal-indu	619	439	389	603	534	600	9.032656	7.549122	7.480131	7.612111	8.754173	8.701331
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.186354
pseudogen	ferritin_hea	3	3	4	19	2	9	0.271957	0.320485	0.477831	1.490033	0.203685	0.810833
protein_co	endogenou	87	62	118	73	83	73	1.693956	1.422596	3.027608	1.229614	1.815558	1.412588
protein_co	synaptojan	251	207	176	414	287	330	6.388553	6.208779	5.903047	9.115744	8.206533	8.347421
protein_co	ADP-ribosy	407	341	211	500	290	383	17.5464	17.32428	11.98701	18.64776	14.04562	16.40976
processed_	-	60	19	33	65	84	121	1.084856	0.404838	0.786266	1.016711	1.706276	2.174283
protein_co	tubulin_tyr	0	0	0	7	1	10	0	0	0	0.11709	0.021722	0.192162

pseudogen	eukaryotic_	3	0	0	0	0	0	0.133465	0	0	0	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.135991	0	0	0
pseudogen	actinin_alp	2	0	0	0	0	0	0.072972	0	0	0	0	0
protein_co	chemokine	0	0	0	0	0	2	0	0	0	0	0	0.032229
pseudogen	peptidylpr	0	0	1	2	2	1	0	0	0.143251	0.188086	0.244254	0.108037
pseudogen	-	7	5	1	4	20	34	0.240641	0.202558	0.045301	0.118958	0.772415	1.161609
pseudogen	-	1	0	0	11	5	2	0.014266	0	0	0.135755	0.080135	0.028356
protein_co	RNA_bindi	198	201	231	540	434	456	2.061825	2.466549	3.169811	4.864557	5.077212	4.71912
pseudogen	-	1	0	0	2	0	1	0.185108	0	0	0.320272	0	0.183965
pseudogen	ras-related_	0	0	0	5	1	0	0	0	0	0.39756	0.103257	0
protein_co	steroid_rec	825	669	579	1218	827	1033	20.17382	19.27824	18.65725	25.76585	22.71898	25.10407
pseudogen	-	0	0	1	2	0	0	0	0	0.17311	0.22729	0	0
protein_co	transmemb	2	1	1	0	4	2	0.022202	0.013082	0.014628	0	0.049885	0.022065
pseudogen	keratin_8_p	2	1	2	0	2	0	0.057922	0.034129	0.076327	0	0.065072	0
pseudogen	-	0	2	0	0	1	1	0	0.253094	0	0	0.120641	0.106722
pseudogen	-	1	4	2	4	5	2	0.066676	0.314296	0.175726	0.230725	0.374533	0.132529
pseudogen	-	1	0	0	0	0	0	0.141176	0	0	0	0	0
protein_co	DnaJ_(Hsp4	76	97	64	220	169	123	1.327017	1.995914	1.472576	3.32314	3.315115	2.134409
pseudogen	ribosomal_	116	130	99	177	102	249	6.43727	8.501473	7.239586	8.497281	6.35906	13.7326
pseudogen	-	2	0	1	0	0	0	0.278637	0	0.183588	0	0	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.049673	0	0
protein_co	chromoson	720	537	453	531	366	486	15.3948	13.53078	12.76364	9.821978	8.791674	10.32731
pseudogen	-	2	0	0	0	3	0	0.173293	0	0	0	0.292026	0
protein_co	voltage-dep	5660	4933	4357	8565	6037	6851	153.4286	157.5825	155.6368	200.8539	183.8485	184.5667
protein_co	zinc_finger_	207	185	159	589	460	539	4.034899	4.249532	4.08408	9.93209	10.07324	10.44145
pseudogen	-	2	1	5	9	1	12	0.080092	0.047192	0.263855	0.311793	0.044989	0.477586
pseudogen	-	0	2	3	0	0	0	0	0.256212	0.429753	0	0	0
protein_co	thioredoxi	1052	949	762	2239	1519	1719	32.81905	34.8886	31.32565	60.42649	53.23743	53.29614
pseudogen	-	0	0	0	1	0	0	0	0	0	0.121806	0	0
pseudogen	-	13	17	5	1	9	10	1.917083	2.954294	0.971633	0.127574	1.49104	1.465572
pseudogen	keratin_18_	1	0	0	1	2	0	0.075094	0	0	0.064963	0.168726	0
pseudogen	solute_carr	2	2	6	6	0	0	0.117516	0.138486	0.464572	0.304987	0	0
pseudogen	-	0	2	0	0	0	1	0	0.15695	0	0	0	0.066181
pseudogen	family_with	1	0	1	11	26	7	0.063708	0	0.083951	0.606243	1.860859	0.443199
pseudogen	-	13	4	8	2	3	4	1.315933	0.477153	1.067125	0.175139	0.341162	0.402402
protein_co	hexosamini	114	119	104	180	99	146	0.873538	1.074561	1.050135	1.193198	0.852239	1.111833
protein_co	NADH_deh	925	808	649	1434	977	1305	27.68254	28.49592	25.59433	37.12585	32.84792	38.81364
pseudogen	ribosomal_	5	5	2	7	1	7	0.298764	0.352075	0.157479	0.361842	0.067129	0.415687
protein_co	leptin_rece	1187	1108	961	2100	1561	1633	13.59605	14.95578	14.50509	20.80868	20.08696	18.58908
protein_co	limb_bud_	321	270	323	260	416	397	5.794088	5.74316	7.682762	4.05991	8.435725	7.121643
protein_co	adenosine_	69	41	38	282	219	234	2.257681	1.5809	1.638445	7.982257	8.050201	7.609201
protein_co	protein_ph	2617	2310	2209	4187	2857	3048	28.31526	29.45343	31.49542	39.19068	34.72771	32.77491
pseudogen	-	0	1	0	5	4	7	0	0.070895	0	0.260221	0.270345	0.418521
pseudogen	-	0	1	0	0	0	0	0	0.081128	0	0	0	0

protein_co	sulfotransfe	0	0	0	0	0	3	0	0	0	0	0	0.066628
protein_co	G-protein_	37	42	26	346	256	292	1.327112	1.775261	1.228893	10.73606	10.31561	10.40874
protein_co	NCK_intera	296	251	191	677	500	613	5.242735	5.238983	4.457941	10.37332	9.949133	10.79037
protein_co	activating_	1455	1276	1063	1551	1141	1338	29.35562	30.33794	28.26157	27.07092	25.86205	26.82835
pseudogen	-	0	1	1	1	1	4	0	0.081874	0.091553	0.060104	0.078052	0.276189
protein_co	three_prim	94	84	72	144	99	119	2.265113	2.38533	2.28628	3.00184	2.680071	2.849828
pseudogen	-	0	0	0	1	0	1	0	0	0	0.089802	0	0.103165
pseudogen	SEC14-like_	23	11	9	31	26	15	0.558296	0.314656	0.287881	0.65097	0.709021	0.361857
protein_co	sphingosin	824	613	634	1062	860	858	5.129145	4.496611	5.200461	5.718805	6.014026	5.307802
pseudogen	ribosomal_	0	1	1	0	0	0	0	0.107012	0.119663	0	0	0
protein_co	solute_carr	1037	751	663	1426	1056	1315	14.0841	12.0198	11.86584	16.75455	16.11251	17.74948
pseudogen	ribosomal_	43	45	48	6	11	9	4.169346	5.141846	6.133036	0.503285	1.198233	0.867265
pseudogen	-	1	1	0	0	0	0	0.096962	0.114263	0	0	0	0
pseudogen	-	0	1	0	8	3	4	0	0.10926	0	0.641666	0.312483	0.368575
pseudogen	high_mobil	17	32	11	89	63	94	1.598574	3.546017	1.363048	7.239969	6.655387	8.784584
pseudogen	phosphatid	93	75	80	88	103	109	5.501131	5.228022	6.235824	4.503133	6.844714	6.407745
protein_co	family_with	1	1	1	1	0	5	0.076284	0.089896	0.100523	0.065993	0	0.379064
protein_co	chloride_in	5916	4842	4172	13681	8587	11413	200.7685	193.6419	186.5721	401.6505	327.3844	384.9257
pseudogen	high_mobil	6	0	2	4	0	5	1.240805	0	0.545026	0.715608	0	1.027618
protein_co	dimethylar	1418	1205	1064	1410	1142	1655	44.47294	44.53626	43.97401	38.25619	40.23785	51.58546
pseudogen	RAB5C_mer	5	0	0	2	8	2	0.456388	0	0	0.157927	0.820357	0.181428
pseudogen	anaphase_p	0	4	0	0	0	0	0	0.448833	0	0	0	0
pseudogen	SERPINE1_r	1	1	5	2	2	9	0.045639	0.053783	0.300704	0.078964	0.102545	0.408212
protein_co	ribosomal_	3194	3337	2430	3330	3718	4310	123.0666	151.5195	123.3805	110.9973	160.9399	165.0412
antisense	-	29	22	25	19	15	7	0.329037	0.294156	0.373785	0.186494	0.1912	0.078932
pseudogen	ribosomal_	0	0	0	0	3	4	0	0	0	0	0.355434	0.419235
pseudogen	ribosomal_	898	709	597	1051	807	889	14.48538	13.47742	12.69003	14.66626	14.62433	14.25164
pseudogen	-	0	1	0	1	1	1	0	0.043445	0	0.031893	0.041418	0.036639
pseudogen	-	0	0	1	0	0	2	0	0	0.143546	0	0	0.216519
pseudogen	-	6	5	3	4	3	5	0.403616	0.396364	0.265934	0.232777	0.226719	0.33427
protein_co	ATPase_H+_	46	18	16	5	11	14	1.533555	0.707166	0.702905	0.144203	0.411987	0.463852
pseudogen	metallothic	0	0	0	5	2	0	0	0	0	1.251336	0.65001	0
protein_co	zinc_finger_	270	243	211	300	269	254	4.029904	4.274096	4.150001	3.873603	4.510578	3.767682
pseudogen	actin_beta_	2	0	2	1	1	0	0.094285	0	0.124244	0.040783	0.052962	0
pseudogen	-	0	0	1	0	0	0	0	0	0.207013	0	0	0
pseudogen	-	0	1	0	0	0	0	0	0.198056	0	0	0	0
pseudogen	-	0	0	0	6	2	5	0	0	0	0.309801	0.134106	0.296584
pseudogen	-	0	0	0	0	2	1	0	0	0	0	0.262008	0.11589
protein_co	general_tra	0	0	0	0	1	0	0	0	0	0	0.03428	0
protein_co	DEAD_(Asp	17	7	18	26	7	23	0.334696	0.162408	0.466991	0.442831	0.154828	0.450027
pseudogen	Obg-like_AT	1	5	3	2	0	0	0.044526	0.262354	0.176022	0.077038	0	0
lincRNA	zinc_finger_	9	2	6	10	12	12	0.864735	0.226453	0.759673	0.831196	1.295301	1.14586
protein_co	zinc_finger_	84	78	88	217	180	169	1.031557	1.128797	1.424071	2.30535	2.483337	2.062578
protein_co	Uncharacte	3	0	3	0	3	0	0.601602	0	0.792765	0	0.675863	0

pseudogen	cofilin_1_(r	1	0	0	3	0	2	0.10546	0	0	0.273699	0	0.209618
pseudogen	-	111	66	90	127	124	91	8.300071	5.815805	8.868214	8.21534	10.41669	6.76254
pseudogen	suppressor_	8	4	2	1	0	5	0.426943	0.251563	0.140652	0.046168	0	0.265192
pseudogen	-	21	40	33	3	4	1	1.492296	3.349677	3.090186	0.184425	0.319334	0.070623
protein_co	epithelial_r	109	99	77	1371	1107	1370	1.110365	1.188452	1.03363	12.08203	12.66882	13.86978
pseudogen	calponin_2	0	0	0	0	2	3	0	0	0	0	0.132169	0.17538
pseudogen	voltage-dep	0	0	0	2	2	0	0	0	0	0.107762	0.139943	0
protein_co	potassium_	310	275	168	137	154	190	5.379124	5.623279	3.841439	2.056522	3.002062	3.276522
pseudogen	ribosomal_	8	5	1	7	2	12	0.750936	0.553083	0.123694	0.568426	0.210908	1.119448
pseudogen	-	1	2	2	2	1	0	0.066845	0.157545	0.17617	0.115654	0.075096	0
lincRNA	-	2	0	0	5	0	0	0.139686	0	0	0.302104	0	0
pseudogen	eukaryotic_	0	0	0	0	0	1	0	0	0	0	0	0.077831
protein_co	chromoson	84	101	78	67	50	78	2.423457	3.433875	2.965415	1.672222	1.620597	2.236456
pseudogen	Y_box_binc	29	22	13	24	19	23	1.574655	1.407723	0.930177	1.127358	1.159018	1.241152
pseudogen	TAF9B_RNA	0	3	1	0	0	0	0	0.250889	0.093516	0	0	0
pseudogen	-	0	0	1	0	5	4	0	0	0.17057	0	0.727089	0.514563
pseudogen	nucleophos	13	10	13	40	13	27	0.790164	0.716277	1.041243	2.103279	0.8877	1.630975
pseudogen	ribosomal_	5	6	0	1	0	1	0.433232	0.612645	0	0.074957	0	0.086111
protein_co	CDNA_FLJ2	32	38	32	47	59	65	0.943269	1.320008	1.242998	1.198524	1.95383	1.904183
protein_co	protein_ph	8	8	4	1	9	7	0.21686	0.255556	0.142884	0.023451	0.274083	0.188581
pseudogen	ribosomal_	3	2	6	0	5	1	0.131913	0.103634	0.347658	0	0.246993	0.043699
pseudogen	-	1	0	0	0	0	0	0.141553	0	0	0	0	0
protein_co	solute_carr	39	43	28	20	8	26	0.489033	0.635403	0.462665	0.216954	0.112697	0.324009
protein_co	leukotriene	68	58	39	132	73	104	0.875909	0.880411	0.661987	1.470914	1.056385	1.331353
antisense	-	9	1	0	7	8	0	0.199945	0.02618	0	0.134533	0.199667	0
protein_co	leukotriene	2	13	9	6	10	17	0.034244	0.262303	0.203063	0.088872	0.192354	0.289275
pseudogen	-	1	0	0	0	1	1	0.064958	0	0	0	0.072977	0.064557
protein_co	deoxyribon	429	354	296	362	370	376	4.80061	4.6682	4.364813	3.504376	4.651467	4.181544
protein_co	Interleukin	1	8	2	3	1	1	0.113122	1.066457	0.298134	0.293583	0.127085	0.112423
protein_co	casein_kina	3512	2963	2232	4339	3308	4114	66.61726	66.23248	55.79063	71.20081	70.49313	77.55435
protein_co	interferon_	17	24	6	9	14	22	0.489661	0.814638	0.227737	0.22426	0.453027	0.629766
protein_co	galactose-1	71	64	48	95	56	86	1.464852	1.556046	1.305003	1.695595	1.297994	1.76337
protein_co	hemoglobi	0	0	1	22	11	12	0	0	0.077001	1.112115	0.722114	0.696875
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.282113
protein_co	claudin_9	0	0	0	34	28	35	0	0	0	0.759592	0.812354	0.898289
pseudogen	selenophos	0	0	0	1	0	0	0	0	0	0.038846	0	0
pseudogen	-	0	0	2	1	1	2	0	0	0.347081	0.113928	0.14795	0.261761
pseudogen	keratin_18_	0	0	0	1	1	0	0	0	0	0.035808	0.046502	0
protein_co	integrin_al	1330	1092	1537	1134	1025	897	8.753297	8.469344	13.32996	6.456484	7.578669	5.867081
protein_co	Uncharacte	4	0	2	5	0	0	3.715157	0	2.447834	4.017448	0	0
processed_	-	11	14	2	27	21	28	0.111948	0.167902	0.026822	0.237711	0.240099	0.283198
pseudogen	coiled-coil-	2	1	5	0	0	0	0.323798	0.190788	1.066717	0	0	0
protein_co	nudix_(nuc	90	63	59	183	147	170	1.605895	1.324714	1.387271	2.824806	2.946734	3.014624
protein_co	zinc_finger_	6	4	2	172	149	143	0.128446	0.10091	0.05642	3.185367	3.583466	3.042381

pseudogen	-	0	0	0	1	1	3	0	0	0	0.104088	0.135173	0.358732
processed_	-	47	24	8	191	119	160	0.938599	0.564808	0.210527	3.299733	2.669798	3.175499
pseudogen	-	0	0	0	0	1	1	0	0	0	0	0.06416	0.056757
pseudogen	-	9	6	11	86	116	75	0.270107	0.212203	0.435032	2.232826	3.911115	2.236992
protein_co	Tax1_(hum	17	11	7	7	7	13	0.653593	0.498377	0.354643	0.232819	0.302347	0.496719
pseudogen	ribosomal_	0	0	0	0	1	0	0	0	0	0	0.074159	0
protein_co	adaptor-rel	142	104	73	390	306	367	2.279448	1.967351	1.544184	5.41588	5.518384	5.854869
pseudogen	-	0	1	0	0	0	0	0	0.052648	0	0	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.190019	0
protein_co	zinc_finger_	11	9	8	311	249	339	0.2521	0.243069	0.241604	6.166	6.41104	7.721283
antisense	-	0	3	1	3	0	0	0	0.427313	0.159277	0.313691	0	0
protein_co	carbohydra	402	319	321	538	543	499	8.003866	7.48465	8.421968	9.266571	12.1457	9.873791
protein_co	transmemb	5	4	0	7	4	6	0.144727	0.136441	0	0.175283	0.130073	0.172599
protein_co	myocyte_e	0	0	0	4	0	0	0	0	0	0.108851	0	0
pseudogen	-	1	3	6	6	10	10	0.198281	0.700986	1.567714	1.029189	2.227562	1.970564
protein_co	glucosidase	131	145	94	169	96	137	1.537072	2.004925	1.453402	1.715429	1.265445	1.597545
pseudogen	-	0	4	1	1	0	0	0	0.284227	0.079457	0.052163	0	0
pseudogen	ribonucleo	4	0	2	0	1	0	0.182084	0	0.119971	0	0.05114	0
protein_co	tubulin_tyr	451	441	327	243	190	286	4.520331	5.20882	4.318931	2.106992	2.139421	2.848849
protein_co	replication_	763	520	480	5191	3926	4546	12.27035	9.854684	10.17205	72.21814	70.93027	72.65598
protein_co	mitochond	1268	979	658	2003	1364	1618	73.0459	66.46092	49.95021	99.82068	88.27546	92.63279
protein_co	zinc_finger_	102	97	65	42	54	61	1.311312	1.469551	1.101169	0.467109	0.779917	0.779373
pseudogen	phosphogly	1	3	1	1	2	1	0.060024	0.212203	0.079097	0.051926	0.134866	0.059653
processed_	-	4	3	0	0	0	0	0.086153	0.076145	0	0	0	0
protein_co	small_integ	581	547	368	860	555	782	11.08023	12.29326	9.248158	14.18842	11.8909	14.82139
lincRNA	urothelial_	0	0	0	333	189	208	0	0	0	6.593617	4.8599	4.731398
protein_co	F-box_prot	26	26	13	59	52	72	0.461437	0.543775	0.30403	0.905845	1.036791	1.269933
pseudogen	-	3	1	0	1	1	0	0.219369	0.086171	0	0.063258	0.082149	0
protein_co	tetraspanin	2665	2056	1596	1565	1132	1619	50.80582	46.18983	40.09442	25.81033	24.24441	30.67416
pseudogen	cleavage_ar	2	4	10	6	0	2	0.028387	0.066904	0.187033	0.073671	0	0.028211
pseudogen	guanine_nu	0	0	0	2	3	0	0	0	0	0.085846	0.167224	0
protein_co	copine_I	3107	2581	2028	2555	1666	2215	74.63143	73.05931	64.19235	53.09265	44.95775	52.87664
protein_co	ADP-ribosy	656	493	424	1042	613	816	14.82257	13.12725	12.62468	20.3681	15.56071	18.32397
pseudogen	-	5	0	0	3	0	0	0.579223	0	0	0.300649	0	0
protein_co	single-pass_	0	0	1	0	1	0	0	0	0.037792	0	0.032219	0
protein_co	WEE1_hom	1	3	0	3	0	0	0.017295	0.061144	0	0.044886	0	0
protein_co	HCG19991	41	31	20	23	23	27	1.023376	0.911843	0.657834	0.496641	0.644953	0.669769
protein_co	Uncharacte	3	3	1	3	2	10	0.413602	0.487404	0.181675	0.357804	0.30977	1.370158
pseudogen	lactate_deh	65	87	87	84	71	65	3.448061	5.43861	6.081569	3.854818	4.231253	3.426767
protein_co	LYR_motif_	645	496	401	962	556	794	22.9328	20.78194	18.78783	29.58935	22.2086	28.05612
protein_co	c-myc_binc	111	141	93	705	401	530	1.818771	2.722584	2.008042	9.993262	7.381567	8.630593
protein_co	-	1	3	1	5	1	10	0.027559	0.09743	0.036316	0.119206	0.030961	0.273889
pseudogen	thioredoxin	2	1	3	1	4	3	0.177654	0.104677	0.351157	0.076844	0.399167	0.264836
protein_co	transmemb	0	0	0	0	0	1	0	0	0	0	0	0.012626

pseudogen	-	260	206	215	400	324	330	8.868981	8.280846	9.664372	11.80384	12.41636	11.18727
protein_co	progressive	51	49	32	5	14	4	0.800709	0.906583	0.662048	0.067911	0.246934	0.062413
pseudogen	-	0	1	1	0	0	0	0	0.084881	0.094916	0	0	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.041303	0
protein_co	ALG3_alph	918	725	539	1622	980	1088	28.63868	26.65357	22.15817	43.77479	34.34673	33.73252
pseudogen	archaelysin	191	155	144	115	69	98	2.95233	2.823386	2.933113	1.537773	1.198201	1.505453
pseudogen	pleckstrin_	307	239	230	169	230	259	3.241501	2.973807	3.200151	1.543681	2.728253	2.717798
pseudogen	prothymos	7	6	11	34	12	35	1.112874	1.124103	2.304493	4.676165	2.143276	5.530005
antisense	-	12	14	12	8	14	3	1.10678	1.521652	1.458466	0.638312	1.450632	0.274986
pseudogen	exportin_t	8	14	5	4	2	1	0.176617	0.364232	0.145461	0.076395	0.049605	0.021941
protein_co	ST7_overla	4	3	0	5	11	11	0.134368	0.118758	0	0.145301	0.415124	0.36723
protein_co	zinc_finger	1	0	1	9	8	15	0.014028	0	0.018485	0.109218	0.126075	0.209118
pseudogen	-	0	0	1	0	0	6	0	0	0.115502	0	0	0.522656
pseudogen	ubiquitin-c	1	1	1	4	0	2	0.12032	0.14179	0.158553	0.416354	0	0.239155
protein_co	SH3_domai	320	392	180	220	199	286	5.329071	7.692982	3.950107	3.169474	3.723091	4.733444
protein_co	Putative_tr	605	519	416	1144	812	974	29.93393	30.26096	27.12292	48.96631	45.135	47.89354
pseudogen	-	18	32	10	13	12	15	0.240459	0.503762	0.176037	0.150236	0.180094	0.199145
pseudogen	eukaryotic_	19	15	9	7	10	2	0.74731	0.695257	0.466471	0.238182	0.441872	0.078178
pseudogen	-	2	1	0	5	3	5	0.134539	0.079273	0	0.290971	0.226719	0.33427
pseudogen	CTAGE_fam	1	1	5	0	4	0	0.022031	0.025962	0.145159	0	0.099003	0
protein_co	chromoson	3	0	1	2	2	7	0.129863	0	0.057043	0.074896	0.097262	0.301143
protein_co	IQ_motif_c	6	0	4	0	0	0	0.217566	0	0.191132	0	0	0
pseudogen	tubulin_be	0	3	1	2	0	0	0	0.455385	0.16974	0.222866	0	0
pseudogen	heterogene	66	50	43	63	64	93	3.632126	3.242605	3.118317	2.999305	3.956818	5.086389
protein_co	chromoson	68	44	37	104	69	82	1.788369	1.363666	1.282286	2.366163	2.038668	2.143245
protein_co	Uncharacte	2	2	13	0	4	4	1.604273	1.890537	13.74125	0	3.604601	3.18873
pseudogen	-	0	0	2	1	6	0	0	0	0.280738	0.092151	0.718019	0
protein_co	Uncharacte	2	3	6	0	0	1	0.022343	0.039494	0.088327	0	0	0.011102
pseudogen	CTAGE_fam	0	0	2	0	0	0	0	0	0.059297	0	0	0
protein_co	fission_1_(r	1554	1274	1025	1355	1050	1660	81.861	79.08653	71.15161	61.74877	62.13902	86.9048
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.096187
pseudogen	ankyrin_rep	151	105	185	97	219	158	4.493586	3.682244	7.254754	2.497186	7.321656	4.672861
pseudogen	-	0	0	2	0	0	0	0	0	0.119663	0	0	0
protein_co	SNRPN_ups	149	95	155	144	231	239	2.457386	1.846366	3.368632	2.05453	4.280043	3.91737
pseudogen	angiogenic_	0	0	0	2	0	2	0	0	0	0.044186	0	0.050761
protein_co	angiogenin	11	7	10	12	9	16	0.476556	0.357377	0.570894	0.449744	0.438039	0.688891
pseudogen	-	6	6	8	0	0	0	0.389272	0.458733	0.683954	0	0	0
pseudogen	-	78	76	50	2	14	9	0.842047	0.966857	0.71129	0.018678	0.169793	0.096559
pseudogen	keratin_8_p	1	2	8	0	2	1	0.036714	0.086529	0.387036	0	0.082491	0.036487
pseudogen	-	2	0	2	4	0	1	0.105776	0	0.139387	0.183013	0	0.052561
pseudogen	phosducin-	2	0	2	0	5	3	0.148087	0	0.195142	0	0.415916	0.220758
pseudogen	ribosomal_	1	0	0	1	1	0	0.117909	0	0	0.102002	0.132463	0
protein_co	chromoson	0	0	0	1	0	0	0	0	0	0.03239	0	0
processed_	RSBN1L_an	65	76	71	137	141	153	1.69599	2.336849	2.441199	3.092385	4.133122	3.967447

protein_co	speedy_hor	61	77	47	101	115	84	1.013941	1.508275	1.029474	1.452336	2.147482	1.387623
protein_co	metallo-be	31	29	16	31	20	39	1.094844	1.206967	0.744638	0.947142	0.793541	1.368878
protein_co	Uncharacte	3	0	0	0	0	1	0.348296	0	0	0	0	0.115382
pseudogen	-	78	46	34	53	36	44	1.75346	1.218614	1.007198	1.030718	0.909186	0.983023
processed_	forkhead_b	1	0	0	58	118	73	0.039508	0	0	1.982341	5.237432	2.866288
protein_co	SOGA_fami	6	6	4	11	9	11	0.026878	0.031674	0.023613	0.042629	0.045294	0.048972
lincRNA	-	13	0	0	1	0	3	1.068685	0	0	0.071116	0	0.245097
antisense	-	25	15	18	7	12	9	0.272723	0.192832	0.258755	0.066061	0.147066	0.097574
pseudogen	-	3	1	0	0	0	0	0.169502	0.066582	0	0	0	0
protein_co	neuralized_	42	31	32	11	17	19	0.346127	0.301062	0.347513	0.078423	0.157393	0.155614
pseudogen	ribosomal_	3	3	5	4	1	0	0.29521	0.347887	0.648358	0.340512	0.11055	0
protein_co	EF-hand_ca	2	1	0	0	4	0	0.150829	0.088871	0	0	0.338894	0
protein_co	HAUS_augn	160	156	162	456	309	382	1.507217	1.731759	2.01097	3.716068	3.270117	3.576258
pseudogen	-	0	1	0	0	1	0	0	0.078673	0	0	0.075001	0
pseudogen	ribosomal_	0	0	0	4	0	0	0	0	0	0.538811	0	0
protein_co	V-set_and_	0	3	2	2	12	13	0	0.063039	0.046994	0.030851	0.240388	0.230375
pseudogen	ribosomal_	91	78	57	108	58	120	6.144937	6.206942	5.072075	6.309033	4.400004	8.053171
pseudogen	-	4	0	2	12	4	3	0.131286	0	0.086501	0.340723	0.147491	0.097856
antisense	KANSL1_an	9	16	5	23	11	19	0.715419	1.498804	0.523748	1.581644	0.982335	1.501001
protein_co	lipocalin-li	8	13	3	0	0	0	0.114282	0.218845	0.056473	0	0	0
protein_co	BBSome_in	316	267	226	250	207	224	3.550372	3.535128	3.346032	2.429908	2.6128	2.501177
pseudogen	keratin_18	0	0	0	0	0	4	0	0	0	0	0	0.163144
pseudogen	leucine_ric	28	18	11	59	49	61	0.300131	0.22737	0.155375	0.547102	0.590063	0.649819
pseudogen	-	0	0	0	4	1	0	0	0	0	0.606608	0.19694	0
antisense	-	4	6	2	1	4	4	0.098084	0.17338	0.064626	0.021213	0.110192	0.097479
pseudogen	-	4	7	4	0	5	16	0.271841	0.560609	0.35822	0	0.381745	1.080648
protein_co	arsenic_(+3	3	0	0	0	0	0	0.066066	0	0	0	0	0
pseudogen	family_with	8	3	7	7	9	12	0.591519	0.261401	0.682043	0.447755	0.747602	0.8818
pseudogen	reticulocall	257	179	179	166	198	209	14.86977	12.20481	13.64768	8.308872	12.8702	12.01785
protein_co	perilipin_5	0	1	0	0	0	0	0	0.025258	0	0	0	0
pseudogen	-	0	0	0	3	6	2	0	0	0	0.188732	0.490186	0.144544
pseudogen	SWI/SNF_re	6	1	2	0	2	0	0.261222	0.051306	0.114742	0	0.097822	0
protein_co	-	0	0	3	0	0	2	0	0	3.875738	0	0	1.948669
pseudogen	-	158	136	149	191	94	236	11.00615	11.16412	13.67728	11.50999	7.356232	16.33805
protein_co	SEC14-like_	0	0	2	0	0	0	0	0	0.081452	0	0	0
protein_co	serine_pep	0	0	0	1	0	0	0	0	0	0.044813	0	0
protein_co	HIG1_hypo	1	0	0	2	1	1	0.142698	0	0	0.246894	0.160312	0.141817
protein_co	notochord_	2	0	0	0	0	3	0.038517	0	0	0	0	0.057418
pseudogen	keratin_42_	0	0	1	0	1	0	0	0	0.024098	0	0.020544	0
protein_co	protein_ph	1408	1130	1093	3898	2136	2420	18.38247	17.38548	18.80426	44.02568	31.32936	31.39975
pseudogen	-	1	3	0	0	2	0	0.043681	0.154425	0	0	0.098145	0
protein_co	StAR-relate	244	175	138	902	629	694	6.580541	5.56182	4.904398	21.04463	19.05774	18.6012
pseudogen	zinc_finger_	1	3	3	0	3	0	0.015381	0.054376	0.060805	0	0.051838	0
pseudogen	ribosomal_	4	3	0	0	0	2	0.541596	0.478678	0	0	0	0.269126

pseudogen	GTF2I_repe	2	0	1	4	1	0	0.035177	0	0.023177	0.060862	0.019759	0
lincRNA	-	0	0	1	0	0	0	0	0	0.113252	0	0	0
lincRNA	maternally_	13	2	4	1	1	4	0.141408	0.025637	0.057336	0.00941	0.01222	0.043241
pseudogen	leucine_ric	0	0	0	6	8	4	0	0	0	0.073929	0.128008	0.05662
pseudogen	-	7	0	5	3	1	1	0.114485	0	0.107759	0.042446	0.018374	0.016254
antisense	-	0	0	0	0	2	8	0	0	0	0	0.299627	1.060233
protein_co	NUT_family	22	19	14	64	53	60	0.210121	0.213849	0.176202	0.528798	0.568685	0.569519
pseudogen	glyceraldeh	0	0	1	0	0	0	0	0	0.071552	0	0	0
protein_co	cytoplasmi	10	24	15	0	0	0	0.108441	0.306699	0.214348	0	0	0
pseudogen	high_mobil	5	2	0	1	1	3	0.980389	0.462131	0	0.169626	0.220281	0.584601
pseudogen	-	0	2	0	0	3	0	0	0.507217	0	0	0.725316	0
protein_co	echinoderm	30	9	25	8	16	9	0.190893	0.067487	0.209625	0.044037	0.114377	0.056914
protein_co	transmemb	0	0	0	9	1	4	0	0	0	0.2338	0.033736	0.119374
pseudogen	nucleophos	0	0	0	5	0	0	0	0	0	0.274245	0	0
pseudogen	solute_carr	0	1	0	0	0	0	0	0.016221	0	0	0	0
pseudogen	polymerase	3	0	0	1	3	0	0.135054	0	0	0.038945	0.151724	0
pseudogen	-	0	0	3	0	2	2	0	0	0.23729	0	0.134866	0.119306
protein_co	defensin_b	0	0	0	0	0	4	0	0	0	0	0	1.131485
pseudogen	-	2	0	0	0	0	3	0.175884	0	0	0	0	0.262196
lincRNA	-	9	14	10	1	1	13	0.371661	0.681301	0.544175	0.035725	0.046393	0.533528
pseudogen	-	1	0	0	0	1	0	0.036187	0	0	0	0.040653	0
pseudogen	heterogene	1	0	0	1	3	9	0.046562	0	0	0.04028	0.156929	0.41647
pseudogen	-	28	23	23	110	82	124	1.457569	1.410932	1.577734	4.953667	4.795502	6.415086
protein_co	zinc_finger_	1206	979	1008	605	621	872	10.50977	10.05392	11.57554	4.561043	6.07976	7.552173
pseudogen	keratin_8_p	0	2	0	0	0	0	0	0.097786	0	0	0	0
pseudogen	ribosomal_	0	0	0	6	0	0	0	0	0	0.324815	0	0
pseudogen	ribosomal_	3	2	1	0	5	3	0.280111	0.220063	0.123039	0	0.524479	0.278381
protein_co	chromoson	2	2	3	0	0	0	0.02189	0.025796	0.043269	0	0	0
protein_co	Rho_guanir	24	11	11	12	8	6	0.283359	0.153048	0.171141	0.122566	0.106112	0.070402
protein_co	chromoson	0	3	0	3	0	6	0	0.195573	0	0.14357	0	0.329869
protein_co	interferon-i	805	775	615	2136	1501	1753	18.73297	21.25296	18.85909	43.00064	39.24103	40.54173
protein_co	Uncharacte	2	2	3	1	2	4	0.066218	0.078033	0.130888	0.028642	0.074391	0.131617
protein_co	calpain_14	3	0	1	7	0	2	0.041577	0	0.018263	0.083925	0	0.027547
protein_co	zinc_finger_	362	319	293	500	540	588	4.249366	4.412791	4.532293	5.077484	7.121285	6.859659
processed_	-	187	162	129	435	269	334	2.0886	2.132239	1.898621	4.203064	3.375321	3.707404
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.069595
antisense	-	1	4	0	3	11	13	0.075738	0.357011	0	0.196562	0.935959	0.978516
pseudogen	-	0	0	0	2	0	0	0	0	0	0.071841	0	0
protein_co	heterogene	1187	933	934	1396	1261	1573	12.30728	11.39987	12.76124	12.5216	14.68843	16.20875
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.119306
protein_co	methyltran	170	98	109	225	163	245	3.135878	2.130313	2.649546	3.590507	3.377901	4.491443
pseudogen	ribosomal_	0	0	0	0	2	0	0	0	0	0	0.234619	0
pseudogen	heterogene	0	0	0	3	0	3	0	0	0	0.143122	0	0.164419
pseudogen	septin_7_p	183	150	173	274	170	193	3.222955	3.11316	4.014986	4.174617	3.363575	3.378081

antisense	-	1	6	7	12	16	10	0.030235	0.213779	0.278894	0.31387	0.543469	0.30048
antisense	-	4	0	2	0	2	6	0.32232	0	0.212369	0	0.181053	0.480494
sense_intrc	-	2	0	2	2	4	4	0.074147	0	0.097708	0.064144	0.166599	0.147378
pseudogen	-	4	3	3	42	18	27	0.026932	0.023803	0.026617	0.244634	0.136152	0.180666
protein_co	membrane	0	0	2	0	0	0	0	0	0.14399	0	0	0
pseudogen	polymerase	124	106	91	161	150	228	1.015262	1.02275	0.981822	1.140369	1.379738	1.855243
pseudogen	-	1	1	2	3	4	2	0.064799	0.076362	0.170779	0.168172	0.291192	0.128798
protein_co	membrane	0	0	0	4	0	2	0	0	0	0.162841	0	0.093536
pseudogen	-	28	22	19	534	336	488	0.807819	0.747973	0.722345	13.32786	10.89041	13.99218
lincRNA	-	4	3	4	0	0	0	0.177208	0.156622	0.233517	0	0	0
pseudogen	cytochrom	0	1	0	0	0	2	0	0.200604	0	0	0	0.338354
protein_co	fer-1-like_6	79	79	71	0	1	2	0.691181	0.814515	0.818574	0	0.009829	0.01739
pseudogen	myosin_ph	20	11	4	10	3	13	0.972286	0.630179	0.256247	0.420559	0.163846	0.628083
pseudogen	keratin_16	0	0	0	14	12	38	0	0	0	0.330678	0.368082	1.031116
pseudogen	DEAD/H_(A	54	72	67	337	291	459	0.727619	1.143272	1.189651	3.928285	4.405063	6.146564
protein_co	mature_T-c	1	5	16	29	26	10	0.023281	0.137176	0.490859	0.584067	0.680024	0.231372
pseudogen	UPF3_regul	4	7	11	9	4	11	0.187071	0.38579	0.677912	0.364126	0.210162	0.511267
processed_	-	5	7	17	10	7	8	0.341996	0.56423	1.532268	0.591717	0.537896	0.543814
protein_co	RAD51_ass	3	3	10	0	0	0	0.042648	0.050259	0.187334	0	0	0
pseudogen	zinc_finger	1	0	1	0	0	0	0.087651	0	0.115502	0	0	0
pseudogen	-	0	0	0	0	4	5	0	0	0	0	0.357213	0.395
processed_	long_interg	0	0	0	0	0	1	0	0	0	0	0	0.023775
pseudogen	apolipopro	0	2	0	0	0	0	0	0.170691	0	0	0	0
pseudogen	keratin_16	0	0	0	17	21	16	0	0	0	0.397641	0.637893	0.429941
pseudogen	split_hand/	0	2	0	0	0	0	0	0.597012	0	0	0	0
pseudogen	serine/argi	2	6	0	10	16	18	0.199777	0.706276	0	0.86413	1.795499	1.786892
processed_	-	0	0	0	4	0	3	0	0	0	0.057213	0	0.049295
protein_co	Uncharacte	2	0	1	1	1	0	0.410395	0	0.2704	0.177515	0.230527	0
protein_co	smoothelin	2	0	0	3	0	4	0.051349	0	0	0.066633	0	0.102064
pseudogen	mediator_c	0	0	1	0	0	3	0	0	0.122177	0	0	0.276431
pseudogen	transmemb	0	0	1	0	1	0	0	0	0.202212	0	0.172394	0
pseudogen	family_with	0	0	0	0	0	1	0	0	0	0	0	0.111235
pseudogen	ubiquitin_s	0	2	0	0	0	0	0	0.039201	0	0	0	0
processed_	long_interg	15	9	9	4	9	4	0.386996	0.27363	0.305979	0.089277	0.260859	0.102562
protein_co	chromoson	3	2	3	12	16	9	0.037117	0.02916	0.048911	0.128438	0.222392	0.110663
pseudogen	deoxyuridi	0	0	0	0	0	9	0	0	0	0	0	0.968357
lincRNA	-	0	0	0	1	0	0	0	0	0	0.095018	0	0
protein_co	CDNA_FLJ2	0	0	0	0	1	2	0	0	0	0	0.037572	0.066474
processed_	HLA-F_anti	6	5	5	0	0	1	0.112044	0.110031	0.123039	0	0	0.018559
protein_co	Uncharacte	0	0	0	0	0	1	0	0	0	0	0	0.011589
protein_co	zinc_finger	180	135	93	478	300	363	4.745707	4.194394	3.231068	10.90233	8.885844	9.511404
protein_co	Rho_guanir	47	43	45	0	2	12	0.300329	0.323799	0.378919	0	0.014357	0.076206
protein_co	TBC1_dom	0	0	0	4	0	0	0	0	0	0.048567	0	0
protein_co	leucine_ric	7	12	11	38	39	30	0.199133	0.402285	0.412357	0.935174	1.246406	0.848158

processed_	-	3	2	3	1	2	3	0.197296	0.155001	0.259987	0.056893	0.147766	0.196077
protein_co	isoprenoid_	22	24	22	37	54	54	0.626521	0.805436	0.825601	0.911544	1.727649	1.528326
antisense	-	0	2	2	0	0	0	0	0.054919	0.061411	0	0	0
pseudogen	coiled-coil-	0	0	0	1	3	0	0	0	0	0.071561	0.278793	0
pseudogen	peptidylpr	19	15	10	38	14	28	2.015789	1.875383	1.398062	3.487692	1.668663	2.952291
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.070813
pseudogen	poly_(ADP-	66	35	66	75	92	80	1.423261	0.889438	1.87551	1.399152	2.228833	1.714511
pseudogen	-	0	1	0	0	0	0	0	0.310387	0	0	0	0
pseudogen	ribosomal_	1	0	0	2	3	0	0.065118	0	0	0.112666	0.219468	0
pseudogen	A_kinase_(F	0	0	0	3	1	0	0	0	0	0.050532	0.021874	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.051718	0
protein_co	-	0	1	0	0	0	0	0	0.034583	0	0	0	0
protein_co	acyl-CoA_sy	2	1	1	4	0	0	0.049431	0.029126	0.032569	0.085526	0	0
protein_co	chromoson	461	406	357	1736	1409	1543	3.597023	3.733149	3.670669	11.71804	12.351	11.96514
protein_co	Uncharacte	12	9	2	9	18	14	0.623446	0.55102	0.136925	0.404505	1.050605	0.722862
protein_co	collagen_ty	10	9	15	0	2	2	0.123781	0.131281	0.244669	0	0.027812	0.024603
protein_co	prohibitin_	4470	3795	2950	7503	4871	6119	155.8934	155.9693	135.5742	226.3697	190.848	212.0852
antisense	-	2	2	0	0	3	0	0.143277	0.168844	0	0	0.241445	0
pseudogen	ribosomal_	32	25	22	33	25	42	2.663698	2.452348	2.413195	2.376358	2.33789	3.474513
pseudogen	guanine_nu	1	0	2	7	1	1	0.032222	0	0.084922	0.195126	0.0362	0.032023
protein_co	Protein_LO	0	0	0	6	3	0	0	0	0	0.139489	0.090572	0
pseudogen	farnesyl_di	0	0	0	1	0	3	0	0	0	0.043329	0	0.14933
processed_	CD27_antis	14	15	16	11	12	2	0.313525	0.395861	0.472171	0.213108	0.301908	0.044513
protein_co	neuralized_	140	124	127	187	235	300	1.425334	1.487707	1.703834	1.646999	2.687854	3.035426
protein_co	glutamate_	6	3	0	9	15	31	0.087361	0.051475	0	0.113364	0.245363	0.44858
pseudogen	peroxiredo	4	0	0	0	2	1	0.359531	0	0	0	0.201956	0.089328
pseudogen	dual_specif	0	2	0	0	0	2	0	0.070855	0	0	0	0.059755
protein_co	chromoson	6	6	6	2	7	4	0.115173	0.135724	0.151769	0.033212	0.150954	0.076308
protein_co	Uncharacte	28	24	31	23	37	32	0.856848	0.865495	1.250093	0.608887	1.272028	0.973208
processed_	-	113	105	91	8	17	21	2.468977	2.703554	2.620082	0.151214	0.417289	0.456003
pseudogen	nucleophos	0	1	0	3	0	0	0	0.069785	0	0.153688	0	0
pseudogen	ribosomal_	0	0	0	0	1	1	0	0	0	0	0.096552	0.085412
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.046357	0
pseudogen	eukaryotic_	0	0	0	2	0	0	0	0	0	0.083575	0	0
pseudogen	interferon_	0	0	0	0	0	3	0	0	0	0	0	0.400615
pseudogen	telomeric_	0	0	0	0	4	0	0	0	0	0	0.213367	0
pseudogen	-	5	4	1	2	4	4	0.52941	0.499102	0.139527	0.183196	0.475807	0.420912
pseudogen	tetratricop	20	17	33	87	58	40	0.174119	0.174411	0.378587	0.655238	0.567276	0.346088
protein_co	UBX_doma	310	263	259	840	608	575	3.238301	3.237564	3.565251	7.590979	7.135232	5.969432
pseudogen	-	0	0	0	2	0	1	0	0	0	0.059287	0	0.034054
protein_co	COBW_dor	3	5	1	10	5	5	0.047752	0.093788	0.020975	0.1377	0.089411	0.079095
protein_co	chromoson	0	3	1	1	0	0	0	0.201467	0.075095	0.049299	0	0
pseudogen	-	1	0	0	6	5	2	0.035844	0	0	0.186048	0.20134	0.071244
pseudogen	-	174	157	131	158	171	181	3.352159	3.564364	3.325688	2.63327	3.701012	3.465481

pseudogen	-	44	34	33	16	92	56	0.647416	0.589545	0.639852	0.203664	1.520785	0.818896
pseudogen	-	71	82	67	58	45	106	0.751612	1.022954	0.934641	0.531161	0.535176	1.115195
antisense	-	3	1	13	1	0	1	0.269649	0.105921	1.539767	0.077757	0	0.089328
pseudogen	olfactory_r	0	0	0	0	0	1	0	0	0	0	0	0.051735
lincRNA	long_interg	0	0	0	3	1	2	0	0	0	0.063229	0.02737	0.048425
pseudogen	-	0	0	0	4	0	0	0	0	0	0.208177	0	0
pseudogen	-	0	3	0	0	1	0	0	0.058598	0	0	0.018621	0
pseudogen	-	4	3	0	1	5	1	0.520305	0.45986	0	0.112528	0.730662	0.129273
protein_co	family_witl	3	2	1	1	2	0	0.163566	0.128502	0.071847	0.047167	0.122504	0
processed_	long_interg	177	131	105	188	147	126	3.57382	3.117007	2.793724	3.283827	3.334462	2.528364
protein_co	peroxisom	1119	906	801	1677	1270	1598	13.10931	12.50792	12.36565	16.99596	16.71485	18.60528
processed_	-	38	33	12	0	3	7	0.684039	0.700032	0.284651	0	0.060669	0.125229
pseudogen	-	9	2	1	1	3	1	0.367362	0.096203	0.053788	0.035311	0.13757	0.040566
protein_co	chromoson	7	16	9	1	6	14	0.155382	0.418534	0.263258	0.019203	0.149625	0.308846
protein_co	ubiquitin-c	2	2	2	31	17	26	0.024527	0.028903	0.03232	0.328878	0.234211	0.316879
pseudogen	ubiquitin_/	3	1	3	1	4	1	0.415767	0.163319	0.547879	0.119892	0.622784	0.137733
pseudogen	cytochrom	0	3	5	3	0	0	0	0.131067	0.244269	0.096216	0	0
pseudogen	-	0	1	0	5	3	0	0	0.052515	0	0.192756	0.150192	0
lincRNA	-	11	6	9	8	8	10	0.732517	0.470851	0.789773	0.460869	0.5985	0.661812
protein_co	HCG20454	1	4	1	4	5	4	0.017189	0.081023	0.02265	0.059479	0.096552	0.06833
antisense	-	0	0	0	2	0	0	0	0	0	0.026306	0	0
protein_co	FAST_kinas	249	181	217	594	604	570	4.586746	3.929081	5.267443	9.465745	12.49946	10.43494
protein_co	golgin_A8_	246	209	185	389	270	371	2.007319	2.009716	1.989243	2.745958	2.475108	3.008602
processed_	DHRS4_ant	89	78	95	59	64	64	1.652086	1.706256	2.323812	0.947453	1.334663	1.18068
pseudogen	-	2	4	6	0	0	0	0.100936	0.237894	0.399027	0	0	0
protein_co	homeobox_	43	52	26	138	96	120	0.679136	0.967829	0.541123	1.885516	1.703368	1.883558
protein_co	G_antigen_	2	2	0	0	0	0	0.196807	0.231925	0	0	0	0
protein_co	chromoson	14	6	12	28	17	10	0.443817	0.224148	0.501293	0.767886	0.605443	0.315054
pseudogen	high_mobil	1	6	4	15	7	8	0.085114	0.601811	0.448638	1.104475	0.669343	0.676708
pseudogen	transmemb	0	0	0	13	3	7	0	0	0	0.37971	0.113793	0.234884
pseudogen	-	0	0	0	0	4	1	0	0	0	0	0.512723	0.113392
protein_co	DEAD_(Asp	3063	2440	2896	7048	6495	5807	30.40087	28.53882	37.87673	60.51569	72.42146	57.27968
pseudogen	-	45	31	27	14	26	9	1.586115	1.28763	1.254067	0.426887	1.029543	0.315264
processed_	-	2	0	3	0	1	0	0.09652	0	0.190784	0	0.054217	0
protein_co	vacuolar_p	625	529	482	458	300	352	12.03204	12.00113	12.2276	7.6276	6.488282	6.734598
protein_co	Uncharacte	0	0	2	0	0	6	0	0	2.114039	0	0	4.783095
pseudogen	nucleophos	0	0	0	0	1	1	0	0	0	0	0.071314	0.063086
pseudogen	-	3	0	0	0	0	0	0.129019	0	0	0	0	0
pseudogen	argininosuc	5	4	11	0	3	1	0.212785	0.200604	0.616878	0	0.143431	0.042294
protein_co	-	18	7	11	4	10	10	0.437328	0.20042	0.352178	0.084073	0.272951	0.24146
pseudogen	transmemb	3	0	1	0	0	0	0.230178	0	0.101106	0	0	0
pseudogen	ribosomal_	0	0	0	0	2	0	0	0	0	0	0.405979	0
processed_	family_witl	0	0	1	1	2	0	0	0	0.048717	0.031982	0.083067	0
protein_co	myosin_ligl	151	163	69	95	57	109	2.704361	3.440189	1.628439	1.471886	1.146863	1.940099

lincRNA	long_interg	42	27	36	3	0	1	0.639862	0.484739	0.722728	0.039539	0	0.015141
pseudogen	actin_gamr	1	3	7	6	18	2	0.047523	0.16801	0.438369	0.246673	0.961011	0.09446
lincRNA	long_interg	6	4	0	0	0	1	0.405678	0.318711	0	0	0	0.067195
protein_co	scratch_ho	6	0	0	0	0	0	0.088802	0	0	0	0	0
antisense	-	0	0	0	1	0	0	0	0	0	0.046168	0	0
pseudogen	proteasom	0	6	3	1	0	2	0	0.505164	0.282442	0.061807	0	0.142008
processed_	miR-17-92_	19	26	33	187	127	165	0.35356	0.570151	0.809205	3.010332	2.654988	3.05143
protein_co	zinc_finger_	305	221	281	321	324	253	2.031581	1.734737	2.466467	1.849704	2.424534	1.674806
antisense	MCM3AP_a	81	69	85	116	83	70	1.688941	1.695452	2.335518	2.092427	1.94427	1.450565
protein_co	Uncharacte	0	1	0	0	0	0	0	0.770219	0	0	0	0
protein_co	aminopept	49	62	52	31	52	52	0.553823	0.825798	0.774486	0.30311	0.660279	0.584101
pseudogen	CTAGE_fam	0	0	0	0	2	0	0	0	0	0	0.050318	0
processed_	-	144	146	153	22	92	104	5.221577	6.238773	7.31081	0.69012	3.747798	3.74785
pseudogen	-	0	0	0	0	4	0	0	0	0	0	0.275671	0
pseudogen	-	2	4	4	17	25	33	0.038899	0.091679	0.102518	0.286033	0.546252	0.637863
antisense	-	20	21	11	8	17	13	0.230278	0.284937	0.166898	0.079685	0.219898	0.148757
protein_co	Sarcoma_a	0	0	0	0	0	1	0	0	0	0	0	0.23384
pseudogen	ribosomal_	2	0	0	0	3	1	0.243407	0	0	0	0.410179	0.120952
protein_co	SKI_family_	0	0	2	0	0	0	0	0	0.046416	0	0	0
protein_co	siah_E3_ub	0	0	0	21	24	6	0	0	0	0.238654	0.354199	0.078334
pseudogen	carboxylest	0	0	0	4	5	16	0	0	0	0.180311	0.292696	0.828568
pseudogen	breakpoint_	0	0	0	2	0	0	0	0	0	0.062867	0	0
pseudogen	calmodulin	6	0	0	0	2	0	0.707452	0	0	0	0.264926	0
lincRNA	long_interg	0	2	0	3	1	0	0	0.177743	0	0.195722	0.084724	0
pseudogen	heterogene	1	1	2	4	1	1	0.034422	0.040564	0.090719	0.119113	0.038671	0.034209
pseudogen	-	21	22	22	17	29	16	0.652825	0.805948	0.901229	0.457182	1.012802	0.494319
protein_co	CDNA_FLJ2	2	9	7	5	0	13	0.044358	0.235228	0.204584	0.095934	0	0.286545
pseudogen	transmemb	0	0	0	25	24	26	0	0	0	0.713379	0.88936	0.852315
pseudogen	phosphatid	113	126	45	308	164	266	2.268613	2.980984	1.1905	5.349284	3.698919	5.307295
pseudogen	interferon-i	0	2	0	2	1	2	0	0.086111	0	0.063215	0.041046	0.072621
protein_co	Uncharacte	0	1	0	4	0	4	0	0.132458	0	0.38895	0	0.446828
protein_co	EF-hand_ca	2	0	0	0	0	0	0.082656	0	0	0	0	0
pseudogen	-	77	59	54	65	65	45	4.378578	3.95368	4.04642	3.197561	4.152454	2.543107
pseudogen	ankyrin_rep	0	0	0	1	0	3	0	0	0	0.012321	0	0.042465
pseudogen	-	0	0	0	0	2	1	0	0	0	0	0.455754	0.201586
pseudogen	G_protein-r	3	1	3	0	7	1	0.092825	0.036463	0.12232	0	0.243326	0.03075
pseudogen	BCL6_corep	0	2	0	0	0	0	0	0.024499	0	0	0	0
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.300652
protein_co	H6_family_	1	0	3	41	41	68	0.027967	0	0.11056	0.991947	1.288174	1.889992
pseudogen	glucuronid	7	10	21	12	13	17	0.306017	0.515175	1.209768	0.453829	0.63847	0.738595
protein_co	glucagon_r	0	0	0	1	0	0	0	0	0	0.02233	0	0
antisense	-	1	0	0	0	0	0	0.112163	0	0	0	0	0
protein_co	chymotryp	1	4	7	2	0	2	0.057358	0.270369	0.529082	0.099239	0	0.114007
protein_co	transmemb	259	274	182	434	286	412	7.621855	9.502078	7.057764	11.04876	9.455315	12.04947

protein_co	transmemb	729	539	594	526	428	404	13.79342	12.01822	14.81036	8.609801	9.097817	7.596882
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.074104
protein_co	Uncharacte	0	1	0	0	0	0	0	0.014332	0	0	0	0
pseudogen	TAF9B_RNA	0	0	0	0	0	1	0	0	0	0	0	0.105439
processed_	hsa-mir-60	17	24	8	1	9	12	0.314574	0.52335	0.195074	0.016008	0.187097	0.220681
pseudogen	leucine_ric	0	2	0	0	0	0	0	0.270077	0	0	0	0
protein_co	family_witl	4	8	4	95	70	82	0.088493	0.208567	0.116612	1.818176	1.739789	1.802905
pseudogen	cofilin_1_(r	0	2	1	6	1	4	0	0.252582	0.141221	0.556262	0.120397	0.426025
protein_co	tumor_nec	159	174	117	63	68	53	2.416772	3.1167	2.343469	0.828404	1.161172	0.800616
protein_co	solute_carr	115	71	93	67	58	52	2.929843	2.131631	3.122226	1.476673	1.660059	1.316617
pseudogen	-	2	9	9	0	3	2	0.063402	0.336221	0.37597	0	0.106843	0.063011
pseudogen	-	0	4	1	0	6	0	0	0.202722	0.056672	0	0.289891	0
processed_	-	224	204	239	150	106	136	7.715538	8.280479	10.84803	4.469639	4.101787	4.655505
pseudogen	butyrophili	0	0	0	1	0	4	0	0	0	0.052703	0	0.242182
pseudogen	zinc_finger_	35	18	28	1	3	4	0.572423	0.34692	0.603451	0.014149	0.055121	0.065016
pseudogen	-	2	0	1	0	7	1	0.053774	0	0.035431	0	0.211443	0.026721
pseudogen	-	1	0	0	0	0	0	0.059888	0	0	0	0	0
protein_co	thiosulfate_	1	0	0	174	125	161	0.065118	0	0	9.80198	9.144514	10.41926
pseudogen	-	11	23	17	6	8	1	1.544697	3.806148	3.145824	0.728895	1.262088	0.13956
processed_	-	11	13	15	17	17	7	0.263507	0.366987	0.473506	0.352299	0.457507	0.166651
lincRNA	-	1	3	2	111	41	61	0.029104	0.102893	0.076705	2.794766	1.340579	1.764407
pseudogen	-	5	5	1	0	1	4	0.211088	0.248755	0.055633	0	0.047429	0.167828
pseudogen	suppressior	0	0	0	23	8	13	0	0	0	0.989084	0.446767	0.642237
pseudogen	MARCKS-lik	0	0	0	1	0	1	0	0	0	0.046925	0	0.053908
protein_co	cytochrom	27	60	25	68	40	58	0.253306	0.663346	0.30907	0.551892	0.421591	0.540779
pseudogen	-	0	4	0	5	1	2	0	0.500102	0	0.458907	0.11919	0.210878
pseudogen	-	0	0	2	0	0	0	0	0	0.071187	0	0	0
protein_co	zinc_finger_	1	2	1	11	12	19	0.013209	0.031132	0.017406	0.125696	0.178072	0.249418
protein_co	Uncharacte	0	0	0	0	6	0	0	0	0	0	5.406902	0
processed_	ciliary_roo	350	299	230	371	314	461	6.706242	6.751332	5.807295	6.149618	6.759116	8.77853
protein_co	chromoson	0	0	0	0	0	1	0	0	0	0	0	0.011538
protein_co	tetratricop	8	7	5	8	7	2	0.113334	0.116862	0.093341	0.098044	0.111408	0.028158
pseudogen	matrix_met	12	2	3	4	0	1	0.565206	0.11101	0.186201	0.162985	0	0.04681
protein_co	ATPase_fam	19	3	12	34	14	26	0.260658	0.0485	0.216937	0.403515	0.215772	0.354487
pseudogen	-	11	25	12	24	18	28	0.761243	2.038815	1.094326	1.436828	1.399433	1.925743
pseudogen	-	3	1	0	0	0	0	0.229845	0.090286	0	0	0	0
pseudogen	-	1	3	3	8	0	4	0.090964	0.321586	0.359605	0.629538	0	0.361609
pseudogen	histone_clu	30	35	26	5	9	1	7.709853	10.59986	8.805074	1.111624	2.598462	0.255408
pseudogen	-	3	0	1	2	5	0	0.167889	0	0.073746	0.096826	0.314355	0
pseudogen	mitochond	0	0	0	0	1	8	0	0	0	0	0.139615	0.988057
pseudogen	ribosomal_	2	0	0	4	1	0	0.169411	0	0	0.293113	0.095161	0
protein_co	immunoglo	0	0	0	4	0	0	0	0	0	0.185233	0	0
pseudogen	-	0	0	0	0	2	1	0	0	0	0	0.164982	0.072974
pseudogen	-	1	1	1	2	0	2	0.070871	0.083518	0.093391	0.122621	0	0.140868

pseudogen	-	3	0	0	0	0	1	0.153009	0	0	0	0	0.050688
pseudogen	nudix_(nuc	0	0	0	7	4	4	0	0	0	0.577644	0.428655	0.3792
pseudogen	high_mobil	0	0	0	3	0	0	0	0	0	0.273699	0	0
pseudogen	-	631	517	554	417	312	277	10.99236	10.61351	12.71762	6.284351	6.106116	4.795687
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.176225	0
pseudogen	-	2	0	5	7	1	0	0.141553	0	0.466332	0.428599	0.079513	0
pseudogen	-	10	2	16	3	14	3	0.20975	0.049436	0.44224	0.054436	0.329898	0.062537
pseudogen	-	0	5	0	0	7	5	0	0.78574	0	0	1.048694	0.662645
pseudogen	R3H_doma	0	0	0	1	0	0	0	0	0	0.021644	0	0
pseudogen	tubulin_be	1	0	0	3	3	1	0.060782	0	0	0.157746	0.204854	0.060406
pseudogen	ribosomal_	0	1	2	0	0	0	0	0.112817	0.252308	0	0	0
processed_	LY86_antis	1	0	0	0	0	0	0.01878	0	0	0	0	0
pseudogen	ribosomal_	27	12	11	32	10	19	1.618807	0.847851	0.869078	1.659756	0.673566	1.132126
pseudogen	-	6	0	1	0	10	5	0.820791	0	0.180267	0	1.536845	0.679768
protein_co	Protein_LO	30	23	18	53	48	65	1.575625	1.42353	1.245773	2.408077	2.832187	3.392771
pseudogen	-	2	0	0	0	0	0	0.217417	0	0	0	0	0
pseudogen	-	5	3	1	1	0	0	0.121648	0.086012	0.03206	0.021047	0	0
protein_co	Protein_LO	10	7	3	3	5	0	0.889765	0.733973	0.351748	0.230919	0.499798	0
protein_co	coiled-coil_	16	11	14	17	11	11	0.21187	0.171652	0.244294	0.194743	0.163641	0.144761
pseudogen	ribosomal_	0	0	0	3	0	3	0	0	0	0.294843	0	0.338717
pseudogen	cytochrom	0	0	1	0	0	0	0	0	0.059474	0	0	0
pseudogen	-	2	4	0	2	0	4	0.322811	0.760826	0	0.279262	0	0.641635
pseudogen	ribosomal_	0	0	1	0	0	0	0	0	0.108328	0	0	0
pseudogen	-	6	0	0	0	0	2	0.612035	0	0	0	0	0.202752
pseudogen	-	0	0	1	1	0	0	0	0	0.205791	0.1351	0	0
protein_co	Uncharacte	0	0	5	0	3	6	0	0	0.811201	0	0.414948	0.73415
pseudogen	-	0	0	2	1	2	3	0	0	0.361468	0.11865	0.308165	0.408917
pseudogen	peptidylpro	4	6	4	4	7	4	0.427806	0.756215	0.563744	0.370092	0.841074	0.425164
protein_co	folliculin_i	666	571	613	539	431	463	5.515204	5.57225	6.689331	3.86135	4.009717	3.810465
pseudogen	-	0	1	0	0	0	1	0	0.125277	0	0	0	0.105651
pseudogen	La_ribonuc	5	0	3	1	0	1	0.906524	0	0.716746	0.156846	0	0.180185
pseudogen	ankyrin_rep	22	39	26	13	16	7	0.442516	0.924438	0.689151	0.22621	0.361556	0.139931
pseudogen	-	0	0	0	3	6	3	0	0	0	0.286841	0.745001	0.329524
pseudogen	-	1	0	1	0	0	0	0.043862	0	0.057799	0	0	0
protein_co	Sp9_transc	7	1	6	40	43	40	0.145101	0.024427	0.163892	0.717289	1.001356	0.824026
pseudogen	chromobo	1	4	1	2	5	0	0.095908	0.452085	0.126383	0.165938	0.538731	0
processed_	-	1	0	0	0	0	0	0.107168	0	0	0	0	0
pseudogen	-	6	4	2	0	1	0	0.636565	0.500102	0.279612	0	0.11919	0
pseudogen	ubiquinol-c	0	0	0	1	0	1	0	0	0	0.118958	0	0.13666
pseudogen	olfactory_r	0	0	0	0	4	0	0	0	0	0	0.26172	0
pseudogen	PRELI_dom	0	4	0	2	0	4	0	0.276358	0	0.101437	0	0.233063
pseudogen	SSX_family	7	6	0	9	5	6	0.655906	0.662525	0	0.72954	0.526336	0.558733
pseudogen	iron-sulfur_	1	1	0	2	2	4	0.136798	0.161209	0	0.236687	0.307369	0.543814
protein_co	synaptoner	0	0	0	0	2	0	0	0	0	0	0.265517	0

pseudogen	-	0	0	0	1	0	0	0	0	0	0.078692	0	0
pseudogen	-	3	14	4	1	0	3	0.191123	1.051057	0.335804	0.055113	0	0.189942
pseudogen	-	0	0	0	0	3	0	0	0	0	0	0.227296	0
pseudogen	-	5	2	0	1	5	0	0.592181	0.27914	0	0.102458	0.665279	0
pseudogen	ribosomal_	4	4	6	0	1	4	0.524168	0.6177	1.036088	0	0.147218	0.520931
protein_co	chemokine	27	24	16	22	18	20	2.136632	2.238125	1.668479	1.506093	1.600249	1.572916
processed_	-	91	64	56	93	76	63	1.269133	1.051848	1.029174	1.122049	1.190772	0.873205
pseudogen	-	3	3	5	3	4	2	0.216086	0.254644	0.47458	0.186934	0.323678	0.143167
pseudogen	prostaglan	2	0	0	0	0	0	0.219672	0	0	0	0	0
pseudogen	-	0	4	0	0	0	0	0	0.469964	0	0	0	0
pseudogen	histone_clu	0	0	0	2	0	0	0	0	0	0.269405	0	0
pseudogen	-	11	20	10	70	41	52	0.511732	1.096445	0.613034	2.817156	2.142805	2.404157
pseudogen	-	0	0	2	3	0	0	0	0	0.184803	0.181982	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.095045	0	0	0
protein_co	-	0	2	0	0	0	0	0	0.135185	0	0	0	0
pseudogen	ribosomal_	2	3	7	5	0	2	0.214336	0.378873	0.988549	0.463552	0	0.213012
pseudogen	chaperonin	0	2	0	0	0	0	0	0.077452	0	0	0	0
pseudogen	-	0	2	0	0	0	1	0	0.271251	0	0	0	0.114378
pseudogen	-	0	0	1	1	0	0	0	0	0.229484	0.150654	0	0
pseudogen	lactate_deh	2	3	2	0	0	1	0.097858	0.172979	0.128952	0	0	0.048627
pseudogen	-	20	15	25	14	22	22	0.867885	0.767062	1.429575	0.525561	1.072517	0.948778
pseudogen	-	1	0	0	2	3	0	0.058305	0	0	0.100879	0.196506	0
pseudogen	histone_clu	0	0	2	0	0	1	0	0	0.526515	0	0	0.198544
pseudogen	-	0	0	0	1	0	1	0	0	0	0.053755	0	0.061754
pseudogen	zinc_finger_	3	0	0	2	9	5	0.184463	0	0	0.106385	0.621699	0.30554
pseudogen	-	0	0	2	3	3	5	0	0	0.484467	0.477072	0.619541	0.913438
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.018711
protein_co	presequenc	63	35	12	110	109	115	4.138068	2.709145	1.038659	6.250471	8.043269	7.506967
pseudogen	zinc_finger_	0	0	0	0	1	1	0	0	0	0	0.043005	0.038043
antisense	-	0	1	0	0	1	8	0	0.040512	0	0	0.038621	0.27332
pseudogen	-	0	1	0	0	0	0	0	0.039188	0	0	0	0
pseudogen	-	40	27	27	0	0	0	0.586441	0.466483	0.521631	0	0	0
pseudogen	-	0	0	0	11	13	2	0	0	0	1.036601	1.59092	0.216519
pseudogen	DnaJ_(Hsp4	0	0	0	0	6	0	0	0	0	0	0.306051	0
pseudogen	keratin_18_	0	1	0	0	0	0	0	0.046316	0	0	0	0
pseudogen	-	5	7	4	11	1	13	0.767261	1.265838	0.80885	1.460255	0.172394	1.982558
pseudogen	POM121_tr	5	0	0	0	0	0	0.1699	0	0	0	0	0
pseudogen	ribosomal_	0	0	0	3	0	0	0	0	0	0.385946	0	0
pseudogen	-	1	3	0	0	0	0	0.118436	0.41871	0	0	0	0
pseudogen	TatD_DNas	34	51	25	18	29	16	0.808623	1.429368	0.783505	0.370342	0.774843	0.378178
pseudogen	-	0	6	3	8	4	3	0	0.633378	0.354128	0.619951	0.402544	0.267076
pseudogen	nephrocan_	0	0	3	5	2	4	0	0	0.152655	0.167027	0.086763	0.153506
pseudogen	-	9	0	0	0	0	0	0.610858	0	0	0	0	0
pseudogen	mortality_f	277	243	206	248	289	220	15.1651	15.67758	14.86167	11.74574	17.77512	11.9701

pseudogen	-	0	1	0	0	0	0	0	0.036293	0	0	0	0
pseudogen	-	5	2	6	2	2	5	0.282804	0.133307	0.447201	0.097861	0.127085	0.281058
protein_co	teneurin_tr	2370	2068	2202	3115	3418	3114	11.51525	11.84084	14.09864	13.09321	18.65718	15.03672
pseudogen	vomeronas	2	1	0	0	0	0	0.113974	0.067156	0	0	0	0
pseudogen	lysophosph	0	0	0	1	0	0	0	0	0	0.065898	0	0
pseudogen	retinoic_ac	3	1	0	5	2	1	0.084346	0.033132	0	0.121612	0.063171	0.027942
pseudogen	-	0	0	0	2	0	0	0	0	0	0.336757	0	0
pseudogen	-	2	1	0	4	5	0	0.064327	0.037903	0	0.111297	0.180668	0
protein_co	Uncharacte	23	5	11	130	135	192	0.60369	0.154655	0.380464	2.951838	3.980788	5.008378
pseudogen	-	4	7	4	10	7	11	0.035807	0.073844	0.047185	0.077442	0.070398	0.097862
pseudogen	-	17	10	2	28	37	58	0.327153	0.226782	0.050718	0.466147	0.799931	1.109275
pseudogen	-	147	117	89	110	82	155	17.41013	16.32967	13.89023	11.27042	10.91057	18.24425
pseudogen	NIP7_nucle	2	0	2	2	2	0	0.205596	0	0.270925	0.17786	0.230974	0
pseudogen	ribosomal_	9	0	1	4	0	0	1.89075	0	0.276838	0.726967	0	0
pseudogen	H2A_histor	0	1	0	2	3	5	0	0.161209	0	0.236687	0.461054	0.679768
lincRNA	long_interg	160	122	102	265	167	237	8.036584	7.22135	6.751285	11.51491	9.423604	11.83067
pseudogen	-	2	6	0	0	3	4	0.219672	0.776611	0	0	0.370182	0.436631
protein_co	Uncharacte	5	18	3	1	2	3	0.179339	0.760826	0.141795	0.031029	0.080591	0.106939
pseudogen	-	0	0	0	3	2	2	0	0	0	0.342635	0.296638	0.262414
pseudogen	-	0	1	1	0	0	0	0	0.064384	0.071995	0	0	0
pseudogen	-	3	1	4	0	8	4	0.420167	0.165047	0.738236	0	1.25875	0.556762
pseudogen	-	0	0	1	0	0	2	0	0	0.113252	0	0	0.170825
pseudogen	-	0	4	0	0	0	0	0	0.337231	0	0	0	0
pseudogen	bromodom	3	3	3	0	4	0	0.104351	0.122972	0.13751	0	0.15631	0
pseudogen	-	0	0	0	3	2	1	0	0	0	0.271535	0.235083	0.10398
pseudogen	-	0	0	1	0	0	0	0	0	0.085599	0	0	0
pseudogen	histone_clu	0	0	0	0	2	4	0	0	0	0	0.341816	0.604759
pseudogen	suppressior	0	3	0	0	0	0	0	0.239646	0	0	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.028322	0
pseudogen	-	0	1	1	0	0	0	0	0.048176	0.053871	0	0	0
protein_co	HCG19881	16	4	4	26	17	17	0.268225	0.079022	0.088364	0.377065	0.320168	0.28323
pseudogen	-	2	0	1	0	0	0	0.344892	0	0.227242	0	0	0
pseudogen	-	1	1	1	0	0	0	0.096784	0.114054	0.127538	0	0	0
pseudogen	-	1	0	0	0	0	0	0.1034	0	0	0	0	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.152064
protein_co	poly(A)_pol	0	0	0	0	3	1	0	0	0	0	0.041865	0.012345
pseudogen	-	0	3	0	0	2	0	0	0.553737	0	0	0.351929	0
protein_co	zinc_finger_	1000	793	548	1194	799	933	24.78511	23.16174	17.89807	25.60107	22.24778	22.9817
pseudogen	tubulin_be	0	0	1	2	1	0	0	0	0.140936	0.185046	0.120153	0
pseudogen	ferritin_hea	2	0	2	0	0	0	0.37815	0	0.498309	0	0	0
pseudogen	-	0	3	1	1	1	1	0	0.312459	0.116466	0.076459	0.099292	0.087836
protein_co	Uncharacte	0	0	4	0	7	1	0	0	0.092647	0	0.138224	0.017468
pseudogen	-	0	0	0	0	1	1	0	0	0	0	0.151724	0.13422
pseudogen	ribosomal_	0	0	0	5	0	0	0	0	0	0.303706	0	0

pseudogen	nucleopho	3	0	0	0	5	1	0.18172	0	0	0	0.340251	0.060199
pseudogen	-	3	0	4	0	3	4	0.14941	0	0.262515	0	0.167853	0.197983
pseudogen	-	1	0	0	0	0	0	0.109609	0	0	0	0	0
pseudogen	-	0	4	0	0	0	0	0	1.223289	0	0	0	0
pseudogen	ferritin_hea	2	7	0	1	2	0	0.200534	0.82711	0	0.08674	0.225288	0
pseudogen	calcyclin_b	3	0	0	0	0	3	0.254117	0	0	0	0	0.252547
protein_co	ribonuclea	0	1	0	0	2	3	0	0.065533	0	0	0.124949	0.165801
pseudogen	-	31	30	29	26	42	41	1.471902	1.678594	1.814471	1.067957	2.240348	1.934687
pseudogen	archaelysin	0	0	0	0	0	1	0	0	0	0	0	0.049777
pseudogen	phosphatid	0	0	0	0	0	3	0	0	0	0	0	0.095315
pseudogen	ribosomal_	1	5	2	15	1	1	0.144253	0.849969	0.380181	1.87189	0.16206	0.143363
pseudogen	-	2	1	2	3	0	3	0.29576	0.174267	0.389739	0.38379	0	0.4409
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.134563
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.185283	0
pseudogen	activating_	0	0	0	1	0	0	0	0	0	0.049406	0	0
pseudogen	-	1	3	1	4	1	12	0.057295	0.202558	0.075501	0.198264	0.064368	0.683299
pseudogen	heat_shock	14	16	10	22	7	11	0.942969	1.269979	0.887574	1.281903	0.529684	0.736329
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.09847	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.149813	0
antisense	-	4	4	4	4	6	3	0.292896	0.34516	0.385966	0.253383	0.493576	0.218316
pseudogen	-	3	3	0	2	0	2	0.234945	0.276869	0	0.1355	0	0.155663
protein_co	family_with	10	2	3	38	23	33	0.200686	0.047299	0.079337	0.659726	0.518554	0.658174
pseudogen	-	0	3	0	0	3	3	0	0.036055	0	0	0.034373	0.030407
pseudogen	ribosomal_	0	0	0	2	0	0	0	0	0	0.214014	0	0
pseudogen	-	9	3	8	9	4	10	0.540214	0.212203	0.632774	0.467336	0.269732	0.596531
protein_co	neuroblast	847	763	701	533	393	449	7.559174	8.024585	8.24411	4.115107	3.94033	3.982419
pseudogen	-	0	2	0	0	0	0	0	0.187915	0	0	0	0
pseudogen	ferritin_hea	6	12	5	8	5	3	0.617988	1.456523	0.678631	0.712823	0.57856	0.307086
protein_co	Uncharacte	124	90	109	179	121	115	3.10975	2.659827	3.602178	3.883469	3.409089	2.866232
pseudogen	ribosomal_	1	4	2	3	0	0	0.095389	0.449641	0.251399	0.247562	0	0
pseudogen	zinc_finger_	12	0	0	0	4	1	0.129335	0	0	0	0.048433	0.010711
pseudogen	-	0	1	0	0	0	0	0	0.452085	0	0	0	0
protein_co	protein_ph	30	12	19	5	1	5	0.914879	0.431252	0.763538	0.131909	0.03426	0.151538
pseudogen	HIG1_hypo	0	0	5	1	0	0	0	0	1.352002	0.177515	0	0
protein_co	family_with	50	30	45	22	20	21	1.011869	0.715456	1.200056	0.385159	0.454709	0.42236
pseudogen	bone_morp	0	0	3	0	3	0	0	0	0.13097	0	0.111657	0
pseudogen	glucosamin	3	0	0	0	0	0	0.482745	0	0	0	0	0
processed_	-	71	61	62	99	47	100	0.939703	0.951413	1.081331	1.133523	0.698842	1.315351
pseudogen	-	2	0	0	0	0	0	0.382245	0	0	0	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.048514	0	0	0
pseudogen	-	0	1	1	2	4	7	0	0.213657	0.238915	0.313691	0.814739	1.261296
pseudogen	patched_d	2	0	0	0	0	0	0.116868	0	0	0	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.04288
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.207958	0

pseudogen	-	0	2	0	8	4	9	0	0.308088	0	0.90467	0.587416	1.169201
pseudogen	-	1	2	1	2	0	1	0.071062	0.167484	0.093642	0.12295	0	0.070623
pseudogen	oligosaccha	4	0	0	0	0	1	0.463379	0	0	0	0	0.115129
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.114378
pseudogen	glyceraldeh	0	0	0	0	5	1	0	0	0	0	0.303139	0.053633
pseudogen	zinc_finger_	13	8	3	33	19	27	0.415349	0.301208	0.126306	0.912109	0.681981	0.85732
pseudogen	ribosomal_	2	2	2	1	5	2	0.285396	0.336322	0.376082	0.123447	0.801562	0.283634
pseudogen	ribosomal_	2	0	0	0	0	0	0.182555	0	0	0	0	0
pseudogen	-	3	0	0	0	4	0	0.159782	0	0	0	0.23934	0
pseudogen	-	4	0	3	1	4	0	0.485697	0	0.480023	0.105043	0.545651	0
protein_co	leucine_ric	1	2	1	0	0	0	0.023624	0.055678	0.03113	0	0	0
protein_co	Homo_sapi	19	10	9	21	9	3	0.484294	0.300374	0.302296	0.463061	0.257719	0.075995
pseudogen	leucine_am	0	0	0	2	0	0	0	0	0	0.311557	0	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.174219
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.184136	0
pseudogen	heterogene	0	0	1	0	0	1	0	0	0.072594	0	0	0.054749
lincRNA	-	10	9	4	21	19	15	0.282956	0.300101	0.149147	0.514044	0.603978	0.421812
protein_co	zinc_finger_	5	3	2	20	9	18	0.114939	0.081269	0.060585	0.397733	0.232429	0.411226
protein_co	vesicle-assc	712	697	516	507	397	501	17.50766	20.19705	16.71986	10.78497	10.96699	12.24321
pseudogen	ribosomal_	0	0	0	1	0	2	0	0	0	0.116241	0	0.267076
pseudogen	-	7	5	9	0	5	9	0.312732	0.263239	0.529848	0	0.250953	0.3996
pseudogen	histone_clu	7	2	10	6	6	4	0.751698	0.253094	1.415077	0.55739	0.723845	0.426889
pseudogen	-	0	0	1	0	0	0	0	0	0.074454	0	0	0
pseudogen	keratin_8_p	0	1	0	2	0	0	0	0.044595	0	0.065474	0	0
pseudogen	FCF1_small	8	2	7	0	0	0	0.878689	0.25887	1.01316	0	0	0
pseudogen	-	0	0	0	10	4	16	0	0	0	0.257442	0.133729	0.473201
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.146557
pseudogen	-	1	4	0	9	3	6	0.072522	0.341851	0	0.564644	0.244422	0.432444
pseudogen	Yes-associat	5	10	10	0	1	0	0.190025	0.447866	0.500813	0	0.042696	0
pseudogen	-	3	5	5	7	8	9	0.242849	0.47697	0.533358	0.490202	0.727534	0.724047
pseudogen	phosphogly	1	0	0	0	0	0	0.069568	0	0	0	0	0
pseudogen	argininosuc	3	0	0	0	0	0	0.128394	0	0	0	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.125871
pseudogen	pyruvate_k	15	16	12	5	2	5	1.11065	1.396089	1.170852	0.320272	0.166366	0.36793
pseudogen	ribosomal_	10	1	3	14	3	1	1.45843	0.171867	0.576556	1.766349	0.491537	0.144942
pseudogen	DEAD_(Asp	0	0	1	0	0	0	0	0	0.034934	0	0	0
pseudogen	-	3	0	0	0	0	0	0.463041	0	0	0	0	0
pseudogen	v-Ki-ras2_K	0	0	0	0	0	1	0	0	0	0	0	0.095315
pseudogen	-	0	0	0	4	2	0	0	0	0	0.65427	0.424828	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.19379
pseudogen	regulator_c	0	0	0	0	1	0	0	0	0	0	0.047054	0
pseudogen	-	0	0	1	6	15	5	0	0	0.058723	0.231308	0.750959	0.22144
pseudogen	-	11	7	3	0	2	5	0.315466	0.236573	0.113375	0	0.064438	0.142508
pseudogen	-	0	0	0	1	0	0	0	0	0	0.08267	0	0

pseudogen	-	1	7	1	0	5	2	0.068135	0.562052	0.089785	0	0.382728	0.135429
pseudogen	olfactory_r	0	0	0	0	1	1	0	0	0	0	0.064789	0.057314
pseudogen	-	0	3	0	0	0	0	0	0.477457	0	0	0	0
pseudogen	-	1	3	2	1	2	2	0.059418	0.21006	0.156595	0.051402	0.133504	0.118101
pseudogen	ribosomal_	27	36	24	62	25	49	2.632425	4.136203	3.08346	5.229341	2.738302	4.747861
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.205524
pseudogen	-	7	6	9	0	0	0	0.419216	0.423446	0.71026	0	0	0
pseudogen	myotubula	29	26	19	97	102	103	0.585095	0.618171	0.505146	1.693024	2.311945	2.065262
pseudogen	ribosomal_	5	1	2	0	0	4	0.487486	0.114895	0.256955	0	0	0.38758
pseudogen	-	4	9	3	9	13	13	0.171469	0.454647	0.169465	0.333757	0.626062	0.553832
pseudogen	-	88	81	52	118	63	130	8.595586	9.323627	6.693156	9.970979	6.913252	12.61961
pseudogen	ribosomal_	16	12	13	10	8	17	1.841426	1.627506	1.971571	0.995628	1.034364	1.944432
pseudogen	-	4	6	5	0	0	1	0.770051	1.361187	1.268423	0	0	0.191324
pseudogen	mitochond	0	0	0	0	2	0	0	0	0	0	0.207958	0
pseudogen	DnaJ_(Hsp4	0	0	0	0	0	3	0	0	0	0	0	0.563722
pseudogen	mesoderm_	2	0	0	0	0	0	0.106521	0	0	0	0	0
pseudogen	-	4	2	0	0	0	3	0.589872	0.347564	0	0	0	0.439672
pseudogen	oligosaccha	0	0	0	1	1	0	0	0	0	0.102002	0.132463	0
antisense	IGBP1_anti	1	0	1	3	5	0	0.103199	0	0.135991	0.26783	0.579687	0
pseudogen	-	0	0	1	5	0	2	0	0	0.075176	0.246761	0	0.113392
processed_	-	5	2	9	19	26	32	0.231994	0.109356	0.55028	0.762646	1.355279	1.475591
protein_co	early_B-cell	246	164	260	60	59	42	2.53129	1.988647	3.525453	0.534098	0.682037	0.429502
protein_co	chromoson	0	4	0	1	3	5	0	0.251057	0	0.046075	0.179505	0.264658
protein_co	chromoson	74	71	69	71	91	77	7.12297	8.053689	8.752121	5.912222	9.840561	7.365967
protein_co	protein_ph	1284	1044	957	1922	1859	2129	22.48635	21.54575	22.08517	29.11859	36.57484	37.05435
protein_co	pregnancy_	0	0	0	2	0	6	0	0	0	0.04671	0	0.160981
protein_co	Fanconi_an	261	263	199	1030	962	1056	5.251843	6.236402	5.27666	17.92964	21.7468	21.11761
protein_co	adaptor-rel	473	373	307	323	212	332	7.347738	6.828234	6.284427	4.340683	3.699793	5.125547
protein_co	chromoson	37	21	40	15	14	22	0.315938	0.211313	0.450086	0.110804	0.1343	0.186695
pseudogen	-	0	0	0	1	0	3	0	0	0	0.027004	0	0.093067
protein_co	keratin_ass	2	1	0	0	0	0	0.089959	0.053006	0	0	0	0
protein_co	plexin_A4	128	103	119	20	25	15	0.491546	0.46612	0.602193	0.066443	0.107856	0.057247
protein_co	CCAAT/enh	6697	5421	4169	563	455	572	162.785	155.2819	133.5368	11.83874	12.42495	13.81783
protein_co	transmemb	0	0	0	0	3	0	0	0	0	0	0.073096	0
polymorph	pregnancy_	0	0	0	0	2	2	0	0	0	0	0.047657	0.042159
protein_co	olfactory_r	0	0	0	0	0	2	0	0	0	0	0	0.097796
protein_co	ariadne_ho	10	22	9	17	6	6	0.331295	0.858905	0.39291	0.487222	0.223314	0.19755
protein_co	chromoson	91	79	74	120	77	82	1.689804	1.728738	1.810762	1.927699	1.60633	1.513277
protein_co	histocompa	1	3	2	25	19	31	0.077626	0.274433	0.204584	1.678846	1.656954	2.391548
protein_co	neuronal_p	3139	2459	2384	68	63	76	28.73129	26.52341	28.75444	0.538438	0.647819	0.691333
protein_co	family_with	139	85	105	275	126	162	2.967257	2.138289	2.953687	5.078508	3.02176	3.436886
protein_co	olfactory_r	0	1	0	0	0	0	0	0.056003	0	0	0	0
protein_co	protein_ph	897	825	786	2567	1876	2008	12.05281	13.06342	13.91724	29.83903	28.31899	26.81447
protein_co	chromoson	5	5	5	22	22	17	0.356265	0.419837	0.46947	1.356091	1.761063	1.203821

protein_co	zinc_finger_	32	36	31	51	24	28	0.759691	1.007156	0.969803	1.047419	0.6401	0.660625
protein_co	tripartite_r	444	366	322	329	239	371	7.331816	7.122242	7.006793	4.699888	4.433794	6.088525
pseudogen	family_with	4	2	1	5	3	8	0.130397	0.076832	0.042958	0.141006	0.109869	0.259183
protein_co	taste_recep	0	1	0	0	0	0	0	0.060395	0	0	0	0
protein_co	tigger_tran	125	123	117	141	80	81	2.703278	3.134678	3.334275	2.637927	1.943657	1.740906
protein_co	FXYD_doma	0	0	0	2	3	7	0	0	0	0.082446	0.160601	0.331502
protein_co	XK_Kell_blo	1	4	2	4	2	0	0.01668	0.078623	0.043959	0.057718	0.037477	0
protein_co	chromoson	23	29	13	28	23	23	0.723066	1.074373	0.538553	0.761502	0.81232	0.7186
protein_co	chromoson	13	9	9	16	21	19	0.304798	0.248667	0.278064	0.324527	0.553142	0.442722
protein_co	solute_carr	74	44	50	179	119	128	1.124464	0.787905	1.001195	2.353044	2.031468	1.933008
protein_co	transmemb	3	2	4	7	3	8	0.122549	0.096277	0.215319	0.247371	0.137676	0.324778
protein_co	apolipopro	6	6	2	2	0	0	0.103501	0.12197	0.045463	0.029846	0	0
protein_co	fatty_acid_	575	463	391	345	199	226	5.728467	5.435739	5.133128	2.973395	2.227269	2.237632
protein_co	olfactory_r	2	2	0	2	2	1	0.113486	0.133736	0	0.098176	0.127494	0.056392
pseudogen	tetratricop	0	0	0	0	1	0	0	0	0	0	0.051361	0
protein_co	chromoson	0	0	0	4	0	1	0	0	0	0.110027	0	0.0316
protein_co	cyclin_L2	2897	2486	2236	2391	1846	2498	34.4497	34.83735	35.03834	24.59685	24.6614	29.52154
protein_co	ubiquitin_/	11155	9237	6232	13568	7562	10213	207.5771	202.5573	152.8171	218.4181	158.0868	188.8743
protein_co	myosin_bir	6	0	5	3	1	2	0.23152	0	0.254239	0.100143	0.04335	0.076697
protein_co	palmitoyl-p	155	145	106	359	245	305	3.726546	4.108184	3.358269	7.466761	6.617439	7.287596
protein_co	chromoson	71	78	39	88	64	79	2.328879	3.01502	1.68573	2.49709	2.358401	2.575285
protein_co	zinc_finger_	47	31	37	20	31	16	0.891518	0.692949	0.924845	0.32819	0.660607	0.301621
protein_co	TGFB1-indu	11	39	14	32	20	46	0.109116	0.455897	0.183003	0.274605	0.222881	0.453484
protein_co	olfactory_r	0	0	0	1	0	0	0	0	0	0.040746	0	0
protein_co	Uncharacte	3	2	2	3	0	1	0.270107	0.212203	0.23729	0.233668	0	0.08948
protein_co	Uncharacte	0	0	0	2	0	0	0	0	0	0.142454	0	0
protein_co	chromoson	0	0	0	0	3	0	0	0	0	0	0.091221	0
protein_co	Uncharacte	3	7	2	0	0	0	0.100014	0.275009	0.087863	0	0	0
protein_co	Uncharacte	3	4	2	0	1	3	0.360143	0.565875	0.316387	0	0.134866	0.357919
protein_co	BTB_(POZ)_	751	773	440	41	66	56	14.9525	18.13679	11.54413	0.706188	1.476273	1.108081
protein_co	family_with	80	72	56	104	101	71	1.910365	2.026124	1.762176	2.148438	2.709548	1.684979
protein_co	Uncharacte	0	0	0	0	4	1	0	0	0	0	0.068838	0.015224
protein_co	RAB6C_mer	5	2	11	9	4	5	0.086027	0.040551	0.249397	0.133958	0.077317	0.085496
protein_co	Uncharacte	10	10	9	5	5	9	0.700278	0.825235	0.830515	0.302903	0.393359	0.626358
protein_co	Protein_LO	0	1	0	6	0	2	0	0.045176	0	0.198981	0	0.076197
protein_co	Uncharacte	6	10	1	7	2	0	0.698123	1.371159	0.153326	0.704599	0.261433	0
protein_co	Uncharacte	18	18	26	0	0	0	1.620643	1.909828	3.084771	0	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.07097	0	0	0
protein_co	HCG18173	0	1	1	0	0	0	0	0.133023	0.148749	0	0	0
lincRNA	-	23	17	45	0	0	0	2.250726	1.960428	5.802861	0	0	0
protein_co	Uncharacte	0	0	0	0	0	2	0	0	0	0	0	0.049706
antisense	-	2	0	0	1	0	2	0.034233	0	0	0.014807	0	0.034021
protein_co	adrenocept	0	0	1	7	17	11	0	0	0.021282	0.097801	0.308447	0.176557
lincRNA	long_interg	389	308	278	330	191	271	18.79019	17.53232	17.69543	13.78982	10.36487	13.0095

antisense	-	2	3	5	1	9	13	0.212188	0.375077	0.699031	0.091781	1.072712	1.370707
protein_co	doublecort	29	31	30	5	16	25	0.824095	1.038121	1.123402	0.122917	0.510797	0.706039
protein_co	chromosor	0	1	0	3	6	0	0	0.024826	0	0.054674	0.142004	0
antisense	-	2	0	0	1	2	3	0.135399	0	0	0.058566	0.152112	0.201844
pseudogen	histone_clu	1	0	0	0	0	0	0.0704	0	0	0	0	0
antisense	-	10	16	10	10	4	9	1.222656	2.30532	1.611161	1.057711	0.549431	1.093595
sense_intrc	PROX1_intı	0	0	0	0	4	0	0	0	0	0	1.038881	0
antisense	-	18	15	6	7	5	19	2.155968	2.117231	0.947013	0.725322	0.672804	2.26169
processed_	SEC22_vesi	1599	1314	1285	1131	893	837	42.15769	40.82544	44.64433	25.7961	26.4502	21.93125
lincRNA	-	2	0	0	7	4	4	0.095561	0	0	0.289343	0.214715	0.189942
lincRNA	-	0	0	0	2	0	1	0	0	0	0.028517	0	0.01638
pseudogen	syndecan_b	1	0	0	0	0	0	0.086223	0	0	0	0	0
antisense	-	0	0	0	0	2	0	0	0	0	0	0.156105	0
processed_	CLDN10_ar	0	0	0	4	0	2	0	0	0	0.204688	0	0.117573
antisense	-	7	4	6	20	11	17	0.466734	0.314296	0.527178	1.153625	0.823974	1.126497
processed_	ribosomal_	0	0	0	6	4	5	0	0	0	0.117988	0.102148	0.112954
lincRNA	-	75	87	96	5	7	14	7.407788	10.12637	12.49492	0.427229	0.776738	1.374248
lincRNA	maternally_	3	4	1	0	0	0	0.060206	0.094599	0.026446	0	0	0
pseudogen	ribosomal_	0	0	0	0	1	3	0	0	0	0	0.106779	0.283379
processed_	long_interg	3	5	4	0	0	0	0.071801	0.141021	0.126154	0	0	0
pseudogen	-	3	0	1	1	1	1	0.456388	0	0.200469	0.131606	0.170908	0.15119
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.150326
pseudogen	-	0	0	0	0	4	0	0	0	0	0	0.282882	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.110359	0	0
pseudogen	MT-ND6_ps	2	4	4	0	0	0	0.219672	0.51774	0.578948	0	0	0
pseudogen	thymosin_b	0	0	1	6	1	0	0	0	0.611959	2.410469	0.521719	0
antisense	-	3	4	4	1	1	3	0.336489	0.52871	0.591214	0.097032	0.126008	0.334411
antisense	-	1	0	0	0	0	0	0.222441	0	0	0	0	0
pseudogen	-	0	0	1	2	0	1	0	0	0.188041	0.246894	0	0.141817
sense_intrc	-	1	0	5	0	0	0	0.217864	0	1.435458	0	0	0
pseudogen	family_with	55	41	43	15	25	17	1.30455	1.146011	1.344006	0.307788	0.666173	0.400734
antisense	-	5	2	3	25	15	11	0.45482	0.214391	0.359605	1.967307	1.532884	0.994424
lincRNA	-	0	0	2	0	0	2	0	0	0.328298	0	0	0.247596
lincRNA	-	5	9	12	20	28	19	0.378691	0.803275	1.197653	1.310412	2.38244	1.430139
protein_co	Uncharacte	1	0	0	0	3	0	0.025489	0	0	0	0.085906	0
antisense	-	0	0	1	0	1	0	0	0	0.126383	0	0.107746	0
pseudogen	vomeronas	4	2	0	11	7	6	0.615593	0.362719	0	1.4645	1.210266	0.917687
lincRNA	long_interg	0	0	0	8	14	15	0	0	0	0.127352	0.289421	0.274317
antisense	-	18	14	10	24	27	20	1.751724	1.605567	1.282413	2.02054	2.95193	1.93434
antisense	NUTM2A_a	441	405	332	591	550	582	9.752288	10.55432	9.674774	11.30625	13.66406	12.79088
pseudogen	transient_r	0	0	1	0	0	1	0	0	0.079276	0	0	0.059789
lincRNA	-	12	17	7	0	1	0	0.981904	1.639245	0.75478	0	0.091926	0
processed_	-	4	0	1	7	16	3	0.078693	0	0.025925	0.119135	0.353629	0.058656
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.186575

antisense	-	1	0	0	0	1	0	0.03268	0	0	0	0.036714	0
protein_co	exosome_c	431	359	352	1211	752	1142	13.4221	13.17482	14.4451	32.62498	26.30935	35.34426
protein_co	vacuolar_p	374	356	298	534	471	488	5.931675	6.653694	6.228118	7.326727	8.392198	7.691928
pseudogen	-	2	2	1	3	4	6	0.159943	0.188483	0.105383	0.207548	0.359371	0.476865
pseudogen	-	2	2	0	7	4	1	0.322811	0.380413	0	0.977416	0.725316	0.160409
pseudogen	ribosomal_	20	17	28	59	44	27	2.316893	2.320769	4.274337	5.912769	5.726347	3.108489
pseudogen	-	132	97	77	51	39	23	4.177054	3.61722	3.210862	1.396141	1.386468	0.723325
protein_co	CMT1A_du	7	8	4	8	9	12	0.483795	0.651569	0.364299	0.478318	0.698803	0.824241
lincRNA	-	0	0	0	3	0	0	0	0	0	0.308757	0	0
pseudogen	ATPase_H+_	3	0	0	0	0	0	0.648257	0	0	0	0	0
sense_intro	AFF2_intro	0	0	0	0	1	0	0	0	0	0	0.134257	0
pseudogen	casein_kina	1	0	0	3	10	5	0.024658	0	0	0.063995	0.277019	0.122529
pseudogen	-	18	17	8	9	2	4	0.312439	0.347735	0.182986	0.135144	0.039001	0.069002
antisense	-	30	32	13	7	0	5	0.752716	0.946165	0.429821	0.151939	0	0.124678
processed_	-	3	1	2	2	0	1	0.199276	0.078278	0.175065	0.114928	0	0.066015
sense_intro	RABGAP1L_	0	1	0	1	0	0	0	0.084651	0	0.062142	0	0
antisense	-	1	13	1	1	1	4	0.063251	0.968985	0.083349	0.054718	0.071058	0.251441
antisense	-	0	0	0	2	0	1	0	0	0	0.184301	0	0.105863
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.258591	0
processed_	-	0	0	0	0	1	0	0	0	0	0	0.094257	0
processed_	long_interg	30	24	25	32	24	38	0.75594	0.712663	0.83012	0.697556	0.679401	0.951611
protein_co	zinc_finger_	51	26	51	162	137	98	0.407854	0.245027	0.537451	1.120759	1.230846	0.778879
pseudogen	MT-ND5_ps	0	1	12	0	3	3	0	0.039139	0.525194	0	0.111937	0.099023
pseudogen	thymosin_b	2	7	5	6	4	7	0.17133	0.706657	0.564428	0.44465	0.384957	0.595952
antisense	-	0	0	0	4	3	2	0	0	0	0.279262	0.271994	0.160409
pseudogen	sphingomy	1	0	0	0	0	0	0.024476	0	0	0	0	0
lincRNA	-	0	0	0	0	1	4	0	0	0	0	0.199584	0.706229
pseudogen	-	3	3	1	15	3	3	0.05507	0.064897	0.02419	0.238205	0.061868	0.05473
processed_	-	4	0	0	0	0	0	0.113243	0	0	0	0	0
sense_intro	DHRSX_int	3	7	4	4	9	6	0.243968	0.670836	0.428653	0.281406	0.822248	0.484922
protein_co	creatine_ki	0	0	1	29	18	19	0	0	0.036506	0.695012	0.560213	0.523112
lincRNA	tissue_diffe	6	1	2	184	180	181	0.085091	0.016712	0.037377	2.257433	2.867845	2.55107
antisense	-	5	7	6	10	3	11	0.596182	0.98359	0.942747	1.031507	0.401864	1.303501
pseudogen	-	7	1	3	8	6	11	0.692686	0.116613	0.391196	0.684843	0.66702	1.081784
pseudogen	trans-golgi_	1	1	5	0	0	0	0.08285	0.097633	0.545879	0	0	0
pseudogen	-	0	0	0	0	3	0	0	0	0	0	0.524788	0
pseudogen	centromere	0	0	0	1	0	0	0	0	0	0.035149	0	0
processed_	-	2	3	0	0	2	3	0.124129	0.219418	0	0	0.139451	0.185044
pseudogen	-	0	5	2	3	5	1	0	0.238303	0.10659	0.104963	0.227181	0.040194
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.112007	0
pseudogen	-	12	6	5	5	7	3	0.902403	0.531714	0.495478	0.325276	0.59138	0.224208
lincRNA	-	0	0	0	0	3	0	0	0	0	0	0.255627	0
pseudogen	RNA_bindi	2	0	0	0	3	0	0.096082	0	0	0	0.161913	0
pseudogen	adenylate_	0	3	0	0	0	0	0	0.289726	0	0	0	0

pseudogen	-	0	0	0	1	1	0	0	0	0	0.327135	0.424828	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.02461	0	0
antisense	-	0	0	0	3	1	2	0	0	0	0.232482	0.100636	0.178051
protein_co	ret_finger_	0	0	0	0	0	1	0	0	0	0	0	0.050835
antisense	-	0	0	0	0	4	0	0	0	0	0	0.207053	0
pseudogen	ubiquitin-li	0	1	4	0	0	1	0	0.026136	0.116905	0	0	0.022042
antisense	-	5	5	3	0	0	0	0.334223	0.393862	0.264255	0	0	0
processed_	-	8	8	5	4	11	10	0.217194	0.25595	0.17888	0.093946	0.335505	0.269816
pseudogen	-	0	0	0	3	2	0	0	0	0	0.501448	0.434131	0
pseudogen	-	0	1	1	0	0	0	0	0.053323	0.059627	0	0	0
antisense	-	0	0	0	0	0	6	0	0	0	0	0	0.769962
pseudogen	-	4	3	2	0	0	7	0.577014	0.509981	0.380181	0	0	1.003538
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.221925	0
pseudogen	ribosomal_	0	0	2	0	0	0	0	0	0.4128	0	0	0
lincRNA	long_interg	4	1	5	12	21	14	0.40336	0.118834	0.664412	1.046832	2.379037	1.403041
pseudogen	ribosomal_	3	0	0	0	0	1	0.433943	0	0	0	0	0.143754
sense_intrc	DIP2A_intr	0	3	1	6	1	2	0	0.437297	0.162998	0.642041	0.138962	0.24586
pseudogen	alcohol_de	2	2	0	0	0	0	0.093124	0.109741	0	0	0	0
lincRNA	-	3	2	4	3	5	10	0.311418	0.244658	0.547163	0.269405	0.583097	1.031648
antisense	-	0	1	2	0	2	0	0	0.080709	0.1805	0	0.153883	0
pseudogen	golgin_A6_	0	0	0	1	0	0	0	0	0	0.035284	0	0
processed_	-	1	0	3	0	0	0	0.107604	0	0.425386	0	0	0
lincRNA	-	0	0	0	1	0	11	0	0	0	0.007579	0	0.095773
pseudogen	NOP2/Sun_	248	235	149	581	267	527	2.739851	3.059498	2.169184	5.552831	3.313871	5.786228
antisense	-	0	0	0	4	0	1	0	0	0	0.226167	0	0.064956
lincRNA	-	0	0	0	1	2	4	0	0	0	0.054849	0.142457	0.252043
lincRNA	-	1	3	1	6	0	0	0.064016	0.226316	0.084357	0.332277	0	0
pseudogen	-	0	4	0	4	0	5	0	0.405774	0	0.297879	0	0.427757
pseudogen	-	2	1	7	8	13	13	0.245097	0.144416	1.130424	0.848128	1.789785	1.583293
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.389734
pseudogen	-	4	2	3	1	4	2	0.172166	0.101443	0.170154	0.037235	0.193418	0.085551
pseudogen	RAD17_hor	3	0	2	3	3	7	0.080335	0	0.070575	0.069498	0.090252	0.186292
antisense	-	0	2	0	0	0	1	0	0.168388	0	0	0	0.071004
lincRNA	-	0	0	0	0	0	3	0	0	0	0	0	0.216816
pseudogen	-	0	0	0	2	0	0	0	0	0	0.099025	0	0
antisense	-	1	0	1	0	2	2	0.092393	0	0.121751	0	0.207595	0.183644
processed_	-	125	90	57	114	84	114	2.225908	1.88863	1.33754	1.756164	1.68045	2.017491
processed_	-	299	284	205	145	74	132	20.8281	23.31331	18.81773	8.737949	5.791076	9.13823
lincRNA	-	2	1	5	0	1	4	0.19791	0.116613	0.651993	0	0.11117	0.393376
pseudogen	-	0	0	0	0	0	4	0	0	0	0	0	0.314114
antisense	-	2	0	2	1	0	0	0.194994	0	0.256955	0.084344	0	0
pseudogen	tumor_sup	2	2	1	644	532	493	0.045307	0.053391	0.029852	12.62067	13.53923	11.09916
processed_	-	0	4	3	3	1	1	0	0.125529	0.105277	0.069113	0.029917	0.026466
processed_	CCDC74B_a	1	0	0	0	0	2	0.028757	0	0	0	0	0.057158

processed_	-	37	44	21	81	71	135	1.410235	1.976285	1.054736	2.670778	3.040166	5.113677
lincRNA	long_interg	164	171	148	158	128	139	6.241785	7.66952	7.422693	5.202176	5.472982	5.257623
antisense	microRNA_	5	7	2	0	3	0	0.099851	0.164736	0.052632	0	0.067306	0
pseudogen	CD99_mole	115	92	73	297	235	253	1.982486	1.868991	1.658326	4.429266	4.551234	4.334534
processed_	-	3	7	4	0	2	4	0.031407	0.086358	0.055182	0	0.023522	0.041617
lincRNA	-	3	1	3	1	1	2	0.173198	0.068035	0.228233	0.049944	0.064859	0.114753
pseudogen	-	0	0	0	0	6	1	0	0	0	0	1.031374	0.152064
antisense	UBE2E1_an	3	10	3	0	6	3	0.204143	0.801899	0.26901	0	0.458683	0.202882
pseudogen	cytochrom	0	3	0	0	0	0	0	0.536284	0	0	0	0
antisense	ENTPD3_an	22	3	15	27	26	24	0.572054	0.091927	0.513973	0.607353	0.759516	0.620205
processed_	-	0	0	0	1	0	0	0	0	0	0.020556	0	0
protein_co	ceramide_s	29	24	20	45	36	81	0.600191	0.585342	0.545452	0.805688	0.837034	1.666043
pseudogen	ribosomal_	0	0	0	1	0	0	0	0	0	0.127219	0	0
processed_	-	27	28	20	31	43	36	0.64679	0.790433	0.631342	0.642428	1.157224	0.857061
lincRNA	-	1	6	0	0	0	0	0.10442	0.738316	0	0	0	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.058395
processed_	-	7	0	4	19	21	35	0.416858	0	0.313896	0.978829	1.404943	2.071419
lincRNA	-	0	1	2	2	7	7	0	0.153287	0.342817	0.225056	1.022927	0.90491
antisense	DIAPH3_an	2	0	2	0	0	1	0.288507	0	0.380181	0	0	0.143363
pseudogen	-	1	0	0	0	0	0	0.14913	0	0	0	0	0
antisense	CDH23_ant	5	0	0	0	0	0	0.700278	0	0	0	0	0
pseudogen	cofilin_1_(r	3	5	3	2	8	14	0.074917	0.147141	0.098722	0.043207	0.224437	0.347451
antisense	-	1	0	0	0	4	0	0.143084	0	0	0	0.642983	0
pseudogen	DAZ_associ	2	0	0	0	0	0	0.210501	0	0	0	0	0
lincRNA	-	2	0	0	0	0	0	0.271492	0	0	0	0	0
pseudogen	barrier_to_	0	0	2	0	0	0	0	0	0.516765	0	0	0
sense_intrc	-	4	5	2	0	0	0	0.850458	1.252766	0.560348	0	0	0
lincRNA	-	0	0	2	0	0	0	0	0	0.331417	0	0	0
lincRNA	-	9	5	2	1	1	1	0.841818	0.551128	0.246513	0.080917	0.105081	0.092958
lincRNA	family_with	2	0	1	9	11	11	0.022566	0	0.014869	0.08785	0.139436	0.123349
lincRNA	-	1	1	0	4	2	3	0.047017	0.055407	0	0.162696	0.105641	0.14018
pseudogen	-	0	0	0	2	0	2	0	0	0	0.263212	0	0.30238
processed_	-	2	3	2	3	5	2	0.0302	0.053384	0.039797	0.039189	0.08482	0.030014
pseudogen	-	0	3	1	3	5	2	0	0.378107	0.140936	0.277569	0.600767	0.212582
pseudogen	nucleopho	0	0	2	0	3	1	0	0	0.195964	0	0.250601	0.073896
protein_co	major_hist	6	6	5	182	166	214	0.203619	0.239953	0.2236	5.343206	6.328848	7.217568
pseudogen	-	1	0	0	0	0	0	0.158982	0	0	0	0	0
pseudogen	-	24	39	11	7	6	7	2.598331	4.975708	1.569317	0.655608	0.729766	0.753166
antisense	ABCC5_ant	0	1	0	0	1	0	0	0.133023	0	0	0.126814	0
lincRNA	-	0	0	4	0	1	1	0	0	0.445061	0	0.094858	0.083914
antisense	-	12	10	12	0	3	7	1.14467	1.124103	1.508395	0	0.321491	0.663601
pseudogen	-	1	6	3	4	7	4	0.114343	0.80848	0.45203	0.395671	0.899204	0.454549
pseudogen	-	0	0	0	1	0	0	0	0	0	0.228995	0	0
lincRNA	-	42	37	34	71	33	83	1.422599	1.476869	1.517563	2.080437	1.25573	2.793964

pseudogen	cyclin_J_ps	1	0	1	0	0	0	0.045521	0	0.059986	0	0	0
pseudogen	SEC13_hon	4	0	0	0	5	6	0.22338	0	0	0	0.313692	0.333
antisense	-	8	7	3	1	2	4	0.80672	0.831836	0.398647	0.087236	0.226575	0.400869
pseudogen	-	0	0	1	0	1	2	0	0	0.227985	0	0.194366	0.343883
pseudogen	developme	0	0	0	0	5	0	0	0	0	0	0.534855	0
pseudogen	-	2	1	0	0	7	0	0.205596	0.121141	0	0	0.808411	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.147172
pseudogen	argininosu	2	11	1	2	3	3	0.086576	0.561132	0.057043	0.074896	0.145894	0.129061
antisense	-	2	5	1	0	0	0	0.186412	0.549188	0.122823	0	0	0
pseudogen	-	3	2	0	0	0	0	0.167712	0.131759	0	0	0	0
lincRNA	-	1	0	2	0	0	0	0.02521	0	0.066441	0	0	0
antisense	-	0	0	0	0	0	16	0	0	0	0	0	1.16435
pseudogen	-	2	7	2	0	4	4	0.121703	0.50197	0.160375	0	0.273452	0.241904
lincRNA	-	1	3	1	0	0	0	0.328826	1.162504	0.433312	0	0	0
antisense	-	14	12	10	0	2	1	0.212675	0.214821	0.200182	0	0.034133	0.015097
antisense	-	17	7	14	21	17	18	0.411145	0.199504	0.446179	0.439368	0.461896	0.432642
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.461054	0
lincRNA	-	5	2	0	0	3	3	0.485697	0.228946	0	0	0.32739	0.289619
pseudogen	AFG3_ATPa	159	160	121	472	394	431	2.530093	3.000312	2.537228	6.49747	7.043436	6.815947
antisense	-	255	179	202	378	352	367	6.726434	5.564227	7.021516	8.625803	10.43125	9.621005
pseudogen	protein-kin	0	0	0	3	2	2	0	0	0	0.064963	0.056242	0.049753
pseudogen	zinc_finger	1	0	0	2	2	1	0.038197	0	0	0.066088	0.085824	0.037961
antisense	-	3	2	1	1	3	0	0.35294	0.277279	0.15503	0.101775	0.396506	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.052093
pseudogen	DEAD/H_(A	0	0	1	0	1	3	0	0	0.042102	0	0.035894	0.095258
pseudogen	-	0	0	2	4	0	4	0	0	0.112431	0.147619	0	0.169586
pseudogen	-	1	0	0	0	2	2	0.093042	0	0	0	0.209054	0.184935
lincRNA	Smith-Mag	0	0	0	0	0	3	0	0	0	0	0	0.279862
pseudogen	heterogene	0	1	1	0	0	6	0	0.036807	0.041158	0	0	0.186244
antisense	-	7	10	11	0	0	0	0.158033	0.266046	0.327248	0	0	0
sense_intrc	-	7	5	1	4	2	10	0.62179	0.523387	0.117052	0.307375	0.199584	0.882786
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.180778	0
pseudogen	-	0	0	0	4	1	2	0	0	0	0.112528	0.036533	0.064636
pseudogen	ATP_syntha	0	0	1	0	0	0	0	0	0.077948	0	0	0
pseudogen	-	8	1	1	9	5	3	1.680666	0.24757	0.276838	1.635675	1.180078	0.626358
pseudogen	-	2	0	1	0	1	0	0.1034	0	0.068128	0	0.058082	0
pseudogen	-	0	0	0	0	0	5	0	0	0	0	0	0.827265
pseudogen	-	0	2	12	3	0	0	0	0.462131	3.10059	0.508877	0	0
pseudogen	-	0	0	0	1	5	0	0	0	0	0.157385	1.021923	0
lincRNA	-	13	5	13	0	0	0	0.564125	0.255687	0.743379	0	0	0
pseudogen	-	0	0	3	0	0	0	0	0	0.438763	0	0	0
antisense	MIR181A2_	4	13	10	1	4	9	0.319885	1.225137	1.053826	0.069183	0.359371	0.715297
lincRNA	-	2	0	1	3	2	3	0.040724	0	0.026832	0.052845	0.045751	0.060709
sense_intrc	-	1	0	0	6	0	4	0.08285	0	0	0.430037	0	0.329352

antisense	TCEAL3_ant	5	0	1	0	2	0	0.733255	0	0.19325	0	0.329506	0
lincRNA	EPB41L4A_	688	726	422	352	226	337	12.2679	15.25547	9.915832	5.429847	4.527301	5.972023
lincRNA	-	0	1	1	2	0	0	0	0.090156	0.100814	0.132367	0	0
pseudogen	high_mobil	0	0	0	2	1	3	0	0	0	0.315855	0.205089	0.544283
antisense	-	9	2	8	8	5	2	0.488185	0.127844	0.57183	0.375401	0.304692	0.107816
processed_	-	0	1	3	15	20	16	0	0.081128	0.272158	0.893347	1.546838	1.094701
lincRNA	-	1	0	0	0	0	0	0.08973	0	0	0	0	0
protein_co	glycolipid_	716	550	482	989	721	714	17.30856	15.66815	15.35429	20.6827	19.58088	17.15362
pseudogen	glyceraldeh	0	2	6	0	3	4	0	0.155387	0.52127	0	0.222201	0.262087
antisense	EGFR_antis	3	7	12	0	3	2	0.056601	0.155636	0.298346	0	0.063588	0.037501
pseudogen	heat_shock	0	0	0	0	1	6	0	0	0	0	0.031891	0.169268
pseudogen	arylsulfatas	0	0	0	0	1	0	0	0	0	0	0.093663	0
processed_	-	4	1	5	0	5	9	0.255445	0.075257	0.420768	0	0.358721	0.571202
pseudogen	-	0	0	0	2	0	0	0	0	0	0.230725	0	0
antisense	-	0	0	0	1	0	0	0	0	0	0.058268	0	0
pseudogen	-	3	5	2	0	0	0	0.384559	0.755299	0.337837	0	0	0
pseudogen	-	18	11	1	11	5	2	0.414501	0.298506	0.030345	0.219134	0.129352	0.045771
lincRNA	-	0	6	0	0	0	0	0	0.505164	0	0	0	0
antisense	-	0	1	0	0	0	4	0	0.129167	0	0	0	0.435727
processed_	small_nucl	1272	1221	1220	3915	2965	2880	7.616031	8.61518	9.625786	20.27852	19.94414	17.13735
antisense	-	4	5	7	0	13	12	0.243687	0.358963	0.56196	0	0.889743	0.726546
pseudogen	ubiquitin-c	3	1	7	19	17	18	0.355309	0.13957	1.09249	1.94671	2.261948	2.118687
lincRNA	-	13	5	9	28	14	26	0.51708	0.234364	0.471728	0.963463	0.625592	1.027773
pseudogen	-	0	0	0	6	4	0	0	0	0	0.179839	0.155696	0
antisense	-	40	40	31	9	31	29	0.580653	0.684264	0.592997	0.113022	0.505553	0.418373
antisense	-	0	0	0	0	0	3	0	0	0	0	0	0.273083
antisense	-	7	12	11	1	21	4	0.513278	1.036915	1.062875	0.063433	1.729909	0.291491
pseudogen	-	0	1	0	0	0	1	0	0.155193	0	0	0	0.130881
pseudogen	-	13	15	3	10	6	5	0.449238	0.610846	0.136612	0.298948	0.232934	0.171717
lincRNA	-	3	0	0	1	0	0	0.160589	0	0	0.046308	0	0
antisense	-	1	0	1	9	6	16	0.121146	0	0.159641	0.943227	0.816603	1.926373
antisense	ELMO1_ant	0	0	0	0	7	1	0	0	0	0	0.788506	0.099648
pseudogen	cytochrom	0	0	0	1	0	0	0	0	0	0.088075	0	0
pseudogen	centromere	0	0	0	7	21	35	0	0	0	0.659655	2.569947	3.789078
sense_overl	-	14	8	22	14	22	13	0.159187	0.107195	0.329638	0.137711	0.281029	0.146903
pseudogen	-	1	1	9	0	0	3	0.122266	0.144083	1.450045	0	0	0.364532
antisense	INHBA_anti	1	1	0	6	1	3	0.017618	0.020761	0	0.091445	0.019792	0.052527
pseudogen	protein_tyr	0	0	1	0	0	0	0	0	0.068128	0	0	0
sense_intro	-	0	0	0	0	2	2	0	0	0	0	0.282546	0.249948
pseudogen	autophagy_	1	0	3	2	0	0	0.127262	0	0.503101	0.220187	0	0
pseudogen	POM121_tr	1	3	0	0	1	0	0.005545	0.019604	0	0	0.00623	0
pseudogen	ubiquitin-c	8	1	2	38	7	13	0.852169	0.125529	0.280738	3.501727	0.837689	1.376223
antisense	-	1	0	0	0	0	1	0.079016	0	0	0	0	0.078528
antisense	-	2	0	0	0	0	0	0.226244	0	0	0	0	0

protein_co	Uncharacte	11	10	4	0	0	0	1.66386	1.782507	0.797295	0	0	0
antisense	-	21	25	14	26	23	17	2.154575	3.022661	1.892802	2.307697	2.651058	1.733409
sense_intrc	AMMECR1_	0	3	1	2	1	0	0	0.333624	0.124355	0.163276	0.106018	0
antisense	-	3	0	0	0	4	4	0.072094	0	0	0	0.107991	0.095532
antisense	-	6	3	18	8	12	4	0.212614	0.125277	0.840521	0.245242	0.477718	0.140868
antisense	HLA_compl	0	0	1	0	0	0	0	0	0.168918	0	0	0
pseudogen	-	0	1	0	1	0	0	0	0.111407	0	0.081784	0	0
antisense	DNAJC27_a	6	12	8	5	4	6	0.068164	0.160655	0.119765	0.04914	0.051052	0.067743
lincRNA	-	0	0	0	5	2	2	0	0	0	0.39011	0.202644	0.179264
lincRNA	long_interg	2	0	0	0	0	2	0.079611	0	0	0	0	0.079119
pseudogen	succinate_d	3	0	7	1	1	1	0.330881	0	1.017381	0.095414	0.123908	0.109613
lincRNA	-	6	3	5	0	0	0	0.145509	0.085737	0.159788	0	0	0
pseudogen	sorting_nex	0	0	0	0	5	0	0	0	0	0	0.356143	0
protein_co	Homo_sapi	8	5	16	16	14	10	0.170846	0.125832	0.450267	0.295596	0.335887	0.212239
antisense	HOXD_clus	24	25	12	5	2	9	0.30002	0.368286	0.197676	0.054072	0.028088	0.111813
antisense	-	4	3	3	2	9	5	0.475874	0.420591	0.470314	0.205838	1.202884	0.591169
antisense	-	4	0	0	1	1	0	0.908858	0	0	0.196562	0.255261	0
antisense	PHEX_antis	0	0	0	0	3	0	0	0	0	0	0.093614	0
pseudogen	-	0	0	0	2	1	0	0	0	0	0.35503	0.230527	0
pseudogen	-	0	1	1	4	0	2	0	0.097481	0.109005	0.286243	0	0.164419
antisense	-	1	3	2	0	1	0	0.059351	0.209824	0.15642	0	0.066677	0
antisense	-	14	4	7	10	6	8	0.557693	0.187773	0.367451	0.344612	0.268514	0.316714
antisense	-	0	0	0	0	1	0	0	0	0	0	0.54069	0
antisense	-	0	5	1	0	1	0	0	0.753475	0.16851	0	0.143662	0
pseudogen	ribosomal_	0	0	1	0	0	0	0	0	0.095566	0	0	0
lincRNA	-	5	0	0	0	0	0	0.505162	0	0	0	0	0
antisense	-	0	6	0	0	1	0	0	0.468494	0	0	0.074438	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.095143
pseudogen	-	2	0	1	0	0	0	0.156168	0	0.102896	0	0	0
lincRNA	-	0	0	0	4	0	0	0	0	0	0.232777	0	0
pseudogen	mitochond	0	0	2	0	0	0	0	0	0.687323	0	0	0
antisense	WARS2_int	8	0	8	0	3	2	0.205596	0	0.270925	0	0.086615	0.051082
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.211727
pseudogen	cytochrom	0	0	0	4	3	4	0	0	0	0.574281	0.559335	0.659737
pseudogen	-	2	1	0	5	1	9	0.211341	0.124526	0	0.457075	0.118714	0.945163
antisense	-	0	0	0	1	1	0	0	0	0	0.107762	0.139943	0
pseudogen	phosducin-	0	4	0	0	2	0	0	0.353472	0	0	0.168487	0
pseudogen	-	0	2	1	1	0	1	0	0.509288	0.284748	0.186934	0	0.214751
lincRNA	-	24	30	17	0	0	0	1.141585	1.68161	1.065567	0	0	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.137835	0
pseudogen	-	4	1	2	3	5	1	0.239011	0.070415	0.157479	0.155075	0.335643	0.059384
antisense	-	0	0	0	0	1	1	0	0	0	0	0.175445	0.155204
antisense	-	0	0	0	0	2	1	0	0	0	0	0.096866	0.042845
pseudogen	-	0	0	0	2	4	0	0	0	0	0.145163	0.377026	0

pseudogen	-	0	5	0	1	0	0	0	0.104818	0	0.015389	0	0
processed_	SLC25A5_a	8	12	9	7	31	27	0.138317	0.244498	0.205052	0.1047	0.60214	0.463938
lincRNA	-	5	1	6	1	0	0	0.181678	0.042819	0.287289	0.031434	0	0
pseudogen	male-specif	23	45	35	83	69	58	0.599234	1.381618	1.201631	1.870723	2.019605	1.501779
antisense	-	6	0	0	5	2	6	0.486441	0	0	0.350681	0.182162	0.483437
lincRNA	-	27	12	11	150	85	92	0.641565	0.33602	0.344433	3.083409	2.269054	2.172573
pseudogen	-	5	1	6	0	0	3	0.179097	0.042211	0.283207	0	0	0.106794
pseudogen	-	0	1	0	2	0	0	0	0.244658	0	0.359207	0	0
pseudogen	mitochond	8	0	1	0	2	0	1.264263	0	0.208249	0	0.35508	0
pseudogen	-	0	1	6	1	2	2	0	0.088745	0.595419	0.065148	0.169206	0.149684
pseudogen	-	3	3	5	4	4	1	0.217268	0.256037	0.477177	0.25061	0.32545	0.071975
pseudogen	-	2	2	0	10	1	3	0.216086	0.254644	0	0.934672	0.121379	0.322127
pseudogen	THAP_dom	0	0	1	1	1	10	0	0	0.266272	0.174805	0.227007	2.00817
pseudogen	-	2	0	0	0	3	0	0.341555	0	0	0	0.575573	0
pseudogen	-	0	0	2	0	0	0	0	0	0.15642	0	0	0
pseudogen	-	1	0	1	0	0	1	0.157095	0	0.207013	0	0	0.156125
antisense	-	24	21	19	25	19	9	3.076474	3.172257	3.209449	2.772331	2.73618	1.146553
antisense	SCEL_antise	0	1	0	0	0	0	0	0.126547	0	0	0	0
pseudogen	MT-ND2_ps	0	0	1	2	0	2	0	0	0.069347	0.091052	0	0.1046
sense_intrc	-	6	0	4	1	3	1	0.133915	0	0.117645	0.019308	0.075222	0.022181
antisense	-	4	5	0	8	3	3	0.098495	0.145088	0	0.170415	0.08299	0.073415
lincRNA	-	0	0	3	0	0	0	0	0	0.591214	0	0	0
protein_co	Uncharacte	2	0	2	0	0	0	0.181305	0	0.238915	0	0	0
lincRNA	-	0	2	0	0	2	0	0	0.057368	0	0	0.05469	0
antisense	-	0	3	0	0	0	0	0	0.866496	0	0	0	0
processed_	-	5	16	6	4	4	1	0.201603	0.760247	0.318796	0.139524	0.181191	0.040072
lincRNA	long_interg	2	1	0	0	0	0	0.044302	0.026104	0	0	0	0
protein_co	chromoson	0	0	0	0	2	0	0	0	0	0	0.03804	0
antisense	-	6	14	7	41	18	28	0.660387	1.815859	1.015266	3.903857	2.22571	3.062772
antisense	-	0	0	0	1	0	2	0	0	0	0.100657	0	0.231271
protein_co	complemer	2	1	1	0	7	1	0.019392	0.011426	0.012777	0	0.076251	0.009636
antisense	GPC6_antis	2	3	0	0	0	6	0.180378	0.318847	0	0	0	0.537793
lincRNA	-	0	0	0	2	0	0	0	0	0	0.045571	0	0
pseudogen	ribosomal_	1	1	2	2	2	3	0.071542	0.084308	0.188549	0.123781	0.160746	0.2133
pseudogen	olfactory_r	0	0	0	1	0	0	0	0	0	0.048774	0	0
processed_	-	0	0	0	0	0	3	0	0	0	0	0	0.069078
antisense	-	3	0	0	0	0	1	0.402083	0	0	0	0	0.1332
pseudogen	-	2	2	1	8	2	4	0.048216	0.056819	0.031768	0.166845	0.054168	0.095836
pseudogen	-	0	3	1	4	1	2	0	1.051479	0.391929	1.029189	0.334134	0.591169
lincRNA	-	3	0	1	0	0	0	0.072258	0	0.031739	0	0	0
pseudogen	-	1	0	0	0	0	0	0.018453	0	0	0	0	0
pseudogen	ribosomal_	6	1	3	2	0	3	0.537472	0.105563	0.354128	0.154988	0	0.267076
antisense	STK24_anti	4	4	2	0	10	6	0.1657	0.195267	0.109176	0	0.465383	0.247014
pseudogen	keratin_18	0	0	1	1	1	0	0	0	0.053705	0.035257	0.045786	0

protein_co	adrenomed	5	9	3	46	17	48	0.154077	0.326827	0.121822	1.22628	0.588528	1.470008
pseudogen	ATP_syntha	0	0	1	0	2	0	0	0	0.296865	0	0.506178	0
antisense	PRKAR2A_a	4	4	4	4	3	4	0.061434	0.072397	0.080955	0.053146	0.051763	0.061055
lincRNA	long_interg	16	8	9	7	2	13	0.719063	0.423686	0.532996	0.27215	0.100978	0.58063
pseudogen	makorin_ri	1	3	4	0	0	0	0.036088	0.127582	0.19022	0	0	0
pseudogen	-	7	11	14	0	4	8	0.104215	0.192988	0.274659	0	0.066902	0.118367
pseudogen	-	0	5	0	0	0	0	0	0.666536	0	0	0	0
pseudogen	-	0	4	0	0	0	0	0	0.223812	0	0	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.150572	0
pseudogen	-	0	0	3	1	4	1	0	0	0.397889	0.08707	0.452288	0.100027
pseudogen	ATP_syntha	1	3	0	0	0	0	0.093042	0.328934	0	0	0	0
pseudogen	ribosomal_	5	7	1	1	1	7	0.660112	1.089063	0.173973	0.114212	0.148319	0.91845
lincRNA	-	6	9	10	0	2	5	0.790164	1.39674	1.735405	0	0.2959	0.654404
pseudogen	complemer	0	3	0	0	0	0	0	0.098871	0	0	0	0
pseudogen	phosphogly	0	0	2	3	3	2	0	0	0.186783	0.183931	0.238859	0.140868
processed_	-	12	4	6	23	21	9	1.212389	0.476242	0.798816	2.010257	2.383577	0.903676
protein_co	ataxin_1-lik	621	511	629	810	969	931	4.171597	4.045188	5.567961	4.707158	7.312798	6.215414
pseudogen	-	0	0	0	2	0	0	0	0	0	0.157927	0	0
protein_co	LOC64421	24	26	8	11	11	11	5.38383	6.873224	2.364857	2.134695	2.772183	2.45235
pseudogen	ribosomal_	0	0	0	1	2	1	0	0	0	0.14967	0.388731	0.171941
pseudogen	-	0	3	1	5	6	1	0	0.101554	0.037853	0.124251	0.193628	0.028548
lincRNA	-	2	0	0	3	0	3	0.079551	0	0	0.103228	0	0.118589
pseudogen	-	5	0	2	0	3	0	0.18921	0	0.099733	0	0.127539	0
processed_	-	1	4	5	4	2	3	0.023425	0.110421	0.154344	0.08106	0.052634	0.069842
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.045751
antisense	-	4	3	1	0	3	0	0.506612	0.447759	0.166898	0	0.426861	0
pseudogen	-	0	0	0	0	5	0	0	0	0	0	0.545651	0
antisense	-	2	9	12	1	1	1	0.185758	0.985069	1.468701	0.080349	0.104344	0.092305
antisense	-	0	0	0	5	5	7	0	0	0	0.485158	0.630041	0.780293
lincRNA	long_interg	0	0	3	2	0	1	0	0	0.079943	0.034988	0	0.020097
pseudogen	keratin_8_p	0	0	0	4	5	1	0	0	0	0.126604	0.205515	0.036361
antisense	-	0	0	0	6	2	1	0	0	0	0.284171	0.123011	0.05441
pseudogen	-	1	1	0	1	0	0	0.070871	0.083518	0	0.06131	0	0
antisense	-	0	0	0	0	5	2	0	0	0	0	0.558984	0.197797
pseudogen	peptidylpro	1	0	0	0	0	0	0.115592	0	0	0	0	0
protein_co	small_integ	414	325	363	472	378	434	4.677245	4.326934	5.404198	4.613121	4.797673	4.872919
antisense	TMLHE_ant	0	2	1	1	3	2	0	0.073311	0.040989	0.026909	0.104834	0.061826
processed_	-	0	0	2	0	3	1	0	0	0.410372	0	0.524788	0.154747
antisense	-	0	1	2	0	0	2	0	0.159152	0.355935	0	0	0.268439
pseudogen	-	49	48	51	129	82	73	2.777418	3.206222	3.809344	6.325545	5.221654	4.112233
pseudogen	-	0	0	0	3	4	0	0	0	0	0.374378	0.648239	0
pseudogen	eukaryotic_	44	47	75	20	15	16	1.259137	1.584986	2.828241	0.495123	0.482237	0.45504
pseudogen	-	0	0	0	0	4	0	0	0	0	0	0.316361	0
pseudogen	high_mobil	3	0	0	1	0	0	0.290353	0	0	0.083727	0	0

pseudogen	-	2	0	0	0	0	0	0.304259	0	0	0	0	0
pseudogen	major_hist	0	0	0	2	1	4	0	0	0	0.056647	0.036782	0.130152
antisense	LPP_antise	1	0	0	0	1	0	0.107168	0	0	0	0.120397	0
lincRNA	-	0	0	0	2	0	0	0	0	0	0.12213	0	0
pseudogen	family_witl	0	0	2	4	2	2	0	0	0.292509	0.384058	0.249375	0.220604
lincRNA	-	0	3	0	0	0	0	0	0.121614	0	0	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.080838	0	0	0
pseudogen	-	0	0	0	2	1	0	0	0	0	0.050973	0.033097	0
antisense	COL18A1_a	26	24	25	2	10	3	2.493598	2.71251	3.159569	0.165938	1.077462	0.285946
lincRNA	-	3	2	0	0	0	0	0.227215	0.178506	0	0	0	0
pseudogen	-	114	89	73	146	146	262	4.382915	4.032322	3.698417	4.855948	6.306089	10.01081
pseudogen	-	6	2	5	1	6	0	0.971394	0.381576	1.066717	0.140058	1.091301	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.2397
antisense	-	20	7	9	3	7	4	1.785531	0.736449	1.058802	0.231698	0.702077	0.354901
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.098962	0
pseudogen	ribosomal_	77	75	45	16	12	12	8.861862	10.17191	6.824669	1.593005	1.551546	1.37254
antisense	-	0	2	0	0	0	0	0	0.214391	0	0	0	0
antisense	ZMIZ1_anti	14	2	6	2	2	2	0.257531	0.043355	0.145441	0.031827	0.041331	0.036563
antisense	patched_d	28	30	33	234	148	157	0.732024	0.924263	1.136883	5.292318	4.346882	4.079213
pseudogen	ribosomal_	8	0	0	0	1	0	0.661762	0	0	0	0.092931	0
pseudogen	-	1	0	0	0	0	0	0.074987	0	0	0	0	0
pseudogen	-	0	0	4	0	0	0	0	0	0.29374	0	0	0
sense_intro	TGFA_intro	0	0	0	2	0	0	0	0	0	0.210087	0	0
processed_	-	0	1	1	0	0	0	0	0.056155	0.062793	0	0	0
pseudogen	-	0	0	0	1	1	0	0	0	0	0.211055	0.274083	0
antisense	-	0	0	0	2	0	0	0	0	0	0.17381	0	0
processed_	-	9	1	1	23	20	19	0.227323	0.029765	0.033284	0.502564	0.567518	0.47694
antisense	-	9	6	9	6	9	6	1.126404	0.884932	1.484325	0.64963	1.265445	0.746299
pseudogen	-	1	3	0	0	1	1	0.141176	0.499102	0	0	0.158602	0.140304
antisense	-	0	1	1	5	10	4	0	0.114683	0.128241	0.420946	1.093307	0.386868
pseudogen	-	4	15	8	16	14	5	1.018096	4.499115	2.683203	3.522993	4.003187	1.264761
pseudogen	-	36	34	26	53	26	64	3.367272	3.747673	3.204674	4.28859	2.732109	5.949292
lincRNA	-	14	9	2	30	15	44	0.369847	0.280184	0.069624	0.685612	0.445179	1.155199
pseudogen	-	0	0	0	1	0	0	0	0	0	0.06755	0	0
lincRNA	-	0	1	0	2	2	0	0	0.136815	0	0.200872	0.260859	0
antisense	-	0	0	0	1	0	0	0	0	0	0.151652	0	0
pseudogen	-	3	0	1	0	0	0	0.122833	0	0.053955	0	0	0
processed_	-	0	0	0	1	1	0	0	0	0	0.025054	0.032536	0
lincRNA	-	1	0	0	0	0	1	0.066676	0	0	0	0	0.066265
antisense	-	7	1	4	0	0	0	1.191598	0.200604	0.897277	0	0	0
processed_	SH3BP5_ar	113	84	110	81	72	56	1.074027	0.940856	1.377731	0.666016	0.768809	0.528974
pseudogen	-	0	0	3	0	0	0	0	0	0.453008	0	0	0
pseudogen	importin_8	0	0	0	0	3	0	0	0	0	0	0.057391	0
antisense	-	0	0	0	10	1	1	0	0	0	0.193899	0.02518	0.022275

pseudogen	-	1	3	0	0	6	2	0.33507	1.184577	0	0	2.258579	0.666001
pseudogen	phospholip	4	6	3	28	8	25	0.372824	0.659025	0.368468	2.257693	0.837689	2.315759
pseudogen	suppressor	0	0	0	2	0	0	0	0	0	0.067401	0	0
pseudogen	-	1	4	0	3	6	2	0.164925	0.777417	0	0.428027	1.111699	0.327813
processed_	RASAL2_an	10	3	6	57	28	33	0.227312	0.080362	0.179725	1.120883	0.715039	0.745497
pseudogen	-	0	1	0	1	0	0	0	0.083406	0	0.061228	0	0
protein_co	zinc_finger	0	0	0	4	0	1	0	0	0	0.087319	0	0.025078
pseudogen	ubiquitin-c	0	0	0	0	0	3	0	0	0	0	0	0.371393
antisense	-	0	1	0	0	0	0	0	0.176736	0	0	0	0
antisense	LAMTOR5_	1	1	2	16	8	10	0.060092	0.070815	0.158373	0.831762	0.540076	0.597208
antisense	-	0	0	0	2	2	0	0	0	0	0.158748	0.206156	0
pseudogen	ribosomal_	0	0	0	0	3	0	0	0	0	0	0.438397	0
sense_intrc	E2F3_intro	3	10	1	1	0	1	0.397057	1.559693	0.174408	0.114497	0	0.131535
pseudogen	olfactory_r	2	0	0	0	1	0	0.118304	0	0	0	0.066454	0
protein_co	Protein_LO	6	9	0	6	1	5	0.275018	0.486138	0	0.237916	0.051494	0.227766
antisense	-	11	11	10	0	0	0	0.247283	0.291408	0.296235	0	0	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.012056
processed_	-	0	0	0	9	19	16	0	0	0	0.142874	0.391696	0.291794
processed_	-	0	0	0	1	0	0	0	0	0	0.021213	0	0
pseudogen	-	0	1	0	4	8	2	0	0.04999	0	0.146791	0.381256	0.084317
pseudogen	FCF1_small	5	3	3	0	2	2	0.474382	0.335418	0.375071	0	0.213175	0.188581
pseudogen	-	9	5	5	14	18	13	0.312439	0.20455	0.228732	0.420449	0.702011	0.448513
antisense	PCOLCE_an	10	6	11	2	3	10	0.208676	0.147547	0.302482	0.036105	0.07033	0.207387
antisense	-	0	0	0	0	2	0	0	0	0	0	0.244757	0
antisense	-	0	0	0	1	3	1	0	0	0	0.083422	0.325005	0.095836
antisense	-	9	1	0	37	34	42	0.356105	0.046628	0	1.266487	1.511346	1.651562
antisense	TEX26_anti	0	0	0	0	2	0	0	0	0	0	0.05794	0
sense_intrc	-	9	8	1	5	5	4	0.954848	1.000204	0.139806	0.458907	0.595951	0.421756
processed_	-	0	0	0	0	5	0	0	0	0	0	0.369875	0
pseudogen	-	9	12	6	3	0	8	0.428094	0.672644	0.376082	0.123447	0	0.378178
lincRNA	-	0	1	0	0	0	0	0	0.026346	0	0	0	0
pseudogen	serine_hyd	4	9	2	0	0	0	0.161405	0.427965	0.106346	0	0	0
pseudogen	high_mobil	0	1	0	0	0	0	0	0.21513	0	0	0	0
pseudogen	farnesyl_di	0	0	0	4	0	0	0	0	0	0.168224	0	0
antisense	-	1	0	3	0	0	1	0.108708	0	0.429753	0	0	0.108037
antisense	-	0	0	0	4	2	4	0	0	0	0.312621	0.202989	0.35914
pseudogen	-	0	1	0	0	0	0	0	0.037136	0	0	0	0
pseudogen	heat_shock	0	0	0	0	4	0	0	0	0	0	0.122127	0
pseudogen	centrin_EF-	1	0	0	4	4	0	0.112881	0	0	0.390609	0.507257	0
lincRNA	-	0	1	3	1	9	12	0	0.142438	0.477831	0.104564	1.222108	1.441481
antisense	-	0	0	0	1	0	1	0	0	0	0.025759	0	0.029592
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.595631
antisense	-	1	0	4	4	1	6	0.082207	0	0.433312	0.284465	0.092354	0.490193
pseudogen	-	1	2	0	0	1	0	0.118172	0.278517	0	0	0.132759	0

antisense	-	0	1	0	0	0	2	0	0.080709	0	0	0	0.136129
antisense	long_interg	0	0	0	1	0	0	0	0	0	0.069287	0	0
pseudogen	double_ho	1	1	0	0	0	0	0.04205	0.049553	0	0	0	0
antisense	SRGAP3_an	4	0	0	0	0	0	0.494776	0	0	0	0	0
pseudogen	BEN_domai	0	0	0	3	0	0	0	0	0	0.060957	0	0
antisense	TMEM72_a	0	0	0	4	0	1	0	0	0	0.055514	0	0.015944
lincRNA	-	88	99	72	174	140	162	7.790648	10.3284	8.399592	13.3261	13.92413	14.2533
lincRNA	-	3	0	2	0	0	0	0.310201	0	0.272513	0	0	0
antisense	COL4A2_an	8	4	3	4	7	6	0.278271	0.163962	0.13751	0.120365	0.273542	0.207414
sense_intro	THRB_intro	0	0	0	18	17	9	0	0	0	0.47	0.576448	0.269969
pseudogen	-	0	0	0	0	3	0	0	0	0	0	0.095212	0
pseudogen	long_interg	0	0	0	0	1	0	0	0	0	0	0.076056	0
pseudogen	-	4	6	7	58	13	31	0.187236	0.330969	0.43178	2.348662	0.683631	1.442118
pseudogen	glycine_cle	6	6	3	10	11	17	0.608517	0.7171	0.400938	0.877374	1.253324	1.713484
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.105651
antisense	-	0	0	0	3	8	9	0	0	0	0.271535	0.940331	0.935823
processed_	long_interg	3	0	0	10	1	10	0.31326	0	0	0.903331	0.11731	1.037752
lincRNA	-	4	0	0	0	0	0	0.316538	0	0	0	0	0
antisense	-	4	0	0	0	1	0	0.512746	0	0	0	0.144009	0
lincRNA	-	1	11	1	5	11	8	0.124567	1.614741	0.164149	0.538811	1.539377	0.990382
processed_	long_interg	1	0	0	0	0	0	0.118969	0	0	0	0	0
lincRNA	long_interg	0	0	0	0	0	2	0	0	0	0	0	0.216965
antisense	OPA1_antis	0	3	1	1	1	0	0	0.380413	0.141795	0.093087	0.120886	0
pseudogen	-	0	0	1	0	3	1	0	0	0.216656	0	0.554123	0.163398
lincRNA	-	0	0	2	0	0	3	0	0	0.327527	0	0	0.370521
pseudogen	ribosomal_	20	21	11	12	26	28	2.152073	2.662891	1.559748	1.117046	3.143036	2.994296
pseudogen	Y_box_binc	49	48	43	67	53	95	2.702197	3.119386	3.124814	3.196382	3.283566	5.206599
pseudogen	-	0	0	0	9	1	13	0	0	0	0.853396	0.123139	1.416113
processed_	-	2	1	3	0	0	0	0.086153	0.050763	0.170293	0	0	0
protein_co	HCG20425	345	247	232	387	353	534	8.197775	6.916413	7.264399	7.955196	9.423249	12.61037
antisense	-	3	1	7	2	8	1	0.24174	0.094958	0.743292	0.139418	0.724212	0.080082
protein_co	chromoson	1082	820	733	1510	1074	1697	77.30385	69.03905	69.0101	93.3284	86.20396	120.494
pseudogen	-	0	2	0	0	0	0	0	0.140513	0	0	0	0
pseudogen	inhibitor_c	4	3	3	11	5	7	0.19699	0.174105	0.194688	0.46864	0.276632	0.342603
antisense	-	0	0	1	0	0	0	0	0	0.135463	0	0	0
sense_intro	TSSC1_intr	2	2	3	0	5	2	0.147468	0.173782	0.29149	0	0.414178	0.146557
pseudogen	BEN_domai	16	18	10	15	6	5	1.721658	2.282478	1.417953	1.396308	0.725316	0.534696
pseudogen	-	0	0	0	0	6	0	0	0	0	0	0.360096	0
antisense	-	12	15	3	5	16	29	0.14052	0.206993	0.046293	0.050651	0.210488	0.337493
pseudogen	-	0	6	0	0	0	0	0	0.483002	0	0	0	0
pseudogen	ribosomal_	7	3	14	6	4	6	0.459216	0.231925	1.210268	0.340512	0.2948	0.391183
pseudogen	vacuolar_p	4	2	1	0	3	2	0.280482	0.165266	0.092402	0	0.236328	0.139375
processed_	-	3	4	7	11	3	8	0.048839	0.076738	0.150167	0.154916	0.054867	0.129432
antisense	-	1	0	0	0	0	3	0.214336	0	0	0	0	0.639037

antisense	-	0	1	0	2	1	0	0	0.08408	0	0.123447	0.080156	0
processed_	-	14	27	21	48	60	75	0.556437	1.264616	1.099872	1.650411	2.679095	2.962503
lincRNA	long_interg	106	90	83	188	149	182	1.707254	1.708213	1.761592	2.619469	2.696049	2.913221
protein_co	apolipopro	1	0	0	0	2	0	0.028945	0	0	0	0.065037	0
pseudogen	keratin_8_p	0	0	0	0	0	1	0	0	0	0	0	0.080945
lincRNA	long_interg	0	0	0	0	0	2	0	0	0	0	0	0.143363
lincRNA	-	8	7	2	10	13	20	0.635928	0.655727	0.209499	0.687671	1.160941	1.580002
pseudogen	succinate-C	2	2	0	0	0	0	0.077286	0.091077	0	0	0	0
pseudogen	-	0	1	0	0	0	0	0	0.287501	0	0	0	0
lincRNA	long_interg	0	0	3	4	0	1	0	0	0.092198	0.080703	0	0.023178
protein_co	proline-rich	13	0	1	2525	2058	2557	0.194197	0	0.019685	32.63043	34.53765	37.9611
sense_intrc	-	13	10	21	46	23	19	1.176467	1.066457	2.504323	3.601281	2.338369	1.708832
pseudogen	-	0	0	3	0	0	0	0	0	0.811201	0	0	0
processed_	-	15	12	7	13	19	14	0.34602	0.32621	0.212786	0.259427	0.492393	0.320957
pseudogen	-	39	27	14	89	65	106	1.670468	1.362839	0.790199	3.297818	3.127779	4.512208
processed_	PGM5_anti	0	0	0	0	1	0	0	0	0	0	0.103979	0
lincRNA	-	3	5	0	4	0	5	0.180276	0.354073	0	0.207941	0	0.298604
lincRNA	-	1	0	0	0	0	0	0.12087	0	0	0	0	0
protein_co	Protein_LO	0	1	0	0	0	0	0	0.089125	0	0	0	0
antisense	KCNC4_ant	1	0	0	1	0	4	0.070777	0	0	0.061228	0	0.281359
pseudogen	-	0	0	1	0	0	0	0	0	0.198191	0	0	0
antisense	-	0	2	0	10	12	16	0	0.264916	0	0.972376	1.51531	1.787314
processed_	-	2	2	6	0	1	0	0.191468	0.225634	0.756925	0	0.107551	0
processed_	-	0	2	2	0	12	2	0	0.047661	0.053295	0	0.272617	0.040194
protein_co	inactivatio	53	45	36	15	26	27	2.969177	2.970844	2.657649	0.726967	1.636374	1.503259
lincRNA	-	0	0	0	0	0	4	0	0	0	0	0	0.628227
pseudogen	-	0	0	0	3	0	0	0	0	0	0.410139	0	0
protein_co	transmemb	0	0	0	0	0	2	0	0	0	0	0	0.066896
antisense	-	0	0	0	2	3	4	0	0	0	0.15631	0.304484	0.35914
antisense	-	0	1	0	0	0	0	0	0.164611	0	0	0	0
pseudogen	protein_ph	6	2	3	0	0	1	0.304259	0.119517	0.200469	0	0	0.050397
pseudogen	-	0	0	0	0	4	3	0	0	0	0	0.697665	0.46288
sense_intrc	-	3	2	3	2	0	0	0.299102	0.234982	0.394143	0.172501	0	0
pseudogen	-	0	6	0	0	1	0	0	0.799843	0	0	0.127085	0
protein_co	Uncharacte	11	9	7	22	14	25	0.377415	0.363895	0.316489	0.652998	0.539639	0.852464
antisense	-	0	0	0	0	0	4	0	0	0	0	0	0.385451
lincRNA	-	0	0	0	2	1	0	0	0	0	0.200872	0.13043	0
pseudogen	-	2	0	0	0	0	0	0.106521	0	0	0	0	0
processed_	-	0	0	0	3	8	3	0	0	0	0.189513	0.656286	0.217713
pseudogen	sorting_ne	0	2	0	0	3	0	0	0.170226	0	0	0.243421	0
pseudogen	-	2	0	3	0	0	1	0.048019	0	0.094916	0	0	0.023861
pseudogen	ubiquitin-c	2	0	2	0	1	2	0.238473	0	0.314249	0	0.133955	0.237
pseudogen	-	1	0	2	0	0	0	0.194636	0	0.512965	0	0	0
lincRNA	-	1	0	0	0	0	0	0.029298	0	0	0	0	0

sense_intrc	-	0	0	0	7	2	1	0	0	0	1.35271	0.501906	0.222
pseudogen	eukaryotic_	14	10	11	4	9	8	0.408811	0.344113	0.423274	0.101046	0.295247	0.232163
antisense	-	22	19	16	16	3	3	0.566765	0.576821	0.543169	0.356585	0.086826	0.076809
antisense	EIF1AX_ant	1	0	0	0	2	3	0.140056	0	0	0	0.314687	0.417572
lincRNA	-	0	0	1	0	1	0	0	0	0.155722	0	0.132759	0
pseudogen	ribosomal_	0	3	3	2	0	3	0	0.388305	0.434211	0.190037	0	0.327473
pseudogen	high_mobil	0	0	1	1	1	0	0	0	0.116856	0.076715	0.099625	0
processed_	-	1	0	1	2	0	0	0.0211	0	0.027805	0.036508	0	0
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.153394
pseudogen	-	0	1	3	3	0	9	0	0.179275	0.601408	0.394818	0	1.360708
antisense	-	1	5	1	0	6	2	0.117909	0.694741	0.155375	0	0.794778	0.234361
antisense	WWC3_ant	0	1	0	0	1	4	0	0.107937	0	0	0.1029	0.364111
antisense	long_interg	2	4	2	41	26	34	0.081323	0.191667	0.107163	1.442208	1.187691	1.373946
pseudogen	-	1	1	0	3	0	2	0.061703	0.072713	0	0.160136	0	0.122643
pseudogen	profilin_1_	1	0	2	3	2	0	0.131694	0	0.347081	0.341783	0.2959	0
pseudogen	death_asso	1	2	2	1	2	3	0.190435	0.448833	0.501894	0.164744	0.427884	0.567778
antisense	GRTP1_ant	0	0	1	1	3	0	0	0	0.080465	0.052825	0.205799	0
antisense	-	0	0	4	0	1	2	0	0	0.393033	0	0.083769	0.148209
lincRNA	-	0	0	0	1	1	0	0	0	0	0.091781	0.11919	0
processed_	-	2	3	8	7	15	9	0.767261	1.356255	4.044248	2.323133	6.464774	3.431351
sense_intrc	-	7	2	2	3	4	8	0.221114	0.074448	0.08325	0.081979	0.141947	0.251141
pseudogen	ribosomal_	0	0	0	2	0	0	0	0	0	0.075576	0	0
pseudogen	SET_pseudo	9	0	0	6	2	7	0.559236	0	0	0.322528	0.139615	0.432275
lincRNA	-	1	0	0	0	0	0	0.175884	0	0	0	0	0
pseudogen	olfactory_r	1	2	3	11	15	8	0.056141	0.132318	0.22194	0.53424	0.946064	0.446355
antisense	-	0	0	2	0	0	1	0	0	0.148908	0	0	0.056152
pseudogen	-	1	0	0	0	0	0	0.036361	0	0	0	0	0
sense_intrc	-	0	0	1	0	2	0	0	0	0.148749	0	0.253629	0
antisense	-	0	0	2	0	6	2	0	0	0.374066	0	0.956717	0.282113
antisense	-	12	6	3	9	8	14	1.065926	0.628064	0.351157	0.691594	0.798334	1.235901
pseudogen	arylsulfatas	0	0	2	4	3	10	0	0	0.114837	0.150778	0.146854	0.433037
protein_co	-	0	1	5	6	4	1	0	0.062891	0.351629	0.27701	0.239822	0.053038
pseudogen	-	0	0	0	0	5	1	0	0	0	0	1.304296	0.230763
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.25972	0
pseudogen	RAN_memb	9	2	1	3	0	2	0.727434	0.190497	0.106509	0.209766	0	0.160654
lincRNA	long_interg	0	0	0	0	1	0	0	0	0	0	0.048751	0
lincRNA	-	0	0	0	2	0	0	0	0	0	0.116241	0	0
pseudogen	proteasom	1	0	0	0	1	0	0.07563	0	0	0	0.084966	0
pseudogen	mortality_f	1	1	0	0	0	2	0.054243	0.063922	0	0	0	0.107816
lincRNA	-	117	84	72	84	32	38	4.193701	3.548117	3.400783	2.604677	1.288578	1.353645
pseudogen	dynein_cyt	2	3	5	5	9	9	0.057607	0.10183	0.18978	0.124589	0.291231	0.257631
antisense	-	669	691	448	163	97	194	12.82314	15.60823	11.3157	2.702832	2.088763	3.695556
antisense	-	10	6	8	3	7	8	0.319499	0.225906	0.336817	0.082919	0.251256	0.254021
antisense	-	0	2	0	0	0	1	0	0.30139	0	0	0	0.127087

antisense	-	0	1	1	0	0	5	0	0.116613	0.130399	0	0	0.49172
pseudogen	-	298	255	195	326	386	486	3.709479	3.740623	3.198646	3.510567	5.398002	6.012327
pseudogen	-	0	5	6	0	0	0	0	1.0295	1.381451	0	0	0
pseudogen	nucleopho	5	4	8	13	8	6	0.305311	0.287833	0.643721	0.686719	0.548797	0.364111
lincRNA	long_interg	0	0	0	6	1	0	0	0	0	0.613378	0.132759	0
lincRNA	-	1	0	1	0	0	0	0.064171	0	0.084562	0	0	0
pseudogen	brain_prot	2	1	2	1	1	3	0.280111	0.165047	0.369118	0.121161	0.157344	0.417572
pseudogen	-	1	0	0	0	2	0	0.037734	0	0	0	0.084784	0
pseudogen	deoxyuridi	1	1	3	0	2	3	0.114591	0.135038	0.453008	0	0.257472	0.34165
lincRNA	-	0	0	0	3	5	10	0	0	0	0.193789	0.419435	0.742088
antisense	-	319	245	217	138	104	104	18.41677	16.66848	16.50887	6.892311	6.74536	5.967133
processed_	long_interg	0	0	0	0	0	2	0	0	0	0	0	0.25479
antisense	AATK_antis	2	0	0	2	0	0	0.067141	0	0	0.058084	0	0
pseudogen	-	0	0	2	0	0	0	0	0	0.586246	0	0	0
pseudogen	-	1	0	0	0	0	0	0.107604	0	0	0	0	0
antisense	-	5	1	0	2	1	0	0.307796	0.072544	0	0.106509	0.069158	0
protein_co	pleckstrin_	597	480	474	369	374	405	6.005277	5.689932	6.28307	3.211058	4.226485	4.048773
pseudogen	zinc_finger_	5	0	0	0	0	0	0.144332	0	0	0	0	0
pseudogen	ribosomal_	5	2	2	0	0	0	0.668447	0.31509	0.35234	0	0	0
lincRNA	long_interg	2	0	2	0	4	0	0.061345	0	0.080838	0	0.137835	0
processed_	-	0	0	0	4	0	6	0	0	0	0.651942	0	1.123432
pseudogen	-	2	3	1	3	1	2	0.168871	0.298506	0.111265	0.219134	0.094858	0.167828
antisense	TBC1D4_an	1	0	0	0	3	0	0.124567	0	0	0	0.41983	0
antisense	-	16	15	12	9	7	16	0.606339	0.669875	0.599255	0.295054	0.298018	0.602595
lincRNA	MIR137_ho	39	17	28	42	58	38	0.782379	0.401891	0.740194	0.728895	1.307163	0.75761
lincRNA	-	22	6	9	2	2	1	0.249081	0.080053	0.134275	0.019589	0.025439	0.011252
sense_intrc	-	4	2	7	11	15	2	0.303822	0.179018	0.700636	0.722795	1.27997	0.150973
antisense	-	0	1	0	0	0	0	0	0.123053	0	0	0	0
antisense	-	3	0	2	1	13	0	0.286168	0	0.251399	0.082521	1.39313	0
pseudogen	heat_shock	0	0	0	10	4	6	0	0	0	0.237669	0.123458	0.163822
lincRNA	-	1	8	2	7	6	14	0.185758	1.751235	0.489567	1.124885	1.252125	2.58455
pseudogen	phospholip	0	0	0	2	0	0	0	0	0	0.346961	0	0
pseudogen	coiled-coil-	1	1	0	0	1	0	0.123984	0.146107	0	0	0.139288	0
pseudogen	-	3	2	1	0	3	1	0.341555	0.268334	0.150029	0	0.383716	0.113148
pseudogen	ADP-ribosy	6	16	13	26	9	17	0.598203	1.879856	1.707952	2.242508	1.008066	1.684442
antisense	-	0	0	0	0	2	0	0	0	0	0	0.130144	0
antisense	TRAPPC12_	52	42	23	12	30	27	3.031863	2.885776	1.767132	0.605272	1.965063	1.564515
antisense	DDX26B_an	0	1	0	0	0	0	0	0.156753	0	0	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.07726
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	2.630703
pseudogen	-	506	472	458	156	286	157	8.765754	9.635801	10.45536	2.337902	5.566136	2.703012
pseudogen	-	0	0	0	2	0	0	0	0	0	0.118191	0	0
pseudogen	suppressior	5	8	1	2	8	7	0.240204	0.452905	0.063306	0.08312	0.431767	0.334209
antisense	-	0	0	0	1	0	0	0	0	0	0.039245	0	0

processed_	-	0	0	1	4	2	2	0	0	0.105224	0.276313	0.179415	0.158715
antisense	-	14	4	8	20	22	24	0.564489	0.190062	0.425062	0.697622	0.99655	0.961719
lincRNA	long_interg	9	2	2	0	0	0	0.273048	0.071505	0.079958	0	0	0
pseudogen	-	4	1	2	0	2	0	0.448652	0.132177	0.295607	0	0.252017	0
pseudogen	ubiquitin-c	2	0	0	0	0	0	0.139686	0	0	0	0	0
processed_	-	0	0	0	0	3	1	0	0	0	0	0.232934	0.068687
antisense	-	0	0	0	0	1	0	0	0	0	0	0.092211	0
antisense	-	0	0	0	4	0	0	0	0	0	0.352299	0	0
antisense	-	0	0	1	0	0	2	0	0	0.126842	0	0	0.191324
lincRNA	-	4	4	0	1	5	8	0.334013	0.393613	0	0.072238	0.469053	0.6639
sense_intrc	-	0	0	2	0	1	0	0	0	0.442941	0	0.188812	0
pseudogen	-	1	0	0	0	2	0	0.286168	0	0	0	0.642983	0
lincRNA	long_interg	0	0	0	0	0	1	0	0	0	0	0	0.091983
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.104186
sense_intrc	-	0	1	0	1	0	1	0	0.03183	0	0.023367	0	0.026844
antisense	-	0	2	0	3	6	2	0	0.189917	0	0.209127	0.543159	0.160165
pseudogen	DnaJ_(Hsp4	0	0	0	0	1	2	0	0	0	0	0.172394	0.305009
antisense	-	1	0	0	0	0	1	0.105671	0	0	0	0	0.105018
antisense	-	32	24	19	24	16	24	2.114996	1.869295	1.654809	1.372252	1.188033	1.576451
antisense	-	0	0	2	0	0	0	0	0	0.228358	0	0	0
lincRNA	-	2	1	0	0	0	0	0.165441	0.097481	0	0	0	0
lincRNA	-	8	8	1	8	3	11	0.490762	0.578334	0.080838	0.424555	0.206753	0.670631
processed_	-	0	0	2	0	0	0	0	0	0.322232	0	0	0
antisense	-	0	0	0	0	5	2	0	0	0	0	0.703025	0.248766
antisense	-	0	0	0	5	0	2	0	0	0	0.284465	0	0.130718
pseudogen	high_mobil	0	0	1	0	0	0	0	0	0.121751	0	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.149067	0	0	0
lincRNA	-	1203	1080	1078	774	593	661	8.982795	9.503349	10.60717	4.999768	4.974502	4.905203
pseudogen	sorting_ne	0	0	0	3	6	7	0	0	0	0.078512	0.203917	0.210456
pseudogen	solute_carr	0	0	0	1	0	0	0	0	0	0.051001	0	0
pseudogen	-	0	1	2	0	7	0	0	0.11705	0.261776	0	0.78111	0
antisense	FREM2_ant	0	0	0	0	5	0	0	0	0	0	0.639526	0
lincRNA	-	0	0	0	3	0	0	0	0	0	0.156846	0	0
pseudogen	-	0	0	0	1	1	0	0	0	0	0.133915	0.173906	0
antisense	-	18	12	6	121	96	141	0.32646	0.256476	0.143398	1.898482	1.956042	2.54148
protein_co	cancer/test	4	0	1	0	5	0	0.07504	0	0.024721	0	0.105379	0
pseudogen	ATPase_H+_	12	2	3	0	6	4	2.811026	0.552104	0.926061	0	1.579007	0.931222
pseudogen	teratocarci	0	0	0	0	1	0	0	0	0	0	0.021947	0
pseudogen	-	18	15	11	28	20	30	1.532054	1.504527	1.233756	2.061687	1.912409	2.537655
antisense	-	103	110	70	59	32	74	7.156066	9.006103	6.4087	3.546109	2.497676	5.109501
IG_V_pseuc	-	0	0	0	1	0	1	0	0	0	0.142676	0	0.163907
lincRNA	surfactant_	26	18	16	88	26	75	1.986242	1.620461	1.610696	5.815734	2.23142	5.694161
lincRNA	-	0	0	0	5	7	4	0	0	0	0.504393	0.91703	0.46356
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.106077

protein_co	Uncharacte	1	0	0	0	0	2	0.043147	0	0	0	0	0.08576
pseudogen	-	2	0	1	0	0	0	0.162645	0	0.107163	0	0	0
pseudogen	TGFB-induc	0	0	3	1	0	4	0	0	0.305533	0.06686	0	0.307235
pseudogen	-	0	2	1	5	3	3	0	0.18242	0.101993	0.334787	0.260859	0.230763
processed_	-	0	1	0	2	0	0	0	0.10398	0	0.152663	0	0
antisense	-	0	0	0	1	0	0	0	0	0	0.084344	0	0
processed_	-	3	5	2	26	17	18	0.055185	0.108387	0.04848	0.41375	0.351317	0.329066
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.124687	0
pseudogen	-	1	0	0	0	1	2	0.050276	0	0	0	0.056482	0.099932
pseudogen	ribosomal_	0	3	3	3	4	5	0	0.391555	0.437845	0.287441	0.497706	0.550356
antisense	-	0	0	0	4	4	4	0	0	0	0.104863	0.136178	0.120467
pseudogen	RNA_bindi	0	0	2	1	1	4	0	0	0.120698	0.039618	0.05145	0.182056
pseudogen	transportin	0	2	1	0	1	0	0	0.109645	0.061303	0	0.052264	0
lincRNA	-	2	1	0	0	0	0	0.050954	0.030023	0	0	0	0
antisense	BOLA3_ant	119	90	87	139	73	108	3.492227	3.11247	3.364415	3.528851	2.406731	3.149843
antisense	MPRIP_ant	2	3	3	0	3	6	0.100077	0.176903	0.197816	0	0.168646	0.298378
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.090714
pseudogen	ribosomal_	2	1	2	1	6	4	0.277178	0.163319	0.365253	0.119892	0.934177	0.550932
pseudogen	-	2	6	1	14	5	0	0.043147	0.152537	0.028428	0.261281	0.121182	0
antisense	-	2	6	0	0	0	1	0.211764	0.748653	0	0	0	0.105228
antisense	-	0	2	0	3	0	2	0	0.191667	0	0.211055	0	0.161641
pseudogen	-	0	0	0	1	0	0	0	0	0	0.100436	0	0
antisense	RFPL1_anti	3	6	5	5	9	1	0.02857	0.067337	0.062748	0.041193	0.096291	0.009465
lincRNA	JPX_transc	275	260	193	534	325	368	6.635722	7.393259	6.136879	11.14704	8.810243	8.824964
pseudogen	-	27	16	24	7	9	11	0.629972	0.439931	0.73791	0.141292	0.235912	0.25507
pseudogen	-	0	0	0	3	0	0	0	0	0	0.616129	0	0
sense_intrc	PLCB1_intr	0	2	1	0	1	1	0	0.334519	0.187033	0	0.159453	0.141056
pseudogen	-	3	0	0	1	0	0	1.557088	0	0	0.449009	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.152502	0
lincRNA	-	89	76	62	116	132	116	5.683653	5.719502	5.217519	6.408532	9.47023	7.362159
protein_co	Rho_GTPas	3299	2775	2432	1395	1200	1207	27.82861	27.5854	27.03383	10.17997	11.37207	10.11873
processed_	-	0	0	0	2	1	2	0	0	0	0.061025	0.039624	0.070105
lincRNA	-	6	3	2	1	0	0	0.574405	0.338451	0.252308	0.082819	0	0
pseudogen	guanylate_l	2	0	0	2	0	2	0.060852	0	0	0.052642	0	0.060476
lincRNA	-	6	0	2	2	1	0	0.160833	0	0.070646	0.046379	0.030114	0
antisense	-	3	0	0	0	4	5	0.371951	0	0	0	0.557151	0.61609
pseudogen	ribosomal_	0	0	1	0	1	1	0	0	0.120282	0	0.102545	0.090714
pseudogen	glyceraldeh	0	3	0	0	0	0	0	0.194556	0	0	0	0
pseudogen	-	0	0	4	2	3	0	0	0	0.350129	0.114928	0.223874	0
lincRNA	CYP4A22_a	0	0	1	2	1	7	0	0	0.075747	0.099455	0.064578	0.39989
pseudogen	-	28	19	13	48	55	26	2.818152	2.253549	1.724188	4.179368	6.218965	2.600694
pseudogen	protocadhe	0	0	0	0	0	1	0	0	0	0	0	0.021634
processed_	long_interg	60	51	47	42	27	61	1.267542	1.269662	1.30841	0.767579	0.640802	1.280709
pseudogen	-	0	0	0	0	3	2	0	0	0	0	0.396506	0.23384

processed_	-	4	11	6	1	6	4	0.355906	1.153387	0.703495	0.076973	0.599757	0.353708
lincRNA	testis-speci	0	0	0	1	2	0	0	0	0	0.238536	0.619541	0
antisense	-	5	3	13	0	0	0	0.473533	0.334818	1.622402	0	0	0
protein_co	chromoson	1	3	4	3	11	3	0.058758	0.207728	0.309715	0.152494	0.726121	0.175186
antisense	-	5	1	0	5	4	0	0.640932	0.15106	0	0.554466	0.576038	0
sense_intrc	-	0	0	0	1	0	0	0	0	0	0.035586	0	0
lincRNA	-	0	0	0	0	1	3	0	0	0	0	0.13548	0.359549
lincRNA	-	2	2	0	1	1	2	0.089201	0.105118	0	0.038584	0.050106	0.08865
processed_	-	0	0	0	0	0	6	0	0	0	0	0	0.246244
antisense	ZNF385D_a	1	0	0	0	1	0	0.075094	0	0	0	0.084363	0
pseudogen	-	0	3	0	2	0	0	0	0.477457	0	0.233668	0	0
lincRNA	-	1	0	0	0	0	0	0.033571	0	0	0	0	0
lincRNA	-	6	2	1	39	32	65	0.584983	0.229789	0.128477	3.289424	3.505026	6.298183
pseudogen	-	0	0	4	2	2	4	0	0	0.236686	0.077691	0.100892	0.178504
pseudogen	-	0	2	2	0	0	3	0	0.945269	1.057019	0	0	1.195774
lincRNA	-	2	0	2	0	1	0	0.210083	0	0.276838	0	0.118008	0
antisense	-	0	0	0	3	0	0	0	0	0	0.291713	0	0
protein_co	C2_calcium	4	2	2	2	12	9	0.120526	0.071016	0.079412	0.052133	0.40621	0.269509
pseudogen	ubiquitin-c	0	0	0	0	1	1	0	0	0	0	0.133654	0.118234
lincRNA	-	0	4	0	0	0	0	0	0.639874	0	0	0	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.055447	0	0
antisense	-	1	1	15	0	2	0	0.021227	0.025015	0.419587	0	0.047695	0
pseudogen	ribosomal_	1	2	2	10	1	2	0.143084	0.337231	0.377099	1.237808	0.160746	0.2844
antisense	NCBP2_ant	7	9	7	11	17	12	0.659407	0.999092	0.868938	0.89642	1.799094	1.123432
pseudogen	-	0	0	0	2	1	0	0	0	0	0.077757	0.050489	0
pseudogen	tripartite_r	0	0	0	0	1	0	0	0	0	0	0.038521	0
pseudogen	-	0	0	0	2	0	2	0	0	0	0.279262	0	0.320817
pseudogen	-	0	0	2	0	0	0	0	0	0.547163	0	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.126276	0
antisense	MTOR_anti	1	1	1	0	2	0	0.075094	0.088493	0.098955	0	0.168726	0
antisense	-	4	0	0	0	0	0	0.271145	0	0	0	0	0
lincRNA	-	0	0	0	3	0	0	0	0	0	0.297395	0	0
protein_co	zinc_finger_	3204	2444	2437	3	0	4	12.77377	11.48246	12.80316	0.010347	0	0.015849
processed_	-	3	3	1	0	0	0	0.115508	0.136119	0.050737	0	0	0
pseudogen	MT-ND2_ps	218	210	182	495	218	611	11.05473	12.54926	12.1618	21.715	12.4193	30.79232
antisense	-	0	4	3	0	0	0	0	0.224618	0.18838	0	0	0
pseudogen	-	0	0	1	0	1	2	0	0	0.067995	0	0.057969	0.102562
lincRNA	-	1	3	0	0	1	0	0.109609	0.387501	0	0	0.123139	0
pseudogen	ribosomal_	1	1	0	1	1	0	0.519029	0.611644	0	0.449009	0.583097	0
lincRNA	-	0	0	1	0	0	0	0	0	0.104907	0	0	0
pseudogen	Shwachma	355	262	254	977	526	678	10.96503	9.536514	10.33832	26.10591	18.25224	20.81233
processed_	-	11	2	2	0	1	12	0.299872	0.064251	0.071847	0	0.030626	0.325113
pseudogen	eukaryotic_	0	2	1	0	4	1	0	0.1289	0.07207	0	0.245768	0.054353
antisense	-	25	13	6	7	10	8	1.888053	1.156976	0.597118	0.457336	0.848444	0.600446

pseudogen	ring_finger_	0	0	1	0	0	0	0	0	0.045009	0	0	0
antisense	-	0	0	0	3	0	0	0	0	0	0.238951	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.085209	0
pseudogen	TAF13_RNA	0	3	1	0	0	0	0	0.654417	0.243928	0	0	0
pseudogen	ribosomal_	0	0	0	0	0	1	0	0	0	0	0	0.072074
protein_co	family_with	106	52	67	96	51	85	1.883768	1.08901	1.56903	1.475896	1.018218	1.50124
antisense	-	0	0	0	0	2	5	0	0	0	0	0.231424	0.51181
antisense	-	0	0	0	2	0	0	0	0	0	0.027068	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.100807	0
pseudogen	importin_7	2	0	2	0	0	1	0.060504	0	0.079729	0	0	0.030065
lincRNA	-	2	0	4	9	0	0	0.186741	0	0.492157	0.726967	0	0
pseudogen	-	1	0	0	3	0	0	0.052941	0	0	0.137397	0	0
lincRNA	family_with	0	0	1	1	0	0	0	0	0.009453	0.006206	0	0
lincRNA	-	4	0	0	0	0	1	0.440258	0	0	0	0	0.109385
pseudogen	-	3	5	7	3	4	7	0.328147	0.644501	1.008973	0.283878	0.491537	0.760947
pseudogen	-	0	5	4	4	2	11	0	0.323924	0.289775	0.190234	0.123522	0.600991
protein_co	solute_carr	391	330	293	608	441	589	3.643071	3.623363	3.597438	4.900692	4.616135	5.454008
lincRNA	-	0	0	1	0	0	0	0	0	0.154003	0	0	0
processed_	-	34	20	36	50	26	50	0.918833	0.636934	1.28202	1.168936	0.789369	1.34288
lincRNA	-	0	1	2	0	0	0	0	0.061526	0.1376	0	0	0
pseudogen	-	0	1	0	0	0	0	0	0.086529	0	0	0	0
pseudogen	-	3	4	2	0	0	0	0.204143	0.32076	0.17934	0	0	0
antisense	-	0	4	0	4	1	15	0	0.43026	0	0.315855	0.102545	1.360708
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.036222	0
pseudogen	-	0	0	5	2	4	0	0	0	0.716255	0.188086	0.488509	0
antisense	FGD5_antis	1269	1115	1086	1770	1538	1531	17.7168	18.34449	19.97967	21.37765	24.12288	21.24265
pseudogen	nucleopho	0	0	0	0	0	1	0	0	0	0	0	0.071877
pseudogen	transcriptio	1	0	0	0	0	0	0.161405	0	0	0	0	0
lincRNA	-	0	0	0	29	24	27	0	0	0	1.459526	1.568596	1.561076
lincRNA	-	0	0	1	0	0	0	0	0	0.088085	0	0	0
processed_	-	1	0	5	0	0	1	0.052365	0	0.345021	0	0	0.052042
lincRNA	-	3	0	1	1	1	3	0.569258	0	0.250048	0.164154	0.213175	0.565742
antisense	-	1	3	1	2	8	3	0.074043	0.261767	0.097571	0.128109	0.665465	0.220758
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.231271
pseudogen	-	0	1	0	0	1	0	0	0.055064	0	0	0.052494	0
antisense	DBH_antise	0	1	1	2	0	0	0	0.029167	0.032615	0.042823	0	0
lincRNA	-	0	0	1	9	1	1	0	0	0.101993	0.602617	0.086953	0.076921
sense_intrc	-	5	5	3	13	4	11	0.59888	0.705744	0.473506	1.347027	0.538244	1.309399
antisense	-	3	2	2	10	2	11	0.328826	0.258334	0.288875	0.948218	0.246277	1.19825
antisense	LEPREL1_ar	6	10	0	1	1	2	0.435131	0.854626	0	0.062738	0.081474	0.144148
pseudogen	-	0	0	2	0	1	2	0	0	0.155202	0	0.066158	0.11705
antisense	-	0	0	1	10	4	9	0	0	0.138694	0.910515	0.47297	0.941404
antisense	PROSER2_a	0	0	0	11	4	6	0	0	0	0.160391	0.075741	0.100504
pseudogen	-	0	0	2	0	0	0	0	0	0.377099	0	0	0

processed_	myocardial	59	36	38	7	20	13	0.305748	0.219847	0.259495	0.031381	0.116437	0.066952
pseudogen	-	6	6	16	16	14	8	0.134996	0.159085	0.474378	0.311425	0.353873	0.178883
lincRNA	-	0	2	1	0	0	0	0	0.222813	0.124577	0	0	0
processed_	-	75	46	45	39	42	41	5.979781	4.322041	4.727933	2.689996	3.762031	3.248759
antisense	-	0	0	0	4	14	5	0	0	0	0.299829	1.362787	0.430557
processed_	-	4	5	7	5	15	12	0.475874	0.700986	1.0974	0.514594	2.004806	1.418806
antisense	-	1	0	2	0	0	0	0.138227	0	0.364299	0	0	0
pseudogen	-	0	2	5	6	3	1	0	0.577664	1.614891	1.272192	0.826054	0.243584
processed_	-	5	0	2	12	3	8	0.296422	0	0.156245	0.615439	0.199807	0.471346
lincRNA	-	4	0	0	0	1	0	0.371516	0	0	0	0.104344	0
pseudogen	DnaJ_(Hsp4	5	5	8	5	0	6	0.837674	0.987148	1.766159	0.724666	0	0.999001
antisense	UBXN7_ant	3	6	4	2	4	2	0.079095	0.186418	0.138971	0.045616	0.118478	0.052404
lincRNA	long_interg	0	0	0	4	6	1	0	0	0	0.191828	0.373671	0.055093
protein_co	family_witl	21	27	25	65	25	68	0.402958	0.610536	0.632143	1.078988	0.538926	1.296758
protein_co	excision_re	95	91	98	300	284	267	0.628046	0.708951	0.853746	1.715743	2.109286	1.75424
pseudogen	ribosomal_	0	2	0	0	0	2	0	0.272435	0	0	0	0.229756
pseudogen	-	4	0	0	0	0	0	0.637843	0	0	0	0	0
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.183324
lincRNA	-	0	4	0	0	0	0	0	0.678127	0	0	0	0
antisense	TRMT2B_ar	0	1	1	1	2	4	0	0.15558	0.173973	0.114212	0.296638	0.524828
pseudogen	non_impri	0	0	2	0	0	0	0	0	0.142958	0	0	0
pseudogen	makorin_ri	8	3	1	12	11	11	0.346302	0.153036	0.057043	0.449376	0.534943	0.473225
antisense	-	0	0	0	1	0	3	0	0	0	0.07447	0	0.256654
pseudogen	-	0	0	0	5	8	3	0	0	0	0.661834	1.375166	0.456191
antisense	RUSC1_ant	93	121	69	109	114	160	2.681652	4.11161	2.621823	2.718998	3.692949	4.585102
lincRNA	-	2	1	0	0	0	3	0.194994	0.114895	0	0	0	0.290685
pseudogen	-	2	3	2	1	0	0	0.172166	0.30433	0.226872	0.07447	0	0
lincRNA	-	3	0	0	0	0	0	0.073292	0	0	0	0	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.024452	0	0
lincRNA	long_interg	9	5	17	13	11	27	0.361784	0.236855	0.900513	0.452077	0.496762	1.078648
lincRNA	-	0	1	1	4	5	8	0	0.088118	0.098536	0.258751	0.420028	0.594509
pseudogen	-	4	16	9	1	7	2	0.239281	1.127914	0.709457	0.05175	0.470431	0.118902
protein_co	Uncharacte	0	0	0	0	1	0	0	0	0	0	0.076154	0
antisense	-	2	2	1	0	0	0	0.216528	0.255165	0.142665	0	0	0
antisense	-	0	0	2	71	39	42	0	0	0.09277	2.162049	1.542261	1.469275
antisense	-	3	1	1	2	1	3	0.300232	0.117935	0.131878	0.173153	0.112431	0.298378
pseudogen	-	72	51	28	293	123	105	1.533287	1.279877	0.785749	5.39786	2.942694	2.222235
pseudogen	-	0	5	4	0	3	1	0	1.050298	0.939573	0	0.600767	0.177152
antisense	-	0	0	1	1	0	0	0	0	0.128477	0.084344	0	0
pseudogen	-	4	5	1	2	1	3	0.485697	0.715456	0.160008	0.210087	0.136413	0.362023
lincRNA	-	8	0	2	0	2	9	0.855612	0	0.281872	0	0.240307	0.956619
antisense	-	0	0	0	1	0	0	0	0	0	0.013244	0	0
lincRNA	-	2	0	3	0	0	0	0.192163	0	0.379836	0	0	0
pseudogen	ribosomal_	4	5	4	1	7	4	0.323798	0.47697	0.426687	0.070029	0.636592	0.321798

protein_co	nucleolar_p	44	43	37	118	93	84	1.967402	2.265771	2.180103	4.564418	4.671673	3.732754
pseudogen	-	0	1	0	0	0	0	0	0.131067	0	0	0	0
pseudogen	calcyclin_b	2	1	3	5	3	2	0.154798	0.09121	0.305979	0.334787	0.260859	0.153842
lincRNA	-	1	0	5	0	2	8	0.012427	0	0.081882	0	0.027923	0.098806
pseudogen	-	0	1	0	0	0	0	0	0.092977	0	0	0	0
antisense	prostate_ca	25	23	17	0	0	1	0.337462	0.365864	0.302391	0	0	0.013415
antisense	-	15	3	13	0	0	1	1.970508	0.464425	2.250428	0	0	0.130556
protein_co	Uncharacte	0	0	0	15	3	0	0	0	0	0.898018	0.233239	0
antisense	-	1	2	1	4	7	7	0.126351	0.297793	0.166499	0.437221	0.993631	0.878994
processed_	-	0	0	0	7	1	4	0	0	0	0.153909	0.028553	0.101035
pseudogen	-	3	0	0	0	0	0	0.405161	0	0	0	0	0
protein_co	neurotroph	5	5	3	10	4	24	0.151433	0.178455	0.119731	0.262007	0.1361	0.72239
antisense	-	1	5	0	4	0	2	0.130076	0.766434	0	0.450112	0	0.258546
processed_	SATB2_anti	18	16	3	9	5	10	0.287549	0.301208	0.063153	0.124378	0.089734	0.158763
antisense	-	0	0	0	0	0	3	0	0	0	0	0	0.353906
antisense	-	3	5	9	0	0	0	0.205463	0.403543	0.81225	0	0	0
antisense	-	0	0	0	0	2	0	0	0	0	0	0.148876	0
protein_co	extracellula	680	667	457	150	139	153	9.362777	10.82253	8.291761	1.786693	2.150105	2.093615
antisense	long_interg	7	10	2	4	11	10	0.664134	1.11806	0.250048	0.328308	1.172464	0.942904
processed_	-	0	0	0	2	1	1	0	0	0	0.288043	0.187031	0.165453
pseudogen	MT-ND1_ps	7	0	4	23	15	10	0.996201	0	0.750143	2.831653	2.398222	1.414356
antisense	-	79	68	57	142	84	105	4.82949	4.898806	4.59181	7.509751	5.769027	6.379302
lincRNA	-	0	2	1	0	0	0	0	0.399921	0.2236	0	0	0
lincRNA	-	15	8	12	14	19	10	0.974374	0.612395	1.027189	0.78673	1.386555	0.645571
pseudogen	-	0	3	1	1	0	2	0	0.57412	0.213998	0.140487	0	0.322786
pseudogen	olfactory_r	0	0	0	5	0	0	0	0	0	0.241555	0	0
antisense	-	2	1	3	0	0	6	0.212614	0.125277	0.420261	0	0	0.633904
antisense	-	0	0	0	0	1	1	0	0	0	0	0.116619	0.103165
lincRNA	-	0	0	0	3	0	0	0	0	0	0.60795	0	0
pseudogen	-	10	5	4	26	17	6	0.90343	0.532319	0.4762	2.032033	1.725411	0.53871
lincRNA	-	0	0	0	2	1	0	0	0	0	0.154988	0.100636	0
lincRNA	-	0	0	0	1	6	5	0	0	0	0.0204	0.158956	0.117181
antisense	-	3	6	2	5	2	1	0.186851	0.440384	0.164149	0.269405	0.139943	0.061899
pseudogen	-	4	0	0	1	0	0	0.119573	0	0	0.02586	0	0
pseudogen	OFD1_pseu	3	3	3	0	0	0	0.129651	0.152786	0.170849	0	0	0
pseudogen	-	0	0	2	0	0	0	0	0	0.683954	0	0	0
pseudogen	chaperonin	6	17	10	5	9	2	0.191699	0.640067	0.421022	0.138198	0.323044	0.063505
antisense	PRICKLE2_a	15	22	17	3	6	10	0.318155	0.549892	0.475151	0.055047	0.142971	0.210793
processed_	-	0	0	0	1	0	0	0	0	0	0.153174	0	0
antisense	-	1	0	0	0	4	2	0.021635	0	0	0	0.097223	0.043003
lincRNA	-	42	48	17	40	9	23	0.685215	0.922839	0.365478	0.564547	0.164956	0.372919
processed_	FGF13_anti	0	0	0	2	3	6	0	0	0	0.107889	0.210162	0.371831
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.079
pseudogen	-	0	0	0	1	0	0	0	0	0	0.087737	0	0

lincRNA	-	0	0	0	1	0	4	0	0	0	0.076459	0	0.351346
pseudogen	-	1	0	0	0	0	0	0.143084	0	0	0	0	0
pseudogen	Y_box_binc	0	0	0	1	0	0	0	0	0	0.048567	0	0
pseudogen	tousled-like	2	1	4	1	1	7	0.033171	0.019545	0.087423	0.014348	0.018633	0.115382
processed_	-	1	1	2	15	17	10	0.023751	0.027989	0.062596	0.308203	0.453607	0.236043
pseudogen	mediator_c	7	7	7	19	10	18	0.240641	0.283581	0.317106	0.565051	0.386207	0.614969
pseudogen	phosphorib	9	4	3	2	1	3	0.391511	0.205054	0.171972	0.075265	0.048871	0.129698
pseudogen	MT-ND4_ps	2	0	0	8	0	0	0.085596	0	0	0.296193	0	0
pseudogen	-	1	0	0	0	0	0	0.112881	0	0	0	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.045567	0	0	0
processed_	long_interg	5	4	5	19	12	10	0.38087	0.359066	0.501894	1.252056	1.026922	0.757037
lincRNA	-	1	0	0	0	0	0	0.064249	0	0	0	0	0
pseudogen	protease_se	0	0	0	6	5	1	0	0	0	0.239785	0.259494	0.045911
pseudogen	-	0	0	2	0	0	0	0	0	0.272513	0	0	0
pseudogen	-	54	52	30	58	33	57	4.63341	5.257961	3.392056	4.305246	3.181046	4.860617
pseudogen	ubiquinol-c	81	90	59	124	122	153	5.197843	6.805934	4.989132	6.883714	8.795227	9.757515
antisense	-	19	25	34	18	4	2	1.749355	2.71251	4.125133	1.433705	0.413746	0.183005
sense_intrc	-	0	0	0	0	2	1	0	0	0	0	0.151724	0.06711
processed_	-	5	5	3	25	19	18	0.087275	0.102848	0.069004	0.377505	0.372582	0.31225
pseudogen	-	0	0	0	1	0	0	0	0	0	0.085287	0	0
lincRNA	-	0	0	0	2	2	1	0	0	0	0.0444	0.05766	0.025504
pseudogen	septin_7_p	0	0	2	0	5	1	0	0	0.22468	0	0.478872	0.084725
protein_co	Uncharacte	0	2	0	3	4	8	0	1.540438	0	1.696256	2.937082	5.196449
pseudogen	-	2	2	0	1	4	3	0.366374	0.431749	0	0.158474	0.823196	0.546167
lincRNA	-	3	1	0	0	0	0	0.447389	0.17574	0	0	0	0
pseudogen	MT-ND3_ps	0	0	0	0	3	0	0	0	0	0	0.811035	0
pseudogen	AT_hook_c	0	0	1	2	0	3	0	0	0.010228	0.013429	0	0.023141
protein_co	HCG16537	0	1	0	12	17	8	0	0.061105	0	0.538283	0.990294	0.412255
lincRNA	-	0	0	1	1	0	0	0	0	0.026739	0.017554	0	0
pseudogen	-	0	0	0	1	0	1	0	0	0	0.134703	0	0.154747
lincRNA	-	0	0	0	1	0	0	0	0	0	0.058047	0	0
lincRNA	BAIAP2_ant	439	414	334	220	277	326	5.208672	5.788552	5.222083	2.258126	3.692252	3.844057
pseudogen	-	0	0	1	0	0	4	0	0	0.187536	0	0	0.565742
pseudogen	ribosomal_	0	0	0	1	0	0	0	0	0	0.100879	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.028091
pseudogen	solute_carr	2	5	10	2	18	8	0.09942	0.2929	0.655054	0.086007	1.005227	0.395223
lincRNA	-	0	1	5	5	0	2	0	0.085697	0.479143	0.314553	0	0.144544
processed_	-	1	0	1	0	2	5	0.087942	0	0.115886	0	0.197594	0.436994
pseudogen	-	0	1	0	0	0	0	0	0.176736	0	0	0	0
antisense	-	2	0	0	6	4	0	0.169411	0	0	0.439669	0.380646	0
pseudogen	Charcot-Le	0	0	0	1	0	0	0	0	0	0.108786	0	0
antisense	-	1	0	0	0	0	0	0.326796	0	0	0	0	0
processed_	AP4B1_ant	2	0	4	0	10	0	0.061062	0	0.16093	0	0.342998	0
protein_co	testis_expr	22	19	23	5	3	28	0.453015	0.461053	0.624098	0.089068	0.0694	0.573004

antisense	long_interg	8	11	14	28	14	17	0.989551	1.603423	2.281977	2.99619	1.945474	2.08981
protein_co	Uncharacte	4	1	6	59	88	84	0.081136	0.023903	0.160375	1.035301	2.005318	1.693326
pseudogen	tripartite_r	1	0	0	0	0	0	0.039626	0	0	0	0	0
pseudogen	transcriptic	0	0	2	0	0	0	0	0	0.415258	0	0	0
pseudogen	heterogene	1	0	1	0	0	0	0.096082	0	0.126612	0	0	0
pseudogen	-	0	0	0	0	3	1	0	0	0	0	0.1228	0.036211
lincRNA	-	0	2	3	0	3	1	0	0.054678	0.091713	0	0.078189	0.023056
antisense	-	1	0	2	0	4	3	0.025343	0	0.066791	0	0.113884	0.075559
pseudogen	-	4	1	2	3	1	1	0.270798	0.07978	0.178423	0.175699	0.076056	0.067281
lincRNA	-	0	0	0	1	0	1	0	0	0	0.049999	0	0.057439
pseudogen	-	466	450	300	672	503	696	13.5776	15.45101	11.51843	16.93829	16.46471	20.15376
pseudogen	ribosomal_	0	0	0	3	3	7	0	0	0	0.370342	0.480937	0.992718
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.039889
pseudogen	-	23	25	17	23	16	23	2.780007	3.560943	2.707707	2.404965	2.172636	2.762838
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.457513
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.194867
antisense	LEMD1_ant	4	0	0	0	0	1	0.076147	0	0	0	0	0.018919
processed_	-	26	18	19	9	7	8	0.31376	0.255979	0.302143	0.093957	0.094901	0.095945
antisense	ZNF32_anti	0	4	3	0	0	1	0	0.575002	0.482235	0	0	0.121231
pseudogen	-	0	2	0	0	0	2	0	0.366987	0	0	0	0.309494
lincRNA	-	0	0	2	2	2	2	0	0	0.231387	0.151904	0.197267	0.174508
pseudogen	mitochond	0	0	0	1	0	0	0	0	0	0.125821	0	0
pseudogen	protein_tyr	0	0	5	0	0	0	0	0	0.830515	0	0	0
processed_	GRM7_anti	2	4	4	8	10	18	0.111808	0.263517	0.294671	0.386897	0.628046	1.000056
pseudogen	general_tra	43	46	27	101	60	83	1.080941	1.362695	0.894401	2.196434	1.694471	2.073583
antisense	ISM1_antis	0	0	2	2	0	0	0	0	0.213998	0.140487	0	0
processed_	-	6	5	3	1	6	6	0.792135	0.777902	0.52192	0.114212	0.889914	0.787243
pseudogen	-	0	1	1	2	3	4	0	0.064584	0.072219	0.094822	0.184708	0.217864
lincRNA	-	1	2	0	1	0	0	0.139686	0.329223	0	0.120841	0	0
pseudogen	phosphose	1	0	0	0	0	0	0.202839	0	0	0	0	0
pseudogen	-	0	1	0	0	0	0	0	0.125277	0	0	0	0
pseudogen	actin_relat	2	1	1	2	4	3	0.198653	0.11705	0.130888	0.171853	0.446348	0.296139
pseudogen	-	3	0	0	0	0	0	0.168423	0	0	0	0	0
processed_	transmemb	16	14	15	102	95	115	0.431951	0.445399	0.53363	2.382197	2.881291	3.085475
antisense	-	2	0	1	1	0	0	0.350603	0	0.231004	0.151652	0	0
processed_	-	0	0	0	3	1	5	0	0	0	0.117836	0.051009	0.225618
pseudogen	SWI/SNF_re	0	1	0	0	0	0	0	0.051179	0	0	0	0
antisense	-	2	4	3	0	2	4	0.159221	0.375265	0.314722	0	0.178875	0.316475
antisense	CFLAR_anti	8	6	9	11	15	10	0.395082	0.349185	0.585699	0.469951	0.832219	0.490803
pseudogen	zinc_finger_	13	16	6	16	11	10	0.422747	0.613147	0.257113	0.450112	0.401864	0.323182
pseudogen	-	13	10	8	5	5	4	0.902009	0.817664	0.731463	0.300124	0.38975	0.275827
protein_co	Protein_LO	28	11	19	0	0	0	0.470886	0.218	0.421062	0	0	0
processed_	-	74	94	58	212	140	152	3.092055	4.628608	3.193584	7.663274	6.571925	6.312025
pseudogen	-	15	12	9	3	0	1	0.541319	0.510329	0.427996	0.093658	0	0.035865

processed_	-	0	1	0	1	0	2	0	0.12837	0	0.094236	0	0.216519
antisense	-	8	3	2	43	21	33	0.621921	0.274836	0.204885	2.891855	1.834059	2.54958
processed_	-	0	0	2	0	0	0	0	0	0.297498	0	0	0
pseudogen	ribosomal_	5	0	4	0	0	2	1.102937	0	1.162721	0	0	0.43845
pseudogen	-	0	0	1	0	0	1	0	0	0.347081	0	0	0.261761
pseudogen	vomeronas	0	1	0	4	3	0	0	0.073139	0	0.214766	0.209177	0
sense_intrc	-	3	10	5	0	0	0	0.297421	1.16831	0.653214	0	0	0
antisense	-	7	0	4	4	6	3	0.985604	0	0.742163	0.487222	0.949084	0.419793
pseudogen	-	0	1	0	3	5	2	0	0.071138	0	0.156667	0.339087	0.119986
pseudogen	ribosomal_	12	9	4	4	7	6	0.974374	0.86118	0.427996	0.280975	0.638545	0.484178
pseudogen	telomeric_	0	0	0	0	0	1	0	0	0	0	0	0.043411
lincRNA	-	9	2	6	0	2	2	0.425039	0.111307	0.373398	0	0.106112	0.09387
antisense	ST7_antiser	2	1	0	0	2	2	0.078373	0.046179	0	0	0.088047	0.077889
antisense	-	0	0	0	4	0	13	0	0	0	0.309976	0	1.157331
processed_	-	57	54	22	19	10	23	1.354415	1.51209	0.688865	0.390565	0.266948	0.543143
processed_	-	15	26	11	30	31	36	1.289148	2.633248	1.245773	2.230466	2.993106	3.074847
lincRNA	-	0	0	2	7	16	6	0	0	0.087041	0.199995	0.593646	0.196933
antisense	PARD3_ant	1	1	1	1	0	0	0.175301	0.206582	0.231004	0.151652	0	0
pseudogen	interferon_	7	0	2	2	1	7	0.701869	0	0.264255	0.173481	0.112644	0.697535
pseudogen	ribosomal_	5	2	1	11	9	8	0.581769	0.274232	0.153326	1.107226	1.176447	0.925082
protein_co	chromoson	2	0	0	0	0	0	0.069843	0	0	0	0	0
antisense	-	2	0	0	0	3	0	0.306017	0	0	0	0.515687	0
sense_intrc	-	0	0	0	15	12	11	0	0	0	1.53003	1.589557	1.288986
pseudogen	RNA_bindi	4	0	0	0	0	0	0.253306	0	0	0	0	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.400511	0
pseudogen	triosephos	31	16	19	10	7	12	2.188228	1.330938	1.767336	0.610652	0.555109	0.841825
antisense	MRPL23_a	0	4	0	1	5	10	0	0.133023	0	0.024413	0.158518	0.280459
processed_	-	49	30	24	61	60	78	1.12105	0.80883	0.72356	1.207318	1.542159	1.773507
pseudogen	solute_carr	0	0	0	10	1	0	0	0	0	0.510579	0.066305	0
lincRNA	-	0	0	0	2	0	0	0	0	0	0.16212	0	0
pseudogen	-	0	0	1	1	7	1	0	0	0.079548	0.052222	0.474722	0.059993
lincRNA	-	1	0	0	0	0	1	0.116868	0	0	0	0	0.116146
pseudogen	ankyrin_re	0	0	0	0	2	0	0	0	0	0	0.04106	0
antisense	-	0	0	0	2	1	0	0	0	0	0.164154	0.106588	0
antisense	-	1	0	1	0	0	0	0.059218	0	0.078035	0	0	0
pseudogen	glyceraldeh	0	0	0	0	0	1	0	0	0	0	0	0.052719
antisense	-	14	4	10	3	2	3	0.7563	0.254644	0.71187	0.140201	0.121379	0.161063
pseudogen	cytochrom	7	7	5	2	8	10	0.248716	0.293097	0.234105	0.061475	0.319334	0.353114
lincRNA	-	0	2	1	0	1	2	0	0.151795	0.08487	0	0.072355	0.128015
antisense	-	0	0	0	4	0	1	0	0	0	0.209127	0	0.060062
pseudogen	-	3	2	7	0	6	0	0.416858	0.327495	1.28174	0	0.936629	0
antisense	-	1	0	0	4	4	4	0.165441	0	0	0.572486	0.743449	0.657676
pseudogen	-	0	0	5	4	2	6	0	0	0.438212	0.230145	0.149437	0.396588
pseudogen	ADAM_met	1	2	4	5	0	1	0.02647	0.062388	0.139527	0.114497	0	0.026307

antisense	-	26	27	12	15	12	21	2.667569	3.264474	1.622402	1.331364	1.383161	2.141269
lincRNA	-	1	0	0	2	0	0	0.085943	0	0	0.148698	0	0
lincRNA	-	10	3	6	0	3	0	0.294444	0.104095	0.232803	0	0.099237	0
pseudogen	UPF3_regul	3	0	0	4	3	4	0.141051	0	0	0.162696	0.158462	0.186906
protein_co	transmemb	262	207	195	491	381	374	6.508935	6.060188	6.383782	10.55245	10.63366	9.234
pseudogen	fat_mass_a	6	0	0	11	5	8	0.368927	0	0	0.58512	0.345389	0.488865
pseudogen	-	1	1	1	3	0	4	0.121146	0.142764	0.159641	0.314409	0	0.481593
pseudogen	-	0	3	0	0	0	2	0	1.155328	0	0	0	0.649556
processed_	-	0	0	3	1	1	2	0	0	0.263922	0.057754	0.075001	0.132696
lincRNA	-	0	0	2	10	7	19	0	0	0.175065	0.574641	0.522373	1.254287
antisense	UPK1A_ant	1	0	3	0	0	0	0.066592	0	0.263258	0	0	0
sense_intro	KIRREL_int	3	6	15	5	8	8	0.270567	0.637694	1.782707	0.39011	0.810575	0.717057
pseudogen	-	0	3	0	0	1	1	0	0.974808	0	0	0.30977	0.274032
lincRNA	-	9	5	6	7	8	7	0.879094	0.575533	0.772287	0.591499	0.877873	0.679517
pseudogen	ribosomal_	6	2	1	8	1	6	0.526776	0.206924	0.115694	0.607614	0.098633	0.523523
antisense	-	1	0	0	0	2	9	0.083241	0	0	0	0.187031	0.744538
processed_	-	0	0	0	0	1	2	0	0	0	0	0.101495	0.17957
antisense	BTBD9_ant	1	0	0	2	5	1	0.094537	0	0	0.163568	0.531035	0.093954
pseudogen	-	0	0	0	19	18	6	0	0	0	0.550746	0.677574	0.1998
pseudogen	-	0	0	1	0	3	4	0	0	0.097163	0	0.248507	0.293114
pseudogen	ribosomal_	0	1	0	0	0	0	0	0.085113	0	0	0	0
pseudogen	-	1	1	2	0	3	2	0.127569	0.150332	0.336209	0	0.429946	0.253562
pseudogen	acylglycero	6	3	4	0	3	2	0.251501	0.148189	0.220945	0	0.141273	0.083316
lincRNA	-	0	2	2	146	102	107	0	0.14645	0.163764	7.848169	7.120356	6.607633
pseudogen	ferritin_hea	3	1	3	2	3	1	0.289823	0.113846	0.381916	0.167149	0.325598	0.096011
processed_	SPANXA2_c	1	3	0	0	0	0	0.031123	0.110031	0	0	0	0
lincRNA	-	2	1	2	0	0	0	0.148711	0.087623	0.195964	0	0	0
pseudogen	ribosomal_	0	0	0	0	2	4	0	0	0	0	0.814739	1.441481
antisense	-	3	1	3	11	12	5	0.033401	0.01312	0.044015	0.105949	0.150097	0.055325
pseudogen	-	0	0	1	0	0	0	0	0	0.080096	0	0	0
lincRNA	-	7	4	2	0	0	0	0.838432	0.564595	0.315671	0	0	0
lincRNA	-	3	0	0	2	0	0	0.258669	0	0	0.149182	0	0
antisense	-	3	11	12	0	0	2	0.085665	0.370154	0.451542	0	0	0.056757
pseudogen	ferritin_ligh	6	7	6	6	4	2	0.601602	0.82711	0.792765	0.520442	0.450575	0.199296
antisense	-	0	0	4	0	2	2	0	0	0.664412	0	0.283219	0.250543
pseudogen	OFD1_pseu	5	2	4	0	0	0	0.230379	0.108595	0.242866	0	0	0
pseudogen	ribosomal_	2	0	0	0	6	3	0.237404	0	0	0	0.800124	0.353906
antisense	-	0	0	2	1	0	1	0	0	0.149707	0.04914	0	0.056453
pseudogen	-	0	0	0	0	3	0	0	0	0	0	0.292505	0
pseudogen	-	4	0	1	1	0	0	0.177953	0	0.058625	0.038486	0	0
pseudogen	-	0	0	3	2	8	8	0	0	0.272158	0.119113	0.618735	0.54735
antisense	SHANK2_ar	0	0	0	2	3	2	0	0	0	0.040674	0.079231	0.046727
lincRNA	-	1	1	0	0	0	0	0.024727	0.02914	0	0	0	0
pseudogen	ubiquitin-c	3	2	1	0	1	0	0.356906	0.280394	0.156771	0	0.133654	0

lincRNA	-	0	1	0	0	0	0	0	0.19743	0	0	0	0
lincRNA	-	0	0	0	9	8	13	0	0	0	0.769011	0.8877	1.276087
antisense	-	3	2	7	17	8	8	0.379052	0.297793	1.165496	1.858189	1.135578	1.004564
antisense	-	2	2	2	1	1	1	0.112044	0.132038	0.147647	0.048464	0.062937	0.055676
antisense	-	2	3	1	3	8	3	0.072423	0.128019	0.047718	0.093979	0.32545	0.107963
lincRNA	-	0	0	1	0	0	2	0	0	0.160375	0	0	0.241904
pseudogen	-	1	1	0	1	1	4	0.105671	0.124526	0	0.091415	0.118714	0.420072
antisense	-	5	9	13	9	6	8	0.44265	0.938946	1.516593	0.689281	0.596748	0.703867
lincRNA	-	0	2	0	0	0	0	0	0.183764	0	0	0	0
lincRNA	-	1	2	5	0	1	0	0.016796	0.039586	0.110665	0	0.018869	0
lincRNA	-	10	11	9	3	12	0	0.11422	0.148061	0.135463	0.029643	0.153983	0
pseudogen	-	1	2	0	0	1	5	0.103199	0.243227	0	0	0.115937	0.512808
pseudogen	immunoglo	2	5	4	5	0	1	0.104938	0.309156	0.276564	0.226952	0	0.052145
lincRNA	-	2	0	0	8	8	10	0.06232	0	0	0.215651	0.280051	0.309677
processed_	ENTPD1_an	3	1	5	7	16	9	0.037449	0.014711	0.082249	0.075594	0.224385	0.111654
processed_	-	31	20	23	1	8	1	1.500156	1.140543	1.466687	0.041864	0.434924	0.048093
pseudogen	-	0	1	0	0	0	0	0	0.05936	0	0	0	0
pseudogen	ankyrin_rep	0	0	0	0	0	1	0	0	0	0	0	0.034729
antisense	LENG8_ant	51	48	44	30	45	97	3.099875	3.43813	3.524207	1.577459	3.072809	5.859429
antisense	-	88	89	71	105	63	140	15.22486	18.14545	16.18691	15.71531	12.24504	24.07179
antisense	-	4	0	1	1	0	4	1.150891	0	0.379148	0.248907	0	1.143784
pseudogen	-	0	0	0	4	2	2	0	0	0	0.288043	0.187031	0.165453
pseudogen	syndecan_b	0	1	0	0	0	0	0	0.070099	0	0	0	0
antisense	-	0	0	1	0	2	0	0	0	0.062456	0	0.106492	0
antisense	FGF12_anti	0	1	0	2	0	3	0	0.214391	0	0.314769	0	0.542413
antisense	family_with	19	23	16	8	5	6	0.383484	0.547052	0.425548	0.139684	0.113374	0.120352
pseudogen	-	1	0	0	0	0	0	0.067873	0	0	0	0	0
pseudogen	transmemb	0	0	1	0	1	1	0	0	0.204584	0	0.174416	0.154293
pseudogen	small_nucl	3	0	1	0	1	1	0.745648	0	0.327527	0	0.27923	0.247014
antisense	-	0	0	3	0	0	0	0	0	1.333056	0	0	0
antisense	-	0	0	0	0	0	4	0	0	0	0	0	0.257912
lincRNA	-	0	2	0	0	0	0	0	0.024698	0	0	0	0
protein_co	heat_shock	92	81	64	172	115	125	4.60792	4.780895	4.224078	7.452613	6.47089	6.222097
pseudogen	-	1	7	0	0	0	0	0.430415	3.550521	0	0	0	0
antisense	Smith-Mag	6	2	4	1	1	4	0.11169	0.043873	0.09812	0.016104	0.020913	0.074
processed_	-	7	2	7	3	6	6	0.314323	0.105832	0.414201	0.116537	0.302676	0.267756
lincRNA	-	0	1	0	0	2	0	0	0.089767	0	0	0.171154	0
processed_	-	366	342	304	495	388	420	5.506224	6.063258	6.026723	6.442301	6.557731	6.279597
antisense	-	3	6	4	5	4	11	0.134482	0.316957	0.236285	0.193899	0.201443	0.490055
lincRNA	-	4	0	0	0	1	6	0.337742	0	0	0	0.094858	0.503484
antisense	-	2	0	0	0	0	0	0.0839	0	0	0	0	0
protein_co	taste_recep	0	2	0	1	4	0	0	0.134167	0	0.049246	0.25581	0
lincRNA	-	0	0	1	0	2	0	0	0	0.17888	0	0.305005	0
protein_co	serine/argi	20	4	6	19	10	1	0.392446	0.092495	0.155144	0.322528	0.220444	0.019501

pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.182476
pseudogen	fatty_acid_	0	1	0	0	0	0	0	0.159559	0	0	0	0
pseudogen	-	0	0	0	7	11	18	0	0	0	0.731946	1.493687	2.162221
pseudogen	keratin_ass	0	0	1	0	0	0	0	0	0.249155	0	0	0
antisense	NAALADL2_	2	0	1	0	0	0	0.102006	0	0.067209	0	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.113939	0
protein_co	phosphogl	3	5	6	0	0	1	0.09465	0.185899	0.249452	0	0	0.031355
lincRNA	-	3	3	0	20	4	14	0.200029	0.235722	0	1.153625	0.299627	0.927704
pseudogen	-	0	0	1	0	6	0	0	0	0.024695	0	0.126321	0
antisense	-	0	0	4	0	0	0	0	0	0.532544	0	0	0
lincRNA	-	0	0	0	1	1	1	0	0	0	0.0579	0.075191	0.066516
antisense	CACTIN_ant	10	2	2	5	5	15	0.276743	0.065225	0.072936	0.119704	0.155452	0.412551
pseudogen	oligosaccha	0	0	5	5	3	3	0	0	0.778608	0.511148	0.398276	0.352326
antisense	-	21	22	18	19	12	6	1.236664	1.52673	1.396818	0.967941	0.793894	0.351151
antisense	-	6	1	2	4	0	0	0.170594	0.033506	0.074934	0.098386	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.122177	0	0	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.02588
antisense	MEIS1_anti	0	0	0	0	3	1	0	0	0	0	0.252373	0.074419
pseudogen	-	14	16	5	13	14	20	1.557088	2.097067	0.732808	1.25081	1.749292	2.210674
sense_intrc	-	93	66	48	77	60	112	9.691954	8.105492	6.591806	6.94196	7.024715	11.59995
processed_	-	1	2	0	1	0	0	0.029428	0.069358	0	0.025458	0	0
antisense	-	7	5	4	12	4	3	0.51045	0.429668	0.384371	0.757007	0.327691	0.217413
lincRNA	-	1	1	3	22	12	21	0.110294	0.129974	0.436021	2.099116	1.486898	2.301865
antisense	-	0	0	0	1	1	0	0	0	0	0.098281	0.127631	0
pseudogen	eukaryotic_	0	0	2	0	0	0	0	0	0.108328	0	0	0
lincRNA	long_interg	0	0	0	4	2	0	0	0	0	0.193244	0.125477	0
antisense	-	1	6	0	9	2	14	0.019739	0.13957	0	0.153688	0.044352	0.274645
processed_	-	4	5	3	0	0	0	0.377476	0.55604	0.373066	0	0	0
lincRNA	-	0	0	0	17	10	33	0	0	0	0.445668	0.340446	0.993854
lincRNA	-	7	9	7	4	7	4	0.660583	1.000873	0.870487	0.326552	0.742124	0.375145
pseudogen	-	0	0	1	6	0	0	0	0	0.079007	0.311204	0	0
lincRNA	-	2	0	0	8	3	6	0.136095	0	0	0.47094	0.229342	0.405764
pseudogen	deoxyuridi	0	0	1	0	0	0	0	0	0.168104	0	0	0
lincRNA	-	0	0	2	0	0	0	0	0	0.202212	0	0	0
antisense	-	1	0	0	0	0	0	0.168602	0	0	0	0	0
antisense	-	4	11	6	2	8	5	0.222675	0.721625	0.440147	0.096317	0.500323	0.276625
pseudogen	-	1	1	1	0	2	1	0.139686	0.164611	0.184072	0	0.313857	0.138823
antisense	-	10	1	2	0	0	1	0.911205	0.10738	0.240149	0	0	0.090558
pseudogen	glutathion	4	0	2	2	3	6	0.48019	0	0.316387	0.207705	0.404598	0.715837
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.070813
protein_co	endogenou	33	25	28	203	127	116	0.45615	0.407231	0.510019	2.427462	1.972178	1.593533
antisense	-	1	0	0	0	0	0	0.092071	0	0	0	0	0
antisense	-	2	1	4	0	2	1	0.32183	0.189628	0.848186	0	0.361556	0.159921
lincRNA	-	1	0	0	0	0	0	0.018881	0	0	0	0	0

antisense	-	0	1	3	5	0	1	0	0.075166	0.252156	0.275897	0	0.06339
processed_	-	0	0	0	0	4	0	0	0	0	0	0.375242	0
antisense	-	0	0	0	0	3	2	0	0	0	0	0.524788	0.309494
pseudogen	iron-sulfur_	0	0	0	0	1	0	0	0	0	0	0.132759	0
processed_	BSN_antise	2	0	1	0	0	3	0.040677	0	0.026801	0	0	0.060639
antisense	-	0	0	0	2	3	0	0	0	0	0.160136	0.311937	0
lincRNA	-	11	7	7	17	11	22	1.218307	0.913628	1.021638	1.628831	1.368693	2.421567
antisense	-	2	0	0	0	0	0	0.277178	0	0	0	0	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.066714	0
pseudogen	-	0	0	3	0	3	1	0	0	0.500693	0	0.426861	0.125871
lincRNA	long_interg	0	1	0	0	0	0	0	0.07171	0	0	0	0
pseudogen	centrosom	2	0	0	6	1	0	0.042833	0	0	0.111162	0.02406	0
pseudogen	interleukin	4	9	3	0	1	3	0.126502	0.335418	0.125024	0	0.035529	0.09429
antisense	-	13	21	13	6	2	2	1.820722	3.465985	2.399266	0.726967	0.314687	0.278381
processed_	differentiat	1544	1244	946	3809	2158	2835	93.09897	88.39446	75.16636	198.688	146.1834	169.8871
pseudogen	-	0	0	0	0	1	1	0	0	0	0	0.236016	0.208786
processed_	-	0	1	6	13	12	11	0	0.116613	0.782392	1.112871	1.334039	1.081784
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.115263	0
antisense	-	0	1	1	4	0	1	0	0.096129	0.107494	0.282274	0	0.081069
pseudogen	RNA_28S_r	14539	16150	20772	2604	17007	9356	1781.734	2332.319	3354.451	276.0656	2341.451	1139.484
antisense	-	0	0	0	0	2	0	0	0	0	0	0.213175	0
pseudogen	Ras-homol	0	2	2	3	7	5	0	0.207959	0.232544	0.228995	0.693886	0.43845
lincRNA	-	8	3	8	24	15	18	0.855612	0.378107	1.127487	2.220553	1.802301	1.913238
pseudogen	HAUS_augn	0	3	2	0	0	0	0	0.163461	0.121857	0	0	0
lincRNA	long_interg	0	0	0	1	0	1	0	0	0	0.050719	0	0.058266
antisense	-	0	0	0	6	1	0	0	0	0	0.628818	0.1361	0
pseudogen	-	0	0	1	0	0	1	0	0	0.285915	0	0	0.215631
protein_co	cytochrom	5	4	8	12	6	9	0.463581	0.437042	0.977419	0.962499	0.624966	0.829293
pseudogen	high_mobil	0	1	2	2	0	1	0	0.209355	0.46821	0.307375	0	0.176557
protein_co	lymphotox	3	0	1	1	3	2	0.10539	0	0.046293	0.030391	0.118399	0.069826
pseudogen	abhydrolas	1	0	5	1	1	2	0.05071	0	0.334115	0.043869	0.056969	0.100793
pseudogen	centromere	0	0	0	2	0	0	0	0	0	0.035531	0	0
pseudogen	-	1	0	0	2	0	1	0.123984	0	0	0.214515	0	0.123218
lincRNA	-	0	0	1	1	0	0	0	0	0.120282	0.078964	0	0
pseudogen	-	3	0	0	0	0	0	0.28412	0	0	0	0	0
pseudogen	-	1	0	1	1	0	0	0.133353	0	0.175726	0.115362	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.207013	0	0	0
pseudogen	neuroblast	11	3	3	3	3	6	0.881015	0.283152	0.316626	0.207862	0.269936	0.477586
antisense	-	10	12	8	5	4	1	0.614878	0.869515	0.648207	0.265963	0.276311	0.061108
pseudogen	-	16	11	15	26	8	20	2.036192	1.649676	2.515503	2.862432	1.143768	2.529522
lincRNA	-	1	1	4	19	5	5	0.069476	0.081874	0.366211	1.141967	0.390262	0.345237
antisense	-	3	8	4	15	22	5	0.177853	0.558905	0.31249	0.769299	1.465252	0.294592
lincRNA	-	0	1	0	0	0	0	0	0.092563	0	0	0	0
antisense	SLC8A1_an	2	1	0	15	16	10	0.113243	0.066725	0	0.734742	1.01777	0.562717

antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.269126
processed_	long_interg	35	56	33	233	140	137	0.818073	1.542478	1.016419	4.711322	3.676216	3.182395
pseudogen	-	0	0	0	1	2	1	0	0	0	0.019091	0.049584	0.021932
antisense	ITGB2_anti	0	6	0	3	5	1	0	0.164034	0	0.060209	0.130315	0.023056
protein_co	chromoson	1554	1268	1100	250	282	214	10.58275	10.17592	9.871316	1.472823	2.157475	1.448341
antisense	-	0	2	0	1	1	1	0	0.306574	0	0.112528	0.146132	0.129273
pseudogen	ferredoxin_	0	0	1	0	0	0	0	0	0.186035	0	0	0
pseudogen	-	2	2	1	0	4	1	0.135226	0.159356	0.089097	0	0.303836	0.067195
protein_co	WD_repeat	1278	1035	835	1946	1437	2105	28.69321	27.38393	24.70413	37.79672	36.2455	46.96886
processed_	long_interg	9	7	7	3	0	2	0.564537	0.517434	0.578605	0.162792	0	0.124678
pseudogen	ribosomal_	3838	3900	2381	2477	2675	4179	664.0116	795.1377	542.8313	370.7317	519.9284	718.5429
antisense	-	0	2	0	1	0	0	0	0.197118	0	0.072352	0	0
antisense	-	1	0	4	0	9	2	0.146246	0	0.770865	0	1.478683	0.290685
lincRNA	-	12	4	3	3	6	7	1.769615	0.695128	0.58298	0.382721	0.994026	1.025901
pseudogen	-	0	0	1	0	0	0	0	0	0.141221	0	0	0
pseudogen	succinate_(	1	0	0	0	0	0	0.113852	0	0	0	0	0
sense_intrc	-	0	0	0	0	1	3	0	0	0	0	0.160312	0.425451
pseudogen	-	1	2	0	4	2	2	0.142698	0.336322	0	0.493789	0.320625	0.283634
lincRNA	-	6	0	0	0	0	0	0.610858	0	0	0	0	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.153618
pseudogen	-	85	87	77	107	51	123	13.97511	16.85631	16.68252	15.21889	9.420099	20.09791
processed_	-	11	13	12	35	32	16	0.159025	0.221475	0.228607	0.437728	0.519724	0.229881
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.197056
lincRNA	-	0	0	0	0	4	0	0	0	0	0	0.837689	0
antisense	-	0	0	0	0	3	0	0	0	0	0	0.345121	0
pseudogen	-	783	702	397	711	462	1079	110.8364	117.1021	74.05354	87.0669	73.47025	151.7929
lincRNA	-	1	2	3	6	1	4	0.025737	0.060659	0.101745	0.133589	0.028914	0.102312
antisense	LMCD1_ant	3	1	0	8	3	3	0.059196	0.023253	0	0.13656	0.066503	0.05883
pseudogen	-	0	3	1	7	8	10	0	0.806738	0.300704	1.381864	2.050894	2.267847
lincRNA	-	1	0	0	1	1	0	0.016606	0	0	0.014366	0.018656	0
lincRNA	-	0	0	0	4	0	0	0	0	0	0.389778	0	0
processed_	-	0	0	0	5	3	0	0	0	0	0.253874	0.197813	0
pseudogen	-	1	1	0	0	0	0	0.124861	0.147141	0	0	0	0
lincRNA	-	0	0	0	2	0	0	0	0	0	0.220718	0	0
pseudogen	ribosomal_	4	1	3	1	1	0	0.421841	0.124278	0.416912	0.091233	0.118478	0
protein_co	zinc_finger_	28	28	33	63	71	45	0.382541	0.450802	0.594113	0.744602	1.089752	0.611002
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.121231
lincRNA	long_interg	0	8	0	0	0	2	0	0.620773	0	0	0	0.130881
pseudogen	-	2	0	1	0	0	0	0.04285	0	0.028233	0	0	0
antisense	IL21_antise	0	1	4	0	0	0	0	0.016646	0.074454	0	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.088085	0	0	0
antisense	-	2	0	0	1	4	7	0.081762	0	0	0.035366	0.183709	0.2844
lincRNA	-	0	1	0	0	0	0	0	0.132458	0	0	0	0
pseudogen	DEAD/H_(A	3	0	0	1	0	3	0.096666	0	0	0.027875	0	0.096069

processed_	-	3	3	5	2	0	5	1.63735	1.929517	3.596045	0.944307	0	2.712064
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.101181
antisense	WDR11_an	1	0	2	0	6	0	0.023613	0	0.062233	0	0.159168	0
antisense	-	0	0	2	0	0	0	0	0	0.347081	0	0	0
antisense	-	0	0	0	2	0	5	0	0	0	0.221251	0	0.635435
pseudogen	-	8	2	4	4	2	4	0.548611	0.161626	0.361468	0.2373	0.154083	0.272612
protein_co	epiplakin_1	5	0	3	529	858	740	0.033101	0	0.026171	3.029589	6.381185	4.868625
antisense	-	0	3	0	0	0	0	0	0.492535	0	0	0	0
antisense	-	0	3	1	0	2	1	0	0.37583	0.140087	0	0.238859	0.105651
antisense	-	1	0	0	0	0	0	0.024453	0	0	0	0	0
antisense	-	0	0	2	2	4	1	0	0	0.252766	0.165938	0.430985	0.095315
processed_	-	0	1	3	0	1	2	0	0.051433	0.172539	0	0.049032	0.08675
antisense	-	0	0	0	0	3	1	0	0	0	0	0.223314	0.06585
antisense	ST7_antiser	7	7	8	11	7	24	0.196182	0.231188	0.295451	0.266696	0.220398	0.668469
sense_intrc	-	12	22	19	1	11	2	1.703196	3.679705	3.553626	0.122785	1.753981	0.282113
pseudogen	calponin_2	5	2	1	0	1	1	0.28835	0.135921	0.075995	0	0.064789	0.057314
pseudogen	SUB1_hom	0	5	1	0	0	0	0	0.81234	0.181675	0	0	0
pseudogen	RNA_bindi	0	0	0	1	1	0	0	0	0	0.043247	0.056162	0
pseudogen	long_interg	0	1	0	0	0	0	0	0.024209	0	0	0	0
antisense	-	1	0	2	0	10	0	0.097858	0	0.257905	0	1.09937	0
pseudogen	-	1	3	4	0	0	0	0.152129	0.537825	0.801877	0	0	0
pseudogen	profilin_1_	0	0	2	0	0	1	0	0	0.349691	0	0	0.131865
antisense	SPATA13_a	0	1	0	0	4	0	0	0.144083	0	0	0.549431	0
antisense	HLA_compl	0	1	4	31	12	23	0	0.060453	0.2704	1.375742	0.69158	1.1726
antisense	-	0	3	0	4	2	1	0	0.389923	0	0.381658	0.247816	0.109613
antisense	-	4	7	6	1	5	2	0.191642	0.395216	0.378805	0.041447	0.269122	0.095229
antisense	-	1	0	0	0	0	1	0.106952	0	0	0	0	0.106291
antisense	-	0	1	0	0	1	0	0	0.10926	0	0	0.104161	0
antisense	-	5	2	2	1	0	2	0.381419	0.179792	0.201047	0.065993	0	0.151626
pseudogen	WAS_prote	309	237	152	454	325	469	9.174855	8.292704	5.94729	11.66164	10.8411	13.83959
pseudogen	-	1	0	0	0	0	0	0.030708	0	0	0	0	0
processed_	-	0	0	1	0	0	0	0	0	0.08385	0	0	0
pseudogen	neuroblast	5	6	9	2	1	5	0.069513	0.0983	0.164882	0.024054	0.015619	0.069084
lincRNA	long_interg	0	0	0	0	1	0	0	0	0	0	0.085454	0
lincRNA	-	0	1	0	0	0	0	0	0.122569	0	0	0	0
sense_intrc	FAM155A_i	1	1	1	0	3	3	0.064641	0.076175	0.085181	0	0.217861	0.192725
processed_	-	8	15	10	32	4	5	0.180918	0.399751	0.298006	0.626042	0.101625	0.112375
antisense	-	2	0	0	2	0	5	0.152129	0	0	0.131606	0	0.377974
antisense	MIS18A_an	9	9	5	10	3	5	0.619596	0.730155	0.453597	0.595564	0.232026	0.342094
antisense	SMIM2_ant	0	5	0	2	1	2	0	0.625128	0	0.183563	0.11919	0.210878
lincRNA	-	0	1	0	0	0	0	0	0.143091	0	0	0	0
pseudogen	HLA_compl	2	0	0	0	0	0	0.106844	0	0	0	0	0
pseudogen	-	0	9	0	0	0	0	0	0.966419	0	0	0	0
protein_co	killin_p53-l	17	11	12	36	23	10	0.210427	0.160455	0.195735	0.385495	0.319838	0.123016

lincRNA	-	0	0	0	2	0	0	0	0	0	0.208651	0	0
antisense	-	1	1	4	0	6	2	0.12032	0.14179	0.634212	0	0.811035	0.239155
antisense	-	8	8	1	10	7	4	0.540214	0.636609	0.088984	0.58417	0.531035	0.268439
antisense	-	28	11	16	22	16	34	1.830059	0.847241	1.37804	1.243921	1.174833	2.208491
pseudogen	-	0	0	0	3	2	9	0	0	0	0.082028	0.071016	0.282702
pseudogen	heat_shock	6	6	3	6	0	5	0.266705	0.314296	0.175726	0.230725	0	0.220882
lincRNA	-	0	0	1	0	0	0	0	0	0.078474	0	0	0
lincRNA	-	0	0	1	0	0	0	0	0	0.11216	0	0	0
antisense	-	0	0	2	0	0	0	0	0	0.252766	0	0	0
pseudogen	keratin_16_	0	0	0	53	50	73	0	0	0	1.54117	1.888124	2.438619
pseudogen	-	2	0	0	3	0	0	0.070919	0	0	0.092027	0	0
processed_	-	0	3	0	0	0	0	0	0.377345	0	0	0	0
pseudogen	-	1	0	0	0	0	2	0.146651	0	0	0	0	0.291491
pseudogen	-	0	0	2	2	0	0	0	0	0.08581	0.056333	0	0
pseudogen	MT-ND4_ps	1	4	2	0	5	4	0.05125	0.241579	0.135069	0	0.28788	0.203733
pseudogen	-	9	9	5	4	6	4	2.853107	3.362213	2.088721	1.09698	2.136859	1.260217
pseudogen	-	0	1	0	3	4	4	0	0.077985	0	0.171746	0.29738	0.26307
lincRNA	long_interg	0	0	0	3	2	0	0	0	0	0.327916	0.283895	0
pseudogen	-	0	0	0	1	0	1	0	0	0	0.097238	0	0.111707
pseudogen	HAUS_augn	1	0	0	0	0	0	0.034133	0	0	0	0	0
protein_co	poly_(ADP-	231	195	193	587	441	497	4.820406	4.795273	5.307179	10.59675	10.33854	10.30713
pseudogen	Nanog_hon	0	0	1	2	0	0	0	0	0.082463	0.108272	0	0
antisense	ARHGEF7_a	0	0	0	0	2	1	0	0	0	0	0.370566	0.163907
processed_	RBM26_ant	13	23	2	24	22	20	0.391932	0.817151	0.079457	0.625953	0.745142	0.599249
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.119577
lincRNA	-	12	10	10	12	8	3	1.132428	1.112081	1.243552	0.979656	0.848141	0.281359
lincRNA	-	7	0	0	0	0	0	0.516858	0	0	0	0	0
antisense	-	0	0	0	2	1	1	0	0	0	0.195722	0.127085	0.112423
pseudogen	-	0	0	2	0	2	0	0	0	0.255076	0	0.217462	0
pseudogen	-	0	1	6	1	3	1	0	0.136815	0.917938	0.100436	0.391289	0.115382
pseudogen	-	0	0	1	0	1	0	0	0	0.166898	0	0.142287	0
antisense	TP73_antis	421	345	277	789	715	769	3.50553	3.385305	3.039388	5.683444	6.688468	6.363669
lincRNA	-	3	0	0	4	3	0	0.230847	0	0	0.266273	0.259343	0
processed_	DLG1_antis	0	0	2	20	4	6	0	0	0.082365	0.540719	0.140439	0.186354
pseudogen	ferritin_hea	1	5	1	4	5	3	0.095908	0.565106	0.126383	0.331876	0.538731	0.285946
pseudogen	peptidylpro	0	0	3	3	0	2	0	0	0.425386	0.279262	0	0.213878
pseudogen	eukaryotic_	3	3	2	3	1	4	0.148433	0.174919	0.130399	0.128408	0.055585	0.196688
pseudogen	-	2	3	3	0	1	2	0.323798	0.572364	0.64003	0	0.181884	0.321798
processed_	-	7	0	0	12	10	13	0.678731	0	0	1.006569	1.089303	1.252715
antisense	HPN_antise	0	0	0	0	0	1	0	0	0	0	0	0.04681
pseudogen	-	0	0	0	1	0	0	0	0	0	0.078692	0	0
processed_	KIF9_antise	22	8	12	30	3	19	0.494986	0.212113	0.355784	0.583921	0.07583	0.424848
pseudogen	-	1	0	0	0	0	0	0.109609	0	0	0	0	0
processed_	-	0	0	0	11	6	6	0	0	0	0.859706	0.608968	0.53871

pseudogen	ribosomal_	3	2	0	0	0	0	0.559236	0.43935	0	0	0	0
processed_	-	0	0	0	13	18	22	0	0	0	0.255202	0.45888	0.496146
antisense	-	3	0	1	0	0	0	0.300232	0	0.131878	0	0	0
antisense	ZMYM4_an	5	0	0	4	1	0	0.576699	0	0	0.399119	0.129577	0
processed_	-	0	0	2	5	18	22	0	0	0.16974	0.278582	1.302392	1.408162
pseudogen	-	0	7	1	0	0	9	0	1.230181	0.196516	0	0	1.333877
pseudogen	-	0	3	2	0	3	5	0	0.291078	0.216993	0	0.277493	0.409129
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.135255
antisense	-	0	0	2	8	2	4	0	0	0.250947	0.658977	0.213942	0.378518
antisense	-	3	8	12	0	0	0	0.306017	0.961661	1.613024	0	0	0
pseudogen	-	0	0	3	0	0	1	0	0	0.570272	0	0	0.143363
pseudogen	FCF1_small	0	1	0	3	9	1	0	0.10926	0	0.240625	0.937449	0.092144
antisense	-	5	6	2	0	4	0	0.393906	0.557033	0.207629	0	0.354023	0
pseudogen	ATP_syntha	3	0	2	18	6	7	0.360143	0	0.316387	1.869343	0.809196	0.835144
protein_co	Uncharacte	5	2	0	0	5	4	0.195066	0.091949	0	0	0.219145	0.155089
lincRNA	long_interg	5	3	4	0	8	7	0.220956	0.15623	0.232932	0	0.397168	0.307428
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.115382
processed_	-	0	0	0	4	0	2	0	0	0	0.074774	0	0.04295
pseudogen	-	4	1	3	18	18	9	1.384078	0.407763	1.367907	5.388107	6.997167	3.094944
protein_co	aldo-keto_r	0	0	1	1	0	0	0	0	0.035075	0.023026	0	0
pseudogen	testis-speci	0	0	2	0	0	0	0	0	0.153833	0	0	0
processed_	STK4_antis	2	1	3	3	2	2	0.051275	0.030212	0.101351	0.066536	0.057604	0.050958
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.122643
antisense	-	6	3	0	0	4	8	0.550513	0.324373	0	0	0.412311	0.729484
lincRNA	-	1	0	1	0	2	0	0.043288	0	0.057043	0	0.097262	0
antisense	-	0	4	0	0	0	0	0	0.469964	0	0	0	0
processed_	-	0	0	1	10	20	17	0	0	0.069278	0.454805	1.18125	0.888221
antisense	-	0	0	1	0	0	0	0	0	0.064536	0	0	0
lincRNA	-	3	1	1	0	0	0	0.24322	0.09554	0.106835	0	0	0
antisense	-	8	7	2	5	0	5	0.500624	0.516211	0.164925	0.270679	0	0.310958
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.063543	0
pseudogen	ubiquitin_s	0	0	0	0	0	1	0	0	0	0	0	0.093453
antisense	-	0	3	5	5	1	11	0	0.321035	0.598313	0.392786	0.102017	0.992718
antisense	-	37	47	28	0	0	0	1.280272	1.916486	1.276714	0	0	0
protein_co	secretory_c	1525	1216	961	2340	1807	2086	27.33074	25.68161	22.6955	36.27943	36.38219	37.154
processed_	-	0	2	3	0	0	0	0	0.30212	0.506755	0	0	0
protein_co	lymphotox	7	3	0	10	11	28	0.266993	0.134844	0	0.329963	0.471351	1.061379
antisense	-	10	3	6	2	14	18	0.612743	0.216624	0.484467	0.106016	0.96373	1.096126
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.261112
lincRNA	-	0	0	0	0	1	1	0	0	0	0	0.019279	0.017055
antisense	microRNA_	3	5	2	2	8	1	0.054336	0.106719	0.047734	0.031337	0.16278	0.018
pseudogen	ribosomal_	2	5	0	2	1	4	0.340457	1.003018	0	0.294527	0.191241	0.676708
sense_intrc	-	0	3	1	3	0	6	0	0.283152	0.105542	0.207862	0	0.477586
processed_	SLC2A1_an	31	25	38	56	55	58	0.533714	0.507217	0.862115	0.834061	1.063797	0.992395

antisense	-	2	0	0	2	2	0	0.38087	0	0	0.329489	0.427884	0
pseudogen	suppressor_	6	12	8	12	14	18	0.202839	0.478067	0.35639	0.350949	0.531713	0.604759
processed_	-	9	7	6	20	17	10	0.625287	0.573116	0.549317	1.202071	1.326891	0.690473
pseudogen	-	0	0	1	0	0	0	0	0	0.1014	0	0	0
lincRNA	-	10	21	13	13	17	26	0.582409	1.441301	0.997715	0.65499	1.112311	1.504912
processed_	SPAG5_ant	13	10	3	40	38	45	0.321454	0.291395	0.097753	0.855654	1.055621	1.105853
lincRNA	-	0	4	0	2	0	0	0	0.151151	0	0.05548	0	0
antisense	-	0	2	0	0	0	1	0	0.34279	0	0	0	0.144544
pseudogen	phosphogl	24	25	29	3	7	4	0.645622	0.792527	1.028016	0.069815	0.211551	0.106939
pseudogen	-	4	6	7	6	3	3	0.542985	0.959811	1.252161	0.704599	0.457507	0.404723
pseudogen	-	0	0	0	0	1	1	0	0	0	0	0.135173	0.119577
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.086679
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.09562	0
pseudogen	-	7	7	4	0	9	2	0.326508	0.38477	0.245862	0	0.471615	0.092712
pseudogen	-	0	0	2	1	2	4	0	0	0.187284	0.061475	0.159667	0.282492
pseudogen	-	1	0	3	0	0	0	0.152129	0	0.601408	0	0	0
lincRNA	CNTN4_ant	0	0	0	0	2	0	0	0	0	0	0.27923	0
antisense	-	0	1	0	0	2	0	0	0.138948	0	0	0.264926	0
pseudogen	-	5	0	0	0	0	0	0.234045	0	0	0	0	0
antisense	-	0	0	1	13	9	7	0	0	0.181203	1.546457	1.390346	0.956619
antisense	-	7	5	5	7	2	9	0.536305	0.451431	0.504799	0.463954	0.172144	0.685277
lincRNA	-	0	0	0	0	2	1	0	0	0	0	0.237904	0.105228
pseudogen	SMT3_supp	0	0	2	0	0	0	0	0	0.547163	0	0	0
pseudogen	-	20	12	2	34	14	29	2.653684	1.876323	0.349691	3.902664	2.086874	3.824079
antisense	-	4	2	2	0	0	0	0.08647	0.05095	0.056973	0	0	0
pseudogen	asparagine-	1	0	1	5	10	6	0.069659	0	0.091794	0.301309	0.782578	0.415374
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.158715
processed_	-	2	0	0	5	4	10	0.029626	0	0	0.064072	0.066565	0.147213
pseudogen	-	2	2	1	0	0	0	0.17133	0.201902	0.112886	0	0	0
lincRNA	-	1	0	0	0	0	0	0.106521	0	0	0	0	0
antisense	-	5	5	5	0	1	5	0.827203	0.974808	1.090051	0	0.185862	0.822095
pseudogen	heterogene	6	6	5	11	4	8	0.339728	0.400349	0.373066	0.538811	0.254442	0.450174
processed_	SOX21_ant	2	4	1	4	0	0	0.068934	0.162468	0.045419	0.119268	0	0
sense_intrc	-	0	0	0	1	3	0	0	0	0	0.120207	0.468314	0
antisense	-	3	4	2	0	1	1	0.222441	0.349511	0.195415	0	0.0833	0.073689
pseudogen	-	2	4	0	0	0	1	0.33507	0.789718	0	0	0	0.1665
pseudogen	-	203	206	192	490	485	462	7.335851	8.772609	9.143038	15.31841	19.68998	16.59228
antisense	-	0	0	1	7	1	3	0	0	0.444352	2.041989	0.378827	1.005364
processed_	long_interg	2	1	2	0	0	0	0.05638	0.03322	0.074295	0	0	0
lincRNA	-	2	0	0	3	0	3	0.304259	0	0	0.394818	0	0.453569
antisense	-	0	1	2	0	0	0	0	0.081128	0.181439	0	0	0
lincRNA	-	7	0	2	0	6	3	0.479414	0	0.1805	0	0.46165	0.204194
pseudogen	heterogene	0	0	0	0	1	0	0	0	0	0	0.089843	0
pseudogen	mediator_c	0	0	1	1	5	2	0	0	0.131381	0.08625	0.560037	0.19817

pseudogen	glutathione	0	0	2	0	0	2	0	0	0.243078	0	0	0.183324
antisense	DNMBP_an	7	3	3	0	3	3	0.182196	0.092017	0.102896	0	0.087723	0.077602
sense_intrc	-	0	7	2	2	6	2	0	0.976989	0.31214	0.204917	0.798334	0.23541
pseudogen	-	0	0	0	0	4	4	0	0	0	0	0.460162	0.407072
antisense	-	2	2	0	0	0	0	0.218313	0.257269	0	0	0	0
lincRNA	-	0	0	0	34	20	20	0	0	0	0.970195	0.741133	0.655627
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.169997
lincRNA	-	0	0	0	6	0	0	0	0	0	0.306006	0	0
antisense	-	0	0	2	2	1	1	0	0	0.266272	0.174805	0.113504	0.100408
pseudogen	-	0	0	0	0	3	0	0	0	0	0	0.325598	0
pseudogen	GRINL1B_c	2	4	3	1	0	0	0.095648	0.22543	0.18906	0.041372	0	0
sense_intrc	-	0	0	0	0	0	5	0	0	0	0	0	1.27704
pseudogen	MT-ND6_ps	0	1	0	0	4	1	0	0.121851	0	0	0.464656	0.102762
sense_intrc	-	0	0	0	7	4	0	0	0	0	0.127574	0.094669	0
lincRNA	-	1	6	1	2	2	6	0.08058	0.569751	0.106185	0.139418	0.181053	0.480494
processed_	-	12	18	16	4	27	25	0.402593	0.711647	0.707359	0.116094	1.017649	0.833556
pseudogen	calreticulin	0	0	0	0	6	3	0	0	0	0	0.377226	0.166852
lincRNA	-	1	0	1	0	0	0	0.015174	0	0.019995	0	0	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.182722	0
pseudogen	-	0	0	0	2	0	0	0	0	0	0.142898	0	0
pseudogen	vesicle_trar	0	0	0	0	1	0	0	0	0	0	0.112858	0
antisense	-	0	0	1	0	0	0	0	0	0.061628	0	0	0
pseudogen	-	0	1	0	0	0	0	0	0.083184	0	0	0	0
sense_intrc	ASH1L_intr	0	3	3	0	0	4	0	0.417775	0.467165	0	0	0.469768
pseudogen	-	335	364	265	178	178	218	9.80931	12.56036	10.22526	4.508963	5.855483	6.343951
pseudogen	-	1	0	0	3	5	0	0.085665	0	0	0.222325	0.481197	0
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.102695
pseudogen	glutamate_	19	0	1	3	0	0	1.079269	0	0.074853	0.147421	0	0
protein_co	Uncharacte	0	0	1	0	0	0	0	0	0.861275	0	0	0
pseudogen	-	0	0	0	0	2	1	0	0	0	0	0.154283	0.068241
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.25972	0
pseudogen	-	22	23	11	21	10	27	0.812205	1.00064	0.535144	0.670695	0.414755	0.990641
processed_	-	15	6	6	2	0	1	0.372649	0.175658	0.196424	0.042983	0	0.02469
pseudogen	-	2	0	0	0	4	0	0.216086	0	0	0	0.485518	0
pseudogen	-	0	4	0	0	0	0	0	0.693197	0	0	0	0
processed_	-	0	0	0	0	1	0	0	0	0	0	0.086322	0
pseudogen	solute_carr	7	8	15	23	22	21	0.111926	0.150741	0.316052	0.318144	0.395189	0.333704
pseudogen	-	101	71	69	45	53	56	0.538365	0.445986	0.484662	0.207506	0.317381	0.296656
pseudogen	coactivator	4	2	1	0	0	0	0.178704	0.105296	0.058872	0	0	0
pseudogen	-	0	0	0	2	0	5	0	0	0	0.253033	0	0.726713
pseudogen	-	0	1	0	0	0	0	0	0.189054	0	0	0	0
antisense	-	1	3	6	0	0	0	0.03372	0.119212	0.266611	0	0	0
pseudogen	-	1	0	0	1	0	0	0.119776	0	0	0.103617	0	0
antisense	SUCLA2_an	3	0	0	4	1	4	0.287723	0	0	0.331876	0.107746	0.381261

pseudogen	-	13	10	3	33	41	33	0.295887	0.268219	0.089978	0.64977	1.048372	0.746459
antisense	-	0	0	1	0	1	1	0	0	0.205791	0	0.175445	0.155204
protein_co	uncharacte	1	3	0	3	0	0	0.103806	0.366987	0	0.269405	0	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.060476
pseudogen	paraspeckle	0	0	1	1	0	5	0	0	0.104907	0.068871	0	0.395594
lincRNA	-	6	4	2	4	12	6	0.373701	0.293589	0.164149	0.215524	0.83966	0.371393
processed_	family_with	0	0	0	0	1	2	0	0	0	0	0.064578	0.114254
pseudogen	proteasom	0	0	0	7	0	0	0	0	0	0.474952	0	0
pseudogen	olfactory_r	0	0	0	0	8	1	0	0	0	0	0.518874	0.057376
antisense	-	7	10	5	16	15	21	0.576341	0.97026	0.542483	1.139631	1.387463	1.718344
antisense	SNAP25_an	2	0	0	3	1	1	0.033016	0	0	0.042843	0.018546	0.016406
antisense	-	3	0	1	2	1	1	0.069385	0	0.030478	0.040017	0.025983	0.022986
lincRNA	-	0	0	0	2	2	0	0	0	0	0.196562	0.255261	0
pseudogen	keratin_8_p	0	0	1	0	0	0	0	0	0.051677	0	0	0
antisense	-	0	0	0	0	3	1	0	0	0	0	0.15931	0.046977
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.11919	0
protein_co	-	2	2	2	16	1	5	0.027878	0.032853	0.036737	0.192939	0.01566	0.069265
lincRNA	-	0	0	1	0	0	0	0	0	0.164925	0	0	0
sense_intro	MACROD2_	0	0	0	0	3	0	0	0	0	0	0.268312	0
antisense	SRGAP3_an	1	0	0	2	3	2	0.09337	0	0	0.161548	0.314687	0.185587
pseudogen	-	0	1	4	5	2	4	0	0.108879	0.487004	0.399641	0.207595	0.367288
lincRNA	-	1	0	0	0	0	0	0.062357	0	0	0	0	0
pseudogen	ribosomal_	1	2	0	0	0	2	0.044007	0.10372	0	0	0	0.087471
antisense	-	2	0	1	0	1	2	0.140801	0	0.09277	0	0.07909	0.139931
lincRNA	-	62	22	19	13	25	37	4.364816	1.825173	1.762636	0.791736	1.977258	2.588723
pseudogen	-	0	0	2	0	1	3	0	0	0.487855	0	0.207958	0.551896
processed_	-	14	5	2	7	5	7	0.285067	0.119976	0.053664	0.123305	0.114377	0.141653
processed_	-	0	0	0	3	0	0	0	0	0	0.182466	0	0
antisense	-	10	5	9	5	14	14	0.58563	0.345065	0.694546	0.253313	0.921087	0.814819
pseudogen	-	0	1	3	0	6	0	0	0.221233	0.742163	0	1.265445	0
processed_	-	0	6	1	4	4	5	0	0.143365	0.026719	0.070163	0.091116	0.100755
lincRNA	-	0	0	0	3	6	1	0	0	0	0.05907	0.15342	0.02262
pseudogen	protein_(pe	2	1	0	2	4	7	0.267379	0.157545	0	0.231308	0.600767	0.930046
lincRNA	-	3	0	1	0	0	0	0.696592	0	0.305979	0	0	0
pseudogen	tripartite_r	0	0	0	10	12	13	0	0	0	0.553127	0.86197	0.826066
pseudogen	-	6	3	0	7	15	6	0.915406	0.539375	0	0.923897	2.571005	0.909753
pseudogen	MT-ND5_ps	9	3	9	7	0	0	0.346523	0.136119	0.456632	0.233158	0	0
pseudogen	ribosomal_	0	0	5	5	2	4	0	0	0.466332	0.306142	0.159027	0.281359
pseudogen	-	0	0	0	0	4	0	0	0	0	0	0.741133	0
protein_co	Uncharacte	2	2	0	0	0	0	0.17647	0.207959	0	0	0	0
processed_	-	6	3	8	2	1	4	0.563202	0.33185	0.98955	0.162407	0.105454	0.373149
processed_	RAPGEF4_a	0	0	1	0	2	0	0	0	0.015084	0	0.025719	0
pseudogen	-	4	1	2	5	9	2	0.560222	0.165047	0.369118	0.605806	1.416093	0.278381
lincRNA	-	0	0	1	2	0	1	0	0	0.019763	0.025948	0	0.014905

lincRNA	HLA_compl	7	0	0	3	0	0	0.308309	0	0	0.114307	0	0
antisense	-	1	0	0	0	5	1	0.125453	0	0	0	0.704691	0.124678
protein_co	chromoson	6	1	0	0	0	0	0.195595	0.038416	0	0	0	0
lincRNA	-	0	1	3	0	0	0	0	0.127582	0.427996	0	0	0
antisense	-	0	0	0	1	0	0	0	0	0	0.017547	0	0
antisense	-	0	0	1	0	3	2	0	0	0.111443	0	0.285028	0.168096
pseudogen	vomeronas	4	0	1	10	8	12	0.224089	0	0.073824	0.484645	0.5035	0.668115
pseudogen	-	0	0	0	1	0	1	0	0	0	0.293583	0	0.33727
processed_	-	0	2	0	12	11	7	0	0.134456	0	0.592227	0.704995	0.396873
protein_co	Homo_sapi	0	0	0	1	1	0	0	0	0	0.02672	0.0347	0
pseudogen	topoisome	0	1	0	2	0	3	0	0.045208	0	0.066375	0	0.114378
pseudogen	-	0	1	2	3	0	2	0	0.130518	0.291897	0.287441	0	0.220142
pseudogen	RAN_memb	0	0	0	0	0	1	0	0	0	0	0	0.080327
pseudogen	cofilin_1_(r	12	0	0	0	7	8	1.296514	0	0	0	0.849656	0.859005
pseudogen	SEC63_hon	0	0	0	0	1	3	0	0	0	0	0.047278	0.125471
antisense	-	3	6	4	4	14	11	0.288245	0.679358	0.506449	0.332478	1.511185	1.050371
processed_	-	0	0	0	0	2	0	0	0	0	0	0.198916	0
processed_	-	146	118	130	0	3	0	10.67595	10.16817	12.52656	0	0.246447	0
antisense	-	0	4	1	0	0	2	0	0.379834	0.106185	0	0	0.160165
lincRNA	-	8	9	8	95	85	100	0.345174	0.457612	0.454854	3.545963	4.120174	4.288024
pseudogen	-	8	2	7	1	6	5	0.543682	0.160174	0.626884	0.058792	0.458094	0.337703
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.1332
antisense	-	4	3	4	2	1	6	0.533411	0.471444	0.702905	0.230725	0.149813	0.795175
pseudogen	-	0	4	2	1	0	0	0	0.335418	0.187536	0.061558	0	0
pseudogen	major_hist	0	0	1	0	0	0	0	0	0.375071	0	0	0
lincRNA	-	0	0	1	3	6	2	0	0	0.123913	0.244044	0.633846	0.186906
protein_co	interferon_	0	0	2	0	0	0	0	0	0.17934	0	0	0
antisense	-	1	0	0	0	5	1	0.080826	0	0	0	0.454015	0.080327
antisense	-	0	2	1	3	0	0	0	0.210769	0.117843	0.232089	0	0
pseudogen	-	0	0	3	0	0	0	0	0	0.486721	0	0	0
pseudogen	-	7	1	3	0	0	1	1.756336	0.295676	0.991895	0	0	0.249356
pseudogen	-	0	0	0	2	0	0	0	0	0	0.136713	0	0
pseudogen	-	0	0	3	0	0	0	0	0	0.917938	0	0	0
lincRNA	-	0	0	0	2	0	0	0	0	0	0.160698	0	0
lincRNA	-	15	7	5	20	14	21	1.035352	0.56938	0.45478	1.194235	1.08561	1.440541
processed_	-	10	4	1	7	3	1	0.888272	0.41871	0.117052	0.537907	0.299375	0.088279
antisense	-	3	1	1	0	9	0	0.296312	0.116395	0.130155	0	0.998663	0
antisense	MFI2_antis	5	7	3	6	12	12	0.278344	0.459216	0.220073	0.288952	0.750485	0.6639
pseudogen	suppressior	0	0	0	4	0	3	0	0	0	0.162985	0	0.140429
antisense	-	1	2	1	1	0	0	0.064484	0.15198	0.084974	0.055784	0	0
pseudogen	prohibitin_	1	0	0	0	0	0	0.064641	0	0	0	0	0
pseudogen	MT-ND1_ps	0	1	0	0	0	0	0	0.305822	0	0	0	0
antisense	-	1	0	0	0	0	2	0.112163	0	0	0	0	0.222941
pseudogen	-	0	0	0	0	2	4	0	0	0	0	0.208687	0.369221

lincRNA	long_interg	4	2	6	1	2	8	0.374141	0.220451	0.73954	0.080917	0.210162	0.743661
lincRNA	-	0	0	0	3	0	0	0	0	0	0.098422	0	0
lincRNA	-	2	0	1	2	0	1	0.060608	0	0.039933	0.052431	0	0.030117
antisense	-	12	16	13	8	9	4	1.628954	2.559497	2.325443	0.939465	1.372521	0.539631
processed_	-	3	2	0	1	0	0	0.030673	0.024097	0	0.008845	0	0
lincRNA	-	0	0	1	0	0	0	0	0	0.027156	0	0	0
protein_co	caspase_16	17	22	16	0	6	4	0.416472	0.635137	0.516526	0	0.165134	0.097388
pseudogen	ribosomal_	1	0	1	2	0	4	0.043717	0	0.057608	0.075638	0	0.173787
processed_	-	6	3	11	11	8	6	0.721923	0.425371	1.744082	1.144973	1.08138	0.717464
antisense	-	0	0	1	0	0	0	0	0	0.02236	0	0	0
pseudogen	-	0	0	0	0	2	2	0	0	0	0	0.672044	0.594509
processed_	-	0	2	0	0	0	0	0	0.337231	0	0	0	0
protein_co	Uncharacte	1	0	1	3	3	0	0.027559	0	0.036316	0.071524	0.092883	0
pseudogen	transducin-	0	0	0	7	1	3	0	0	0	0.544299	0.100978	0.267983
pseudogen	MT-ND1_ps	1	0	0	0	0	1	0.060435	0	0	0	0	0.060062
pseudogen	peptidylpro	0	0	1	0	0	0	0	0	0.141795	0	0	0
pseudogen	-	0	2	2	0	0	0	0	0.501106	0.560348	0	0	0
processed_	-	0	2	0	2	0	8	0	0.241345	0	0.177172	0	0.814144
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.110302
pseudogen	gem_(nucle	7	0	0	31	18	32	0.50835	0	0	1.947553	1.468541	2.309533
antisense	-	0	4	0	0	0	0	0	0.4091	0	0	0	0
pseudogen	protein_tyr	0	1	0	0	0	0	0	0.058198	0	0	0	0
antisense	-	0	0	2	11	7	5	0	0	0.35868	1.295085	1.070261	0.676273
processed_	RNF144A_a	220	238	150	37	37	47	3.942796	5.0265	3.542482	0.573649	0.744959	0.837123
antisense	-	0	0	0	2	3	4	0	0	0	0.120207	0.234157	0.276189
pseudogen	-	5	1	1	7	4	2	0.361619	0.085229	0.095305	0.437968	0.325005	0.143754
protein_co	chromoson	0	0	0	10	7	4	0	0	0	0.563332	0.512093	0.258864
pseudogen	OFD1_pseu	2	8	4	7	4	0	0.035083	0.165375	0.092463	0.106227	0.078828	0
antisense	NLGN1_ant	1	0	1	0	0	0	0.064958	0	0.085599	0	0	0
antisense	long_interg	2	6	1	11	5	4	0.065806	0.232645	0.043358	0.313106	0.184823	0.130799
pseudogen	-	0	0	2	3	0	2	0	0	0.332206	0.327135	0	0.250543
pseudogen	activating_	0	2	0	0	1	1	0	0.118159	0	0	0.056322	0.049824
pseudogen	nucleophos	0	0	0	10	2	3	0	0	0	0.553127	0.143662	0.190631
lincRNA	long_interg	3	1	1	0	0	0	0.259515	0.101941	0.113992	0	0	0
lincRNA	-	11	3	8	3	7	9	1.2605	0.405115	1.208022	0.297395	0.90115	1.024949
lincRNA	HLA_compl	341	364	337	223	241	228	3.815063	4.799056	4.968349	2.158317	3.029099	2.535081
pseudogen	glyceraldeh	18	12	9	8	8	13	0.948197	0.744928	0.624746	0.364568	0.47344	0.68058
lincRNA	-	2	0	2	0	0	0	0.255137	0	0.336209	0	0	0
pseudogen	-	0	0	0	2	3	2	0	0	0	0.290787	0.566437	0.334057
antisense	EFCAB14_a	6	0	3	2	2	6	0.635292	0	0.41858	0.183196	0.237904	0.631369
pseudogen	-	1	1	1	0	0	0	0.051852	0.061105	0.068328	0	0	0
processed_	-	2	2	5	0	8	5	0.184143	0.217001	0.606637	0	0.827491	0.457513
pseudogen	-	2	6	2	0	0	1	0.178855	0.632308	0.235687	0	0	0.088875
pseudogen	ubiquitin_l	1	0	0	0	0	0	0.229182	0	0	0	0	0

lincRNA	-	3	4	2	10	5	0	0.300232	0.471741	0.263755	0.865764	0.562154	0
pseudogen	collagen_ty	0	6	1	4	0	3	0	0.14331	0.026709	0.070136	0	0.06043
protein_co	mitochond	18	9	20	11	19	38	4.603565	2.71251	6.740414	2.433758	5.459142	9.658618
protein_co	Uncharacte	0	0	0	0	1	4	0	0	0	0	0.076546	0.270857
lincRNA	-	3	8	6	0	0	0	0.166481	0.523168	0.438763	0	0	0
pseudogen	-	0	4	0	0	0	0	0	0.324514	0	0	0	0
lincRNA	-	7	5	8	40	14	18	0.561495	0.472634	0.845616	2.775691	1.26161	1.434929
antisense	-	61	57	36	19	15	18	2.437283	2.683849	1.895455	0.656739	0.673312	0.714757
protein_co	orosomucc	0	0	0	4	0	0	0	0	0	0.186934	0	0
pseudogen	-	0	0	0	1	0	1	0	0	0	0.031241	0	0.03589
pseudogen	lysophosph	0	0	0	1	1	1	0	0	0	0.065803	0.085454	0.075595
antisense	KDM5B_an	106	109	81	68	57	83	7.502333	9.09126	7.55458	4.163537	4.532256	5.83819
antisense	-	6	0	1	0	0	0	0.416858	0	0.091553	0	0	0
pseudogen	-	2	3	0	0	0	3	0.411992	0.728261	0	0	0	0.614172
lincRNA	-	1	3	1	0	2	0	0.068135	0.240879	0.089785	0	0.153091	0
protein_co	chromoson	906	684	502	1261	730	976	29.01666	25.81561	21.18643	34.93794	26.26583	31.06553
antisense	-	8	15	20	38	27	34	0.221279	0.488932	0.728979	0.909278	0.839002	0.934628
pseudogen	-	2	1	0	5	3	3	0.16116	0.094958	0	0.348546	0.27158	0.240247
pseudogen	-	1	0	0	0	1	0	0.055727	0	0	0	0.062606	0
antisense	-	0	0	3	2	0	6	0	0	0.078298	0.034268	0	0.118101
pseudogen	glucuronid	261	186	198	151	180	186	2.761311	2.318968	2.760418	1.382021	2.139421	1.955678
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.079839
antisense	-	1	0	0	0	0	0	0.0839	0	0	0	0	0
antisense	-	11	4	2	0	1	1	1.32654	0.568453	0.317828	0	0.13548	0.11985
lincRNA	-	34	40	30	21	36	78	1.366738	1.894844	1.589141	0.730279	1.625765	3.116094
pseudogen	-	0	0	0	2	0	0	0	0	0	0.073396	0	0
pseudogen	-	0	1	1	0	1	2	0	0.078673	0.087974	0	0.075001	0.132696
pseudogen	-	3	0	0	6	0	3	0.261652	0	0	0.452707	0	0.260036
pseudogen	-	0	0	0	0	3	0	0	0	0	0	0.740364	0
processed_	-	3	0	4	0	2	2	0.07774	0	0.13659	0	0.058224	0.051507
pseudogen	-	0	1	0	0	0	2	0	0.222813	0	0	0	0.375815
antisense	-	204	183	130	268	208	262	23.99992	25.37101	20.15384	27.27579	27.49109	30.63307
pseudogen	ribosomal_	0	0	0	0	4	0	0	0	0	0	0.670151	0
antisense	-	1	4	0	2	5	6	0.270107	1.273219	0	0.467336	1.517243	1.610634
antisense	-	1	0	1	2	0	0	0.083372	0	0.109863	0.144249	0	0
antisense	-	1	4	5	0	4	4	0.027177	0.128106	0.179064	0	0.122127	0.108037
protein_co	Uncharacte	1	0	0	3	2	0	0.11534	0	0	0.299339	0.259154	0
antisense	-	1	1	0	1	2	9	0.135399	0.159559	0	0.117133	0.304225	1.211065
pseudogen	-	0	0	0	7	3	1	0	0	0	0.14173	0.078881	0.02326
sense_intro	ITPKB_intro	0	0	3	0	0	2	0	0	0.280549	0	0	0.141056
antisense	family_witl	0	0	0	0	3	0	0	0	0	0	0.076743	0
antisense	-	2	0	0	0	0	0	0.087434	0	0	0	0	0
lincRNA	-	2	0	4	0	10	2	0.175592	0	0.462775	0	0.986334	0.174508
antisense	-	29	28	22	32	24	13	0.730394	0.831045	0.730158	0.697224	0.679078	0.325396

antisense	-	41	39	37	59	46	80	3.164112	3.546824	3.762743	3.938973	3.988181	6.135749
antisense	-	15	11	9	20	24	19	0.818675	0.70749	0.647288	0.944307	1.471569	1.030584
lincRNA	-	3	0	0	1	0	0	0.258249	0	0	0.07447	0	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.109734	0
antisense	-	0	0	0	0	2	0	0	0	0	0	0.213558	0
pseudogen	-	4	3	0	2	1	0	0.622835	0.55048	0	0.269405	0.174929	0
pseudogen	chaperonin	96	119	58	165	103	127	3.864894	5.645734	3.077012	5.746631	4.65857	5.081357
pseudogen	chromodor	2	6	3	2	8	0	0.069981	0.247407	0.138328	0.060541	0.314479	0
processed_	-	4	9	1	18	13	6	0.208429	0.552647	0.068665	0.811398	0.761011	0.310713
pseudogen	-	1	5	0	0	1	3	0.153898	0.906798	0	0	0.172895	0.458843
pseudogen	prothymos	9	8	3	0	3	5	1.784528	1.869295	0.783857	0	0.668269	0.985282
antisense	-	0	5	0	0	0	0	0	0.663699	0	0	0	0
pseudogen	cathepsin_l	0	0	1	0	0	0	0	0	0.177515	0	0	0
lincRNA	-	0	0	0	0	6	0	0	0	0	0	0.606897	0
lincRNA	long_interg	0	0	0	0	1	0	0	0	0	0	0.085454	0
lincRNA	-	0	0	0	0	1	2	0	0	0	0	0.168487	0.298097
lincRNA	-	18	3	2	0	0	0	1.183774	0.232501	0.173325	0	0	0
pseudogen	ADP-ribosy	3	0	3	0	0	2	0.411459	0	0.542202	0	0	0.272612
processed_	-	21	16	28	12	20	24	0.595799	0.534943	1.046823	0.294527	0.63747	0.676708
antisense	-	11	14	16	10	20	7	0.924367	1.386394	1.771766	0.726967	1.888124	0.584601
lincRNA	-	0	0	0	0	2	3	0	0	0	0	0.103617	0.137493
antisense	thiosulfate_	18	8	15	36	19	29	0.99058	0.518817	1.087785	1.713888	1.17468	1.586078
antisense	-	7	8	8	15	15	9	0.181305	0.244179	0.273046	0.336098	0.436467	0.231667
pseudogen	-	2	3	6	0	7	4	0.148294	0.262133	0.586246	0	0.583097	0.294757
pseudogen	SDA1_dom	13	11	6	4	4	3	0.216835	0.216215	0.131878	0.057718	0.074954	0.04973
antisense	-	11	17	22	20	30	17	1.203204	2.191305	3.171058	1.892517	3.686524	1.848014
protein_co	chromoson	16	3	15	0	2	0	1.25676	0.27769	1.552595	0	0.176486	0
lincRNA	-	16	26	6	6	8	6	0.375302	0.718689	0.185458	0.121752	0.210814	0.139869
pseudogen	tubulin_be	0	0	0	0	1	0	0	0	0	0	0.044887	0
processed_	-	5	1	4	12	11	17	0.511013	0.12044	0.538713	1.060979	1.263002	1.726716
protein_co	oligosaccha	2067	1947	1390	1151	1233	1257	195.0607	216.5221	172.8538	93.96531	130.7198	117.8892
pseudogen	-	2	0	2	0	1	1	0.146044	0	0.19245	0	0.082036	0.072571
lincRNA	-	0	0	0	0	3	3	0	0	0	0	0.331035	0.292843
antisense	-	0	3	4	0	1	0	0	0.500436	0.746131	0	0.159027	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.022125
sense_intrc	-	0	1	4	6	0	4	0	0.155969	0.697633	0.686984	0	0.526141
antisense	-	20	15	6	76	46	60	0.780841	0.69013	0.308687	2.5669	2.01762	2.328055
antisense	-	0	0	0	0	2	1	0	0	0	0	0.299627	0.132529
pseudogen	RAB11_fam	52	21	21	12	15	11	1.56239	0.743554	0.831458	0.311911	0.506322	0.328465
processed_	-	4	3	1	7	0	1	0.115655	0.102219	0.038101	0.175091	0	0.028735
sense_intrc	-	1	0	0	0	0	0	0.045249	0	0	0	0	0
pseudogen	thymosin_b	3	2	0	1	0	0	1.203204	0.945269	0	0.346961	0	0
pseudogen	ribosomal_	0	0	0	1	0	0	0	0	0	0.074835	0	0
pseudogen	eukaryotic_	11	11	9	2	7	7	0.419259	0.494071	0.45203	0.065945	0.299735	0.265154

antisense	-	24	22	24	42	56	30	0.775692	0.83793	1.022173	1.174331	2.033365	0.963627
pseudogen	death_asso	1	0	0	1	0	0	0.103806	0	0	0.089802	0	0
antisense	-	0	0	0	0	2	3	0	0	0	0	0.147218	0.195349
pseudogen	-	6	3	2	1	0	2	0.183187	0.107937	0.080465	0.026412	0	0.060685
pseudogen	-	0	0	2	3	0	7	0	0	0.128006	0.126052	0	0.337888
pseudogen	-	4	0	0	13	6	7	0.349446	0	0	0.982485	0.58887	0.607753
pseudogen	-	4	4	3	15	6	8	0.26942	0.317495	0.266272	0.874025	0.454015	0.535512
lincRNA	-	4	12	18	2	13	0	0.386431	1.366155	2.291495	0.167149	1.410925	0
lincRNA	-	3	0	0	0	0	0	0.484216	0	0	0	0	0
lincRNA	-	19	4	14	18	14	16	1.418729	0.351976	1.377554	1.162737	1.174419	1.187341
lincRNA	-	516	462	329	2	1	0	33.68379	35.54024	28.30101	0.112944	0.073337	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.096011
lincRNA	-	0	0	0	3	5	0	0	0	0	0.166946	0.361336	0
sense_intrc	IMMP2L_in	0	1	0	0	0	0	0	0.112007	0	0	0	0
lincRNA	-	0	0	0	2	0	0	0	0	0	0.216033	0	0
antisense	KIAA1984_	14	8	9	10	11	7	0.310634	0.209179	0.263147	0.191948	0.274197	0.154358
antisense	ITPKB_anti	1	0	2	0	0	0	0.098403	0	0.259343	0	0	0
lincRNA	-	0	0	0	6	8	3	0	0	0	0.109045	0.188812	0.062636
pseudogen	-	1	0	0	0	1	0	0.132352	0	0	0	0.14869	0
pseudogen	small_nucl	0	0	1	0	0	0	0	0	0.310059	0	0	0
antisense	-	5	1	0	2	0	1	0.362114	0.085346	0	0.125305	0	0.071975
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.088427
processed_	-	0	0	0	0	3	0	0	0	0	0	0.167853	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.101322	0
pseudogen	-	1	2	0	1	0	2	0.162396	0.382747	0	0.140487	0	0.322786
antisense	-	5	3	10	0	0	0	0.601602	0.425371	1.585529	0	0	0
pseudogen	signal_pept	9	17	12	10	14	21	0.380566	0.847118	0.668658	0.365806	0.665066	0.882504
processed_	-	0	2	0	0	0	0	0	0.072334	0	0	0	0
protein_co	chromoson	328	303	198	249	188	183	8.328367	9.066418	6.625002	5.46951	5.362817	4.617924
pseudogen	phosphorib	0	0	1	2	0	0	0	0	0.060664	0.07965	0	0
antisense	MACC1_ant	0	0	0	1	0	1	0	0	0	0.071673	0	0.082338
pseudogen	ribosomal_	14	5	5	5	0	0	4.751115	1.999607	2.236003	1.467914	0	0
antisense	-	3	2	1	0	2	0	0.199777	0.15695	0.087753	0	0.149625	0
antisense	-	2	0	2	0	1	3	0.190093	0	0.250497	0	0.106779	0.283379
lincRNA	-	18	13	7	65	34	48	0.296312	0.252189	0.151848	0.925662	0.628788	0.785284
pseudogen	hexokinase	0	0	1	0	0	0	0	0	0.025489	0	0	0
antisense	-	1	0	0	2	6	4	0.067355	0	0	0.116537	0.454015	0.267756
antisense	-	2	0	1	1	5	3	0.219217	0	0.144437	0.094822	0.615693	0.326795
pseudogen	-	3	2	0	0	0	0	0.156168	0.12269	0	0	0	0
lincRNA	-	2	0	0	0	0	0	0.270798	0	0	0	0	0
lincRNA	zinc_finger_	43	38	46	77	37	46	0.981657	1.022309	1.383834	1.520705	0.948947	1.043659
processed_	-	15	8	8	163	139	131	0.393906	0.24757	0.276838	3.702987	4.10077	3.418869
antisense	-	2	2	3	0	0	0	0.130076	0.153287	0.257113	0	0	0
pseudogen	-	4	3	1	11	8	12	0.743031	0.656713	0.244783	1.767677	1.669499	2.215328

antisense	-	0	3	1	4	0	0	0	0.431252	0.160745	0.42211	0	0
antisense	HOX_transc	117	146	109	0	0	0	2.558487	3.762333	3.140933	0	0	0
lincRNA	-	12	7	3	8	1	6	1.228805	0.844708	0.404816	0.708687	0.11504	0.610608
pseudogen	FCF1_small	52	42	49	83	72	95	4.72201	4.494485	5.863466	6.520256	7.345225	8.573473
lincRNA	-	0	0	0	1	0	0	0	0	0	0.132367	0	0
processed_	-	1	0	1	0	0	0	0.076284	0	0.100523	0	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.160746	0
processed_	-	29	23	24	27	18	29	1.503711	1.405404	1.639881	1.211137	1.048547	1.494425
pseudogen	-	3	1	9	6	3	8	0.175495	0.068937	0.693778	0.303639	0.197158	0.465097
pseudogen	-	9	4	0	0	0	0	1.015925	0.532092	0	0	0	0
antisense	-	0	0	0	0	6	0	0	0	0	0	0.72238	0
pseudogen	proteasom	13	5	3	5	2	6	1.010621	0.45806	0.307327	0.336262	0.174672	0.46356
pseudogen	-	7	0	3	0	0	0	1.464771	0	0.827233	0	0	0
pseudogen	-	1	1	1	0	0	0	0.197541	0.23279	0.260311	0	0	0
protein_co	proline-rich	73	61	40	25	23	22	1.18877	1.17061	0.858361	0.352191	0.420777	0.356047
antisense	TTC3_antis	2	3	4	0	0	1	0.09652	0.170614	0.254378	0	0	0.047962
lincRNA	-	0	3	1	0	0	0	0	0.224148	0.083549	0	0	0
antisense	-	0	2	0	4	6	5	0	0.198371	0	0.291249	0.567338	0.418236
antisense	-	0	0	0	0	0	3	0	0	0	0	0	0.172883
lincRNA	-	0	5	0	2	1	5	0	0.519898	0	0.152663	0.099127	0.43845
protein_co	ADP-ribosy	7	12	5	8	7	12	0.168679	0.340761	0.158769	0.166769	0.1895	0.287378
antisense	TNKS2_anti	8	7	9	3	4	11	0.695448	0.7171	1.030984	0.22561	0.390646	0.950336
pseudogen	-	1	0	4	1	0	2	0.153452	0	0.80885	0.13275	0	0.305009
lincRNA	-	1	0	1	0	0	0	0.10401	0	0.137059	0	0	0
processed_	-	8	8	7	24	17	22	0.464395	0.547261	0.535464	1.205234	1.108652	1.269199
protein_co	dihydrofola	575	444	410	3292	2777	2829	7.771527	7.071777	7.302258	38.49119	42.1661	37.99978
lincRNA	-	0	0	1	0	0	0	0	0	0.083649	0	0	0
antisense	SRGAP3_an	2	2	2	0	1	0	0.089051	0.104942	0.117348	0	0.050022	0
protein_co	suppressor	0	3	0	1	8	4	0	0.204327	0	0.049999	0.51944	0.229756
pseudogen	-	5	1	1	0	10	0	0.53584	0.126291	0.141221	0	1.203966	0
pseudogen	-	0	0	2	0	0	2	0	0	0.169947	0	0	0.128171
pseudogen	-	0	2	0	0	0	0	0	1.434201	0	0	0	0
antisense	-	0	1	0	4	1	10	0	0.100302	0	0.294527	0.09562	0.845885
antisense	-	0	0	0	0	3	0	0	0	0	0	0.183946	0
processed_	-	1	3	5	1	3	2	0.030762	0.108753	0.202682	0.026612	0.103677	0.061144
lincRNA	-	0	6	0	4	0	0	0	0.12277	0	0.060084	0	0
antisense	-	4	6	4	12	6	7	0.10442	0.184579	0.1376	0.270999	0.175964	0.181607
pseudogen	eukaryotic_	0	0	0	0	1	0	0	0	0	0	0.033153	0
antisense	-	0	6	2	0	5	5	0	0.784751	0.292509	0	0.623437	0.55151
protein_co	Uncharacte	5	6	4	2	0	1	0.576699	0.815526	0.607959	0.19956	0	0.114628
lincRNA	-	2	0	0	0	0	0	0.142506	0	0	0	0	0
processed_	-	15	22	12	32	10	26	0.351068	0.606777	0.370097	0.647907	0.262935	0.604759
antisense	-	2	10	3	0	1	4	0.132187	0.778873	0.261286	0	0.074252	0.262742
pseudogen	mitochond	106	112	65	114	83	77	3.183066	3.963372	2.572101	2.961472	2.800057	2.297948

lincRNA	-	4	4	3	0	4	2	0.070706	0.083323	0.06988	0	0.079434	0.035135
antisense	NLGN4Y_ar	10	1	1	9	3	4	0.995131	0.11727	0.131134	0.774794	0.335391	0.395594
lincRNA	THRB_antis	0	0	0	13	7	7	0	0	0	0.489626	0.342378	0.302877
processed_	-	204	161	141	389	422	425	1.634872	1.5205	1.489044	2.696908	3.7994	3.384949
pseudogen	family_witl	0	0	1	0	0	0	0	0	0.138145	0	0	0
lincRNA	-	7	5	2	0	0	0	0.673794	0.567161	0.253685	0	0	0
antisense	-	74	28	30	46	39	32	4.185506	1.8663	2.236003	2.250801	2.478163	1.798771
antisense	-	2	1	0	2	1	0	0.246811	0.145426	0	0.213515	0.138639	0
protein_co	Uncharacte	7	4	0	0	0	1	0.551469	0.371356	0	0	0	0.078295
pseudogen	mitochond	0	0	2	0	0	0	0	0	0.62568	0	0	0
pseudogen	high_mobil	5	6	7	6	3	0	0.51499	0.728261	0.950084	0.534618	0.347136	0
antisense	-	0	0	1	2	0	1	0	0	0.063364	0.083195	0	0.047788
pseudogen	poly(A)_bin	0	1	0	2	25	3	0	0.031085	0	0.045639	0.740856	0.078646
antisense	-	1	0	0	0	2	6	0.076726	0	0	0	0.172394	0.457513
pseudogen	-	0	0	5	0	0	0	0	0	0.840521	0	0	0
pseudogen	adenylate_l	10	10	8	6	9	7	1.020058	1.202076	1.075349	0.529467	1.031374	0.709631
sense_intrc	BACH1_int	4	6	4	3	0	3	0.262734	0.464425	0.34622	0.170467	0	0.195834
pseudogen	-	1	0	6	3	6	1	0.019464	0	0.15389	0.050513	0.131197	0.019343
processed_	MIR4500_h	14	16	7	0	0	0	0.443817	0.597727	0.292421	0	0	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.142586
pseudogen	-	1	0	0	0	0	0	0.343773	0	0	0	0	0
pseudogen	-	0	4	2	2	2	0	0	0.111407	0.062289	0.040892	0.053103	0
pseudogen	-	1	0	1	0	0	0	0.204405	0	0.269356	0	0	0
protein_co	Uncharacte	2	0	0	0	0	1	0.063746	0	0	0	0	0.031676
antisense	-	0	1	3	0	7	2	0	0.092426	0.310059	0	0.616787	0.155893
antisense	-	1	3	0	4	0	1	0.095561	0.33784	0	0.330678	0	0.094971
antisense	PCDH9_ant	0	0	1	4	0	0	0	0	0.129672	0.340512	0	0
antisense	-	2	3	14	4	9	4	0.285396	0.504483	2.632577	0.493789	1.442812	0.567267
lincRNA	-	3	1	1	7	0	4	0.27478	0.107937	0.120698	0.554658	0	0.364111
lincRNA	-	0	0	0	3	0	0	0	0	0	0.038551	0	0
antisense	-	0	0	0	0	0	6	0	0	0	0	0	1.39068
pseudogen	-	0	0	0	0	6	3	0	0	0	0	0.458683	0.202882
lincRNA	-	0	1	0	0	0	0	0	0.145766	0	0	0	0
processed_	-	11	11	11	7	5	9	0.82956	0.977586	1.093157	0.456684	0.423618	0.674539
pseudogen	-	0	5	0	0	1	0	0	0.968754	0	0	0.184708	0
antisense	-	2	3	1	0	2	3	0.253306	0.447759	0.166898	0	0.284574	0.377613
lincRNA	-	24	5	14	1	0	5	4.098658	1.006254	3.1506	0.147738	0	0.848614
pseudogen	eukaryotic_	0	0	1	0	0	1	0	0	0.077861	0	0	0.058721
lincRNA	-	0	1	0	0	0	0	0	0.071382	0	0	0	0
processed_	UBAC2_ant	25	12	11	10	29	43	0.775806	0.438835	0.449822	0.268458	1.011021	1.326145
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.121877	0
pseudogen	ST6_(alpha	0	0	1	0	0	0	0	0	0.083449	0	0	0
pseudogen	RAS_p21_p	11	9	6	19	9	15	0.182384	0.17585	0.131093	0.272527	0.167643	0.247169
lincRNA	-	15	9	5	18	7	18	1.760787	1.244988	0.773429	1.827894	0.92313	2.099896

lincRNA	-	0	3	0	0	0	0	0	0.305323	0	0	0	0
pseudogen	-	6	7	6	6	1	8	0.310201	0.426479	0.408769	0.268353	0.058082	0.411047
antisense	-	0	0	0	0	3	6	0	0	0	0	0.160891	0.284657
protein_co	-	6	5	2	3	3	5	0.245286	0.240879	0.107743	0.106098	0.137782	0.203143
processed_	-	10	2	11	13	5	5	0.288507	0.067998	0.4182	0.324461	0.16206	0.143363
pseudogen	-	2	5	0	4	0	0	0.232708	0.685579	0	0.402628	0	0
processed_	-	4	0	3	3	3	0	0.326796	0	0.322978	0.212032	0.275351	0
processed_	-	7	2	3	0	0	0	0.197226	0.066405	0.111384	0	0	0
sense_intro	AKT3_intro	0	6	2	0	3	0	0	0.724036	0.269877	0	0.345121	0
pseudogen	solute_carr	0	0	1	2	0	0	0	0	0.067209	0.088245	0	0
pseudogen	UDP_glucu	0	3	0	0	0	0	0	0.219418	0	0	0	0
lincRNA	-	0	2	0	7	2	5	0	0.507217	0	1.303221	0.483544	1.069391
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.535819	0
processed_	-	2	0	1	23	37	28	0.094622	0	0.062344	0.941354	1.966585	1.316527
pseudogen	olfactory_r	9	6	2	6	10	2	0.163566	0.128502	0.047898	0.094333	0.204174	0.036124
antisense	HLA_compl	0	0	0	0	0	2	0	0	0	0	0	0.172505
sense_intro	-	1	1	0	0	0	5	0.028961	0.034129	0	0	0	0.143912
antisense	-	0	0	0	3	4	1	0	0	0	0.506999	0.877873	0.194148
pseudogen	-	1	3	0	10	1	5	0.169141	0.597965	0	1.463224	0.190019	0.84048
pseudogen	SMT3_supp	0	0	1	0	0	3	0	0	0.243928	0	0	0.551896
pseudogen	-	1	1	1	6	3	3	0.062801	0.074007	0.082756	0.325971	0.211658	0.187239
pseudogen	-	0	0	1	0	0	0	0	0	0.071699	0	0	0
antisense	-	0	3	3	0	1	2	0	0.409547	0.457965	0	0.130144	0.230258
antisense	-	47	51	34	159	81	110	5.995727	7.666926	5.715546	17.54705	11.60855	13.94589
pseudogen	-	0	1	0	5	0	4	0	0.042967	0	0.15771	0	0.144942
pseudogen	ribosomal_	0	1	1	0	0	0	0	0.070976	0.079367	0	0	0
pseudogen	MT-ND1_ps	0	2	4	6	0	5	0	0.132177	0.295607	0.291095	0	0.278676
pseudogen	-	1	0	0	0	1	6	0.120595	0	0	0	0.13548	0.719099
pseudogen	-	234	244	197	629	312	484	4.809081	5.909397	5.335158	11.18304	7.203605	9.885559
pseudogen	actin_beta_	0	2	0	6	0	0	0	0.114578	0	0.252336	0	0
pseudogen	exosome_c	8	2	1	0	0	0	0.847056	0.249551	0.139527	0	0	0
pseudogen	-	1	0	0	0	1	4	0.06472	0	0	0	0.072709	0.257281
pseudogen	ribosomal_	2	0	0	0	2	0	0.304259	0	0	0	0.341816	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.129911
pseudogen	-	0	0	0	1	0	0	0	0	0	0.064415	0	0
antisense	-	0	0	0	2	0	1	0	0	0	0.038198	0	0.021941
pseudogen	-	4	5	2	1	5	3	0.158863	0.234012	0.104671	0.034358	0.22309	0.118411
pseudogen	aldo-keto_r	12	1	1	17	18	9	0.694308	0.068183	0.076244	0.850909	1.170018	0.517515
processed_	-	1	0	3	1	0	0	0.012884	0	0.050934	0.011146	0	0
pseudogen	-	0	0	4	0	2	0	0	0	0.451542	0	0.192479	0
pseudogen	-	0	0	0	3	1	0	0	0	0	0.220187	0.095314	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.153842
processed_	-	4	1	0	1	4	3	0.248258	0.073139	0	0.053692	0.278902	0.185044
antisense	-	23	26	18	10	15	20	0.585687	0.780222	0.604011	0.220293	0.429119	0.506148

antisense	-	14	8	6	67	33	70	0.529032	0.356247	0.298772	2.19024	1.400932	2.628825
antisense	-	7	1	1	0	0	1	0.844162	0.142113	0.158914	0	0	0.11985
pseudogen	high_mobil	0	0	1	0	5	5	0	0	0.225043	0	0.959289	0.848614
pseudogen	deoxyuridi	0	0	0	1	1	0	0	0	0	0.097444	0.126545	0
pseudogen	-	0	3	0	1	0	3	0	0.054999	0	0.013458	0	0.046383
pseudogen	-	1	0	0	3	0	1	0.309596	0	0	0.80349	0	0.307685
processed_	-	4	1	1	9	7	6	0.149868	0.044153	0.049372	0.291713	0.294644	0.223414
pseudogen	-	1	0	0	0	5	3	0.072127	0	0	0	0.405149	0.215044
antisense	-	0	5	0	0	2	2	0	0.589676	0	0	0.224862	0.198919
pseudogen	-	0	0	0	1	0	0	0	0	0	0.303304	0	0
antisense	-	1	2	0	2	2	0	0.032619	0.07688	0	0.056437	0.073291	0
pseudogen	olfactory_r	0	0	1	0	3	0	0	0	0.069347	0	0.177364	0
pseudogen	-	3	0	1	0	0	0	0.456388	0	0.200469	0	0	0
pseudogen	calmodulin	19	22	30	11	30	19	2.286088	3.119386	4.756587	1.144973	4.055176	2.27197
antisense	-	3	1	1	0	1	0	0.090446	0.035528	0.039729	0	0.03387	0
pseudogen	abhydrolas	0	0	2	0	0	0	0	0	0.153495	0	0	0
lincRNA	-	2	2	0	0	0	0	0.151911	0.179018	0	0	0	0
antisense	-	0	0	0	0	1	1	0	0	0	0	0.133955	0.1185
pseudogen	-	2	0	0	0	2	0	0.104626	0	0	0	0.117541	0
antisense	MED4_anti	2	1	4	8	0	0	0.195354	0.115107	0.514858	0.675999	0	0
pseudogen	-	0	1	0	3	0	1	0	0.253609	0	0.558523	0	0.213878
antisense	-	0	0	0	4	0	2	0	0	0	0.200214	0	0.115003
protein_co	ribosomal_	13227	11259	8352	12347	8591	14320	1001.789	1004.898	833.5664	808.983	730.9837	1077.873
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.096395	0
pseudogen	-	21	26	23	58	25	32	3.768681	5.49858	5.439171	9.004531	5.040332	5.707287
pseudogen	-	0	0	0	0	5	0	0	0	0	0	0.898428	0
sense_intrc	AGBL5_intr	3	33	23	5	25	22	0.468504	6.073142	4.733202	0.6755	4.38613	3.414481
antisense	VIM_antise	34	20	28	43	35	56	1.332342	0.923579	1.445871	1.4577	1.540827	2.180893
antisense	-	16	24	3	17	21	16	0.385201	0.680903	0.095175	0.354062	0.567983	0.382822
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.112906
pseudogen	eukaryotic_	8	8	7	20	19	18	0.348296	0.410446	0.401598	0.753271	0.929311	0.778826
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.077602
lincRNA	coiled-coil_	1	0	1	0	0	0	0.030762	0	0.040536	0	0	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.116661
sense_intrc	ANKRD10_i	81	86	121	83	120	78	11.28479	14.11933	22.2141	10.00345	18.78187	10.79973
processed_	EPHA1_ant	1	3	1	2	11	11	0.01055	0.037298	0.013903	0.018254	0.130378	0.115336
antisense	KCNQ5_ant	0	0	1	0	0	0	0	0	0.063364	0	0	0
lincRNA	-	0	0	0	1	0	2	0	0	0	0.130481	0	0.299795
pseudogen	t-complex_	2	0	0	0	1	0	0.065765	0	0	0	0.036942	0
antisense	-	0	0	0	1	0	2	0	0	0	0.055852	0	0.128327
pseudogen	nucleosom	3	0	2	1	3	0	0.145843	0	0.128124	0.042056	0.163846	0
TR_C_gene	T_cell_rece	12	6	6	32	23	23	0.65225	0.384319	0.429753	1.504687	1.404462	1.242426
antisense	-	0	0	0	4	4	8	0	0	0	0.309976	0.402544	0.712204
pseudogen	ribosomal_	0	0	0	0	4	0	0	0	0	0	0.402544	0

pseudogen	-	1	0	0	0	1	2	0.073022	0	0	0	0.082036	0.145142
lincRNA	-	0	0	0	1	0	0	0	0	0	0.140058	0	0
processed_	-	0	0	0	1	0	0	0	0	0	0.027196	0	0
lincRNA	-	97	98	77	166	108	202	0.978334	1.164793	1.02339	1.448394	1.223738	2.024774
pseudogen	-	0	0	3	0	0	0	0	0	0.431525	0	0	0
pseudogen	ADAM_met	109	78	59	139	149	109	2.212641	1.865891	1.578234	2.440969	3.397972	2.198977
antisense	-	2	0	1	0	6	2	0.190093	0	0.125248	0	0.640674	0.188919
processed_	-	6	0	0	21	3	21	0.09086	0	0	0.275108	0.051038	0.316045
lincRNA	-	0	0	2	0	0	0	0	0	0.375071	0	0	0
antisense	-	6	1	1	1	0	2	0.743902	0.146107	0.16338	0.107257	0	0.246436
pseudogen	-	0	0	0	1	0	0	0	0	0	0.223409	0	0
pseudogen	prostaglan	0	1	0	0	0	0	0	0.129167	0	0	0	0
sense_intrc	-	2	1	2	1	4	3	0.244531	0.144083	0.322232	0.105771	0.549431	0.364532
pseudogen	serpin_pep	3	2	1	3	0	2	0.12716	0.0999	0.055855	0.110005	0	0.08425
pseudogen	-	97	79	74	66	131	153	2.033773	1.951933	2.044548	1.19712	3.085681	3.188099
lincRNA	long_interg	13	15	5	10	0	3	0.284629	0.387021	0.144258	0.189408	0	0.065278
pseudogen	-	0	0	0	1	0	0	0	0	0	0.145393	0	0
pseudogen	-	0	0	1	5	1	1	0	0	0.074693	0.245176	0.063679	0.056332
pseudogen	keratin_18	4	1	1	7	5	3	0.164413	0.048438	0.054164	0.248907	0.230885	0.122548
lincRNA	-	0	1	0	0	0	0	0	0.070177	0	0	0	0
antisense	long_interg	0	2	0	0	0	0	0	0.209004	0	0	0	0
antisense	-	0	0	0	0	2	0	0	0	0	0	0.206156	0
lincRNA	-	0	0	0	5	6	5	0	0	0	0.53008	0.826054	0.608959
pseudogen	-	1	2	2	0	0	4	0.217864	0.513479	0.574183	0	0	0.866075
lincRNA	testis-speci	11	10	12	0	1	7	0.357709	0.383217	0.514226	0	0.036533	0.226227
pseudogen	high_mobil	0	0	0	0	1	0	0	0	0	0	0.19629	0
pseudogen	protein_ph	0	0	0	1	3	0	0	0	0	0.027408	0.106779	0
protein_co	long_interg	0	5	3	0	1	0	0	0.213657	0.143349	0	0.040737	0
lincRNA	-	0	0	0	8	7	2	0	0	0	0.12933	0.146958	0.037144
pseudogen	WW_doma	0	1	0	0	1	0	0	0.080918	0	0	0.077141	0
pseudogen	heterogene	0	0	0	0	0	1	0	0	0	0	0	0.054636
antisense	-	0	0	0	0	0	3	0	0	0	0	0	0.163229
pseudogen	suppressior	0	0	1	1	0	0	0	0	0.063886	0.04194	0	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.030769	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.14869	0
antisense	-	1	3	4	0	0	0	0.096784	0.342163	0.510152	0	0	0
processed_	-	0	2	0	0	1	0	0	0.276052	0	0	0.131584	0
antisense	-	0	0	0	0	0	8	0	0	0	0	0	1.838045
pseudogen	-	40	30	34	84	73	93	4.623668	4.086532	5.178934	8.399799	9.479786	10.68364
sense_intrc	REV3L_intr	0	0	7	0	0	0	0	0	1.278385	0	0	0
antisense	-	1	0	4	3	0	3	0.174723	0	0.920967	0.453455	0	0.520931
pseudogen	fatty_acid_	0	0	0	0	5	0	0	0	0	0	1.739062	0
lincRNA	-	7	4	6	0	0	0	1.950458	1.313426	2.203051	0	0	0
processed_	-	0	0	0	0	2	1	0	0	0	0	0.232328	0.102762

pseudogen	tubulin_be	2	3	2	1	5	3	0.145642	0.257446	0.191921	0.062997	0.40905	0.217114
antisense	-	0	0	3	0	0	0	0	0	0.473506	0	0	0
protein_co	orosomucc	1	1	0	0	0	1	0.053154	0.062638	0	0	0	0.052825
lincRNA	-	0	0	0	2	0	0	0	0	0	0.111569	0	0
pseudogen	keratin_8_p	70	73	55	121	103	125	2.652734	3.26006	2.746586	3.966834	4.385125	4.707771
lincRNA	-	1	1	0	3	2	1	0.081952	0.096575	0	0.212688	0.184136	0.081446
lincRNA	-	0	5	8	2	0	0	0	0.426729	0.763483	0.125305	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.140304
sense_intrc	ACAP2_intr	8	6	6	16	3	9	0.613809	0.542502	0.606637	1.062004	0.258591	0.68627
pseudogen	-	1	0	0	0	0	0	0.097677	0	0	0	0	0
antisense	-	2	0	0	0	0	0	0.399555	0	0	0	0	0
sense_intrc	-	1	2	2	0	1	5	0.109382	0.257801	0.288278	0	0.122884	0.543534
sense_intrc	GK_introni	0	0	0	0	0	2	0	0	0	0	0	0.265058
antisense	-	7	10	11	7	3	7	0.381262	0.641849	0.789502	0.329828	0.183568	0.378908
antisense	-	0	0	2	10	11	3	0	0	0.314249	1.031507	1.473502	0.3555
pseudogen	-	1	5	0	0	0	0	0.102998	0.606885	0	0	0	0
pseudogen	-	28	9	17	48	16	27	2.173531	0.823298	1.738967	3.223383	1.395329	2.082961
antisense	HYI_antiser	7	2	0	0	1	0	0.679976	0.228946	0	0	0.10913	0
antisense	LRRC3_anti	1	1	0	0	0	3	0.067527	0.079576	0	0	0	0.201329
pseudogen	-	16	17	12	32	26	33	0.491332	0.615192	0.485591	0.850096	0.896969	1.007113
processed_	-	0	0	0	0	1	3	0	0	0	0	0.112858	0.299511
pseudogen	-	1	0	0	1	4	0	0.089883	0	0	0.077757	0.403911	0
lincRNA	-	2	0	0	0	0	0	0.232708	0	0	0	0	0
lincRNA	long_interg	0	0	2	0	0	0	0	0	0.086824	0	0	0
pseudogen	capicua_tra	6	1	5	5	1	12	0.129387	0.025413	0.142084	0.093277	0.024226	0.257177
antisense	-	0	0	2	0	5	0	0	0	0.243928	0	0.519894	0
antisense	-	0	0	0	1	0	0	0	0	0	0.068459	0	0
pseudogen	olfactory_r	0	0	0	0	1	0	0	0	0	0	0.064298	0
lincRNA	-	4	0	11	2	5	2	0.307796	0	1.115401	0.133136	0.432238	0.152948
pseudogen	MHC_class_	1	0	1	0	3	0	0.065118	0	0.08581	0	0.219468	0
pseudogen	major_hist	0	0	0	0	0	1	0	0	0	0	0	0.042602
antisense	-	0	0	0	0	0	3	0	0	0	0	0	0.307086
pseudogen	-	0	2	0	0	1	0	0	0.280394	0	0	0.133654	0
lincRNA	-	0	0	0	5	4	2	0	0	0	0.349077	0.362658	0.160409
lincRNA	long_interg	7	5	6	11	8	10	0.138021	0.116178	0.155896	0.187631	0.177209	0.195955
pseudogen	OFD1_pseu	0	0	0	0	1	0	0	0	0	0	0.050446	0
antisense	-	0	0	0	6	0	0	0	0	0	0.505135	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.430638	0	0	0
pseudogen	-	1	3	3	2	0	3	0.215207	0.760826	0.850772	0.372349	0	0.641635
pseudogen	nucleophos	0	0	0	1	0	0	0	0	0	0.053629	0	0
pseudogen	Ral_GTPase	9	7	19	19	6	5	0.076455	0.070076	0.212693	0.139631	0.057262	0.042213
pseudogen	-	4	0	0	0	0	0	0.624672	0	0	0	0	0
pseudogen	-	3	3	3	0	0	0	0.254117	0.299461	0.334864	0	0	0
lincRNA	-	0	1	0	0	0	0	0	0.106282	0	0	0	0

lincRNA	-	0	0	0	4	7	1	0	0	0	0.183196	0.416331	0.052614
pseudogen	ankyrin_rep	0	0	0	0	0	1	0	0	0	0	0	0.055383
antisense	-	13	15	10	5	5	15	0.941495	1.280186	0.954354	0.313262	0.406812	1.079632
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.022955	0
pseudogen	phosphatid	0	0	0	0	0	1	0	0	0	0	0	0.046977
pseudogen	-	0	0	2	0	0	1	0	0	0.547163	0	0	0.20633
lincRNA	-	0	0	0	0	1	1	0	0	0	0	0.110963	0.098161
antisense	-	1	6	0	0	0	2	0.112881	0.798137	0	0	0	0.224367
pseudogen	-	5	2	2	9	6	29	0.605732	0.285527	0.319283	0.943227	0.816603	3.49155
protein_co	serine_pept	0	0	0	0	3	1	0	0	0	0	0.405518	0.119577
pseudogen	ribosomal_	2	2	3	1	9	1	0.213903	0.252072	0.422808	0.092523	1.08138	0.106291
pseudogen	ring_finger_	0	0	0	4	2	4	0	0	0	0.109045	0.070805	0.125272
antisense	LYST_antise	2	4	3	0	0	1	0.203228	0.478984	0.401708	0	0	0.100987
pseudogen	-	0	3	0	0	0	0	0	1.207504	0	0	0	0
antisense	-	3	2	7	4	8	10	0.690535	0.542502	2.12323	0.796503	2.068728	2.287567
pseudogen	regulator_c	2	1	1	2	3	3	0.191468	0.112817	0.126154	0.165638	0.322654	0.285429
protein_co	protein_ass	2	0	0	2	1	0	0.05042	0	0	0.043618	0.028322	0
lincRNA	-	0	0	0	0	0	3	0	0	0	0	0	0.060546
antisense	ALG13_ant	10	5	4	3	3	4	2.714923	1.599685	1.431042	0.704599	0.915014	1.079263
pseudogen	ATP_synthe	3	0	0	0	1	0	0.119506	0	0	0	0.044752	0
antisense	-	1	1	0	2	0	2	0.071931	0.084766	0	0.124454	0	0.142973
pseudogen	-	0	0	0	4	0	2	0	0	0	0.161834	0	0.092958
pseudogen	-	0	2	0	1	0	0	0	0.402501	0	0.147738	0	0
antisense	-	2	0	1	0	0	0	0.061883	0	0.040773	0	0	0
antisense	-	0	0	6	0	1	0	0	0	0.563364	0	0.080048	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.096014	0	0
pseudogen	-	0	0	0	3	0	0	0	0	0	0.18668	0	0
pseudogen	-	0	4	0	0	4	1	0	2.228133	0	0	2.12414	0.469768
sense_intro	-	5	6	4	2	3	13	1.050417	1.485422	1.107354	0.363483	0.708047	2.714217
pseudogen	ubiquitin-c	2	0	3	0	3	0	0.253914	0	0.501894	0	0.427884	0
pseudogen	-	15	4	2	13	13	8	1.980336	0.622321	0.347947	1.484753	1.928147	1.049657
sense_intro	MYCBP2_ar	2	2	0	0	1	1	0.247388	0.291531	0	0	0.138962	0.12293
pseudogen	-	3	0	1	3	0	4	0.818675	0	0.359605	0.70823	0	1.084826
processed_	-	6	5	3	0	1	0	0.198777	0.195206	0.13097	0	0.037219	0
antisense	-	0	2	0	0	0	0	0	0.186232	0	0	0	0
processed_	-	0	0	0	0	1	0	0	0	0	0	0.038975	0
pseudogen	-	1	1	4	0	0	0	0.055963	0.065949	0.294982	0	0	0
lincRNA	-	1	1	0	1	2	0	0.094034	0.110813	0	0.081348	0.211282	0
antisense	-	5	2	3	2	5	10	0.600238	0.282938	0.47458	0.207705	0.67433	1.193062
pseudogen	SSU72_RNA	0	0	0	0	1	0	0	0	0	0	0.102017	0
lincRNA	-	0	0	0	0	0	4	0	0	0	0	0	0.404723
protein_co	NK1_home	0	0	0	3	2	7	0	0	0	0.08696	0.075286	0.2331
lincRNA	-	4	0	0	0	0	0	0.932881	0	0	0	0	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.025766

lincRNA	long_interg	0	0	0	13	4	26	0	0	0	1.283159	0.512723	2.948201
lincRNA	SACS_antis	0	7	5	0	1	4	0	0.213657	0.170654	0	0.029098	0.102963
pseudogen	-	0	0	0	1	0	0	0	0	0	0.030512	0	0
processed_	-	8	0	3	0	2	2	0.191295	0	0.09453	0	0.053727	0.047529
pseudogen	-	1	0	1	10	0	0	0.31326	0	0.4128	2.709994	0	0
lincRNA	-	1	0	0	0	0	0	0.026234	0	0	0	0	0
pseudogen	ribosomal_	4	3	9	0	0	3	0.448652	0.396532	1.330232	0	0	0.334411
sense_intrc	-	0	6	4	4	4	9	0	0.558696	0.416497	0.273426	0.35508	0.706756
processed_	ACVR2B_an	4	2	5	12	4	16	0.084133	0.049573	0.138584	0.21835	0.094519	0.334456
pseudogen	msh_home	0	0	0	2	3	0	0	0	0	0.118497	0.230825	0
antisense	-	1	7	7	5	8	5	0.078664	0.648907	0.725621	0.340259	0.706995	0.390892
pseudogen	succinate-C	0	0	0	0	1	3	0	0	0	0	0.043829	0.116317
pseudogen	peroxiredo	3	11	2	0	3	2	0.208156	0.89943	0.182866	0	0.23385	0.137914
pseudogen	-	0	0	4	0	1	2	0	0	1.102977	0	0.235083	0.415921
pseudogen	-	0	2	0	1	0	3	0	0.253609	0	0.093087	0	0.320817
pseudogen	golgin_A2_	3	0	1	1	0	1	0.204405	0	0.089785	0.058943	0	0.067714
lincRNA	-	0	0	1	0	1	0	0	0	0.165316	0	0.140938	0
lincRNA	-	0	0	1	0	3	0	0	0	0.121327	0	0.310309	0
pseudogen	MT-ND5_ps	2	3	1	1	0	0	0.092716	0.163891	0.061089	0.040104	0	0
pseudogen	methyltran	1	5	1	0	3	0	0.083372	0.491242	0.109863	0	0.280989	0
lincRNA	-	0	0	1	0	0	0	0	0	0.150352	0	0	0
lincRNA	-	0	3	3	0	0	0	0	0.351811	0.393402	0	0	0
pseudogen	-	0	0	0	0	0	5	0	0	0	0	0	2.769161
pseudogen	-	1	0	1	3	4	0	0.1034	0	0.136256	0.268353	0.464656	0
antisense	HOXB_clust	73	60	48	11	5	11	3.028756	2.933592	2.624324	0.394818	0.233056	0.453569
pseudogen	ribosomal_	43	39	14	47	30	31	1.772946	1.894954	0.760659	1.67644	1.389624	1.270277
protein_co	nicotinami	9	5	6	5	9	4	0.189526	0.124081	0.166499	0.091088	0.212921	0.083714
lincRNA	long_interg	349	287	189	71	27	34	6.547274	6.34489	4.672311	1.152276	0.569047	0.633904
lincRNA	-	1	0	6	0	0	0	0.054354	0	0.429753	0	0	0
pseudogen	-	0	1	0	0	0	0	0	0.073311	0	0	0	0
lincRNA	-	0	0	0	1	1	0	0	0	0	0.109305	0.141947	0
lincRNA	-	15	19	21	7	5	3	0.757743	1.131075	1.397928	0.305909	0.283759	0.150613
pseudogen	-	0	0	0	1	0	3	0	0	0	0.081493	0	0.280858
pseudogen	-	14	5	7	10	3	1	1.692178	0.712189	1.114938	1.045637	0.407369	0.120123
antisense	MAST4_ant	1	0	1	2	5	5	0.068135	0	0.089785	0.117887	0.382728	0.338572
pseudogen	ubiquitin-c	0	0	0	0	0	1	0	0	0	0	0	0.142973
pseudogen	plakophilin	0	0	0	0	4	2	0	0	0	0	0.110243	0.048762
antisense	-	0	0	0	0	0	5	0	0	0	0	0	0.346601
pseudogen	-	1	2	0	0	0	0	0.118436	0.27914	0	0	0	0
pseudogen	-	1	0	0	1	0	0	0.096082	0	0	0.08312	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.19325	0	0	0
pseudogen	asparagine_	0	0	0	3	0	0	0	0	0	0.898018	0	0
antisense	-	2	7	3	6	1	0	0.047017	0.193923	0.092935	0.122022	0.02641	0
protein_co	-	1	0	0	0	0	0	0.014951	0	0	0	0	0

antisense	-	0	0	0	1	1	7	0	0	0	0.152156	0.197594	1.223583
sense_intrc	SOS1_intro	21	20	19	44	31	30	0.933468	1.047653	1.112932	1.691983	1.548072	1.325291
lincRNA	-	0	1	0	0	0	0	0	0.111208	0	0	0	0
pseudogen	-	0	3	0	0	0	0	0	0.161626	0	0	0	0
pseudogen	lysyl-tRNA_	0	0	1	0	0	1	0	0	0.039819	0	0	0.030031
pseudogen	-	0	0	0	1	0	6	0	0	0	0.094236	0	0.649556
processed_	-	0	0	1	0	0	0	0	0	0.042384	0	0	0
pseudogen	eukaryotic_	2	3	0	0	0	0	0.032252	0.05701	0	0	0	0
antisense	-	0	1	0	0	0	0	0	0.031912	0	0	0	0
lincRNA	-	0	1	0	0	0	0	0	0.03503	0	0	0	0
lincRNA	-	0	0	1	0	0	0	0	0	0.074693	0	0	0
antisense	-	0	0	0	0	0	6	0	0	0	0	0	0.614172
pseudogen	-	1	0	0	0	0	0	0.087506	0	0	0	0	0
processed_	-	3	0	2	0	0	0	0.070494	0	0.061929	0	0	0
antisense	-	13	3	5	25	9	15	1.433819	0.389923	0.726701	2.38536	1.115173	1.644189
protein_co	Uncharacte	48	68	87	22	67	47	1.845438	3.080876	4.407702	0.731718	2.89389	1.795832
antisense	-	5	2	1	4	2	0	0.843009	0.397374	0.222176	0.583426	0.378827	0
pseudogen	-	2	1	3	7	3	0	0.22338	0.13162	0.44154	0.676355	0.37643	0
antisense	-	1	1	0	0	0	0	0.017061	0.020106	0	0	0	0
antisense	-	6	2	1	0	3	2	0.639127	0.251057	0.140369	0	0.35901	0.211727
antisense	-	1	0	3	0	1	4	0.092879	0	0.367175	0	0.104344	0.369221
pseudogen	ribosomal_	0	0	0	2	1	5	0	0	0	0.254438	0.165211	0.730751
pseudogen	-	0	0	0	3	0	0	0	0	0	0.174583	0	0
pseudogen	dynein_ligh	0	0	0	7	2	0	0	0	0	1.086754	0.403227	0
pseudogen	mitochond	0	1	1	1	0	0	0	0.105921	0.118444	0.077757	0	0
processed_	-	1	0	1	1	0	1	0.027445	0	0.036166	0.023742	0	0.027275
lincRNA	-	1	5	1	0	0	0	0.193923	1.142632	0.255543	0	0	0
lincRNA	-	1	14	3	0	0	0	0.11264	1.858358	0.445298	0	0	0
lincRNA	-	1	0	0	0	0	0	0.17301	0	0	0	0	0
antisense	UBE2Q1_ar	5	3	5	0	0	5	0.612743	0.433248	0.807445	0	0	0.608959
antisense	-	0	0	0	3	0	2	0	0	0	0.371342	0	0.2844
pseudogen	small_nucl	0	0	0	1	0	0	0	0	0	0.182466	0	0
pseudogen	-	24	16	18	29	37	5	2.989609	2.348715	2.95468	3.125102	5.177903	0.618989
pseudogen	-	0	3	0	0	0	1	0	0.17266	0	0	0	0.048537
pseudogen	-	0	0	2	0	0	2	0	0	0.564885	0	0	0.426025
pseudogen	-	1	0	0	0	1	0	0.041328	0	0	0	0.046429	0
pseudogen	ATPase_am	3	1	1	0	0	1	0.10129	0.039788	0.044492	0	0	0.033555
pseudogen	ribosomal_	0	0	0	3	0	0	0	0	0	0.318048	0	0
lincRNA	X_inactive_	0	0	5	0	0	3	0	0	0.018097	0	0	0.008189
pseudogen	-	2	3	0	4	11	1	0.077626	0.137216	0	0.134308	0.479644	0.038573
protein_co	zinc_finger_	155	143	97	126	103	135	3.274483	3.560034	2.700335	2.302738	2.444541	2.834356
pseudogen	cyclin_B1_i	0	0	0	0	0	1	0	0	0	0	0	0.06271
pseudogen	DEAD/H_(A	16	5	4	6	4	7	0.35294	0.129974	0.116272	0.114497	0.099127	0.153458
antisense	-	0	0	2	0	3	2	0	0	0.288278	0	0.368652	0.217413

pseudogen	-	4	3	1	2	2	2	0.537472	0.475033	0.177064	0.232482	0.301908	0.267076
pseudogen	-	0	0	0	1	1	3	0	0	0	0.118343	0.153685	0.407861
antisense	-	0	0	2	2	0	0	0	0	0.281304	0.184673	0	0
protein_co	PET100_ho	9	19	12	19	9	28	0.262517	0.653095	0.461245	0.479438	0.294922	0.811677
pseudogen	-	0	0	1	0	0	0	0	0	0.189574	0	0	0
antisense	-	5	7	9	5	8	9	0.157188	0.259331	0.372844	0.135982	0.282546	0.281191
antisense	-	10	14	9	5	4	3	0.269694	0.444946	0.319852	0.116655	0.121194	0.080409
antisense	EMX2_opp	0	0	0	7	20	10	0	0	0	0.166628	0.618253	0.273462
antisense	-	14	24	21	14	16	22	0.946582	1.912268	1.871046	0.818882	1.215344	1.4783
processed_	-	57	23	26	57	49	42	0.897572	0.426805	0.539514	0.776484	0.866841	0.657284
pseudogen	-	4	2	3	1	0	0	0.246237	0.145088	0.24336	0.053255	0	0
antisense	-	1	5	0	0	0	0	0.079971	0.471206	0	0	0	0
lincRNA	-	1	1	4	0	0	0	0.064484	0.07599	0.339894	0	0	0
pseudogen	-	0	3	0	0	0	0	0	0.531714	0	0	0	0
antisense	-	0	1	1	3	0	0	0	0.106464	0.11905	0.234465	0	0
pseudogen	-	0	1	0	0	0	1	0	0.107195	0	0	0	0.090402
antisense	STEAP3_an	24	1	5	4	22	11	0.394836	0.019387	0.108395	0.056928	0.40661	0.179849
antisense	-	0	0	0	7	2	3	0	0	0	0.787696	0.292265	0.387819
pseudogen	-	0	1	1	0	1	1	0	0.133593	0.149386	0	0.127357	0.112664
pseudogen	-	0	0	0	1	0	0	0	0	0	0.051459	0	0
antisense	OGFR_antis	5	7	5	0	4	9	0.396265	0.653764	0.52218	0	0.356143	0.708872
antisense	-	41	46	42	20	67	55	2.863563	3.786063	3.865512	1.208414	5.257106	3.817642
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.308587
pseudogen	-	0	1	0	0	0	0	0	0.318305	0	0	0	0
pseudogen	heterogene	0	0	1	0	0	0	0	0	0.072444	0	0	0
lincRNA	-	15	28	11	9	15	22	0.695372	1.529647	0.671976	0.360937	0.781207	1.013581
antisense	-	0	3	0	0	3	1	0	0.217885	0	0	0.207716	0.06125
pseudogen	glycerol_ki	0	3	2	0	1	1	0	0.083854	0.062512	0	0.026647	0.023573
antisense	-	0	0	0	2	3	0	0	0	0	0.232482	0.452862	0
antisense	-	0	0	1	0	2	0	0	0	0.15299	0	0.260859	0
lincRNA	-	2	0	0	0	0	0	0.17647	0	0	0	0	0
antisense	-	4	8	4	3	1	0	0.468504	1.104208	0.617374	0.303975	0.131584	0
pseudogen	-	3	5	1	0	0	0	0.214626	0.421539	0.094275	0	0	0
pseudogen	-	2	0	2	1	0	2	0.079372	0	0.104593	0.034332	0	0.078882
lincRNA	KIF25_anti	0	0	0	10	5	4	0	0	0	0.16386	0.106397	0.075297
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.098344
pseudogen	Ras-homol	0	0	0	2	1	5	0	0	0	0.129375	0.084006	0.371568
pseudogen	-	1	7	7	0	3	0	0.215207	1.775261	1.985134	0	0.725316	0
antisense	-	27	12	14	16	20	26	2.251034	1.178981	1.538088	1.153988	1.873257	2.154276
pseudogen	tyrosine_3-	3	0	3	5	3	3	0.215207	0	0.283591	0.310291	0.241772	0.213878
pseudogen	-	3	0	1	2	0	1	0.55339	0	0.243078	0.319156	0	0.183324
pseudogen	-	9	8	2	19	9	25	0.358517	0.375547	0.104986	0.654762	0.402771	0.98973
pseudogen	-	4	0	0	0	0	0	1.73577	0	0	0	0	0
pseudogen	-	1	0	1	0	1	1	0.054298	0	0.071552	0	0.061001	0.053963

antisense	-	0	0	1	33	36	29	0	0	0.044294	0.959596	1.35945	0.968767
antisense	-	29	15	35	5	5	12	0.511592	0.311835	0.813634	0.076306	0.099093	0.210386
antisense	-	0	1	0	1	0	1	0	0.082306	0	0.060421	0	0.069412
pseudogen	MT-ND2_ps	0	0	1	0	2	1	0	0	0.073824	0	0.125875	0.055676
processed_	-	3	1	3	0	4	0	0.293573	0.115319	0.386857	0	0.439748	0
processed_	ZRANB2_an	6	3	7	7	6	13	0.357709	0.210769	0.549936	0.361027	0.401864	0.770251
lincRNA	-	0	0	0	6	1	1	0	0	0	0.262709	0.05686	0.0503
processed_	-	6	2	2	14	13	10	0.171423	0.067337	0.075298	0.346025	0.417262	0.28394
processed_	TOB1_antis	3	5	5	2	0	4	0.11756	0.230895	0.258191	0.0678	0	0.155778
lincRNA	-	0	0	0	1	1	3	0	0	0	0.089802	0.116619	0.309494
lincRNA	-	11	5	12	0	9	8	0.252318	0.135155	0.362721	0	0.231925	0.182371
antisense	-	3	0	2	0	1	1	0.501019	0	0.440147	0	0.187621	0.165975
pseudogen	high_mobil	4	3	4	2	3	0	0.363232	0.321035	0.47865	0.157115	0.306051	0
pseudogen	-	7	4	13	19	12	14	0.41827	0.28166	1.023615	0.982144	0.805543	0.831373
antisense	-	12	12	8	0	0	2	1.484327	1.749189	1.303987	0	0	0.24586
antisense	-	1	15	0	0	0	0	0.122549	2.166241	0	0	0	0
sense_intrc	-	11	11	17	0	0	0	0.917088	1.080732	1.867678	0	0	0
sense_intrc	ALMS1_int	1	0	4	9	16	11	0.025126	0	0.132441	0.195629	0.451644	0.274682
antisense	SNAP47_an	0	1	0	0	2	8	0	0.036527	0	0	0.069644	0.246436
pseudogen	ankyrin_re	0	0	0	5	0	0	0	0	0	0.042446	0	0
lincRNA	-	3	1	1	0	0	0	0.063784	0.025055	0.028017	0	0	0
lincRNA	-	1	1	0	1	0	0	0.070588	0.083184	0	0.061065	0	0
pseudogen	farnesyltra	0	2	5	0	0	0	0	0.196807	0.550184	0	0	0
lincRNA	-	0	0	1	0	0	0	0	0	0.03773	0	0	0
lincRNA	-	192	177	148	0	4	0	22.53807	24.48476	22.89349	0	0.527503	0
pseudogen	-	1	0	0	0	1	1	0.038142	0	0	0	0.04285	0.037906
protein_co	Homo_sapi	0	0	0	1	0	0	0	0	0	0.026846	0	0
pseudogen	-	0	0	2	0	1	2	0	0	0.715521	0	0.305005	0.539631
lincRNA	long_interg	0	0	0	0	2	0	0	0	0	0	0.194684	0
pseudogen	adenylate_	1	5	5	7	9	5	0.07973	0.469787	0.525326	0.48282	0.806149	0.39619
antisense	BIRC6_anti	0	0	0	0	2	0	0	0	0	0	0.170663	0
pseudogen	-	0	0	1	0	0	0	0	0	0.217331	0	0	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.285946
protein_co	CDGSH_iro	191	161	126	350	228	416	4.347261	4.318325	3.779094	6.891495	5.82997	9.409908
lincRNA	-	0	0	0	0	4	1	0	0	0	0	0.535819	0.1185
sense_intrc	-	0	1	0	0	1	1	0	0.095981	0	0	0.091501	0.080945
antisense	-	4	3	0	0	1	0	0.566214	0.500436	0	0	0.159027	0
pseudogen	heat_shock	0	0	0	2	6	5	0	0	0	0.054425	0.212035	0.15631
sense_intrc	CDC42_int	0	3	4	9	12	2	0	0.270467	0.403256	0.595651	1.031374	0.152064
pseudogen	leucine_ric	3	1	2	11	8	14	0.117213	0.046043	0.102972	0.371799	0.351149	0.543614
pseudogen	ribosomal_	8	9	7	7	7	13	0.324791	0.43059	0.374496	0.245853	0.319273	0.524527
antisense	-	54	42	23	55	38	39	4.298968	3.940278	2.412865	3.787879	3.398624	3.085636
pseudogen	-	0	2	1	1	0	3	0	0.392376	0.219381	0.144022	0	0.496359
pseudogen	methylthio	1	5	4	1	4	0	0.063631	0.374926	0.3354	0.055047	0.285942	0

pseudogen	-	0	0	0	0	3	0	0	0	0	0	0.845629	0
antisense	PRRT3_anti	19	8	15	7	1	3	1.638239	0.812869	1.704315	0.522137	0.096866	0.257072
antisense	-	7	6	10	0	2	3	0.513278	0.518458	0.96625	0	0.164753	0.218618
antisense	-	7	1	1	15	0	0	0.350271	0.058968	0.065939	0.649323	0	0
processed_	TMEM254_	5	4	6	25	15	25	0.084814	0.079959	0.134117	0.366861	0.28585	0.421452
pseudogen	-	3	2	0	2	3	0	0.303677	0.238576	0	0.175139	0.341162	0
antisense	-	0	0	0	1	3	7	0	0	0	0.097032	0.378025	0.780293
TR_V_gene	T_cell_rece	0	0	0	0	0	2	0	0	0	0	0	0.193434
processed_	-	0	0	0	2	4	2	0	0	0	0.034358	0.089236	0.03947
pseudogen	-	1	0	0	0	0	0	0.077061	0	0	0	0	0
lincRNA	-	0	0	2	0	0	1	0	0	0.195689	0	0	0.073792
lincRNA	-	0	0	0	0	1	5	0	0	0	0	0.103979	0.459913
lincRNA	-	2	13	4	2	1	1	0.241189	1.847473	0.635656	0.208651	0.13548	0.11985
pseudogen	-	1	0	2	0	0	0	0.248549	0	0.655054	0	0	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.29738	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.139375
pseudogen	endothelin	1	2	6	1	0	0	0.071833	0.169302	0.567951	0.062142	0	0
antisense	-	91	71	56	151	91	174	1.806386	1.660866	1.464846	2.593039	2.029362	3.432638
pseudogen	eukaryotic_	2	0	0	0	0	0	0.423528	0	0	0	0	0
antisense	FGF12_anti	0	0	0	0	6	0	0	0	0	0	0.615268	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.063314
antisense	-	6	2	1	0	0	0	0.644312	0.253094	0.141508	0	0	0
antisense	HOXB_clust	17	11	12	4	7	4	1.119399	0.853563	1.041243	0.227855	0.517825	0.261761
processed_	-	0	0	1	0	0	0	0	0	0.132378	0	0	0
pseudogen	-	2	3	2	6	2	1	0.115466	0.204104	0.152155	0.299666	0.129718	0.057376
antisense	-	0	2	3	0	1	1	0	0.207959	0.348816	0	0.099127	0.08769
pseudogen	MT-ND1_ps	0	0	0	0	0	4	0	0	0	0	0	0.221533
pseudogen	-	2	1	0	0	0	0	0.303387	0.178761	0	0	0	0
pseudogen	-	2	2	0	1	3	0	0.09337	0.110031	0	0.040387	0.157344	0
antisense	SMIM12_ar	18	11	14	32	30	72	1.323525	0.953146	1.356508	2.035507	2.478163	5.261405
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.318873
pseudogen	-	2	0	1	1	0	1	0.225281	0	0.148433	0.097444	0	0.111945
antisense	-	2	0	3	2	1	0	0.151911	0	0.300272	0.131417	0.085331	0
antisense	-	35	22	16	102	76	104	3.326633	2.464147	2.003972	8.386873	8.115206	9.823808
pseudogen	-	1	0	0	0	0	0	0.437529	0	0	0	0	0
pseudogen	CCR4-NOT_	0	0	0	0	2	0	0	0	0	0	0.081362	0
sense_intro	SMYD3_int	0	7	4	0	8	1	0	1.209734	0.773	0	1.318026	0.145745
protein_co	chromosor	0	0	0	1	10	0	0	0	0	0.053069	0.689176	0
pseudogen	-	7	2	3	4	3	15	0.783482	0.263796	0.442473	0.387306	0.377226	1.668522
pseudogen	-	15	15	8	13	6	14	0.781609	0.921079	0.549317	0.58601	0.351236	0.724997
sense_intro	-	0	4	0	0	0	0	0	0.223612	0	0	0	0
pseudogen	-	5	2	6	9	1	6	0.278637	0.131343	0.44061	0.433884	0.062606	0.332299
pseudogen	ATPase_H+_	2	5	3	0	1	4	0.17133	0.504755	0.338657	0	0.096239	0.340544
pseudogen	-	233	214	155	177	128	184	26.02374	28.16661	22.81289	17.10212	16.06101	20.42402

pseudogen	ferritin_hea	0	0	1	0	0	0	0	0	0.128006	0	0	0
pseudogen	ribosomal_	5	1	2	5	2	2	0.207449	0.048893	0.109347	0.179463	0.093222	0.082467
sense_intrc	-	1	0	0	3	0	0	0.043359	0	0	0.112528	0	0
pseudogen	heat_shock	3	3	1	5	2	0	0.290885	0.34279	0.127772	0.419404	0.217861	0
pseudogen	-	0	0	2	0	0	0	0	0	0.05642	0	0	0
pseudogen	prohibitin_	8	7	11	13	9	14	0.513367	0.52935	0.930177	0.72168	0.648828	0.892844
antisense	-	1	0	0	0	0	0	0.140801	0	0	0	0	0
pseudogen	-	1	0	0	0	0	0	0.143861	0	0	0	0	0
lincRNA	-	0	2	0	0	0	0	0	0.327495	0	0	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.10115	0
pseudogen	-	0	3	0	0	0	0	0	0.547261	0	0	0	0
pseudogen	SPATA31_s	0	0	0	0	5	0	0	0	0	0	0.076349	0
pseudogen	prohibitin_	0	0	0	3	0	2	0	0	0	0.164154	0	0.125721
pseudogen	-	0	0	0	0	2	2	0	0	0	0	0.111274	0.098436
processed_	-	3	3	2	0	0	0	0.148156	0.174593	0.130155	0	0	0
lincRNA	MIRLET7D_	1	0	0	0	0	0	0.040913	0	0	0	0	0
antisense	XXYLT1_ant	5	2	3	1	4	5	0.337634	0.159152	0.266951	0.058417	0.303449	0.335549
pseudogen	SSU72_RNA	0	0	0	0	1	0	0	0	0	0	0.101668	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.030411	0	0
pseudogen	phosphogly	0	0	1	0	0	1	0	0	0.123475	0	0	0.093122
pseudogen	-	1	0	0	0	0	1	0.150401	0	0	0	0	0.149472
pseudogen	-	3	6	15	1	9	6	0.17301	0.407763	1.139923	0.04989	0.583097	0.343883
antisense	-	1	0	0	0	0	0	0.17301	0	0	0	0	0
antisense	-	2	0	0	4	7	2	0.223852	0	0	0.387306	0.880193	0.22247
pseudogen	-	12	17	12	13	7	8	1.450438	2.421442	1.911323	1.359328	0.950528	0.960987
processed_	NAALADL2_	0	0	0	0	0	3	0	0	0	0	0	0.382184
pseudogen	-	12	19	7	11	14	33	1.809949	3.377114	1.391291	1.435293	2.372259	4.94662
pseudogen	-	0	1	1	3	3	3	0	0.503127	0.562607	1.108038	1.438933	1.272921
sense_intrc	STARD13_i	15	9	5	2	0	0	1.756891	1.242234	0.771718	0.20265	0	0
pseudogen	capicua_tra	1	0	0	0	0	0	0.019399	0	0	0	0	0
pseudogen	barrier_to_	4	1	0	0	3	1	0.802136	0.236317	0	0	0.675863	0.199296
lincRNA	-	0	6	1	1	0	0	0	0.689367	0.128477	0.084344	0	0
pseudogen	-	0	1	0	0	0	0	0	0.14342	0	0	0	0
pseudogen	-	2	3	2	2	1	0	0.115214	0.20366	0.151824	0.099671	0.064718	0
processed_	ELOVL2_an	0	0	0	1	2	7	0	0	0	0.050719	0.13173	0.407861
antisense	FEZF1_antis	0	0	0	0	0	4	0	0	0	0	0	0.079328
antisense	-	4	4	7	5	4	2	0.101663	0.119804	0.234442	0.109935	0.114212	0.050518
pseudogen	-	0	0	1	0	0	0	0	0	0.152655	0	0	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.277925	0
antisense	-	0	0	0	0	10	0	0	0	0	0	1.383161	0
lincRNA	long_interg	2	2	0	0	0	0	0.24174	0.284875	0	0	0	0
processed_	-	0	0	0	0	0	3	0	0	0	0	0	0.319519
pseudogen	high_mobil	0	0	0	3	1	0	0	0	0	0.304649	0.131876	0
pseudogen	high_mobil	3	2	5	14	15	17	0.581769	0.457053	1.277716	2.348662	3.267908	3.276333

processed_	-	0	5	0	0	0	1	0	0.150115	0	0	0	0.02532
antisense	-	0	0	2	9	10	3	0	0	0.286502	0.846386	1.221271	0.324111
pseudogen	MT-ND4_ps	0	0	0	0	0	1	0	0	0	0	0	0.110071
pseudogen	Fanconi_an	0	0	0	0	0	1	0	0	0	0	0	0.037581
pseudogen	-	21	17	8	9	16	14	1.093177	1.042863	0.548777	0.4053	0.935708	0.724284
pseudogen	triosephos	1	3	4	8	9	16	0.0704	0.248887	0.371081	0.487222	0.711813	1.119448
pseudogen	ribosomal_	0	0	0	0	2	0	0	0	0	0	0.090734	0
lincRNA	Down_sync	9	3	6	1	7	6	0.289823	0.113846	0.254611	0.027858	0.253243	0.192022
pseudogen	-	0	1	0	1	0	0	0	0.130518	0	0.095814	0	0
pseudogen	golgin_A6_	94	80	69	18	28	18	2.12942	2.135652	2.059763	0.352752	0.712591	0.405243
pseudogen	mediator_c	0	0	0	0	1	0	0	0	0	0	0.154083	0
pseudogen	-	15	21	15	22	12	20	0.921247	1.519887	1.213978	1.168882	0.827971	1.220744
lincRNA	-	0	0	1	0	0	0	0	0	0.136523	0	0	0
lincRNA	-	1	0	0	1	0	0	0.018212	0	0	0.015755	0	0
antisense	-	2	3	1	0	0	0	0.040944	0.072376	0.026977	0	0	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.672044	0
pseudogen	serine_paln	11	16	11	0	2	0	2.23123	3.824535	2.940215	0	0.455754	0
pseudogen	retinoblast	0	0	3	0	1	0	0	0	0.113498	0	0.032254	0
lincRNA	-	3	0	0	0	0	0	0.319563	0	0	0	0	0
pseudogen	transcriptic	7	11	12	14	9	14	0.394241	0.730069	0.890595	0.682111	0.56945	0.783614
pseudogen	olfactory_r	0	0	0	0	1	0	0	0	0	0	0.062278	0
pseudogen	transcriptic	1	0	0	0	0	0	0.161405	0	0	0	0	0
processed_	-	1	4	4	1	0	2	0.136095	0.641519	0.71736	0.117735	0	0.270509
processed_	long_interg	0	1	4	0	0	2	0	0.023175	0.10366	0	0	0.039089
antisense	-	0	2	6	1	0	5	0	0.246105	0.825601	0.090333	0	0.518876
lincRNA	endogenou	1	0	0	6	14	11	0.022123	0	0	0.114832	0.347958	0.241853
antisense	-	2	0	1	0	0	0	0.096608	0	0.063653	0	0	0
pseudogen	-	2	5	0	0	4	0	0.38087	1.122081	0	0	0.855769	0
antisense	-	0	1	0	0	0	0	0	0.200604	0	0	0	0
antisense	-	1	0	0	3	0	4	0.06221	0	0	0.161453	0	0.247305
lincRNA	-	4	5	2	0	2	4	0.168871	0.248755	0.111265	0	0.094858	0.167828
processed_	-	0	4	0	9	1	0	0	0.149342	0	0.246673	0.035593	0
pseudogen	transcriptic	3	0	0	1	0	0	0.215792	0	0	0.062227	0	0
pseudogen	leucine_ric	2	0	4	0	6	2	0.019449	0	0.051259	0	0.06555	0.019329
pseudogen	cardiotropl	1	1	0	2	0	0	0.087651	0.103291	0	0.151652	0	0
pseudogen	ribosomal_	0	0	1	1	0	0	0	0	0.095566	0.062738	0	0
protein_co	ankyrin_rep	3	1	0	417	220	264	0.042095	0.016535	0	5.061793	3.467984	3.68145
processed_	-	7	29	13	5	13	13	0.141176	0.689236	0.345494	0.087236	0.294547	0.260565
pseudogen	-	1	1	1	0	0	0	0.069476	0.081874	0.091553	0	0	0
pseudogen	proliferatic	2	0	0	8	2	1	0.089579	0	0	0.309976	0.100636	0.044513
pseudogen	-	5	0	1	0	3	0	0.853887	0	0.225043	0	0.575573	0
antisense	PROX1_ant	2	0	0	3	2	1	0.020421	0	0	0.026499	0.022942	0.010147
sense_intrc	-	1	1	3	1	1	2	0.125156	0.147489	0.494775	0.108272	0.140605	0.248766
pseudogen	ATP_syntha	0	0	0	0	2	0	0	0	0	0	0.279887	0

pseudogen	olfactory_r	2	0	0	0	0	0	0.113001	0	0	0	0	0
lincRNA	PSMG3_ant	123	69	102	37	43	49	1.142211	0.755087	1.248177	0.297239	0.448599	0.452217
pseudogen	-	0	1	0	0	0	0	0	0.255687	0	0	0	0
pseudogen	-	2	0	3	0	0	1	0.191468	0	0.378463	0	0	0.095143
pseudogen	-	0	0	0	1	0	0	0	0	0	0.068255	0	0
antisense	-	1	0	2	0	0	0	0.106521	0	0.280738	0	0	0
lincRNA	-	0	2	2	0	0	1	0	0.302853	0.338657	0	0	0.127704
antisense	-	12	13	6	0	0	0	0.852741	1.088645	0.561852	0	0	0
protein_co	PPP5_tetra	12	15	17	13	0	11	0.228769	0.336988	0.427071	0.214399	0	0.20841
antisense	THAP7_ant	31	25	26	16	24	54	0.714174	0.678718	0.789315	0.318878	0.621158	1.236361
pseudogen	-	2	6	0	9	12	3	0.186084	0.657867	0	0.724412	1.254325	0.277403
lincRNA	-	0	0	0	0	4	0	0	0	0	0	0.110756	0
pseudogen	collagen_ty	0	1	0	0	0	0	0	0.014452	0	0	0	0
pseudogen	nitric_oxid	0	0	0	1	2	1	0	0	0	0.013782	0.035797	0.015833
processed_	LIMD1_ant	0	0	0	0	1	1	0	0	0	0	0.038721	0.034254
lincRNA	-	0	0	0	4	2	14	0	0	0	0.350278	0.227441	1.408407
antisense	-	0	0	0	1	1	1	0	0	0	0.070352	0.091361	0.08082
pseudogen	brain_abun	0	0	0	2	8	9	0	0	0	0.137741	0.7155	0.71207
antisense	-	1	4	5	0	1	1	0.069204	0.32621	0.455969	0	0.077746	0.068777
lincRNA	-	2	7	1	0	0	0	0.129917	0.535846	0.085599	0	0	0
sense_intrc	AOAH_intrc	0	1	0	0	0	0	0	0.108879	0	0	0	0
lincRNA	long_interg	3	1	4	1	1	8	0.118525	0.046558	0.208249	0.034178	0.044385	0.314114
lincRNA	long_interg	0	0	4	0	0	0	0	0	0.53153	0	0	0
antisense	-	0	0	0	0	2	0	0	0	0	0	0.105641	0
processed_	-	349	426	358	338	396	363	2.139464	3.077486	2.891993	1.7925	2.727242	2.211545
lincRNA	-	25	32	12	3	9	17	1.74148	2.626852	1.101526	0.180785	0.70432	1.176893
pseudogen	carcinoemb	3	0	0	0	0	0	0.360961	0	0	0	0	0
lincRNA	-	2	12	5	5	8	4	0.10142	0.7171	0.334115	0.219343	0.455754	0.201586
pseudogen	family_with	4	3	5	5	1	4	0.30646	0.270858	0.504799	0.331396	0.086072	0.304568
antisense	ZNF32_anti	11	11	8	5	4	6	0.643482	0.758304	0.616692	0.253033	0.262877	0.348822
pseudogen	splicing_fa	0	2	7	6	5	0	0	0.084479	0.330632	0.186048	0.20134	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.144009	0
pseudogen	-	0	0	0	1	3	0	0	0	0	0.038071	0.148319	0
pseudogen	-	3	0	2	1	3	0	0.372824	0	0.327527	0.107509	0.418844	0
pseudogen	-	5	1	3	1	8	0	0.235922	0.055604	0.186533	0.040819	0.424071	0
pseudogen	GTF2I_repe	0	3	0	6	2	4	0	0.077149	0	0.11327	0.049032	0.08675
pseudogen	prohibitin_	0	0	0	0	3	1	0	0	0	0	0.22001	0.064876
lincRNA	FTX_transc	109	107	84	66	108	86	2.222013	2.570461	2.256494	1.163931	2.473392	1.742321
pseudogen	ribosomal_	1	0	0	1	0	0	0.059551	0	0	0.051517	0	0
pseudogen	-	0	1	0	3	0	1	0	0.125277	0	0.275897	0	0.105651
lincRNA	-	0	0	0	3	0	0	0	0	0	0.390332	0	0
lincRNA	-	0	0	0	0	1	2	0	0	0	0	0.108138	0.191324
pseudogen	tRNA_splici	0	0	1	0	3	0	0	0	0.19487	0	0.498402	0
lincRNA	-	22	19	13	9	2	6	0.326888	0.332688	0.254539	0.115686	0.033385	0.088601

protein_co	-	0	0	0	0	1	0	0	0	0	0	1.321687	0
pseudogen	high_mobil	2	0	0	2	0	0	0.175592	0	0	0.151904	0	0
antisense	-	1	0	2	0	2	1	0.10546	0	0.277941	0	0.236956	0.104809
antisense	HM13_anti	3	8	2	3	1	2	0.324791	1.020658	0.28533	0.280975	0.121628	0.21519
lincRNA	-	6	1	9	6	0	0	0.120138	0.023596	0.23747	0.103931	0	0
pseudogen	ubiquinol-(	2	0	0	4	0	0	0.386431	0	0	0.668597	0	0
lincRNA	-	3	1	2	18	21	19	0.31326	0.123053	0.2752	1.625997	2.4635	1.97173
pseudogen	-	2	0	0	1	0	1	0.088235	0	0	0.038166	0	0.043845
pseudogen	ribosomal_	15	16	7	26	20	23	2.406409	3.02486	1.479827	3.608399	3.604601	3.66704
antisense	DNM3_opp	179	162	178	20	25	28	16.68387	17.79368	21.86244	1.612638	2.617778	2.59365
pseudogen	-	0	0	9	3	1	2	0	0	0.947013	0.207235	0.089707	0.158715
pseudogen	-	2	0	0	7	2	7	0.047227	0	0	0.142994	0.053056	0.164272
antisense	USP12_ant	6	0	0	1	0	7	1.138516	0	0	0.164154	0	1.320066
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.050639
lincRNA	-	0	0	2	0	0	0	0	0	0.173541	0	0	0
antisense	-	7	0	1	6	0	0	1.773143	0	0.333796	1.314801	0	0
lincRNA	-	1	2	0	0	0	0	0.116354	0.274232	0	0	0	0
pseudogen	-	0	5	2	4	0	1	0	0.099661	0.044577	0.058529	0	0.01681
protein_co	proline-rich	0	2	0	0	0	1	0	0.136665	0	0	0	0.057628
processed_	KLHL7_anti	0	0	0	14	9	35	0	0	0	0.250072	0.208769	0.718211
pseudogen	YY1_transc	1	0	2	0	0	0	0.079253	0	0.208872	0	0	0
pseudogen	transportin	0	0	0	0	1	0	0	0	0	0	0.022317	0
lincRNA	family_with	3	0	3	5	2	7	0.078161	0	0.102997	0.112694	0.058539	0.181249
pseudogen	carcinoemb	0	0	0	0	0	1	0	0	0	0	0	0.017445
pseudogen	poly(A)_bin	3	8	0	2	1	1	0.34602	1.087368	0	0.19956	0.129577	0.114628
antisense	ENO1_antis	5	0	0	0	0	0	0.580493	0	0	0	0	0
pseudogen	D-dopachro	1	4	5	2	0	1	0.138227	0.651569	0.910748	0.239159	0	0.137373
antisense	-	0	1	1	0	0	0	0	0.23454	0.262268	0	0	0
antisense	-	6	9	4	0	0	0	0.698123	1.234043	0.613304	0	0	0
antisense	-	1	2	1	0	0	0	0.40413	0.952484	0.532544	0	0	0
processed_	-	0	3	0	0	1	0	0	0.306825	0	0	0.097502	0
pseudogen	-	2	2	3	0	0	0	0.267379	0.31509	0.52851	0	0	0
antisense	-	35	58	29	0	6	3	0.608917	1.189119	0.664849	0	0.117271	0.051871
pseudogen	F-box_and_	3	0	5	6	8	9	0.13029	0	0.28615	0.225425	0.390326	0.388455
pseudogen	-	5	0	0	3	0	1	0.733255	0	0	0.3806	0	0.145745
pseudogen	-	0	0	1	5	1	5	0	0	0.085181	0.279603	0.07262	0.321209
pseudogen	-	4	9	7	0	0	0	0.318922	0.845617	0.735456	0	0	0
pseudogen	-	205	158	105	191	174	176	21.40612	19.44233	14.44802	17.25363	20.41185	18.26444
pseudogen	-	2	0	0	0	0	0	0.29576	0	0	0	0	0
processed_	-	65	58	35	99	99	105	1.293185	1.359823	0.917593	1.703905	2.212746	2.07609
antisense	-	1	0	1	2	3	0	0.09112	0	0.120074	0.157655	0.307105	0
sense_intrc	-	17	10	9	9	15	18	0.939454	0.651229	0.655396	0.430261	0.931251	0.988573
lincRNA	-	364	294	271	915	703	857	5.927567	5.641954	5.815395	12.89019	12.86114	13.86965
processed_	-	0	0	1	0	2	0	0	0	0.159641	0	0.272201	0

processed_	-	0	7	1	13	4	3	0	0.280304	0.044777	0.382147	0.152698	0.101311
antisense	-	0	0	0	0	1	0	0	0	0	0	0.086072	0
antisense	-	0	2	1	0	0	0	0	0.257801	0.144139	0	0	0
antisense	-	2	1	2	2	2	0	0.143084	0.084308	0.188549	0.123781	0.160746	0
antisense	MEIS1_anti	1	1	1	0	1	0	0.076726	0.090417	0.101106	0	0.086197	0
antisense	-	0	2	0	0	0	0	0	0.194354	0	0	0	0
pseudogen	ras_homol	1	0	1	0	1	0	0.085251	0	0.11234	0	0.095774	0
pseudogen	synaptoson	1	0	0	1	1	2	0.215207	0	0	0.186174	0.241772	0.427757
pseudogen	-	0	3	6	1	7	3	0	0.381188	0.852504	0.093277	0.847926	0.321471
pseudogen	vomeronas	0	2	0	7	14	8	0	0.150332	0	0.386256	1.003208	0.507123
pseudogen	-	2	1	0	0	1	4	0.619193	0.364841	0	0	0.347812	1.230738
protein_co	ankyrin_re	62	39	43	31	46	52	2.87169	2.128715	2.624515	1.24214	2.393606	2.39364
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.070199
processed_	-	2	0	2	0	0	1	0.046501	0	0.061276	0	0	0.023107
pseudogen	-	0	0	1	0	0	2	0	0	0.091194	0	0	0.137553
pseudogen	phosphose	1	0	0	0	0	0	0.047652	0	0	0	0	0
pseudogen	SWI/SNF_re	3	3	0	4	0	0	0.129651	0.152786	0	0.149547	0	0
pseudogen	major_hist	4	0	0	3	2	0	0.204208	0	0	0.132494	0.114708	0
protein_co	YY2_transc	33	37	22	39	17	34	0.637378	0.842155	0.559939	0.651644	0.368877	0.652637
antisense	-	0	0	0	7	4	4	0	0	0	0.340693	0.25282	0.223652
pseudogen	-	2	8	9	1	8	1	0.126502	0.596298	0.750143	0.054718	0.568468	0.06286
pseudogen	-	0	1	0	0	0	0	0	0.252582	0	0	0	0
pseudogen	-	2	0	1	0	0	1	0.18287	0	0.120489	0	0	0.090871
lincRNA	-	0	0	4	0	0	0	0	0	0.47458	0	0	0
lincRNA	-	3	0	5	2	8	6	0.063428	0	0.139304	0.036581	0.190019	0.126072
pseudogen	-	0	0	1	0	0	1	0	0	0.188041	0	0	0.141817
lincRNA	-	29	18	16	0	0	0	2.896771	2.118829	2.106061	0	0	0
sense_intro	-	0	4	0	0	2	1	0	0.588563	0	0	0.280547	0.12409
processed_	-	0	2	1	5	2	2	0	0.184853	0.103353	0.339251	0.176225	0.155893
antisense	-	3	2	0	7	3	2	0.201552	0.158344	0	0.406843	0.226431	0.133538
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.126476
pseudogen	ribulose-5-p	0	2	2	0	0	0	0	0.184579	0.2064	0	0	0
lincRNA	-	3	2	0	6	3	7	0.125453	0.098559	0	0.217056	0.140938	0.290915
pseudogen	ribosomal_	0	0	0	0	1	0	0	0	0	0	0.157761	0
lincRNA	-	10	3	18	0	0	0	0.816991	0.288832	1.937869	0	0	0
lincRNA	-	0	1	0	0	0	0	0	0.180311	0	0	0	0
processed_	ZNF674_an	63	70	36	121	102	132	1.749886	2.29126	1.31767	2.907486	3.182867	3.643785
pseudogen	-	0	0	0	4	1	0	0	0	0	0.269802	0.087593	0
antisense	-	0	0	1	0	0	0	0	0	0.183588	0	0	0
pseudogen	glutamic-o	3	0	0	0	0	0	0.126957	0	0	0	0	0
processed_	-	4	3	0	7	6	10	0.118569	0.104795	0	0.179503	0.199807	0.294592
lincRNA	-	0	2	0	0	0	1	0	0.246105	0	0	0	0.103775
pseudogen	-	0	0	0	2	0	0	0	0	0	0.123447	0	0
lincRNA	-	0	0	0	0	2	2	0	0	0	0	0.127768	0.113027

pseudogen	centaurin_	4	0	3	2	1	1	0.087578	0	0.086555	0.037882	0.024597	0.021759
pseudogen	F-box_and_	8	1	5	8	0	0	0.287332	0.042325	0.236646	0.248569	0	0
pseudogen	-	1	1	1	3	8	8	0.04104	0.048363	0.05408	0.106509	0.368843	0.326289
protein_co	stathmin_d	0	0	0	19	13	5	0	0	0	0.417352	0.370833	0.126173
lincRNA	long_interg	0	1	0	0	0	2	0	0.034776	0	0	0	0.058656
lincRNA	-	11	9	3	10	8	7	0.789093	0.760826	0.283591	0.620581	0.644725	0.499049
antisense	-	0	0	0	0	1	0	0	0	0	0	0.224437	0
pseudogen	-	3	1	0	15	6	10	0.045443	0.017851	0	0.196562	0.102105	0.150541
antisense	-	2	0	6	1	2	4	0.021193	0	0.083783	0.009167	0.023809	0.042125
sense_intrc	-	38	39	24	42	23	25	3.364143	4.068765	2.799864	3.216646	2.287535	2.199584
pseudogen	ribosomal_	0	0	1	0	0	0	0	0	0.15199	0	0	0
antisense	MAGEA8_a	1	0	0	0	0	0	0.111221	0	0	0	0	0
pseudogen	family_with	1	0	0	1	1	0	0.082463	0	0	0.071338	0.092642	0
pseudogen	ribosomal_	0	0	0	1	0	0	0	0	0	0.068052	0	0
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.121933
antisense	-	0	5	0	5	1	1	0	0.131898	0	0.096826	0.025148	0.022247
pseudogen	peptidylpr	4	2	5	0	4	0	0.415223	0.244658	0.683954	0	0.466478	0
antisense	-	14	11	21	5	3	6	1.807741	1.673817	3.573241	0.558523	0.43519	0.769962
lincRNA	-	1	1	1	0	4	0	0.087074	0.102611	0.114742	0	0.391289	0
antisense	-	0	0	0	3	7	2	0	0	0	0.214682	0.650518	0.164419
sense_intrc	-	0	6	0	6	9	15	0	0.229226	0	0.168275	0.327791	0.483289
lincRNA	long_interg	0	0	0	0	0	2	0	0	0	0	0	0.03182
antisense	-	7	3	2	5	4	0	0.468504	0.236616	0.176393	0.2895	0.300763	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.046213	0
antisense	-	0	7	1	0	0	1	0	0.373899	0.059729	0	0	0.045046
pseudogen	-	6	1	7	18	2	3	1.048337	0.2059	1.611693	2.720727	0.39258	0.520931
processed_	MIR205_hc	0	0	0	586	535	637	0	0	0	8.016176	9.504067	10.0105
lincRNA	-	4	0	1	2	2	2	0.433055	0	0.142665	0.187317	0.243255	0.21519
lincRNA	-	1	0	1	0	1	0	0.113852	0	0.150029	0	0.127905	0
pseudogen	-	0	2	3	2	8	3	0	0.127452	0.213779	0.093563	0.486014	0.161228
sense_intrc	-	1	2	1	0	0	0	0.145442	0.34279	0.191657	0	0	0
pseudogen	-	0	1	0	0	0	0	0	0.061466	0	0	0	0
pseudogen	-	0	0	0	0	4	18	0	0	0	0	1.35945	5.411731
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.173644
lincRNA	-	5	0	0	5	0	0	0.149298	0	0	0.129157	0	0
pseudogen	-	4	3	2	5	3	9	0.398802	0.352473	0.262762	0.431251	0.336022	0.891764
pseudogen	-	0	2	4	4	2	7	0	0.222416	0.497421	0.326552	0.212035	0.656503
pseudogen	destrin_(ac	30	18	43	12	36	17	3.415548	2.415009	6.451228	1.181907	4.604587	1.923524
pseudogen	DEAD_(Asp	1	0	0	0	0	0	0.476946	0	0	0	0	0
pseudogen	-	0	2	0	0	2	0	0	0.266046	0	0	0.253629	0
protein_co	heat_shock	2313	1908	1703	3234	2374	3403	22.79883	22.16269	22.12007	27.57655	26.28855	33.33562
pseudogen	family_with	2	1	2	4	3	6	0.048726	0.02871	0.064209	0.084305	0.082111	0.145276
pseudogen	-	0	0	0	1	2	3	0	0	0	0.091781	0.23838	0.316317
pseudogen	-	2	3	2	2	0	1	0.142314	0.251563	0.187536	0.123115	0	0.070718

pseudogen	cell_divisio	9	3	4	14	8	9	0.317646	0.124775	0.186035	0.427456	0.317205	0.315684
pseudogen	cubilin_(int	0	0	0	0	1	0	0	0	0	0	0.033227	0
lincRNA	-	3	7	0	0	0	0	0.134482	0.369783	0	0	0	0
lincRNA	long_interg	0	0	0	0	2	2	0	0	0	0	0.047297	0.04184
lincRNA	-	0	0	1	0	2	0	0	0	0.166103	0	0.283219	0
antisense	-	186	170	100	416	341	353	2.80542	3.021628	1.987558	5.428018	5.778145	5.291385
lincRNA	long_interg	16	3	5	3	3	7	0.536111	0.118458	0.22077	0.08696	0.112929	0.2331
pseudogen	ribosomal_	0	1	0	0	0	0	0	0.083742	0	0	0	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.067351	0	0
pseudogen	-	0	0	0	1	4	1	0	0	0	0.026306	0.136648	0.030221
antisense	-	0	0	0	0	3	1	0	0	0	0	0.412073	0.121511
pseudogen	olfactory_r	0	0	0	0	4	0	0	0	0	0	0.250162	0
antisense	-	8	3	4	7	8	9	0.46747	0.206582	0.308006	0.353855	0.525174	0.522656
pseudogen	-	1	0	0	0	4	0	0.151693	0	0	0	0.681672	0
lincRNA	-	1	1	1	0	0	0	0.095734	0.112817	0.126154	0	0	0
lincRNA	-	0	0	0	1	1	0	0	0	0	0.178902	0.232328	0
antisense	-	1	0	1	4	3	5	0.028679	0	0.037792	0.099239	0.096656	0.142508
pseudogen	-	4	0	0	0	5	5	0.2524	0	0	0	0.354445	0.313552
antisense	-	5	2	0	3	5	2	0.290247	0.136815	0	0.150654	0.326074	0.115382
pseudogen	nucleopho	0	2	2	14	10	16	0	0.147838	0.165316	0.759697	0.704691	0.997423
pseudogen	-	2	6	4	5	0	0	0.185433	0.655563	0.48871	0.401041	0	0
antisense	-	5	1	7	1	7	5	0.719307	0.169532	1.327019	0.124454	1.131335	0.714865
antisense	HLA_compl	369	375	359	439	434	372	4.017941	4.811888	5.151176	4.135278	5.309039	4.025592
antisense	-	0	0	0	2	5	2	0	0	0	0.044791	0.145418	0.051456
lincRNA	-	7	8	7	3	19	8	0.68374	0.920852	0.901002	0.253499	2.084949	0.776591
pseudogen	-	5	4	6	16	19	23	0.704003	0.663699	1.113244	1.94889	3.005432	3.218413
pseudogen	testis-speci	0	0	3	3	1	7	0	0	0.272513	0.178902	0.077443	0.479555
antisense	-	0	0	0	0	3	5	0	0	0	0	0.227586	0.335549
pseudogen	-	0	0	0	1	0	0	0	0	0	0.068767	0	0
antisense	-	0	0	3	1	1	0	0	0	0.233843	0.051172	0.066454	0
antisense	-	2	0	2	7	6	3	0.042712	0	0.056283	0.129323	0.143951	0.063672
lincRNA	-	58	44	57	0	7	7	3.031172	2.709832	3.925476	0	0.410989	0.363572
antisense	-	51	71	22	191	106	150	3.976422	6.523606	2.260371	12.88305	9.2849	11.62313
lincRNA	-	0	2	2	0	2	1	0	0.067998	0.076036	0	0.064824	0.028673
processed_	-	4	15	15	2	6	2	0.117061	0.517311	0.578468	0.050635	0.197267	0.058169
pseudogen	basic_trans	3	0	0	0	0	0	0.318922	0	0	0	0	0
processed_	-	2	0	0	0	0	0	0.106844	0	0	0	0	0
pseudogen	spermatoge	0	0	1	0	0	0	0	0	0.159277	0	0	0
sense_intro	-	2	6	5	16	20	18	0.133353	0.471444	0.439315	0.9229	1.498134	1.192762
antisense	-	0	0	0	3	0	0	0	0	0	0.177745	0	0
pseudogen	major_hist	0	1	0	0	1	0	0	0.138639	0	0	0.132169	0
processed_	-	0	0	0	0	1	0	0	0	0	0	0.061001	0
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.235937
processed_	highly_acce	0	1	0	1	0	0	0	0.113226	0	0.08312	0	0

sense_intrc	TCF7L1_int	6	7	2	2	4	0	0.69355	0.953524	0.304643	0.199995	0.51944	0
protein_co	-	0	0	0	0	2	1	0	0	0	0	2.478163	1.096126
pseudogen	high_mobil	0	0	0	0	2	4	0	0	0	0	0.194366	0.343883
lincRNA	-	5	0	0	1	0	2	0.995131	0	0	0.172176	0	0.395594
processed_	MORF4L2_	13	13	17	13	20	12	0.329929	0.388802	0.568541	0.28542	0.570239	0.30267
lincRNA	-	4	2	1	0	0	0	0.577014	0.339988	0.190091	0	0	0
processed_	-	18	40	15	5	4	9	0.402423	1.053847	0.441913	0.096704	0.100466	0.199969
antisense	-	1	2	0	0	0	0	0.038728	0.091277	0	0	0	0
pseudogen	ribosomal_	1	0	0	0	0	0	0.073837	0	0	0	0	0
pseudogen	Y_box_binc	7	5	7	2	7	6	0.370958	0.312251	0.488832	0.09169	0.416748	0.316
pseudogen	eukaryotic_	0	0	1	4	1	0	0	0	0.103353	0.271401	0.088112	0
antisense	-	0	0	1	0	0	0	0	0	0.090484	0	0	0
protein_co	HCG20258	0	0	0	0	0	8	0	0	0	0	0	0.407072
processed_	-	6	8	11	3	2	1	0.288507	0.453317	0.696999	0.124793	0.10804	0.047788
lincRNA	long_interg	13	20	12	21	24	22	0.518248	0.939574	0.630391	0.72423	1.074866	0.871618
pseudogen	-	2	2	1	13	7	14	0.189413	0.223212	0.1248	1.065091	0.744779	1.317704
processed_	-	19	5	8	4	12	11	1.701995	0.527815	0.944342	0.309976	1.207633	0.97928
antisense	-	3	4	5	19	15	12	0.237404	0.373021	0.5214	1.300716	1.333541	0.94375
antisense	-	0	3	1	0	0	0	0	0.397374	0.148117	0	0	0
antisense	FARP1_anti	0	5	0	0	0	1	0	0.965754	0	0	0	0.162892
pseudogen	interferon_	0	0	0	6	9	16	0	0	0	0.522421	1.017649	1.600427
lincRNA	-	7	6	7	8	12	6	0.546588	0.552104	0.72027	0.5404	1.052671	0.465611
antisense	-	1	4	4	3	8	14	0.064249	0.302853	0.338657	0.166744	0.577436	0.893928
pseudogen	keratin_8_	0	0	0	5	3	9	0	0	0	0.158255	0.123309	0.327247
pseudogen	zinc_finger_	29	36	13	340	178	188	0.461048	0.674462	0.272349	4.676165	3.179193	2.970403
pseudogen	heterogene	5	0	1	0	0	0	0.282503	0	0.074454	0	0	0
antisense	-	2	1	0	0	3	0	0.198653	0.11705	0	0	0.334761	0
lincRNA	-	0	2	0	0	0	2	0	0.199322	0	0	0	0.168096
protein_co	phospholip	0	0	0	123	126	100	0	0	0	2.860978	3.805975	2.67212
lincRNA	-	0	0	0	1	0	0	0	0	0	0.088586	0	0
sense_over	-	0	0	0	1	0	0	0	0	0	0.099563	0	0
lincRNA	-	0	1	0	0	0	0	0	0.102611	0	0	0	0
antisense	CCDC147_a	0	0	3	0	0	2	0	0	0.263258	0	0	0.132362
pseudogen	S-phase_kir	2	2	3	11	8	3	0.216528	0.255165	0.427996	1.030241	0.973021	0.322786
pseudogen	-	1	0	5	1	0	5	0.050807	0	0.334757	0.043953	0	0.252467
pseudogen	ribosomal_	0	0	1	0	0	6	0	0	0.288278	0	0	1.304481
lincRNA	-	14	9	8	0	2	5	0.364572	0.276188	0.274523	0	0.05851	0.1294
pseudogen	proteasom	0	1	0	5	1	0	0	0.047335	0	0.173744	0.045126	0
lincRNA	-	4	2	3	0	0	0	0.387137	0.228109	0.382614	0	0	0
antisense	ITPR1_anti	2	1	0	5	6	5	0.123406	0.072713	0	0.266893	0.415916	0.306609
lincRNA	-	0	2	0	0	0	1	0	0.053232	0	0	0	0.022446
antisense	-	0	0	0	2	0	0	0	0	0	0.340512	0	0
protein_co	chromoson	2	0	0	0	0	0	0.028213	0	0	0	0	0
pseudogen	zinc_finger_	0	0	0	1	0	1	0	0	0	0.022472	0	0.025817

pseudogen	-	48	65	36	34	57	54	1.155602	1.844112	1.1421	0.708123	1.541668	1.292023
processed_	APCDD1L_a	0	0	0	5	1	2	0	0	0	0.08707	0.022614	0.040011
antisense	-	1	0	0	0	0	2	0.104626	0	0	0	0	0.207961
pseudogen	-	0	0	2	0	0	3	0	0	0.445772	0	0	0.504288
processed_	long_interg	40	35	26	0	1	2	2.50312	2.581053	2.144025	0	0.070303	0.124383
pseudogen	ribosomal_	1	0	1	0	0	0	0.168067	0	0.221471	0	0	0
lincRNA	-	0	1	0	0	0	0	0	0.030567	0	0	0	0
antisense	-	18	3	9	16	11	12	0.734159	0.144194	0.483721	0.564547	0.504033	0.486416
pseudogen	ribosomal_	4	4	1	0	0	0	0.302088	0.355993	0.09952	0	0	0
antisense	TBL1XR1_a	0	0	0	0	3	0	0	0	0	0	0.430985	0
antisense	-	21	43	21	86	82	123	0.441701	1.065821	0.582054	1.564841	1.937634	2.571128
pseudogen	ribosomal_	0	5	0	0	0	0	0	0.164611	0	0	0	0
lincRNA	-	13	7	4	24	19	20	1.039627	0.659689	0.42153	1.660383	1.707013	1.589548
antisense	-	8	0	3	0	4	3	0.51089	0	0.252461	0	0.286977	0.190401
pseudogen	ribosomal_	1	2	0	0	4	5	0.153452	0.361668	0	0	0.689576	0.762522
sense_intro	-	0	0	2	7	3	2	0	0	0.583793	1.341391	0.74656	0.440285
antisense	-	0	1	1	1	0	1	0	0.171395	0.191657	0.125821	0	0.144544
pseudogen	actin_gamr	12	11	14	3	9	3	0.587146	0.634256	0.902667	0.126984	0.494717	0.14588
pseudogen	voltage-dep	0	1	0	0	0	3	0	0.072968	0	0	0	0.184611
pseudogen	activating_	1	1	0	0	0	0	0.049339	0.058143	0	0	0	0
pseudogen	-	1	5	3	2	2	4	0.151693	0.893807	0.599684	0.262458	0.340836	0.603026
pseudogen	-	0	0	1	1	1	0	0	0	0.025258	0.016582	0.021534	0
lincRNA	-	6	3	0	24	11	4	0.355309	0.209355	0	1.229501	0.731807	0.23541
pseudogen	-	1	0	1	0	0	1	0.104834	0	0.138145	0	0	0.104186
antisense	-	0	5	0	3	1	3	0	0.468376	0	0.206301	0.089303	0.237
pseudogen	-	1	0	0	1	1	2	0.131694	0	0	0.113928	0.14795	0.261761
pseudogen	-	0	0	0	3	0	4	0	0	0	0.449009	0	0.687765
protein_co	Protein_LO	1	0	0	1	0	3	0.049339	0	0	0.042683	0	0.147104
pseudogen	-	0	0	2	0	0	0	0	0	0.894401	0	0	0
lincRNA	-	0	0	0	0	3	0	0	0	0	0	0.84164	0
antisense	-	189	179	148	225	132	136	4.052591	4.523047	4.181841	4.173655	3.179757	2.898141
lincRNA	-	0	0	0	1	0	0	0	0	0	0.039618	0	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.086965
pseudogen	NADH_deh	0	0	2	0	1	0	0	0	0.277941	0	0.118478	0
pseudogen	ring_finger_	0	0	1	0	1	6	0	0	0.069073	0	0.058887	0.312559
antisense	FGF12_anti	0	0	1	0	0	0	0	0	0.120282	0	0	0
pseudogen	-	0	2	0	0	0	0	0	0.244179	0	0	0	0
protein_co	major_hist	2	0	4	133	95	130	0.021071	0	0.055533	1.21219	1.12442	1.36116
antisense	-	1	0	4	0	0	1	0.077969	0	0.410977	0	0	0.077488
pseudogen	-	2	16	2	2	2	1	0.204405	1.927034	0.269356	0.17683	0.229637	0.101572
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.162948	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.126814	0
lincRNA	-	0	1	0	0	0	0	0	0.099661	0	0	0	0
lincRNA	-	0	5	0	0	0	0	0	0.65949	0	0	0	0

antisense	-	9	12	21	7	9	11	0.229072	0.359929	0.704341	0.154131	0.257348	0.278247
pseudogen	-	0	0	0	3	0	1	0	0	0	0.43618	0	0.167029
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.174798
pseudogen	-	0	3	2	2	0	2	0	1.199764	0.894401	0.587165	0	0.674539
pseudogen	-	0	0	2	0	0	0	0	0	0.424093	0	0	0
processed_	-	0	0	0	0	1	2	0	0	0	0	0.044024	0.077889
antisense	-	6	2	0	0	0	0	0.635292	0.249551	0	0	0	0
lincRNA	-	1	0	0	0	1	0	0.055378	0	0	0	0.062213	0
lincRNA	-	2	1	0	0	2	8	0.200155	0.117935	0	0	0.224862	0.795676
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.048559
antisense	WASH_and	5	0	0	2	11	0	0.245097	0	0	0.084813	0.605773	0
sense_intrc	-	1	3	1	0	0	0	0.078431	0.277279	0.103353	0	0	0
antisense	-	3	2	4	9	7	9	0.288245	0.226453	0.506449	0.748076	0.755592	0.859395
pseudogen	La_ribonuc	0	2	0	0	0	0	0	0.091814	0	0	0	0
pseudogen	-	5	0	1	12	11	6	0.213128	0	0.05617	0.442502	0.526759	0.254174
pseudogen	translocase	0	0	0	17	13	17	0	0	0	2.639259	2.620973	3.031996
pseudogen	-	2	0	0	0	0	1	0.228687	0	0	0	0	0.113637
processed_	-	1	0	0	14	9	11	0.016952	0	0	0.20531	0.1714	0.18532
lincRNA	long_interg	0	0	1	9	2	3	0	0	0.023949	0.1415	0.040835	0.054185
lincRNA	-	0	0	0	3	9	19	0	0	0	0.096082	0.374324	0.699068
pseudogen	-	0	0	0	1	0	0	0	0	0	0.036875	0	0
pseudogen	-	14	5	10	12	7	1	0.950223	0.399921	0.894401	0.704599	0.533758	0.067454
pseudogen	peroxiredo	6	11	6	9	9	25	0.519879	1.123183	0.685073	0.674616	0.876077	2.152784
pseudogen	high_mobil	0	0	0	3	0	0	0	0	0	0.510768	0	0
processed_	long_interg	0	3	1	0	2	2	0	0.163747	0.061035	0	0.10407	0.092063
lincRNA	-	0	0	0	0	3	0	0	0	0	0	0.321491	0
lincRNA	-	1	0	0	0	0	0	0.170777	0	0	0	0	0
lincRNA	-	0	1	1	0	0	0	0	0.116178	0.129913	0	0	0
protein_co	ribosomal_	41140	36217	23442	27862	20598	30210	1963.925	2037.418	1474.654	1150.63	1104.675	1433.247
pseudogen	-	0	0	1	1	1	4	0	0	0.201628	0.132367	0.171896	0.608255
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.067889
pseudogen	-	0	0	2	0	0	2	0	0	0.397512	0	0	0.299795
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.078464	0
lincRNA	-	1	0	0	0	0	0	0.064327	0	0	0	0	0
antisense	-	1	1	0	6	0	1	0.102203	0.12044	0	0.530489	0	0.101572
antisense	-	0	0	0	0	7	0	0	0	0	0	1.460812	0
lincRNA	-	2	0	0	4	2	3	0.113729	0	0	0.196773	0.127768	0.16954
lincRNA	family_with	0	0	1	0	3	0	0	0	0.011437	0	0.02925	0
antisense	-	4	7	7	12	8	12	0.583372	1.203069	1.345297	1.514013	1.310764	1.739307
lincRNA	long_interg	0	0	0	3	5	2	0	0	0	0.234066	0.506609	0.179264
pseudogen	ribosomal_	0	0	2	0	0	0	0	0	0.284168	0	0	0
pseudogen	up-regulate	0	2	0	0	0	0	0	0.704946	0	0	0	0
pseudogen	patched_d	0	2	0	0	0	3	0	0.103548	0	0	0	0.130989
processed_	-	2	3	3	4	6	0	0.068091	0.120362	0.134592	0.117811	0.229489	0

pseudogen	ribosomal_	0	0	0	1	1	6	0	0	0	0.092523	0.120153	0.637746
pseudogen	-	0	1	0	0	0	0	0	0.252582	0	0	0	0
pseudogen	-	0	0	2	2	9	0	0	0	0.17911	0.117584	0.687142	0
antisense	-	9	9	10	31	19	22	1.683636	1.984062	2.465134	5.016841	3.993083	4.090138
pseudogen	eukaryotic_	0	0	0	1	0	0	0	0	0	0.206301	0	0
processed_	-	14	0	7	34	41	46	0.37815	0	0.249155	0.794471	1.244139	1.23482
pseudogen	-	0	1	0	0	0	0	0	0.290175	0	0	0	0
lincRNA	-	4	5	5	0	0	1	0.071614	0.105492	0.117963	0	0	0.017793
sense_intrc	-	4	0	0	0	0	0	0.474807	0	0	0	0	0
pseudogen	-	1	1	1	0	0	1	0.083372	0.098248	0.109863	0	0	0.082857
pseudogen	fumarylace	25	12	4	27	16	36	1.371528	0.775806	0.289174	1.28142	0.986129	1.962804
sense_intrc	-	10	11	9	18	18	21	6.15593	7.979826	7.300809	9.585817	12.44845	12.84762
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.106588	0
antisense	-	6	1	13	21	12	11	0.206666	0.040591	0.59006	0.62575	0.464353	0.376548
lincRNA	-	0	0	1	1	0	0	0	0	0.164536	0.108016	0	0
processed_	deleted_in_	90	127	87	169	172	191	3.68214	6.123062	4.690422	5.981464	7.905609	7.766061
antisense	-	11	18	7	22	20	4	0.281465	0.542764	0.236029	0.486987	0.574924	0.101719
lincRNA	-	18	13	13	36	18	34	1.593542	1.356255	1.516593	2.757125	1.790245	2.991434
antisense	-	8	7	2	0	0	0	0.94749	0.976989	0.31214	0	0	0
sense_intrc	-	0	0	0	0	2	0	0	0	0	0	0.233697	0
pseudogen	-	0	2	1	0	0	2	0	0.093325	0.052179	0	0	0.078705
antisense	-	8	0	3	1	3	0	0.295347	0	0.145948	0.031938	0.124427	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.130716	0
pseudogen	-	2	0	0	1	0	0	0.619193	0	0	0.26783	0	0
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.137254
antisense	-	8	4	4	0	12	3	0.353529	0.208306	0.232932	0	0.595752	0.131755
lincRNA	-	1	4	8	0	1	1	0.118969	0.560789	1.254171	0	0.133654	0.118234
antisense	long_interg	1	0	0	0	0	0	0.027191	0	0	0	0	0
antisense	AGBL5_ant	3	0	1	0	1	0	0.390228	0	0.171409	0	0.146132	0
antisense	-	9	3	7	1	2	1	0.163398	0.064185	0.16747	0.015706	0.040793	0.018043
pseudogen	-	6	0	0	0	0	0	1.076766	0	0	0	0	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.086253
antisense	-	2	2	2	0	2	0	0.153675	0.181096	0.202506	0	0.172644	0
lincRNA	-	0	0	0	2	0	0	0	0	0	0.125994	0	0
pseudogen	SPATA31_s	0	0	1	0	0	0	0	0	0.017371	0	0	0
antisense	DLG3_antis	0	1	1	0	2	1	0	0.144416	0.161489	0	0.275351	0.121792
processed_	-	6	2	0	0	0	0	0.931513	0.36591	0	0	0	0
pseudogen	-	0	5	1	3	1	6	0	0.886189	0.198191	0.390332	0.168966	0.89683
antisense	-	12	12	2	15	11	8	1.104856	1.302005	0.242655	1.194754	1.1378	0.732022
pseudogen	2-oxoglutar	4	6	1	1	0	0	0.133018	0.23513	0.043821	0.028768	0	0
lincRNA	-	0	1	0	0	0	0	0	0.074805	0	0	0	0
processed_	-	3	0	1	0	0	0	0.294662	0	0.129431	0	0	0
protein_co	disrupted_i	24	15	24	1	0	3	0.412795	0.304034	0.543963	0.014879	0	0.051281
lincRNA	-	0	0	0	1	0	0	0	0	0	0.046496	0	0

pseudogen	-	0	1	0	0	1	0	0	0.184035	0	0	0.175445	0
pseudogen	-	0	1	1	5	3	7	0	0.063145	0.070611	0.231776	0.180595	0.372772
pseudogen	ribosomal_	1	0	0	0	0	0	0.112163	0	0	0	0	0
lincRNA	-	0	0	2	5	4	3	0	0	0.158373	0.259926	0.270038	0.179162
processed_	long_interg	3	0	2	0	1	0	0.068517	0	0.060193	0	0.025658	0
antisense	-	0	0	0	1	0	0	0	0	0	0.102688	0	0
pseudogen	Nanog_hon	4	4	4	2	0	6	0.240915	0.283903	0.317467	0.104207	0	0.35914
processed_	-	0	0	0	0	0	1	0	0	0	0	0	0.090093
pseudogen	-	2	1	0	0	2	0	0.649583	0.382747	0	0	0.729766	0
pseudogen	-	2	1	0	4	1	6	0.687545	0.405115	0	1.189582	0.386207	2.049898
antisense	-	2	2	1	0	1	0	0.032281	0.038041	0.021269	0	0.018133	0
lincRNA	-	1	1	2	4	0	3	0.096784	0.114054	0.255076	0.33491	0	0.28856
lincRNA	-	0	0	0	4	0	0	0	0	0	0.61682	0	0
pseudogen	poly(A)_bin	3	3	2	0	1	2	0.268736	0.316689	0.236086	0	0.100636	0.178051
lincRNA	-	0	0	0	0	2	1	0	0	0	0	0.141273	0.062487
processed_	-	12	14	13	0	0	1	0.245856	0.338014	0.350976	0	0	0.020361
lincRNA	-	0	3	0	0	0	0	0	0.121377	0	0	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.102722	0
processed_	-	27	23	35	10	4	5	0.407819	0.409392	0.696638	0.130667	0.067876	0.075056
antisense	-	1	0	0	1	1	0	0.098039	0	0	0.084813	0.110141	0
pseudogen	high_mobil	2	0	0	0	3	0	0.399555	0	0	0	0.673312	0
processed_	-	3	11	6	7	6	10	0.129229	0.558393	0.340586	0.260856	0.290362	0.428105
sense_intro	ARHGEF9_i	0	2	1	0	1	0	0	0.316689	0.177064	0	0.150954	0
antisense	-	17	15	13	18	17	23	0.893741	0.929311	0.900618	0.81865	1.004062	1.201711
lincRNA	-	6	4	1	4	3	6	0.208566	0.163855	0.045806	0.120286	0.117155	0.207278
protein_co	tetraspanin	5	0	0	2	0	3	0.069132	0	0	0.023922	0	0.041223
pseudogen	-	0	3	0	1	1	0	0	0.127495	0	0.031198	0.040515	0
lincRNA	-	1	2	2	6	4	14	0.092393	0.217758	0.243502	0.47957	0.41519	1.285509
pseudogen	-	0	1	2	0	3	4	0	0.10278	0.229863	0	0.29395	0.346715
pseudogen	-	0	1	0	0	0	0	0	0.173782	0	0	0	0
pseudogen	embigin_ps	5	2	4	11	14	7	0.29314	0.138179	0.309029	0.557905	0.922107	0.407861
antisense	-	11	6	15	2	4	2	1.406645	0.90417	2.527655	0.221251	0.574647	0.254174
antisense	-	8	3	1	6	8	6	0.379166	0.167559	0.062456	0.24601	0.425969	0.282618
pseudogen	-	1	0	0	0	0	0	0.023169	0	0	0	0	0
antisense	DLX6_antis	0	0	0	145	146	207	0	0	0	1.334038	1.744372	2.187848
pseudogen	microRNA_	1	3	3	2	4	3	0.112401	0.397374	0.444352	0.194475	0.505103	0.335121
lincRNA	-	4	0	1	0	0	0	0.074043	0	0.024393	0	0	0
antisense	-	0	0	0	0	4	3	0	0	0	0	0.514943	0.34165
antisense	TMEM44_a	15	13	16	62	9	37	0.709665	0.72479	0.997509	2.537562	0.478359	1.739696
lincRNA	-	4	13	2	4	2	8	0.027794	0.10645	0.018313	0.024045	0.015613	0.055245
processed_	-	8	3	3	0	0	1	0.840333	0.371356	0.415258	0	0	0.104393
pseudogen	-	0	0	2	0	0	0	0	0	0.455969	0	0	0
pseudogen	diazepam_b	8	2	5	11	16	13	0.15821	0.04661	0.130301	0.188191	0.355478	0.255503
pseudogen	-	0	3	2	0	0	0	0	0.432248	0.322232	0	0	0

pseudogen	ribosomal_	0	0	0	0	1	0	0	0	0	0	0.200932	0
antisense	-	30	19	26	39	26	48	1.691406	1.262372	1.931678	1.902191	1.646831	2.689536
pseudogen	double_C2	42	44	33	10	12	25	1.911885	2.360327	1.979526	0.3938	0.613681	1.130998
antisense	-	1	0	3	0	0	0	0.029249	0	0.11563	0	0	0
sense_intrc	ITCH_intro	2	0	3	2	0	4	0.509048	0	1.006201	0.440374	0	1.011809
pseudogen	-	0	0	0	5	0	5	0	0	0	0.191307	0	0.219775
pseudogen	-	0	3	0	0	0	1	0	0.244338	0	0	0	0.068687
pseudogen	-	0	0	0	1	0	0	0	0	0	0.096622	0	0
processed_	-	3	3	3	13	6	5	0.147058	0.173299	0.193787	0.551283	0.330422	0.243584
lincRNA	-	1	0	0	0	0	4	0.160915	0	0	0	0	0.639685
pseudogen	-	0	0	1	1	0	4	0	0	0.337021	0.221251	0	1.016697
lincRNA	-	0	0	0	25	15	11	0	0	0	1.017753	0.793012	0.514448
pseudogen	-	1	3	3	10	1	4	0.072029	0.254644	0.284748	0.623114	0.08092	0.286335
lincRNA	-	0	0	0	6	9	5	0	0	0	0.127455	0.248276	0.122018
pseudogen	-	0	1	1	0	2	2	0	0.030582	0.034198	0	0.05831	0.051582
lincRNA	-	0	0	0	2	8	1	0	0	0	0.21809	1.132875	0.125272
antisense	-	1	0	0	0	2	4	0.155252	0	0	0	0.348832	0.617174
pseudogen	methylenet	0	0	0	0	1	6	0	0	0	0	0.021518	0.114213
pseudogen	-	0	7	0	4	5	1	0	0.573116	0	0.240414	0.390262	0.069047
lincRNA	-	0	0	0	0	7	0	0	0	0	0	0.714119	0
pseudogen	high_mobil	2	0	2	0	8	2	0.176765	0	0.232932	0	0.794336	0.175673
pseudogen	ubiquitin-c	6	3	0	3	0	3	1.226432	0.722638	0	0.530489	0	0.609429
antisense	-	7	5	5	2	7	9	0.655906	0.552104	0.617374	0.16212	0.73687	0.8381
protein_co	cytochrom	0	3	0	0	1	0	0	0.085776	0	0	0.027258	0
antisense	-	1	1	1	21	7	3	0.093042	0.109645	0.122607	1.690294	0.73169	0.277403
processed_	-	1	0	0	0	0	0	0.108043	0	0	0	0	0
pseudogen	-	0	0	0	0	1	6	0	0	0	0	0.150954	0.801229
protein_co	olfactory_r	0	0	0	1	0	0	0	0	0	0.04366	0	0
sense_intrc	SIK3_intro	14	22	11	1	18	8	0.299828	0.555231	0.310435	0.018527	0.433077	0.170272
pseudogen	keratin_17	0	0	0	0	1	2	0	0	0	0	0.047128	0.083382
antisense	IPO9_antis	5	0	0	0	0	2	0.315501	0	0	0	0	0.125421
pseudogen	-	0	0	1	0	0	0	0	0	0.077257	0	0	0
processed_	-	1	2	9	4	2	3	0.018256	0.043026	0.216507	0.063171	0.041018	0.054428
pseudogen	small_nucl	0	0	1	0	0	0	0	0	0.276838	0	0	0
pseudogen	NADH_deh	0	0	0	0	6	0	0	0	0	0	1.982531	0
pseudogen	MT-ND5_ps	2	1	1	5	1	0	0.303387	0.178761	0.199895	0.656145	0.170418	0
processed_	TRAF3IP2_a	117	95	81	184	105	117	2.827064	2.705082	2.579108	3.846188	2.850284	2.809605
antisense	-	26	37	15	5	5	11	0.987422	1.655915	0.750681	0.164272	0.213328	0.415175
pseudogen	SET_pseudo	1	0	0	1	2	3	0.065038	0	0	0.056264	0.146132	0.193909
pseudogen	glyceraldeh	0	0	0	1	0	0	0	0	0	0.047313	0	0
antisense	IDH1_antis	0	0	2	1	5	9	0	0	0.28533	0.093658	0.608138	0.968357
processed_	-	4	1	1	0	0	0	0.053761	0.015838	0.017711	0	0	0
antisense	NEBL_antis	1	0	0	0	2	7	0.080092	0	0	0	0.179957	0.557184
protein_co	pregnancy_	0	0	0	54	23	42	0	0	0	0.873901	0.483373	0.780845

protein_co	TAP_bindin	1909	1553	1224	1209	989	1063	26.88597	25.77498	22.71622	14.73021	15.64823	14.87862
antisense	-	1	1	0	2	0	0	0.218764	0.257801	0	0.378503	0	0
pseudogen	high_mobil	1	3	0	0	0	0	0.088976	0.31456	0	0	0	0
pseudogen	ribosomal_	0	1	0	2	3	8	0	0.107565	0	0.157927	0.307634	0.725711
pseudogen	-	1	0	2	1	1	2	0.055436	0	0.146101	0.047957	0.062278	0.110186
antisense	PHKA1_ant	0	0	0	0	1	0	0	0	0	0	0.099458	0
sense_intrc	HS1BP3_in	3	0	3	0	2	0	0.264705	0	0.348816	0	0.198253	0
pseudogen	-	4	1	0	10	4	5	0.231436	0.068183	0	0.500534	0.260004	0.287508
antisense	-	48	44	33	61	44	50	1.800969	1.945471	1.631601	1.979967	1.854671	1.864424
antisense	-	0	1	0	0	0	0	0	0.135038	0	0	0	0
pseudogen	-	8	4	8	2	8	5	0.814477	0.479906	1.073281	0.17615	0.915014	0.505904
lincRNA	-	1	0	0	0	0	2	0.149974	0	0	0	0	0.298097
pseudogen	-	3	0	0	0	0	3	0.742163	0	0	0	0	0.73758
antisense	-	3	3	2	1	0	0	0.155404	0.183134	0.136523	0.044813	0	0
antisense	-	23	8	11	6	4	11	2.221976	0.91077	1.400358	0.501448	0.434131	1.056121
lincRNA	-	1	0	0	2	2	1	0.038927	0	0	0.067351	0.087465	0.038687
lincRNA	long_interg	0	0	1	0	0	0	0	0	0.011556	0	0	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.097074
pseudogen	-	1	0	0	0	0	0	0.172446	0	0	0	0	0
pseudogen	ribosomal_	0	0	0	0	2	0	0	0	0	0	0.163171	0
pseudogen	-	24	21	18	19	27	8	3.850254	3.970128	3.80527	2.636907	4.866211	1.275492
antisense	-	0	0	1	0	0	0	0	0	0.410372	0	0	0
pseudogen	protein_ph	0	0	1	3	0	0	0	0	0.035039	0.069009	0	0
pseudogen	annexin_A2	119	126	75	169	109	173	4.809144	6.000652	3.994081	5.908408	4.94876	6.948268
processed_	-	7	7	2	8	4	19	0.810912	0.955611	0.30531	0.801731	0.520577	2.187455
pseudogen	-	1	14	7	0	0	0	0.088088	1.453292	0.812551	0	0	0
protein_co	family_witl	0	0	0	0	2	3	0	0	0	0	0.048611	0.064504
antisense	-	0	5	4	6	22	4	0	0.366555	0.327912	0.322907	1.537568	0.247305
pseudogen	CAP1_pseu	1	0	0	0	1	1	0.037573	0	0	0	0.042211	0.037341
processed_	-	1	0	0	0	0	0	0.042763	0	0	0	0	0
antisense	-	0	0	0	3	0	0	0	0	0	0.262709	0	0
protein_co	HCG17865	0	0	1	1	0	0	0	0	0.038779	0.025458	0	0
pseudogen	-	0	2	0	0	0	0	0	0.497113	0	0	0	0
processed_	LEF1_antis	10	14	6	33	26	44	0.157562	0.259949	0.124577	0.449811	0.46023	0.688994
pseudogen	-	0	0	0	2	2	1	0	0	0	0.072295	0.093885	0.041526
pseudogen	LSM12_hor	4	9	8	6	4	10	0.360143	0.954914	0.94916	0.467336	0.404598	0.894797
pseudogen	-	8	0	2	3	5	4	0.443485	0	0.146101	0.143871	0.311392	0.220373
lincRNA	-	0	0	0	0	3	0	0	0	0	0	0.354023	0
sense_intrc	-	3	1	1	0	0	0	0.337204	0.132458	0.148117	0	0	0
pseudogen	-	3	0	0	0	0	1	0.939781	0	0	0	0	0.311326
sense_intrc	-	13	22	11	0	2	0	0.959879	1.914268	1.070287	0	0.165902	0
pseudogen	-	0	1	1	0	0	0	0	0.047085	0.052652	0	0	0
protein_co	SCAN_dom	15	37	15	98	61	50	0.162829	0.473313	0.214568	0.920298	0.743906	0.53941
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.14869	0

antisense	-	13	19	10	0	3	6	0.15004	0.258419	0.152089	0	0.038899	0.068822
processed_	-	2	6	3	2	2	0	0.031806	0.112444	0.062869	0.027515	0.035732	0
processed_	-	0	0	0	0	3	4	0	0	0	0	0.261624	0.308587
lincRNA	-	0	5	2	0	1	0	0	0.350887	0.156948	0	0.066902	0
pseudogen	nucleopho	0	0	5	0	0	0	0	0	0.390612	0	0	0
pseudogen	-	2	1	2	1	4	1	0.363856	0.214391	0.479473	0.157385	0.817538	0.180804
pseudogen	-	0	0	0	3	1	0	0	0	0	0.228234	0.098797	0
processed_	-	2	3	4	1	0	1	0.048974	0.086569	0.129072	0.021184	0	0.024336
antisense	-	1	0	0	6	7	6	0.152129	0	0	0.789636	1.196355	0.907139
protein_co	transmemb	1	0	2	2	1	2	0.034693	0	0.091433	0.060025	0.038975	0.068957
antisense	-	4	0	1	0	0	0	0.373481	0	0.123039	0	0	0
pseudogen	mitochond	0	1	0	0	0	0	0	0.122089	0	0	0	0
lincRNA	-	4	2	0	1	0	4	0.271841	0.160174	0	0.058792	0	0.270162
lincRNA	-	1	2	0	0	0	0	0.030183	0.071138	0	0	0	0
sense_intro	LARGE_intr	1	0	2	0	0	0	0.094876	0	0.250048	0	0	0
sense_intro	RPS6KA2_i	9	7	8	4	0	2	0.822917	0.754256	0.963914	0.3164	0	0.181741
pseudogen	ribosomal_	1	0	0	4	0	0	0.13471	0	0	0.466147	0	0
antisense	-	5	0	2	9	15	20	0.322026	0	0.16974	0.501448	1.085327	1.280147
pseudogen	-	5	0	0	1	4	1	0.743553	0	0	0.128649	0.668269	0.147792
lincRNA	-	216	205	142	151	169	186	3.738233	4.180936	3.238439	2.26075	3.285855	3.199154
pseudogen	-	0	0	0	1	0	0	0	0	0	0.303304	0	0
pseudogen	MT-CO3_ps	0	0	0	2	0	0	0	0	0	0.53566	0	0
lincRNA	-	2	2	3	2	4	6	0.191815	0.226042	0.379148	0.165938	0.430985	0.571892
antisense	-	9	10	6	8	1	2	0.790164	1.034622	0.694162	0.607614	0.098633	0.174508
pseudogen	-	0	0	0	2	0	2	0	0	0	0.007755	0	0.008909
protein_co	translation	190	167	119	500	241	325	14.62033	15.14353	12.06661	33.28409	20.83386	24.85402
pseudogen	-	2	0	0	0	0	0	0.231689	0	0	0	0	0
lincRNA	-	2	6	0	2	0	3	0.113243	0.400349	0	0.097966	0	0.168815
lincRNA	-	1	0	0	1	0	1	0.007726	0	0	0.006684	0	0.007679
lincRNA	BACH1_ant	1	1	0	5	1	3	0.219672	0.25887	0	0.950185	0.246788	0.654947
protein_co	malignant_	631	627	503	1278	869	934	29.56263	34.61691	31.05392	51.79735	45.73856	43.48807
antisense	-	0	0	0	0	5	0	0	0	0	0	0.37219	0
pseudogen	-	0	4	3	3	0	3	0	1.279748	1.073281	0.704599	0	0.809447
antisense	-	3	0	0	3	0	1	0.317012	0	0	0.274245	0	0.105018
pseudogen	-	2	3	0	1	0	2	0.272892	0.482379	0	0.118038	0	0.271206
pseudogen	double_ho	1	0	2	0	0	0	0.076837	0	0.202506	0	0	0
lincRNA	long_interg	0	1	0	5	0	3	0	0.107565	0	0.394818	0	0.272142
pseudogen	-	1	0	0	3	0	0	0.210083	0	0	0.545225	0	0
pseudogen	fer_(fps/fes	0	3	1	5	1	0	0	0.236019	0.087974	0.28877	0.075001	0
pseudogen	suppressio	1	2	3	3	4	4	0.048436	0.114159	0.191482	0.125706	0.217661	0.192549
processed_	-	0	4	0	4	2	2	0	0.043552	0	0.031971	0.020759	0.018364
antisense	-	27	25	16	32	16	26	0.411459	0.448962	0.321305	0.421867	0.273925	0.393772
antisense	USP12_ant	5	4	1	0	3	0	0.987705	0.93116	0.260311	0	0.665775	0
pseudogen	ribosomal_	2	8	11	5	0	3	0.35412	1.669237	2.566542	0.765868	0	0.5279

pseudogen	-	0	0	0	1	0	3	0	0	0	0.064324	0	0.221688
pseudogen	-	8	7	8	7	7	4	0.344892	0.35563	0.454484	0.261069	0.339032	0.171381
pseudogen	ferritin_hea	11	9	14	16	3	7	1.054984	1.017191	1.769359	1.327505	0.323239	0.667207
processed_	-	0	0	2	0	0	0	0	0	0.034173	0	0	0
antisense	-	42	37	33	7	8	4	2.745089	2.84981	2.842208	0.395793	0.587416	0.259822
antisense	-	0	0	0	4	6	9	0	0	0	0.255147	0.497013	0.659508
protein_co	MT-RNR2-li	0	0	0	0	0	3	0	0	0	0	0	0.128223
pseudogen	-	5	4	2	0	0	0	0.270107	0.254644	0.142374	0	0	0
pseudogen	prohibitin_	8	3	0	0	0	6	0.636884	0.281448	0	0	0	0.474713
lincRNA	-	0	0	0	3	2	6	0	0	0	0.259239	0.224437	0.595631
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.055972
pseudogen	ferritin_ligh	0	0	1	0	0	0	0	0	0.261286	0	0	0
pseudogen	-	5	7	1	2	6	8	1.31694	2.172707	0.347081	0.455711	1.775401	2.094092
lincRNA	long_interg	21	13	10	3	5	8	0.307116	0.224044	0.192716	0.037955	0.082149	0.116274
pseudogen	-	1	1	0	0	4	0	0.166481	0.196188	0	0	0.748125	0
processed_	-	8	1	4	12	6	6	0.231183	0.034054	0.152322	0.299993	0.19479	0.172317
protein_co	achaete-scu	0	3	0	2	0	0	0	0.092381	0	0.045211	0	0
pseudogen	colony_stir	0	0	0	0	1	0	0	0	0	0	0.152112	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.079513	0
pseudogen	basic_trans	0	0	0	0	4	1	0	0	0	0	0.505103	0.111707
pseudogen	integrator_	8	3	2	1	4	0	0.301873	0.133402	0.099449	0.032644	0.169568	0
pseudogen	ferritin_hea	1	5	2	3	2	1	0.099513	0.586351	0.262268	0.258265	0.223594	0.098899
lincRNA	-	9	8	12	20	25	13	0.082391	0.086305	0.144762	0.158392	0.257115	0.118275
pseudogen	MT-ND1_ps	0	0	0	0	0	1	0	0	0	0	0	0.056092
antisense	GNG12_ant	63	45	57	19	33	28	1.494302	1.257817	1.781589	0.389865	0.879348	0.660033
pseudogen	transcriptio	0	0	0	0	2	0	0	0	0	0	0.404598	0
antisense	-	2	1	1	4	2	1	0.267379	0.157545	0.17617	0.462615	0.300383	0.132864
antisense	-	217	178	189	119	96	65	12.14397	11.73892	13.93791	5.761173	6.035611	3.61513
antisense	-	0	0	0	0	1	0	0	0	0	0	0.069481	0
sense_intro	family_with	5	3	1	0	5	4	0.121257	0.085737	0.031958	0	0.136225	0.096407
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.139191
pseudogen	-	4	4	3	3	1	4	0.216306	0.254904	0.213779	0.140344	0.060752	0.214971
antisense	-	1	0	0	0	0	0	0.094034	0	0	0	0	0
processed_	-	0	0	0	4	3	1	0	0	0	0.205376	0.200031	0.058984
lincRNA	-	0	0	0	4	0	4	0	0	0	0.393969	0	0.452594
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.113504	0
pseudogen	-	5	2	11	3	5	0	0.515994	0.243227	1.495899	0.26783	0.579687	0
lincRNA	-	3	0	0	4	8	1	0.286168	0	0	0.330082	0.857311	0.0948
lincRNA	-	0	0	0	0	0	3	0	0	0	0	0	0.207961
pseudogen	-	3	0	0	0	0	0	0.062553	0	0	0	0	0
pseudogen	ribosomal_	0	2	0	0	0	2	0	0.268334	0	0	0	0.226297
pseudogen	-	8	2	7	0	0	0	0.80672	0.237668	0.930177	0	0	0
antisense	-	2	4	0	2	0	5	0.11804	0.278206	0	0.102116	0	0.293278
pseudogen	-	15	6	10	18	7	10	0.930967	0.438835	0.817858	0.966448	0.488079	0.616812

processed_	-	7	3	1	6	18	22	0.524911	0.265104	0.098815	0.389226	1.516383	1.639531
antisense	-	3	1	2	1	0	1	0.46989	0.184579	0.4128	0.1355	0	0.155663
antisense	VIPR1_anti	0	0	0	8	4	7	0	0	0	0.452335	0.293708	0.454689
antisense	-	0	0	0	0	2	3	0	0	0	0	0.148319	0.196811
lincRNA	-	1	0	0	0	0	0	0.093206	0	0	0	0	0
antisense	-	1	0	0	1	0	0	0.097139	0	0	0.084035	0	0
pseudogen	-	2	0	0	0	0	0	0.215207	0	0	0	0	0
pseudogen	-	29	17	11	24	37	50	4.264691	2.946087	2.131656	3.05326	6.112803	7.307507
pseudogen	MT-CYB_ps	0	0	0	0	2	0	0	0	0	0	0.104619	0
pseudogen	G_protein-	1	5	1	0	0	0	0.048749	0.287236	0.064239	0	0	0
antisense	-	2	1	2	0	0	1	0.101226	0.059644	0.133391	0	0	0.0503
pseudogen	-	0	2	0	0	0	0	0	0.323252	0	0	0	0
pseudogen	ribosomal_	11	20	6	22	8	5	0.734364	1.573461	0.527843	1.270588	0.600009	0.331741
pseudogen	spindle_an	0	0	0	0	0	2	0	0	0	0	0	0.269816
lincRNA	long_interg	494	340	331	513	362	640	51.78782	42.00362	45.72603	46.52443	42.63422	66.67919
pseudogen	-	0	0	0	2	0	1	0	0	0	0.083195	0	0.047788
pseudogen	transmemb	3	2	3	1	3	0	0.232537	0.182687	0.306427	0.067055	0.261241	0
processed_	-	0	0	4	0	5	4	0	0	0.103315	0	0.1101	0.077918
lincRNA	-	2	6	0	0	0	0	0.209253	0.739775	0	0	0	0
lincRNA	-	0	1	0	0	2	1	0	0.191373	0	0	0.364883	0.161393
pseudogen	-	0	0	1	0	0	0	0	0	0.048514	0	0	0
pseudogen	-	2	0	0	1	0	3	0.31326	0	0	0.1355	0	0.466989
protein_co	chromoson	257	226	178	41	59	39	4.642046	4.810518	4.236733	0.640653	1.197229	0.700085
pseudogen	-	0	2	4	0	0	2	0	0.382747	0.855991	0	0	0.322786
pseudogen	ribosomal_	12	7	7	0	11	5	1.212389	0.833424	0.931952	0	1.24854	0.502042
antisense	-	67	49	48	120	64	69	4.428273	3.816478	4.180571	6.861259	4.752133	4.532296
lincRNA	-	0	0	1	0	0	5	0	0	0.094275	0	0	0.3555
antisense	-	13	7	15	175	105	146	0.976217	0.619453	1.484325	11.36852	8.858115	10.89596
lincRNA	-	1	0	0	0	0	0	0.118702	0	0	0	0	0
pseudogen	-	7	2	9	11	11	2	0.495437	0.166812	0.839398	0.673513	0.874646	0.140679
lincRNA	-	12	6	5	6	0	0	0.524601	0.309105	0.28804	0.226914	0	0
pseudogen	-	3	1	0	2	2	7	0.452487	0.177743	0	0.260962	0.338894	1.049283
antisense	LARS2_anti	0	1	0	0	2	0	0	0.1085	0	0	0.206873	0
pseudogen	-	3	2	4	4	4	6	0.149974	0.117824	0.263506	0.172989	0.224649	0.298097
lincRNA	-	9	0	0	0	0	0	0.146022	0	0	0	0	0
pseudogen	bone_morp	0	0	0	1	0	3	0	0	0	0.045167	0	0.155663
lincRNA	-	0	0	0	0	4	4	0	0	0	0	0.35089	0.310407
pseudogen	-	0	0	0	0	5	3	0	0	0	0	0.799407	0.424307
pseudogen	translation	0	0	0	0	1	3	0	0	0	0	0.098962	0.262633
lincRNA	-	4	1	0	7	2	8	0.52809	0.15558	0	0.799482	0.296638	1.049657
pseudogen	eukaryotic_	37	19	26	47	19	39	2.88911	1.748329	2.675288	3.17485	1.666729	3.026472
sense_intrc	NCKAP5_in	0	0	0	0	1	1	0	0	0	0	0.107357	0.094971
pseudogen	-	0	1	2	2	3	6	0	0.048139	0.107659	0.070677	0.137676	0.243584
antisense	-	995	850	1278	38	67	78	94.57143	95.20569	160.0673	3.124521	7.154195	7.367856

pseudogen	-	1	0	1	0	0	0	0.124275	0	0.163764	0	0	0
processed_	-	7	0	1	3	3	16	0.494116	0	0.093018	0.183196	0.237904	1.122433
pseudogen	-	0	0	0	0	1	2	0	0	0	0	0.024435	0.043233
sense_intrc	RASA3_intr	12	14	4	0	5	1	1.671821	2.298495	0.73435	0	0.782578	0.138458
pseudogen	microfibrill	6	1	1	0	1	7	0.253104	0.049711	0.055588	0	0.047391	0.293465
antisense	OSBPL10_a	0	2	1	0	8	3	0	0.217001	0.121327	0	0.827491	0.274508
pseudogen	-	0	2	0	0	0	0	0	0.146795	0	0	0	0
pseudogen	nucleopho	6	0	5	2	0	1	0.367221	0	0.403256	0.105893	0	0.060825
pseudogen	ribosomal_	0	0	1	0	5	1	0	0	0.139248	0	0.593572	0.105018
pseudogen	-	5	6	2	10	9	5	0.257245	0.363777	0.135594	0.445082	0.520198	0.255656
processed_	-	1	0	0	1	0	6	0.067613	0	0	0.058492	0	0.403173
pseudogen	-	1	0	0	0	0	0	0.007567	0	0	0	0	0
antisense	-	3	0	0	1	0	1	0.287723	0	0	0.082969	0	0.095315
antisense	-	1	2	0	4	2	1	0.118172	0.278517	0	0.408919	0.265517	0.117442
antisense	-	3	0	1	0	0	0	0.089985	0	0.039526	0	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.06125
lincRNA	-	441	326	299	169	85	128	38.59005	33.61719	34.47805	12.79341	8.356121	11.13157
pseudogen	-	0	0	0	1	0	0	0	0	0	0.033503	0	0
antisense	-	0	2	1	4	3	1	0	0.154425	0.086341	0.226727	0.220826	0.065116
pseudogen	-	0	0	1	0	2	2	0	0	0.066064	0	0.112644	0.099648
antisense	-	146	118	108	163	83	112	11.92806	11.36073	11.62721	11.5204	7.618057	9.093786
pseudogen	olfactory_r	0	0	0	1	0	2	0	0	0	0.049193	0	0.113027
processed_	-	0	0	0	1	3	8	0	0	0	0.08707	0.339216	0.800214
pseudogen	ribosomal_	0	0	2	0	0	0	0	0	0.463543	0	0	0
sense_intrc	-	27	16	28	2	12	9	2.561661	1.788895	3.500666	0.164154	1.279052	0.848614
pseudogen	-	17	12	8	10	18	22	3.020124	2.512258	1.87284	1.536876	3.592505	3.884259
pseudogen	-	1	0	0	0	0	0	0.040913	0	0	0	0	0
pseudogen	-	139	179	89	165	169	236	7.681418	11.657	6.48114	7.88812	10.4921	12.96129
protein_co	chromoson	1	0	0	0	0	1	0.074147	0	0	0	0	0.073689
pseudogen	general_tra	28	37	35	43	16	25	0.563845	0.878032	0.928762	0.749088	0.361968	0.500324
antisense	-	10	13	12	10	11	17	0.274022	0.419793	0.433312	0.237054	0.338631	0.46296
pseudogen	-	0	0	0	0	1	7	0	0	0	0	0.118714	0.735126
pseudogen	ribosomal_	143	159	92	151	75	178	17.89731	23.45071	15.1731	16.34902	10.54538	22.14019
pseudogen	-	2	0	1	0	1	0	0.052391	0	0.034519	0	0.029429	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.232806
processed_	-	1	0	0	0	0	0	0.123406	0	0	0	0	0
processed_	-	7	2	1	3	5	9	0.257352	0.08665	0.048447	0.095414	0.206514	0.328838
pseudogen	eukaryotic_	3	0	6	5	5	3	0.114674	0	0.302224	0.165339	0.214715	0.113965
lincRNA	-	34	35	25	24	12	30	1.505012	1.825728	1.458263	0.919042	0.596748	1.31975
pseudogen	-	0	0	2	1	2	1	0	0	0.261286	0.085766	0.222756	0.098528
antisense	-	9	13	4	3	5	16	0.858503	1.461334	0.502798	0.247562	0.535819	1.516801
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.164298	0
pseudogen	translocase	1	7	2	3	1	0	0.199026	1.641782	0.524536	0.516529	0.223594	0
lincRNA	-	55	50	43	54	22	42	0.964796	1.033594	0.993977	0.819464	0.433555	0.732203

antisense	-	0	0	0	2	0	0	0	0	0	0.089978	0	0
lincRNA	-	1	0	0	0	0	0	0.095561	0	0	0	0	0
antisense	-	1	5	1	0	3	0	0.090964	0.535977	0.119868	0	0.306577	0
pseudogen	-	2	0	1	0	0	0	0.09042	0	0.059576	0	0	0
pseudogen	-	5	0	1	4	0	0	0.73734	0	0.194327	0.510294	0	0
sense_intrc	-	4	0	3	0	1	5	0.268056	0	0.264924	0	0.075286	0.333
pseudogen	phosphorib	11	12	10	31	16	38	0.621506	0.798989	0.744539	1.515225	1.015597	2.133761
pseudogen	MT-ND2_ps	0	0	0	0	0	3	0	0	0	0	0	0.242461
antisense	-	5	2	2	3	0	1	0.078758	0.037125	0.041513	0.04088	0	0.015654
pseudogen	neurofilam	3	0	6	0	0	0	0.161405	0	0.425386	0	0	0
pseudogen	-	53	43	51	42	80	41	0.51053	0.488114	0.647367	0.349992	0.865734	0.392499
antisense	-	17	14	12	65	30	33	2.233243	2.167316	2.077319	7.38692	4.427488	4.308347
antisense	-	1	2	3	0	0	0	0.066845	0.157545	0.264255	0	0	0
antisense	-	3	0	7	3	5	6	0.308994	0	0.950084	0.267309	0.57856	0.614172
pseudogen	-	6	11	4	0	0	1	1.484327	3.206846	1.303987	0	0	0.24586
antisense	-	14	15	6	28	18	24	1.325893	1.674089	0.748801	2.294042	1.915146	2.258922
lincRNA	-	0	0	0	3	3	0	0	0	0	0.310852	0.403683	0
protein_co	golgin_A8_	8	4	10	0	1	5	0.212082	0.124963	0.34934	0	0.029783	0.131733
antisense	IDI2_antise	3	0	0	6	10	0	0.150686	0	0	0.260715	0.564288	0
pseudogen	lactate_deh	0	0	2	0	3	6	0	0	0.124689	0	0.159453	0.282113
protein_co	Uncharacte	0	2	0	6	4	6	0	0.200604	0	0.44179	0.382482	0.507531
lincRNA	long_interg	144	141	91	1174	724	849	2.790448	3.219865	2.32374	19.68079	15.76155	16.35041
lincRNA	-	22	23	6	0	0	0	2.072423	2.553234	0.744804	0	0	0
antisense	-	8	7	10	1	1	2	0.273951	0.28248	0.45125	0.029624	0.038471	0.068065
antisense	ATP11A_an	2	0	1	4	1	1	0.048304	0	0.031826	0.083575	0.027133	0.024003
sense_intrc	ARID4B_int	9	0	2	2	2	2	1.029091	0	0.301353	0.197835	0.256915	0.227275
sense_intrc	-	0	0	0	8	9	0	0	0	0	0.793055	1.158622	0
antisense	-	12	3	9	10	1	6	0.589325	0.173621	0.582439	0.424851	0.055172	0.292843
processed_	-	4	0	2	4	0	1	0.399555	0	0.263258	0.345652	0	0.099272
antisense	-	2	0	0	0	0	0	0.228194	0	0	0	0	0
lincRNA	-	0	3	1	0	0	0	0	0.40424	0.150677	0	0	0
pseudogen	-	0	0	2	4	0	1	0	0	0.30531	0.400866	0	0.115129
pseudogen	NUT_family	0	0	0	0	0	1	0	0	0	0	0	0.030986
pseudogen	MAP/microc	0	0	2	3	6	3	0	0	0.080791	0.079558	0.206633	0.091397
sense_intrc	-	10	12	11	1	10	4	0.793718	1.122418	1.150519	0.068664	0.891693	0.315527
antisense	-	8	6	5	4	0	0	0.078884	0.06972	0.064969	0.034121	0	0
pseudogen	-	1	3	1	2	3	0	0.132022	0.466741	0.173973	0.228423	0.444957	0
pseudogen	-	2	0	5	0	0	0	0.061452	0	0.202447	0	0	0
pseudogen	tripartite_r	1	5	5	0	0	0	0.040107	0.236317	0.264255	0	0	0
lincRNA	-	0	0	0	2	0	0	0	0	0	0.072181	0	0
processed_	-	0	0	0	0	1	1	0	0	0	0	0.05543	0.049035
pseudogen	-	0	0	0	3	0	0	0	0	0	0.048243	0	0
antisense	-	4	7	1	1	2	0	0.231689	0.477805	0.076327	0.050108	0.130144	0
processed_	-	29	22	27	5	7	8	1.210796	1.082437	1.485496	0.180595	0.328337	0.33195

processed_	-	1	1	3	20	16	11	0.053911	0.063531	0.213126	0.932768	0.969058	0.589363
antisense	-	3	3	1	8	1	3	0.200029	0.235722	0.087863	0.46145	0.074907	0.198794
lincRNA	-	3	0	0	0	0	0	0.271957	0	0	0	0	0
pseudogen	ras_homol	1	1	11	5	2	1	0.088235	0.10398	1.278994	0.381658	0.198253	0.08769
pseudogen	ankyrin_re	0	0	1	3	0	0	0	0	0.039956	0.078692	0	0
pseudogen	-	4	1	3	0	1	0	0.615593	0.18136	0.608401	0	0.172895	0
antisense	-	1	4	1	1	0	0	0.148294	0.699022	0.195415	0.128288	0	0
antisense	-	0	0	0	1	3	3	0	0	0	0.023307	0.090803	0.080327
pseudogen	eukaryotic_	1	1	1	0	2	0	0.053802	0.063402	0.070898	0	0.120886	0
processed_	-	4	1	1	12	9	14	0.087074	0.025653	0.028686	0.225981	0.2201	0.302877
antisense	-	0	5	3	1	8	2	0	0.414812	0.278311	0.060903	0.632723	0.139931
pseudogen	-	0	2	2	2	0	0	0	0.765494	0.855991	0.56195	0	0
protein_co	Uncharacte	22	19	12	6	5	9	0.703747	0.716234	0.505836	0.166038	0.179686	0.286119
pseudogen	mitochond	0	0	0	0	1	0	0	0	0	0	0.158181	0
pseudogen	ribosomal_	6	1	0	0	2	1	0.698123	0.137116	0	0	0.261433	0.115635
antisense	-	0	4	1	0	5	0	0	0.330969	0.092524	0	0.394403	0
pseudogen	-	0	3	0	0	0	0	0	1.641782	0	0	0	0
processed_	-	0	0	0	0	2	2	0	0	0	0	0.266111	0.23541
pseudogen	ferritin_he	0	1	0	0	1	1	0	0.133023	0	0	0.126814	0.112183
pseudogen	DnaJ_(Hsp	7	11	8	3	1	0	1.430838	2.649672	2.15485	0.530489	0.229637	0
pseudogen	SCAN_dom	0	0	0	0	0	2	0	0	0	0	0	0.099272
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.152064
pseudogen	crystallin_	0	0	0	5	0	2	0	0	0	0.361761	0	0.166237
antisense	-	0	1	0	0	0	0	0	0.043935	0	0	0	0
antisense	-	0	0	0	0	3	0	0	0	0	0	0.278793	0
protein_co	tumor_nec	0	0	1	14	1	0	0	0	0.041625	0.382568	0.035487	0
antisense	-	20	19	6	22	17	7	0.448843	0.502487	0.177439	0.42712	0.42861	0.156125
antisense	COL4A2_an	8	0	1	6	10	0	0.784311	0	0.129191	0.508877	1.101406	0
pseudogen	-	29	18	16	52	44	56	2.147257	1.5706	1.561136	3.330829	3.660056	4.120821
pseudogen	ribosomal_	23	13	12	51	21	29	1.36507	0.909238	0.938519	2.618547	1.400218	1.710546
antisense	-	76	82	44	80	66	50	2.351558	2.989944	1.794029	2.141387	2.29422	1.537523
pseudogen	-	0	0	2	0	1	1	0	0	0.341977	0	0.145774	0.128956
processed_	-	0	0	2	0	0	0	0	0	0.042013	0	0	0
antisense	-	0	0	1	0	0	0	0	0	0.07542	0	0	0
pseudogen	-	2	0	0	0	1	0	0.260793	0	0	0	0.146492	0
antisense	LMLN_anti	0	0	1	0	0	0	0	0	0.128715	0	0	0
protein_co	family_wit	8	13	3	39	20	25	0.281227	0.538539	0.138971	1.186027	0.789853	0.873407
lincRNA	-	2	0	0	0	0	0	0.066259	0	0	0	0	0
pseudogen	-	0	1	0	3	0	0	0	0.159969	0	0.352299	0	0
pseudogen	solute_carr	0	1	0	0	1	0	0	0.070976	0	0	0.067663	0
pseudogen	-	2	0	0	0	0	0	0.132352	0	0	0	0	0
protein_co	-	0	2	1	0	4	0	0	0.179275	0.100235	0	0.341816	0
pseudogen	capicua_tr	1	0	1	1	0	0	0.018827	0	0.024809	0.016287	0	0
pseudogen	leucine_zip	0	0	0	0	1	2	0	0	0	0	0.172895	0.305896

lincRNA	-	8	17	7	0	0	0	0.470587	1.178435	0.542603	0	0	0
protein_co	LYR_motif_	44	31	20	26	11	15	0.82486	0.684851	0.494074	0.421661	0.23167	0.279466
processed_	SMG7_anti	11	4	17	5	8	4	0.259284	0.111109	0.528039	0.101957	0.211847	0.093703
pseudogen	-	0	0	1	0	0	1	0	0	0.077687	0	0	0.05859
pseudogen	secretory_t	4	1	1	0	0	0	0.140148	0.041289	0.04617	0	0	0
pseudogen	CTAGE_fam	3	6	2	0	3	1	0.066066	0.15571	0.058039	0	0.074221	0.021886
antisense	-	0	1	0	0	0	1	0	0.145088	0	0	0	0.122358
pseudogen	high_mobil	6	1	1	0	0	3	1.176467	0.231066	0.258383	0	0	0.584601
antisense	-	1	1	0	0	0	0	0.067014	0.078972	0	0	0	0
pseudogen	-	0	0	0	3	1	1	0	0	0	0.794201	0.343791	0.304127
pseudogen	-	0	0	0	1	0	2	0	0	0	0.127574	0	0.293114
pseudogen	phosphoryl	6	0	3	0	0	1	0.511507	0	0.337021	0	0	0.084725
antisense	GPC5_antis	0	0	0	0	2	0	0	0	0	0	0.296638	0
pseudogen	ribosomal_	45	52	37	17	18	25	4.901944	6.67523	5.311196	1.602019	2.202812	2.706484
sense_intrc	-	0	0	0	0	4	3	0	0	0	0	0.629375	0.417572
antisense	-	0	0	1	0	0	3	0	0	0.026496	0	0	0.059948
pseudogen	cytochrom	6	6	2	20	4	1	1.080428	1.273219	0.47458	3.115572	0.809196	0.178959
processed_	-	0	0	0	0	0	1	0	0	0	0	0	0.020089
pseudogen	-	3	0	2	7	5	14	0.127774	0	0.11225	0.257918	0.239243	0.592596
processed_	-	14	4	6	9	17	13	0.989551	0.333179	0.558851	0.550321	1.349921	0.913194
antisense	-	6	6	7	1	3	1	0.474807	0.559531	0.72996	0.068459	0.266708	0.078646
antisense	-	0	6	0	3	2	2	0	0.725439	0	0.266273	0.230527	0.20393
antisense	-	1	4	1	0	0	1	0.032842	0.154808	0.043277	0	0	0.032639
pseudogen	-	0	0	1	0	1	0	0	0	0.055677	0	0.047467	0
pseudogen	high_mobil	1	0	0	3	0	0	0.196078	0	0	0.508877	0	0
pseudogen	-	0	0	0	2	1	0	0	0	0	0.134308	0.087208	0
pseudogen	DEAD_(Asp	4	4	2	0	4	2	0.108597	0.127975	0.071552	0	0.122002	0.053963
lincRNA	long_interg	241	211	106	99	78	84	5.426959	5.599239	3.145431	1.92858	1.973255	1.879872
antisense	-	0	0	0	2	0	0	0	0	0	0.162696	0	0
pseudogen	-	9	2	4	10	2	9	0.211201	0.055308	0.123694	0.203009	0.052727	0.209896
antisense	HLA_compl	4	7	1	2	4	8	0.279004	0.575381	0.091915	0.120682	0.313444	0.554562
pseudogen	-	0	0	0	3	4	0	0	0	0	0.415096	0.718742	0
pseudogen	heat_shock	3	1	2	2	0	1	0.082377	0.032359	0.072369	0.047509	0	0.027289
lincRNA	small_nucl	335	371	209	688	463	645	5.691667	7.428064	4.679245	10.11221	8.837404	10.89091
pseudogen	high_mobil	0	1	0	0	0	0	0	0.228526	0	0	0	0
pseudogen	polymerase	3	4	3	3	0	1	0.337921	0.530959	0.445298	0.292333	0	0.111945
antisense	CYP1B1_an	39	26	36	13	21	15	1.175127	0.923211	1.429413	0.338865	0.710868	0.449181
lincRNA	long_interg	30	24	41	32	9	14	0.761011	0.717444	1.370529	0.702235	0.256485	0.352945
antisense	-	2	0	0	0	0	2	0.25888	0	0	0	0	0.257281
lincRNA	-	0	0	0	3	1	0	0	0	0	0.1903	0.082377	0
pseudogen	ribosomal_	5	0	1	3	0	0	0.357227	0	0.094147	0.185421	0	0
processed_	-	16	14	11	52	33	23	0.587825	0.606126	0.532544	1.652702	1.362044	0.83978
processed_	-	3	0	1	32	30	26	0.088629	0	0.03893	0.817838	0.995691	0.763373
processed_	-	0	0	2	9	6	0	0	0	0.043918	0.129742	0.112325	0

antisense	NALCN_ant	3	1	0	2	0	0	0.055806	0.021921	0	0.032185	0	0
pseudogen	ribulose-5-p	1	3	2	0	3	2	0.087942	0.310902	0.231772	0	0.296392	0.174798
pseudogen	histone_de	0	0	2	0	7	5	0	0	0.099804	0	0.297805	0.188176
lincRNA	family_with	8	3	3	1	3	2	0.235949	0.104269	0.116596	0.025515	0.099403	0.058623
pseudogen	solute_carr	0	0	0	0	0	1	0	0	0	0	0	0.067889
antisense	small_nucl	2797	2322	1686	2043	1563	2177	62.82391	61.46131	49.9028	39.69757	39.44033	48.59601
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.220604
pseudogen	-	0	0	0	1	0	0	0	0	0	0.20265	0	0
antisense	-	1	0	1	4	1	0	0.094876	0	0.125024	0.328308	0.106588	0
protein_co	NPIP-like_p	1	1	0	1	0	0	0.034222	0.040328	0	0.029605	0	0
pseudogen	crystallin_z	12	9	1	2	6	2	0.670847	0.592914	0.073668	0.096724	0.376827	0.111117
processed_	-	2	2	0	1	6	1	0.029885	0.035217	0	0.012927	0.100721	0.01485
antisense	-	9	17	6	7	2	7	0.134482	0.299348	0.118143	0.090486	0.033574	0.103951
antisense	CASK_antis	3	0	0	1	0	1	0.308394	0	0	0.08893	0	0.102163
pseudogen	family_with	0	2	0	0	0	0	0	0.177996	0	0	0	0
antisense	-	0	2	2	0	0	0	0	0.294977	0.32985	0	0	0
pseudogen	-	2	0	0	3	4	0	0.16622	0	0	0.215693	0.373475	0
lincRNA	-	0	1	1	0	0	0	0	0.02057	0.023001	0	0	0
antisense	endogenou	10	8	8	93	95	110	0.189753	0.17889	0.200038	1.52663	2.025166	2.074389
processed_	-	4	1	7	13	2	1	0.079016	0.023279	0.182218	0.222159	0.044385	0.019632
lincRNA	-	0	0	2	1	0	0	0	0	0.311443	0.10223	0	0
sense_intro	TTLL7_intro	3	1	5	1	5	8	0.054373	0.021358	0.119417	0.015679	0.101807	0.144099
lincRNA	-	0	0	1	0	0	0	0	0	0.16974	0	0	0
processed_	-	0	0	0	6	0	1	0	0	0	0.382721	0	0.073279
processed_	ZFY_antiser	0	0	2	1	1	2	0	0	0.279053	0.091598	0.118952	0.210456
pseudogen	-	0	1	1	0	0	0	0	0.162046	0.181203	0	0	0
antisense	-	0	1	0	0	2	2	0	0.090812	0	0	0.173147	0.15317
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.626358
processed_	-	1	1	1	0	0	0	0.023529	0.027728	0.031006	0	0	0
lincRNA	-	0	4	0	1	2	1	0	0.526479	0	0.096622	0.250953	0.111
pseudogen	-	3	0	1	4	1	2	0.34303	0	0.150677	0.395671	0.128458	0.227275
lincRNA	-	0	0	1	0	0	0	0	0	0.106672	0	0	0
lincRNA	-	0	1	0	1	10	0	0	0.034892	0	0.025615	0.332639	0
pseudogen	-	1	0	0	0	0	0	0.014441	0	0	0	0	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.17754	0
antisense	-	0	0	4	164	112	127	0	0	0.074873	2.015299	1.78731	1.792859
antisense	-	2	0	4	0	0	0	0.280854	0	0.740194	0	0	0
antisense	HOXB_clust	1	6	2	127	112	156	0.071253	0.503804	0.187788	7.828346	8.965414	11.04683
lincRNA	-	0	0	0	2	1	0	0	0	0	0.191627	0.124427	0
antisense	-	1	0	1	0	1	0	0.093206	0	0.122823	0	0.104711	0
pseudogen	-	3	3	0	0	0	0	0.341555	0.402501	0	0	0	0
antisense	-	0	0	0	7	4	3	0	0	0	0.179202	0.132981	0.088229
pseudogen	RAB1C_mer	0	0	0	0	1	1	0	0	0	0	0.098145	0.086822
pseudogen	-	1	3	0	0	0	0	0.234252	0.828156	0	0	0	0

lincRNA	long_interg	25	14	11	9	1	9	2.967545	1.958359	1.720619	0.924193	0.133354	1.061719
pseudogen	vomeronas	0	0	0	0	1	0	0	0	0	0	0.061569	0
pseudogen	CTAGE_fam	7	15	7	5	32	16	0.131274	0.331497	0.172987	0.081117	0.674187	0.298202
lincRNA	-	1	0	1	2	1	0	0.076504	0	0.100814	0.132367	0.085948	0
pseudogen	-	0	0	0	0	0	4	0	0	0	0	0	0.274747
pseudogen	-	0	1	0	0	0	0	0	0.354476	0	0	0	0
lincRNA	-	891	846	899	419	390	390	10.78181	12.064	14.33536	4.386227	5.301853	4.690167
lincRNA	-	0	0	0	2	0	0	0	0	0	0.164448	0	0
antisense	-	0	0	1	0	1	3	0	0	0.173973	0	0.148319	0.393621
antisense	UBE2E2_an	0	0	0	0	2	0	0	0	0	0	0.23838	0
lincRNA	-	0	0	0	2	0	0	0	0	0	0.147501	0	0
pseudogen	high_mobil	0	0	0	0	0	1	0	0	0	0	0	0.163907
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.083534	0
pseudogen	-	0	3	0	0	1	0	0	0.496454	0	0	0.157761	0
antisense	ADIRF_anti	2	4	4	34	12	10	0.147468	0.347564	0.388653	2.16875	0.994026	0.732786
pseudogen	-	8	2	6	8	16	14	0.633076	0.18651	0.62568	0.54767	1.422443	1.101041
pseudogen	-	0	0	1	0	0	0	0	0	0.361468	0	0	0
antisense	-	2	0	0	0	1	0	0.052862	0	0	0	0.029693	0
pseudogen	olfactory_r	0	0	0	2	0	0	0	0	0	0.100546	0	0
processed_	-	109	87	91	99	41	62	3.76915	3.54522	4.146609	2.961523	1.592758	2.13068
pseudogen	-	0	0	0	2	0	0	0	0	0	0.077298	0	0
pseudogen	-	0	0	1	0	3	0	0	0	0.152655	0	0.390433	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.299627	0
pseudogen	-	0	0	4	1	2	0	0	0	0.412191	0.06765	0.175704	0
pseudogen	transmemb	0	0	0	1	0	0	0	0	0	0.134703	0	0
protein_co	ring_finger_	7	7	4	5	7	17	0.246565	0.290562	0.185664	0.152358	0.277	0.595102
processed_	-	0	1	1	0	3	0	0	0.114683	0.128241	0	0.327992	0
antisense	-	0	0	0	6	4	4	0	0	0	0.533579	0.461949	0.408653
pseudogen	-	0	2	0	1	0	4	0	0.292214	0	0.107257	0	0.492872
lincRNA	-	1	1	6	0	0	0	0.05902	0.069552	0.466644	0	0	0
pseudogen	-	3	0	0	1	0	0	0.493239	0	0	0.142233	0	0
pseudogen	maestro_he	0	0	0	0	0	1	0	0	0	0	0	0.020043
pseudogen	sorting_nex	1	1	1	14	2	6	0.096784	0.114054	0.127538	1.172184	0.217462	0.577119
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.138458
lincRNA	long_interg	2	0	0	0	1	0	0.074617	0	0	0	0.041914	0
processed_	-	0	0	0	2	0	0	0	0	0	0.032435	0	0
antisense	-	36	34	19	49	40	68	2.806886	3.123981	1.952139	3.305076	3.503736	5.269154
protein_co	histone_clu	0	2	0	0	1	1	0	0.256212	0	0	0.122127	0.108037
pseudogen	-	0	3	1	2	2	7	0	0.108124	0.040302	0.052916	0.068719	0.212766
pseudogen	CCR4-NOT_	0	0	0	0	0	2	0	0	0	0	0	0.123507
antisense	-	67	59	55	51	68	41	5.407083	5.611092	5.849056	3.560586	6.165187	3.288378
pseudogen	-	31	11	14	11	19	5	1.815454	0.759143	1.080405	0.557288	1.250047	0.291007
protein_co	nuclear_po	1	0	3	2	0	4	0.037654	0	0.148855	0.065148	0	0.149684
lincRNA	long_interg	18	13	29	67	49	47	0.322156	0.274185	0.683954	1.037365	0.985233	0.835991

processed_	-	0	0	0	0	5	1	0	0	0	0	0.379795	0.067195
antisense	-	5	5	8	1	2	0	0.540214	0.636609	1.138992	0.093467	0.242759	0
pseudogen	-	0	0	1	1	2	4	0	0	0.057183	0.03754	0.097502	0.172505
antisense	-	3	1	2	6	2	0	0.728546	0.286182	0.64003	1.26052	0.545651	0
processed_	-	7	7	4	80	40	71	0.120516	0.142021	0.090749	1.191516	0.77367	1.214828
pseudogen	ribosomal_	1	0	1	0	0	0	0.109609	0	0.144437	0	0	0
antisense	-	0	0	0	3	0	3	0	0	0	0.242322	0	0.278381
pseudogen	-	4	5	2	2	0	1	0.144155	0.212348	0.094981	0.062354	0	0.035816
pseudogen	high_mobil	3	6	1	1	0	0	0.371951	0.876643	0.16338	0.107257	0	0
pseudogen	small_nucl	0	0	2	7	7	16	0	0	0.500095	1.149076	1.492227	3.017293
pseudogen	-	1	0	5	0	0	0	0.14913	0	0.982581	0	0	0
protein_co	glutathione	6437	5339	3856	6421	4294	5710	297.3658	290.6528	234.7358	256.6097	222.853	262.152
protein_co	Beta/gamm	32	34	92	1	20	5	0.397585	0.497813	1.506271	0.010748	0.279164	0.061739
pseudogen	-	0	0	0	2	0	0	0	0	0	0.220718	0	0
antisense	-	2	2	1	0	0	0	0.225761	0.266046	0.148749	0	0	0
antisense	-	1	1	1	1	3	4	0.027247	0.032109	0.035905	0.023571	0.091831	0.108315
pseudogen	RAS_p21_p	8	1	10	0	0	0	0.353234	0.052033	0.581846	0	0	0
antisense	XXYLT1_ant	4	0	0	0	4	2	0.491332	0	0	0	0.551981	0.244149
antisense	OSTN_antis	2	0	0	0	0	0	0.205596	0	0	0	0	0
pseudogen	-	0	2	0	0	0	0	0	0.264355	0	0	0	0
pseudogen	H2B_histor	1	0	1	0	0	0	0.145442	0	0.191657	0	0	0
lincRNA	-	2	0	0	2	1	1	0.127262	0	0	0.110094	0.071485	0.063238
pseudogen	mitochond	2	0	0	0	0	1	0.238473	0	0	0	0	0.1185
pseudogen	ubiquitin_s	2	0	0	6	2	1	0.022362	0	0	0.058035	0.025122	0.011112
pseudogen	profilin_1_	5	1	7	9	19	18	0.62578	0.147489	1.154475	0.974445	2.671495	2.238896
antisense	-	0	2	2	0	2	1	0	0.366987	0.410372	0	0.349858	0.154747
antisense	-	2	3	5	0	6	5	0.071014	0.125529	0.233948	0	0.23934	0.176439
pseudogen	ubiquitin-c	8	10	11	12	13	23	0.808259	1.190606	1.464496	1.04883	1.475548	2.309395
antisense	TLR8_antis	0	2	0	0	0	1	0	0.092495	0	0	0	0.039002
antisense	-	2	0	3	0	4	0	0.244531	0	0.483348	0	0.549431	0
antisense	-	0	0	0	0	3	4	0	0	0	0	0.498402	0.587866
pseudogen	ATPase_H+_	0	0	0	0	1	0	0	0	0	0	0.17754	0
pseudogen	endoplasm	0	6	2	0	2	0	0	0.530207	0.19763	0	0.168487	0
antisense	-	0	2	1	3	0	0	0	0.319119	0.178423	0.351398	0	0
processed_	CHRM3_an	0	0	1	1	3	1	0	0	0.028697	0.01884	0.073397	0.021643
lincRNA	-	0	2	0	0	0	0	0	0.143255	0	0	0	0
lincRNA	-	0	0	0	5	3	0	0	0	0	0.348546	0.27158	0
antisense	-	0	4	0	3	2	2	0	0.128304	0	0.070641	0.061158	0.054102
antisense	-	0	0	2	0	0	4	0	0	0.218694	0	0	0.329869
pseudogen	-	111	138	107	58	46	54	2.235242	3.274822	2.839358	1.010398	1.040659	1.080699
lincRNA	-	0	0	0	8	6	1	0	0	0	0.406199	0.395627	0.05833
pseudogen	adenylate_	0	1	0	0	0	0	0	0.092839	0	0	0	0
pseudogen	NFKB_activ	0	4	0	25	22	31	0	0.050516	0	0.231776	0.264873	0.330169
antisense	-	4	9	4	0	1	6	0.525469	1.393274	0.69244	0	0.147583	0.783336

processed_	-	23	17	4	0	0	0	0.535463	0.466399	0.122715	0	0	0
lincRNA	-	0	0	0	54	37	16	0	0	0	1.058708	0.942041	0.36037
lincRNA	-	14	15	15	7	5	5	0.84997	1.073183	1.200056	0.367652	0.341032	0.301686
pseudogen	-	2	2	1	4	0	3	0.121703	0.14342	0.080188	0.21057	0	0.181428
pseudogen	-	0	2	0	0	0	0	0	0.332735	0	0	0	0
processed_	-	0	0	1	0	2	0	0	0	0.045067	0	0.076842	0
pseudogen	eukaryotic_	24	41	28	34	29	38	1.169967	2.355338	1.798685	1.433852	1.588215	1.841007
antisense	-	0	0	0	0	1	0	0	0	0	0	0.054817	0
antisense	HOXA_tran	99	72	55	85	60	77	5.895566	5.052774	4.316064	4.378973	4.014123	4.557122
lincRNA	-	5	0	0	0	2	2	0.492933	0	0	0	0.221512	0.195955
antisense	-	0	0	0	0	2	0	0	0	0	0	0.144887	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.037172	0
pseudogen	angiogenic_	0	2	1	0	1	0	0	0.154234	0.086234	0	0.073518	0
protein_co	BTB_(POZ)_	10	7	13	28	8	7	0.173919	0.143467	0.297938	0.421278	0.15631	0.120992
protein_co	Uncharacte	6	12	0	0	3	1	0.385025	0.907458	0	0	0.216276	0.063775
processed_	STXBP5_an	16	10	13	2	9	0	0.289394	0.213146	0.309847	0.031294	0.182878	0
pseudogen	ribosomal_	1	0	0	0	0	0	0.157095	0	0	0	0	0
antisense	-	30	42	21	120	65	68	3.415548	5.635021	3.1506	11.81907	8.313838	7.694098
pseudogen	ST6_(alpha-	2	5	0	7	0	3	0.212188	0.625128	0	0.64247	0	0.316317
pseudogen	-	0	1	0	0	0	0	0	0.048475	0	0	0	0
processed_	-	1	0	0	0	0	0	0.112881	0	0	0	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.089707	0
pseudogen	eukaryotic_	440	402	342	375	227	303	16.80666	18.09514	17.21432	12.39148	9.741005	11.50221
antisense	-	8	2	1	0	0	0	0.190435	0.056104	0.031368	0	0	0
antisense	-	0	0	3	0	0	0	0	0	0.594573	0	0	0
antisense	-	0	0	1	2	0	11	0	0	0.120489	0.1582	0	0.999576
pseudogen	-	0	0	2	0	0	0	0	0	1.098634	0	0	0
lincRNA	-	4	9	7	34	29	45	0.103603	0.274701	0.238915	0.761821	0.843836	1.158333
processed_	-	12	3	6	0	0	0	0.138983	0.040946	0.091573	0	0	0
protein_co	transmemb	0	5	9	84	93	99	0	0.311939	0.62787	3.847108	5.53126	5.208791
sense_intro	SYNJ2_intr	0	1	0	0	0	2	0	0.104153	0	0	0	0.175673
antisense	SRGAP2_an	0	0	0	1	0	5	0	0	0	0.021028	0	0.120785
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.035053
antisense	ZNF197_an	6	5	5	8	2	8	0.509865	0.500704	0.559898	0.588108	0.190934	0.675622
pseudogen	-	2	3	0	1	0	1	0.566214	1.000873	0	0.244914	0	0.281359
processed_	-	1	4	2	0	0	0	0.106952	0.504143	0.281872	0	0	0
pseudogen	-	0	0	0	2	3	0	0	0	0	0.254438	0.495633	0
antisense	-	0	0	3	0	0	0	0	0	0.66231	0	0	0
lincRNA	-	4	8	5	3	0	0	0.33244	0.783519	0.547592	0.215693	0	0
pseudogen	RAN_memb	3	3	0	0	0	0	0.222753	0.262501	0	0	0	0
antisense	-	34	47	28	40	53	61	1.742492	2.838551	1.89097	1.773433	3.051523	3.106928
lincRNA	long_interg	43	26	24	3	15	11	3.080464	2.194967	2.265655	0.185922	1.207224	0.783159
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.167067	0
protein_co	Uncharacte	8	4	0	3	9	4	0.745648	0.43935	0	0.241896	0.9424	0.370521

antisense	-	3	1	2	0	5	3	0.345267	0.135625	0.303319	0	0.646477	0.343135
pseudogen	-	1	0	0	0	0	3	0.193923	0	0	0	0	0.578176
antisense	-	8	12	5	23	13	21	0.502406	0.888082	0.41378	1.249555	0.917185	1.31067
pseudogen	NFU1_iron-	0	0	0	0	1	1	0	0	0	0	0.126814	0.112183
pseudogen	-	4	0	0	0	0	0	0.33991	0	0	0	0	0
processed_	-	20	12	12	15	8	9	0.65521	0.463275	0.518044	0.425114	0.294435	0.293024
pseudogen	keratin_8_p	13	1	1	7	11	17	0.480274	0.043536	0.048683	0.223721	0.456549	0.624172
pseudogen	-	0	0	0	0	4	2	0	0	0	0	0.347812	0.153842
lincRNA	-	0	0	0	5	0	0	0	0	0	0.435351	0	0
processed_	-	0	0	0	0	0	1	0	0	0	0	0	0.09263
pseudogen	-	1	0	0	3	1	4	0.082463	0	0	0.214014	0.092642	0.327813
pseudogen	keratin_8_p	0	0	0	0	1	1	0	0	0	0	0.04099	0.036261
antisense	-	0	0	0	6	8	4	0	0	0	0.477902	0.827491	0.366011
pseudogen	-	0	0	0	0	3	0	0	0	0	0	0.154885	0
pseudogen	-	0	0	0	4	2	5	0	0	0	0.187317	0.121628	0.268988
pseudogen	cytochrom	3	3	5	0	0	0	0.105953	0.124859	0.232699	0	0	0
antisense	-	0	0	4	0	1	3	0	0	0.29068	0	0.061954	0.164419
processed_	-	21	15	12	8	10	7	0.372324	0.313401	0.280361	0.122703	0.199183	0.123342
pseudogen	-	0	0	0	5	0	0	0	0	0	0.39756	0	0
sense_intrc	ERI3_intron	7	12	3	2	14	10	0.598687	1.209455	0.33811	0.147977	1.345174	0.849985
pseudogen	jumping_tr	0	3	0	0	0	0	0	0.757746	0	0	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.093663	0
processed_	-	3	1	0	0	0	0	0.281103	0.110421	0	0	0	0
protein_co	twist_basic	439	400	298	11	19	20	19.76284	21.22032	17.67811	0.428391	0.96092	0.894797
pseudogen	-	0	0	7	0	0	10	0	0	0.676375	0	0	0.728726
protein_co	-	0	0	1	0	0	0	0	0	0.090838	0	0	0
antisense	DCUN1D2_	5	10	2	10	7	7	0.802136	1.890537	0.422808	1.387846	1.26161	1.116056
pseudogen	DEAD/H_(A	0	0	0	1	0	0	0	0	0	0.027707	0	0
pseudogen	-	0	0	0	3	0	1	0	0	0	0.362524	0	0.138823
antisense	-	7	11	5	10	11	15	0.265654	0.491946	0.250048	0.328308	0.468986	0.565742
pseudogen	cytochrom	18	33	24	10	9	16	0.741586	1.602175	1.302972	0.356412	0.416563	0.655117
pseudogen	phosphogl	0	0	0	5	6	5	0	0	0	0.336757	0.524788	0.386868
lincRNA	-	1	1	0	0	0	0	0.083767	0.098715	0	0	0	0
pseudogen	-	8	0	0	3	3	2	1.097223	0	0	0.35595	0.462248	0.272612
processed_	-	0	3	6	7	0	2	0	0.353138	0.789773	0.604891	0	0.198544
antisense	-	3	0	0	0	0	3	0.323468	0	0	0	0	0.321471
antisense	-	0	5	6	0	0	0	0	0.417589	0.560348	0	0	0
lincRNA	-	4	0	0	1	0	0	0.415223	0	0	0.089802	0	0
sense_intrc	ARHGEF7_i	1	0	1	0	0	1	0.065847	0	0.08677	0	0	0.06544
pseudogen	olfactory_r	3	3	0	0	0	0	0.169141	0.199322	0	0	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.112906
pseudogen	-	0	0	1	0	0	0	0	0	0.484467	0	0	0
antisense	-	1	0	0	17	6	4	0.131042	0	0	1.927182	0.883306	0.520931
antisense	SPIN4_anti	0	1	0	0	0	0	0	0.14645	0	0	0	0

pseudogen	-	0	6	6	2	1	2	0	0.580351	0.648961	0.142012	0.092211	0.163144
antisense	RNASEH2B_	13	14	12	5	8	8	0.866792	1.100036	1.054357	0.288406	0.599254	0.530116
pseudogen	-	0	5	2	1	1	2	0	1.151065	0.514858	0.169	0.219468	0.388296
lincRNA	-	1	0	0	0	2	0	0.137509	0	0	0	0.308966	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.558459	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.053692	0	0
pseudogen	-	0	1	0	0	0	0	0	0.068558	0	0	0	0
pseudogen	estrogen_re	3	3	4	0	0	0	0.292492	0.344684	0.51391	0	0	0
antisense	-	0	0	3	0	4	1	0	0	0.106617	0	0.121194	0.026803
lincRNA	-	1	0	0	0	0	0	0.030744	0	0	0	0	0
antisense	GAS6_antis	3	1	2	3	0	0	0.205463	0.080709	0.1805	0.177745	0	0
pseudogen	-	0	0	0	3	0	0	0	0	0	0.492461	0	0
antisense	SLC26A4_a	0	1	0	14	4	5	0	0.016921	0	0.173904	0.064525	0.071351
processed_	-	0	0	2	0	0	0	0	0	0.172043	0	0	0
pseudogen	-	2	1	0	0	0	0	0.094117	0.055456	0	0	0	0
antisense	MYCN_opp	0	0	0	11	15	15	0	0	0	0.383692	0.679466	0.601074
lincRNA	-	5	11	9	5	2	4	0.064926	0.168326	0.154003	0.056167	0.029176	0.05162
lincRNA	long_interg	12	7	4	0	0	1	0.198034	0.136133	0.086987	0	0	0.016401
pseudogen	-	2	0	0	0	0	0	0.334013	0	0	0	0	0
pseudogen	-	4	2	0	1	7	1	0.055552	0.032732	0	0.012014	0.109216	0.013802
lincRNA	-	10	9	27	2	11	15	0.483038	0.512308	1.718621	0.083575	0.59693	0.720083
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.021387	0
pseudogen	-	23	19	12	18	12	21	2.515791	2.449105	1.729668	1.703265	1.47461	2.282841
pseudogen	-	1	1	2	0	0	0	0.083372	0.098248	0.219727	0	0	0
antisense	-	7	2	2	0	1	0	0.307031	0.103377	0.115598	0	0.049276	0
pseudogen	proteasom	2	0	0	0	0	0	0.645622	0	0	0	0	0
pseudogen	capicua_tra	0	0	0	0	2	2	0	0	0	0	0.053703	0.047507
lincRNA	-	0	0	2	0	2	0	0	0	0.203095	0	0.173147	0
processed_	-	8	5	7	8	10	8	0.269249	0.198308	0.310453	0.232925	0.378105	0.267586
antisense	-	0	0	0	1	0	0	0	0	0	0.068153	0	0
antisense	UFL1_antis	0	0	0	1	2	0	0	0	0	0.083575	0.217065	0
antisense	-	5	2	8	0	5	4	0.925542	0.436278	1.95142	0	1.039789	0.735861
sense_intrc	-	0	0	0	1	0	0	0	0	0	0.08707	0	0
processed_	-	8	15	5	3	4	9	0.502406	1.110102	0.41378	0.162985	0.282211	0.561716
protein_co	Uncharacte	2	0	0	0	0	0	0.076394	0	0	0	0	0
protein_co	interferon_	0	0	0	10	1	0	0	0	0	0.64963	0.084363	0
processed_	-	3	17	7	5	1	4	0.052193	0.348535	0.160481	0.075253	0.019545	0.069161
antisense	-	0	0	0	1	0	0	0	0	0	0.064054	0	0
pseudogen	-	1	0	0	15	4	4	0.04195	0	0	0.544361	0.188513	0.166764
lincRNA	ENOX1_ant	3	4	0	6	2	4	0.040651	0.063873	0	0.070334	0.030446	0.053866
protein_co	histone_clu	43	15	30	14	52	43	3.219891	1.323643	2.960252	0.906909	4.374466	3.200006
antisense	-	0	0	1	6	3	8	0	0	0.18215	0.717476	0.465869	1.098988
pseudogen	-	4	0	1	0	0	0	0.575446	0	0.189574	0	0	0
pseudogen	-	12	6	10	19	13	11	0.924734	0.544871	1.015477	1.266636	1.125454	0.842437

processed_	-	0	0	0	13	15	27	0	0	0	0.804575	1.205593	1.919702
pseudogen	-	0	0	1	20	19	15	0	0	0.036128	0.474354	0.585211	0.408706
pseudogen	eukaryotic_	1	0	1	0	0	0	0.065602	0	0.086448	0	0	0
pseudogen	DPH3_KTI1	0	0	0	2	0	0	0	0	0	0.086905	0	0
antisense	PCDH9_ant	1	0	0	0	0	0	0.121424	0	0	0	0	0
pseudogen	cytochrom	0	0	0	2	1	2	0	0	0	0.283585	0.184136	0.325784
sense_intro	KCNQ5_int	0	2	2	2	0	0	0	0.221626	0.247827	0.162696	0	0
antisense	-	5	0	3	0	2	2	0.525208	0	0.415258	0	0.236016	0.208786
antisense	-	1	1	1	0	0	0	0.129757	0.152911	0.170988	0	0	0
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.171381
antisense	LATS2_anti	0	0	0	3	0	2	0	0	0	0.2174	0	0.1665
lincRNA	-	0	3	1	1	0	0	0	0.462131	0.172255	0.113084	0	0
antisense	POU6F2_ar	0	0	0	4	4	2	0	0	0	0.356412	0.462848	0.204724
lincRNA	-	44	27	31	1	1	1	0.656355	0.474632	0.609372	0.012905	0.016759	0.014825
antisense	-	1	0	1	0	1	3	0.095389	0	0.1257	0	0.107164	0.2844
antisense	-	1	0	0	0	1	0	0.014859	0	0	0	0.016693	0
lincRNA	testis-speci	247	216	206	363	403	431	2.474721	2.550293	2.719765	3.146291	4.536108	4.29157
pseudogen	-	0	1	0	0	2	1	0	0.159969	0	0	0.305005	0.134908
antisense	DLG5_antis	0	0	4	13	3	7	0	0	0.573004	1.222558	0.366381	0.756259
pseudogen	-	0	1	0	0	0	0	0	0.076738	0	0	0	0
pseudogen	-	0	3	2	0	0	0	0	0.483626	0.360534	0	0	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.044089	0
antisense	YEATS2_ant	6	18	5	3	8	2	0.170046	0.601167	0.186733	0.073553	0.254715	0.056332
protein_co	Uncharacte	0	0	0	1	0	0	0	0	0	0.036406	0	0
pseudogen	poly(A)_bin	5	2	5	0	8	4	0.220037	0.10372	0.289955	0	0.395517	0.174943
antisense	EZR_antiser	0	0	0	0	4	6	0	0	0	0	1.09633	1.454766
antisense	-	2	0	0	0	0	0	0.213042	0	0	0	0	0
lincRNA	-	22	10	20	9	22	17	1.720387	0.921532	2.060954	0.608848	1.932748	1.32118
processed_	-	0	7	6	2	1	3	0	0.184735	0.177064	0.038747	0.025159	0.066769
lincRNA	-	43	40	21	46	9	16	2.526596	2.769711	1.626003	2.338235	0.594099	0.934323
lincRNA	-	13	3	0	21	10	31	1.265134	0.34405	0	1.767972	1.093307	2.998227
processed_	-	0	0	0	0	6	5	0	0	0	0	1.505719	1.110001
antisense	-	10	13	0	9	0	3	0.787812	1.206905	0	0.613378	0	0.234884
pseudogen	-	27	27	24	36	12	40	1.923832	2.267118	2.253457	2.219059	0.96058	2.83252
pseudogen	zinc_finger_	0	0	2	0	0	0	0	0	0.32985	0	0	0
lincRNA	-	0	0	0	0	0	4	0	0	0	0	0	0.34501
antisense	-	0	0	0	3	0	0	0	0	0	0.173481	0	0
processed_	-	0	0	0	0	0	2	0	0	0	0	0	0.128171
pseudogen	-	1	0	2	0	0	0	0.060504	0	0.159459	0	0	0
processed_	-	2	0	0	0	2	2	0.073072	0	0	0	0.082092	0.072621
protein_co	ribosomal_	17092	13603	8542	12217	10001	13866	594.1349	557.2293	391.279	367.3836	390.5572	479.0193
lincRNA	-	0	0	0	10	28	15	0	0	0	0.92523	3.364294	1.594365
pseudogen	metallothi	3	0	1	1	0	2	0.853887	0	0.375071	0.246231	0	0.565742
processed_	-	0	2	0	9	15	13	0	0.055089	0	0.181982	0.39388	0.301979

antisense	-	27	31	38	16	44	69	1.429407	1.93402	2.651005	0.732782	2.61694	3.630369
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.047581	0
pseudogen	ferritin_ligl	0	0	0	0	0	3	0	0	0	0	0	0.296696
antisense	-	3	0	1	0	0	0	0.367646	0	0.161489	0	0	0
pseudogen	-	47	35	13	24	28	46	4.822145	4.231726	1.757602	2.130182	3.227375	4.6904
pseudogen	basic_trans	0	1	2	4	2	9	0	0.125026	0.279612	0.367125	0.23838	0.948951
pseudogen	-	25	26	27	36	26	27	2.896116	3.549411	4.121682	3.607791	3.38375	3.108489
pseudogen	ubiquitin-c	11	8	17	18	20	16	0.87048	0.746042	1.772759	1.232258	1.778054	1.258333
lincRNA	-	37	57	29	22	12	25	2.872165	5.214224	2.966474	1.477384	1.046497	1.928668
pseudogen	-	21	24	32	9	40	15	0.414064	0.557656	0.831443	0.153516	0.886047	0.293933
lincRNA	-	0	0	0	3	1	0	0	0	0	0.241471	0.104527	0
pseudogen	-	0	0	0	0	4	0	0	0	0	0	0.699717	0
lincRNA	-	2	0	0	0	3	0	0.274306	0	0	0	0.462248	0
lincRNA	-	1	0	0	0	1	0	0.069659	0	0	0	0.078258	0
pseudogen	-	1	0	3	0	0	0	0.155709	0	0.615558	0	0	0
pseudogen	-	23	23	17	1	3	2	0.674968	0.795409	0.657415	0.025387	0.098907	0.05833
antisense	-	2	1	2	0	0	0	0.062467	0.036807	0.082317	0	0	0
pseudogen	GDP_dissoc	0	2	5	0	0	0	0	0.205223	0.573711	0	0	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.08493
lincRNA	-	0	1	0	0	0	0	0	0.082089	0	0	0	0
pseudogen	SET_pseudo	2	2	4	1	6	5	0.188402	0.22202	0.496536	0.081493	0.634974	0.468097
pseudogen	-	0	0	0	0	3	1	0	0	0	0	0.287323	0.084725
pseudogen	-	1	1	0	3	0	0	0.141176	0.166367	0	0.366391	0	0
pseudogen	glyceraldeh	0	0	2	0	0	0	0	0	0.337837	0	0	0
antisense	DDX39B_ar	3	0	0	2	0	8	0.307796	0	0	0.177515	0	0.815722
pseudogen	-	47	36	36	72	19	90	2.792623	2.520716	2.818718	3.700922	1.268286	5.314551
pseudogen	-	0	0	2	0	0	0	0	0	0.701139	0	0	0
pseudogen	-	0	5	1	0	2	0	0	1.294351	0.289474	0	0.493576	0
lincRNA	-	0	0	1	0	1	0	0	0	0.113436	0	0.096709	0
pseudogen	chitinase_a	0	0	0	0	1	2	0	0	0	0	0.052494	0.092876
antisense	-	1	0	2	2	2	0	0.12944	0	0.341141	0.223956	0.290836	0
pseudogen	-	2	4	1	0	1	0	0.169955	0.400563	0.11198	0	0.095467	0
processed_	-	0	0	0	7	4	9	0	0	0	0.483548	0.358829	0.714218
processed_	-	22	4	16	25	10	8	0.721624	0.154616	0.691581	0.709401	0.3685	0.260788
pseudogen	transmemb	1	0	0	0	0	0	0.117386	0	0	0	0	0
pseudogen	ribosomal_	0	3	2	0	0	2	0	0.236915	0.176616	0	0	0.1332
lincRNA	-	0	6	0	0	0	0	0	0.919721	0	0	0	0
pseudogen	-	11	18	19	10	13	4	1.878551	3.622513	4.275814	1.477384	2.494151	0.678891
pseudogen	-	8	6	6	7	1	0	1.331849	1.177127	1.316288	1.008152	0.187031	0
pseudogen	-	0	4	4	0	0	0	0	1.459362	1.63189	0	0	0
pseudogen	-	3	2	1	0	0	0	0.229845	0.180572	0.10096	0	0	0
pseudogen	-	1	2	1	4	3	11	0.071062	0.167484	0.093642	0.2459	0.2395	0.776852
antisense	-	2	1	0	0	0	0	0.168602	0.099344	0	0	0	0
pseudogen	-	0	3	0	1	6	0	0	0.979912	0	0.239785	1.868353	0

processed_	-	18	18	6	38	27	32	0.428865	0.505391	0.18838	0.78324	0.722705	0.757718
pseudogen	MT-ND4_ps	2	0	2	0	1	7	0.077912	0	0.102669	0	0.043764	0.271007
pseudogen	taste_recep	0	0	0	0	1	0	0	0	0	0	0.063272	0
protein_co	P_antigen_	0	0	0	0	0	1	0	0	0	0	0	0.095488
antisense	-	141	159	101	653	417	415	2.439438	3.241715	2.302644	9.773427	8.105051	7.135566
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.192725
antisense	-	5	7	8	0	10	4	0.458761	0.75687	0.967255	0	1.030778	0.364742
pseudogen	-	1	3	0	0	0	1	0.141176	0.499102	0	0	0	0.140304
antisense	-	0	2	1	0	0	0	0	0.263239	0.14718	0	0	0
pseudogen	-	7	2	5	2	3	8	0.950223	0.319937	0.894401	0.234866	0.457507	1.079263
pseudogen	keratin_19_	3	0	0	0	0	0	0.168423	0	0	0	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.199895	0	0	0
pseudogen	-	1	0	0	0	0	0	0.175884	0	0	0	0	0
pseudogen	ribosomal_	0	5	2	0	3	0	0	0.509704	0.227985	0	0.291549	0
pseudogen	rhomboid_	0	0	0	0	4	2	0	0	0	0	0.122568	0.054213
protein_co	tripartite_r	927	676	722	991	990	1034	14.11049	12.12596	14.4822	13.04966	16.9296	15.64201
lincRNA	-	5	1	4	8	16	13	0.247157	0.058252	0.260554	0.342102	0.888529	0.638639
lincRNA	-	2	3	2	0	5	1	0.299949	0.530207	0.395259	0	0.842435	0.149048
sense_intrc	-	0	5	6	0	1	0	0	1.039795	1.395266	0	0.198253	0
pseudogen	ribosomal_	0	0	0	2	0	0	0	0	0	0.193653	0	0
antisense	-	6	5	8	2	2	1	0.671556	0.65949	1.179929	0.193653	0.251484	0.111235
lincRNA	-	0	0	0	0	4	0	0	0	0	0	0.51944	0
antisense	-	0	0	0	2	2	0	0	0	0	0.132367	0.171896	0
pseudogen	-	0	0	0	0	1	2	0	0	0	0	0.263168	0.465611
pseudogen	nucleosom	1	0	0	0	0	0	0.046156	0	0	0	0	0
lincRNA	-	16	18	8	1	2	3	1.869881	2.478983	1.232023	0.101101	0.262587	0.348437
lincRNA	-	6	7	7	3	2	3	0.126401	0.173782	0.194327	0.054674	0.047335	0.06281
pseudogen	RNA_bindi	4	0	0	6	0	4	0.421841	0	0	0.547397	0	0.419235
antisense	-	119	116	117	157	115	161	21.79923	25.04144	28.24327	24.88037	23.66689	29.31094
pseudogen	-	0	1	0	0	0	0	0	0.222813	0	0	0	0
lincRNA	-	0	0	0	7	19	1	0	0	0	0.550846	1.941654	0.090402
pseudogen	transcripti	1	1	1	0	0	0	0.178855	0.210769	0.235687	0	0	0
antisense	-	179	164	97	377	330	472	7.851233	8.476875	5.606494	14.30504	16.26102	20.57484
antisense	-	0	0	0	2	2	0	0	0	0	0.157115	0.204034	0
pseudogen	-	2	0	1	1	5	2	0.31326	0	0.2064	0.1355	0.879821	0.311326
pseudogen	heat_shock	0	5	0	6	4	0	0	0.170179	0	0.149915	0.129789	0
antisense	-	0	0	0	0	3	0	0	0	0	0	0.634974	0
antisense	-	2	1	2	8	1	0	0.262084	0.154425	0.345363	0.906909	0.147218	0
pseudogen	aminoacyl_	0	0	0	0	0	2	0	0	0	0	0	0.112303
lincRNA	-	0	0	1	0	0	0	0	0	0.088757	0	0	0
antisense	-	0	1	0	2	0	3	0	0.116178	0	0.170573	0	0.293933
antisense	ETV5_antis	3	0	1	0	1	0	0.283612	0	0.124577	0	0.106207	0
processed_	-	6	8	2	4	2	5	0.35099	0.551494	0.154173	0.202426	0.131438	0.290685
lincRNA	-	0	0	4	0	4	1	0	0	0.330632	0	0.281876	0.062339

pseudogen	-	2	0	0	0	0	0	0.112881	0	0	0	0	0
antisense	-	9	1	0	0	1	2	1.085351	0.142113	0	0	0.13548	0.2397
antisense	-	18	1	6	0	1	0	2.819343	0.184579	1.238401	0	0.175964	0
processed_	-	1	3	0	0	0	2	0.183187	0.647623	0	0	0	0.364111
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.012994
lincRNA	-	0	2	3	0	2	0	0	0.180572	0.30288	0	0.172144	0
pseudogen	-	0	0	1	0	0	1	0	0	0.102593	0	0	0.077374
antisense	-	17	24	18	11	6	9	0.979322	1.629277	1.366419	0.548191	0.388308	0.515263
protein_co	transmemb	0	0	0	76	71	92	0	0	0	1.364452	1.655347	1.897488
lincRNA	-	2	11	6	0	1	0	0.145642	0.943968	0.575763	0	0.08181	0
lincRNA	-	0	0	0	0	0	3	0	0	0	0	0	0.076846
antisense	ZFX_antiser	3	3	0	2	3	0	0.38087	0.448833	0	0.219659	0.427884	0
pseudogen	-	33	34	19	35	12	15	0.833915	1.012498	0.632698	0.765137	0.340674	0.376712
lincRNA	-	1	0	0	3	0	3	0.098587	0	0	0.25586	0	0.293933
sense_intrc	KCNH1_int	0	0	0	8	5	5	0	0	0	0.58529	0.475047	0.42024
antisense	BOK_antise	0	0	0	1	0	1	0	0	0	0.071227	0	0.081826
protein_co	Uncharacte	0	2	0	0	2	2	0	0.742711	0	0	0.708047	0.626358
pseudogen	-	0	0	2	0	1	4	0	0	0.082903	0	0.035339	0.125048
lincRNA	-	2	0	0	0	0	0	0.35412	0	0	0	0	0
antisense	-	4	11	9	7	7	10	0.088235	0.285944	0.261612	0.13358	0.173471	0.219225
pseudogen	superoxide	2	0	0	0	1	0	0.188402	0	0	0	0.105829	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.051809	0	0
lincRNA	-	0	0	0	0	4	0	0	0	0	0	0.233927	0
antisense	-	0	0	0	8	1	2	0	0	0	0.725527	0.117774	0.208372
processed_	-	0	0	6	10	3	15	0	0	0.335669	0.367273	0.143086	0.632888
pseudogen	-	1	0	4	3	0	0	0.207612	0	1.094326	0.538811	0	0
pseudogen	-	1	0	0	3	4	2	0.169683	0	0	0.440374	0.762512	0.33727
pseudogen	-	1	1	0	0	0	0	0.181928	0.214391	0	0	0	0
pseudogen	cytochrom	0	0	4	0	1	5	0	0	1.153112	0	0.245768	1.087067
antisense	-	1	5	4	1	9	12	0.061274	0.36104	0.322978	0.053008	0.619541	0.730751
processed_	-	0	0	0	1	0	0	0	0	0	0.109045	0	0
protein_co	zinc_finger	40	25	15	29	35	39	0.640932	0.472062	0.316722	0.401988	0.630041	0.62105
antisense	-	0	0	0	2	3	1	0	0	0	0.640544	1.247747	0.36793
pseudogen	-	19	14	8	12	15	23	3.944623	3.425209	2.188652	2.155243	3.498583	4.745581
pseudogen	H2B_histor	0	2	0	5	0	2	0	0.271251	0	0.497814	0	0.228757
antisense	-	9	0	6	1	4	2	0.12774	0	0.11222	0.012279	0.063781	0.028211
lincRNA	-	2	6	3	0	2	0	0.101226	0.357865	0.200086	0	0.113721	0
sense_intrc	BACH1_int	0	0	0	0	1	0	0	0	0	0	0.146492	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.045983	0	0
lincRNA	long_interg	0	0	1	0	0	0	0	0	0.139527	0	0	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.051939
lincRNA	-	1	0	0	0	0	0	0.118436	0	0	0	0	0
pseudogen	ribosomal_	0	0	0	6	0	0	0	0	0	1.021537	0	0
pseudogen	-	3	4	2	3	0	0	0.247003	0.388104	0.216993	0.213681	0	0

pseudogen	suppressior	1	0	0	2	2	1	0.051549	0	0	0.08919	0.115825	0.051231
lincRNA	-	1	1	2	4	1	0	0.0314	0.037003	0.082756	0.108657	0.035276	0
pseudogen	ribosomal_	2	3	0	1	1	1	0.191468	0.338451	0	0.082819	0.107551	0.095143
pseudogen	mitochond	1	2	0	0	0	0	0.138953	0.327495	0	0	0	0
processed_	-	2	11	9	57	10	28	0.064327	0.416929	0.381452	1.585989	0.361336	0.895014
pseudogen	-	5	2	6	2	3	5	0.33592	0.158344	0.531193	0.116241	0.226431	0.333845
pseudogen	breast_carc	1	0	0	2	1	5	0.078547	0	0	0.135902	0.088243	0.390312
pseudogen	-	0	0	5	2	0	0	0	0	0.451835	0.11865	0	0
antisense	JAZF1_anti	0	1	1	0	0	0	0	0.016935	0.018937	0	0	0
pseudogen	-	0	0	0	1	0	3	0	0	0	0.06131	0	0.211301
pseudogen	-	19	8	19	8	33	39	0.627498	0.311355	0.826889	0.228566	1.224395	1.280067
pseudogen	-	4	3	1	9	5	7	0.202065	0.178591	0.066568	0.393311	0.283759	0.35143
lincRNA	-	0	0	1	6	6	0	0	0	0.034434	0.135633	0.176138	0
antisense	-	2	0	1	0	1	0	0.049019	0	0.032298	0	0.027535	0
pseudogen	-	3	7	5	3	5	4	0.175301	0.482024	0.385007	0.151652	0.328234	0.232292
pseudogen	ribosomal_	1	0	8	5	1	2	0.12032	0	1.268423	0.520442	0.135173	0.239155
pseudogen	-	0	0	3	0	0	1	0	0	0.272868	0	0	0.068597
antisense	-	3	0	3	0	0	1	0.23322	0	0.307327	0	0	0.07726
lincRNA	-	23	12	28	0	0	0	1.583411	0.973541	2.540146	0	0	0
pseudogen	profilin_1_	11	10	11	0	8	3	1.448634	1.551934	1.908946	0	1.1836	0.392642
pseudogen	TatD_DNas	3	0	2	6	0	1	0.178253	0	0.156595	0.30841	0	0.059051
pseudogen	sorting_nex	0	0	0	22	55	14	0	0	0	1.586734	5.151457	1.159995
antisense	RNF219_an	3	3	3	1	3	14	0.039696	0.046779	0.052309	0.011447	0.044596	0.184103
antisense	-	37	30	18	3	15	14	0.744231	0.711106	0.477105	0.052202	0.338958	0.279862
pseudogen	-	0	2	0	3	3	5	0	0.196497	0	0.216373	0.280989	0.414284
pseudogen	C-terminal_	13	20	16	12	13	15	0.517468	0.938161	0.839258	0.413223	0.581344	0.593392
sense_intrc	-	0	0	0	0	1	0	0	0	0	0	0.04482	0
lincRNA	-	9	11	5	3	10	21	0.295943	0.426252	0.216656	0.08534	0.369416	0.68627
antisense	-	2	3	1	2	0	1	0.153009	0.270467	0.100814	0.132367	0	0.076032
lincRNA	-	2	0	0	0	0	0	0.324791	0	0	0	0	0
antisense	-	9	0	0	2	8	0	0.753907	0	0	0.144933	0.75286	0
protein_co	uncharacte	15	7	2	2	2	6	0.627263	0.344956	0.110211	0.072352	0.093959	0.249356
protein_co	RNA_bindi	1	2	5	0	0	0	0.027559	0.064953	0.181581	0	0	0
pseudogen	zinc_finger_	94	106	83	84	93	86	1.699028	2.257801	1.976904	1.313454	1.888447	1.54483
pseudogen	solute_carr	0	0	0	0	1	1	0	0	0	0	0.068442	0.060546
pseudogen	ubiquitin-c	0	0	0	2	0	2	0	0	0	0.269405	0	0.309494
lincRNA	-	0	0	1	0	0	2	0	0	0.029762	0	0	0.044893
antisense	-	3	1	5	2	4	3	0.181305	0.071219	0.398192	0.104564	0.27158	0.180185
lincRNA	-	31	41	32	153	118	130	3.688024	5.748083	5.016685	15.74659	15.77114	15.3704
protein_co	Uncharacte	28	40	28	24	42	61	0.560858	0.944196	0.739074	0.415881	0.945134	1.214324
protein_co	zinc_finger_	0	0	0	3	21	10	0	0	0	0.065489	0.595326	0.250782
processed_	-	0	0	0	1	0	1	0	0	0	0.020837	0	0.023937
pseudogen	-	0	0	1	0	0	1	0	0	0.161116	0	0	0.121511
processed_	MAGI2_ant	266	305	275	225	242	229	3.125928	4.223809	4.25858	2.287404	3.194933	2.674499

pseudogen	-	1	0	1	0	0	1	0.34602	0	0.455969	0	0	0.343883
antisense	-	0	3	1	0	0	0	0	0.647623	0.241395	0	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.131584	0
protein_co	phospholip	37	5	9	23	18	47	0.757177	0.120579	0.242702	0.40718	0.413825	0.95588
pseudogen	zinc_finger_	0	4	2	1	9	4	0	0.203052	0.113529	0.037265	0.435544	0.171242
sense_intrc	-	0	1	0	0	1	3	0	0.095103	0	0	0.090665	0.240613
antisense	-	0	0	1	1	0	0	0	0	0.085599	0.056195	0	0
antisense	-	0	4	9	2	4	6	0	0.46645	1.173588	0.171211	0.44468	0.590064
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.388774
processed_	RPL34_anti	5	1	0	0	6	11	0.071291	0.016803	0	0	0.09611	0.155872
lincRNA	-	0	0	0	14	9	13	0	0	0	0.83055	0.693372	0.885988
antisense	-	20	22	13	17	18	9	0.609217	0.789718	0.52182	0.447975	0.615976	0.272455
pseudogen	ribosomal_	1	4	1	42	14	15	0.086505	0.407763	0.113992	3.143062	1.36056	1.28956
pseudogen	-	21	32	12	9	19	16	1.561462	2.803943	1.175786	0.578919	1.587138	1.182338
pseudogen	forty-two-t	1	0	0	0	0	0	0.057482	0	0	0	0	0
processed_	-	4	0	3	0	0	3	0.094834	0	0.093726	0	0	0.070686
pseudogen	prostaglan	4	0	4	4	4	2	0.438435	0	0.57775	0.379287	0.492554	0.217864
lincRNA	-	0	0	0	1	0	0	0	0	0	0.116537	0	0
lincRNA	-	0	3	1	2	0	0	0	0.272435	0.101548	0.13333	0	0
pseudogen	NADH_deh	0	3	0	0	0	0	0	1.063427	0	0	0	0
lincRNA	-	1	1	0	0	0	0	0.137509	0.162046	0	0	0	0
pseudogen	-	4	1	5	0	11	4	0.548611	0.161626	0.903669	0	1.69491	0.545223
pseudogen	-	12	6	1	5	0	0	0.341005	0.200927	0.037447	0.122917	0	0
protein_co	family_witl	232	238	232	585	422	495	5.046142	6.100361	6.649582	11.00754	10.31177	10.70006
lincRNA	-	11	5	3	2	8	5	2.164873	1.159623	0.778029	0.340512	1.768801	0.977956
pseudogen	-	4	0	0	2	0	0	0.533411	0	0	0.230725	0	0
pseudogen	API5_pseu	1	2	0	0	0	3	0.03506	0.082633	0	0	0	0.104531
pseudogen	thiopurine_	0	1	0	0	5	0	0	0.085934	0	0	0.409614	0
pseudogen	ribosomal_	0	0	0	2	0	0	0	0	0	0.123948	0	0
antisense	-	0	0	0	1	2	0	0	0	0	0.144476	0.375242	0
lincRNA	-	2	0	0	0	0	0	0.053557	0	0	0	0	0
pseudogen	cathepsin_l	1	1	4	1	0	0	0.054748	0.064517	0.288576	0.047362	0	0
antisense	SYNE1_anti	1	0	0	0	0	0	0.095734	0	0	0	0	0
lincRNA	-	2	5	2	0	0	0	0.194279	0.572364	0.256012	0	0	0
pseudogen	chaperonin	31	43	28	66	49	50	0.44332	0.724655	0.527653	0.816512	0.787229	0.710617
pseudogen	fatty_acid_	0	0	0	0	0	4	0	0	0	0	0	0.535512
protein_co	multiciliate	0	0	0	0	5	0	0	0	0	0	0.142219	0
pseudogen	-	0	0	1	0	2	0	0	0	0.697633	0	1.189518	0
pseudogen	-	2	8	2	3	1	9	0.188067	0.886504	0.247827	0.244044	0.105641	0.841077
lincRNA	MAPKAPK5	70	54	75	107	81	116	1.621825	1.474371	2.289823	2.144631	2.108337	2.670998
antisense	-	0	4	0	14	25	13	0	0.493184	0	1.267163	2.938533	1.351744
processed_	jerky_homo	768	673	657	843	851	882	4.549478	4.698102	5.12862	4.320071	5.663422	5.192525
antisense	SNRK_antis	2	0	4	1	1	0	0.141176	0	0.372071	0.061065	0.079301	0
pseudogen	ribosomal_	9	2	3	18	19	13	0.536564	0.140513	0.235687	0.928356	1.27257	0.770251

antisense	-	0	0	0	0	0	3	0	0	0	0	0	0.437236
lincRNA	-	35	36	12	21	28	17	3.536135	4.28618	1.597632	1.835452	3.178102	1.706944
lincRNA	long_interg	51	38	24	59	43	51	1.517701	1.332622	0.941157	1.518907	1.437585	1.508329
antisense	MED14_ant	0	1	1	1	0	12	0	0.069552	0.077774	0.051058	0	0.703867
pseudogen	-	2	0	1	0	0	0	0.299102	0	0.197071	0	0	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.059868	0	0
pseudogen	-	22	14	15	5	7	8	7.371531	5.528027	6.623096	1.449332	2.635009	2.664003
antisense	PCCA_antis	12	5	9	3	3	0	1.340278	0.658098	1.324619	0.289866	0.37643	0
pseudogen	olfactory_r	0	0	0	3	0	0	0	0	0	0.12675	0	0
lincRNA	-	1	4	0	0	0	0	0.029893	0.14091	0	0	0	0
pseudogen	high_mobil	35	28	29	46	58	63	6.787307	6.398741	7.410752	7.717032	12.63591	12.1417
processed_	-	3	7	15	8	4	5	0.09914	0.272606	0.653214	0.228709	0.148504	0.164214
lincRNA	-	2	2	2	0	0	0	0.237404	0.279766	0.31284	0	0	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.129911
antisense	-	7	4	6	5	7	25	0.470288	0.316689	0.531193	0.290602	0.528339	1.669227
processed_	SDCBP2_an	39	21	36	20	20	46	1.140088	0.723436	1.386791	0.505786	0.65683	1.336414
pseudogen	nuclear_un	0	0	0	5	5	1	0	0	0	0.262308	0.340641	0.060268
lincRNA	long_interg	0	0	1	3	0	0	0	0	0.32448	0.639054	0	0
lincRNA	-	2	1	0	7	4	3	0.055963	0.032974	0	0.169446	0.125742	0.083426
antisense	-	2	9	0	0	0	0	0.165959	0.880078	0	0	0	0
antisense	-	6	0	2	2	8	7	0.480554	0	0.211084	0.138575	0.71983	0.557184
lincRNA	-	2	2	0	1	0	0	0.249134	0.293589	0	0.107762	0	0
pseudogen	-	0	0	0	7	1	3	0	0	0	0.376724	0.069889	0.185478
antisense	high_mobil	0	3	0	3	1	0	0	0.560369	0	0.411367	0.178072	0
antisense	-	1	2	2	0	2	0	0.110064	0.259408	0.290076	0	0.247301	0
pseudogen	UPF3_regul	0	3	1	2	2	4	0	0.243385	0.090719	0.119113	0.154684	0.273675
lincRNA	-	0	0	0	2	6	3	0	0	0	0.148217	0.577436	0.255408
lincRNA	-	6	2	0	0	0	2	0.30252	0.118834	0	0	0	0.100217
protein_co	NPIP-like_p	0	0	0	1	8	1	0	0	0	0.038358	0.398499	0.044065
pseudogen	ATP_synth	0	0	1	0	0	0	0	0	0.053747	0	0	0
pseudogen	histone_de	2	0	2	0	2	0	0.073275	0	0.096558	0	0.08232	0
pseudogen	keratin_18_	4	0	2	8	0	1	0.164031	0	0.108076	0.283804	0	0.040754
sense_intrc	-	1	3	3	1	1	6	0.115845	0.409547	0.457965	0.100216	0.130144	0.690775
processed_	growth_arr	6359	5926	3833	4910	3315	4591	198.2637	217.7324	157.481	132.4338	116.1146	142.2562
pseudogen	-	13	6	13	5	3	2	1.240059	0.674462	1.634095	0.412603	0.321491	0.1896
pseudogen	eukaryotic_	2	1	1	4	3	5	0.227703	0.134167	0.150029	0.393969	0.383716	0.565742
protein_co	major_hist	107	81	96	58	55	55	3.661724	3.266584	4.329202	1.717089	2.114528	1.870571
pseudogen	-	6	14	6	31	18	21	0.374141	1.028773	0.493027	1.67228	1.260974	1.301408
pseudogen	-	0	0	0	0	4	0	0	0	0	0	0.386835	0
antisense	-	4	0	1	11	4	17	0.368285	0	0.121327	0.876153	0.413746	1.555546
lincRNA	-	3	2	3	2	2	0	0.036595	0.02875	0.048223	0.021105	0.027408	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.064871	0	0
pseudogen	-	0	0	1	0	2	1	0	0	0.056306	0	0.096006	0.042465
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.070623

protein_co	WAS_prote	44	32	18	95	51	46	0.548999	0.470518	0.295955	1.025429	0.714888	0.570409
antisense	-	86	63	56	129	149	157	1.197823	1.034051	1.02782	1.554343	2.331468	2.173219
antisense	-	0	0	0	7	2	0	0	0	0	0.763315	0.283219	0
lincRNA	-	1	0	6	1	2	5	0.057733	0	0.456466	0.049944	0.129718	0.286881
protein_co	chromoson	14	6	7	0	6	3	2.008601	1.014435	1.323423	0	0.967088	0.427757
antisense	-	31	38	16	25	17	15	3.834511	5.539097	2.607973	2.67517	2.362361	1.84395
pseudogen	-	4	0	0	0	0	0	0.878689	0	0	0	0	0
lincRNA	long_interg	0	0	0	2	0	2	0	0	0	0.086905	0	0.099837
pseudogen	heat_shock	0	0	0	5	1	4	0	0	0	0.293583	0.076251	0.269816
antisense	-	3	2	0	3	5	2	0.337921	0.26548	0	0.292333	0.632723	0.22389
processed_	-	0	0	0	0	0	5	0	0	0	0	0	0.254666
pseudogen	ribosomal_	92	114	83	135	65	170	6.050399	8.835032	7.192984	7.680562	4.802403	11.11104
pseudogen	protein-L-is	0	0	0	0	1	1	0	0	0	0	0.126008	0.11147
pseudogen	mortality_f	0	0	0	0	1	0	0	0	0	0	0.061252	0
pseudogen	-	1	1	0	6	7	7	0.12087	0.142438	0	0.627382	0.950528	0.840864
lincRNA	-	5	13	7	0	0	0	0.06515	0.199616	0.120193	0	0	0
pseudogen	supervillin_	12	20	16	2	11	1	0.245097	0.481387	0.430638	0.035339	0.252406	0.020299
pseudogen	-	0	1	1	2	0	0	0	0.169072	0.18906	0.248233	0	0
processed_	-	2	1	3	9	5	4	0.046501	0.027399	0.091915	0.181023	0.130601	0.092427
antisense	-	2	5	8	2	0	1	0.187402	0.552104	0.987799	0.16212	0	0.093122
pseudogen	X-ray_repai	0	0	0	2	3	0	0	0	0	0.050273	0.09793	0
antisense	-	2	2	0	0	2	2	0.130076	0.153287	0	0	0.146132	0.129273
pseudogen	prohibitin_	2	0	0	0	1	3	0.139318	0	0	0	0.078258	0.207687
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.157057
processed_	-	40	26	32	2	0	3	0.902275	0.69113	0.951182	0.039028	0	0.067253
pseudogen	-	1	0	0	2	0	3	0.040693	0	0	0.070406	0	0.121324
antisense	-	1	0	0	0	2	2	0.076174	0	0	0	0.171154	0.151407
pseudogen	-	0	3	0	0	0	0	0	0.542502	0	0	0	0
antisense	long_interg	0	0	2	0	0	0	0	0	0.29436	0	0	0
protein_co	HCG20447	2	0	0	0	1	0	0.026464	0	0	0	0.014865	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.015289	0
antisense	-	6	8	9	4	1	5	0.107713	0.169244	0.212909	0.062121	0.020168	0.089207
lincRNA	long_interg	0	3	3	0	3	5	0	0.086851	0.097118	0	0.082797	0.122074
pseudogen	phosphatid	0	0	3	2	0	0	0	0	0.32149	0.140703	0	0
pseudogen	eukaryotic_	5	5	6	10	13	9	0.201144	0.237035	0.31807	0.348016	0.587528	0.359823
lincRNA	MIR155_ho	40	36	18	17	18	17	1.323525	1.403724	0.784837	0.486613	0.669104	0.559024
antisense	-	0	0	0	0	2	2	0	0	0	0	0.243754	0.215631
pseudogen	MT-ND5_ps	2	0	1	0	3	1	0.060435	0	0.039819	0	0.101842	0.030031
pseudogen	olfactory_r	0	0	0	0	2	1	0	0	0	0	0.249375	0.110302
processed_	-	1	5	4	8	13	23	0.017461	0.102882	0.092036	0.120841	0.255009	0.399117
lincRNA	-	0	0	0	1	0	0	0	0	0	0.062824	0	0
lincRNA	-	1	0	0	0	0	0	0.064327	0	0	0	0	0
pseudogen	testis_expr	4	3	5	10	6	2	0.143472	0.126804	0.236325	0.310291	0.241772	0.071293
processed_	long_interg	170	125	128	163	91	149	4.207559	3.645847	4.174708	3.490052	2.530298	3.665027

sense_intrc	-	3	2	3	2	0	0	0.063708	0.05005	0.083951	0.036742	0	0
lincRNA	-	3	5	1	10	8	5	0.266482	0.523387	0.117052	0.768438	0.798334	0.441393
pseudogen	-	3	11	4	6	0	3	0.334364	1.444768	0.58748	0.578512	0	0.332299
pseudogen	cell_divisio	0	0	0	0	3	0	0	0	0	0	0.325598	0
antisense	-	2	4	3	0	1	3	0.266035	0.627012	0.525854	0	0.149437	0.396588
pseudogen	-	1	7	3	0	2	0	0.05626	0.464096	0.222412	0	0.12641	0
antisense	-	0	4	4	0	3	2	0	0.661939	0.740194	0	0.473283	0.27912
antisense	-	4	9	4	14	8	6	0.245381	0.650625	0.323352	0.742972	0.551341	0.365799
pseudogen	succinate_(	1	0	1	1	0	0	0.104626	0	0.137872	0.090512	0	0
protein_co	-	0	1	0	0	4	0	0	0.047954	0	0	0.182862	0
lincRNA	-	0	0	0	3	0	0	0	0	0	0.186427	0	0
pseudogen	fatty_acid_	29	24	13	81	34	60	3.762963	3.669866	2.22285	9.09243	4.956326	7.73736
protein_co	shisa_homo	0	0	0	0	0	1	0	0	0	0	0	0.108259
pseudogen	-	1	2	0	2	3	0	0.044789	0.105563	0	0.077494	0.150954	0
protein_co	TBC1_dom	12	6	3	12	22	14	0.239462	0.141096	0.078888	0.207157	0.493204	0.277647
pseudogen	ferritin_hea	11	2	9	12	2	5	1.413473	0.302853	1.523955	1.333949	0.288718	0.63852
lincRNA	-	3	1	3	0	0	0	0.34983	0.137418	0.460991	0	0	0
processed_	-	1	0	5	34	10	14	0.030391	0	0.200239	0.893894	0.341423	0.422845
pseudogen	-	0	0	2	0	0	0	0	0	0.17617	0	0	0
pseudogen	-	10	1	3	0	0	0	1.236939	0.145766	0.488995	0	0	0
lincRNA	-	0	0	1	0	0	0	0	0	0.086555	0	0	0
pseudogen	-	0	0	1	3	2	1	0	0	0.089326	0.175924	0.152307	0.067368
processed_	-	1	0	2	13	13	20	0.02281	0	0.060115	0.256521	0.333127	0.453374
antisense	-	3	3	0	0	2	0	0.312644	0.368431	0	0	0.234157	0
pseudogen	-	0	0	1	1	0	7	0	0	0.151659	0.099563	0	0.800649
pseudogen	eukaryotic_	1	2	0	4	0	7	0.043394	0.102275	0	0.15016	0	0.301884
pseudogen	-	0	0	0	1	0	0	0	0	0	0.115362	0	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.068128	0
antisense	-	20	31	14	31	23	43	0.384327	0.702003	0.354514	0.515342	0.496532	0.821199
pseudogen	-	0	0	1	3	0	1	0	0	0.132127	0.260221	0	0.099648
processed_	-	3	0	0	0	0	0	0.200281	0	0	0	0	0
lincRNA	-	2	0	0	0	0	0	0.202839	0	0	0	0	0
antisense	-	0	0	0	26	23	19	0	0	0	1.631194	1.873899	1.369407
antisense	-	11	6	10	0	4	12	0.289008	0.18577	0.34622	0	0.118066	0.313334
antisense	-	0	0	0	0	4	1	0	0	0	0	0.545651	0.120674
antisense	-	0	5	0	0	1	0	0	0.488932	0	0	0.093222	0
pseudogen	-	4	1	3	4	3	3	0.154685	0.045572	0.152878	0.133817	0.130334	0.115297
antisense	-	0	0	1	0	0	0	0	0	0.10475	0	0	0
pseudogen	trans-23-en	26	31	7	45	28	34	2.998836	4.21355	1.063928	4.490089	3.628161	3.897337
pseudogen	peptidylpro	0	0	0	0	0	3	0	0	0	0	0	0.312559
lincRNA	-	0	0	2	0	0	0	0	0	0.059373	0	0	0
antisense	MLIP_antis	0	0	0	1	0	0	0	0	0	0.029856	0	0
lincRNA	-	0	2	1	6	0	3	0	0.27363	0.15299	0.602617	0	0.346145
pseudogen	voltage-dep	3	6	1	1	7	0	0.190207	0.448295	0.083549	0.054849	0.498601	0

pseudogen	ribosomal_	2	0	0	0	0	0	0.222909	0	0	0	0	0
antisense	-	2	0	4	4	1	1	0.124129	0	0.327143	0.214766	0.069726	0.061681
lincRNA	-	0	0	0	1	0	0	0	0	0	0.040387	0	0
processed_	-	0	5	0	0	0	0	0	0.744484	0	0	0	0
pseudogen	glyceraldeh	1	0	1	4	1	0	0.056201	0	0.074059	0.194475	0.063138	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.153842
antisense	-	2	4	2	5	2	2	0.108708	0.256212	0.143251	0.235107	0.122127	0.108037
antisense	ZRANB2_an	2	5	2	3	9	16	0.174435	0.513902	0.229863	0.226354	0.881851	1.386861
pseudogen	-	1	2	1	11	5	5	0.058758	0.138486	0.077429	0.559143	0.330055	0.291976
pseudogen	-	1	3	4	0	1	11	0.174148	0.615668	0.917938	0	0.195644	1.903798
pseudogen	coiled-coil-	2	2	1	0	2	0	0.229182	0.270077	0.151003	0	0.257472	0
antisense	-	0	3	0	2	0	3	0	0.487404	0	0.238536	0	0.411047
pseudogen	-	2	3	1	0	1	1	0.327808	0.579453	0.215985	0	0.184136	0.162892
pseudogen	ribosomal_	0	0	2	0	2	0	0	0	0.202506	0	0.172644	0
lincRNA	-	2	0	0	1	0	0	0.13153	0	0	0.056893	0	0
antisense	-	7	5	0	6	1	3	0.388864	0.327323	0	0.288346	0.062409	0.165627
pseudogen	-	0	1	0	0	0	0	0	0.031509	0	0	0	0
antisense	-	5	2	4	0	0	0	0.376536	0.17749	0.396946	0	0	0
protein_co	ankyrin_rep	5	3	6	17	14	11	0.131432	0.092931	0.207835	0.386585	0.413437	0.287366
lincRNA	-	6	0	0	5	8	9	0.24472	0	0	0.176421	0.36657	0.364812
pseudogen	-	2	2	2	0	0	5	0.084234	0.099264	0.111	0	0	0.209284
antisense	long_interg	951	682	631	474	423	401	9.721353	8.215569	8.499832	4.191674	4.857755	4.073805
protein_co	zinc_finger_	41	51	31	72	58	64	0.611259	0.896022	0.609029	0.928618	0.971446	0.948268
pseudogen	-	5	3	0	7	2	3	0.894274	0.632308	0	1.083082	0.401864	0.533251
lincRNA	-	0	0	0	5	0	2	0	0	0	0.328543	0	0.150973
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.304127
antisense	-	6	14	8	0	8	2	0.175592	0.482824	0.308516	0	0.263022	0.058169
lincRNA	-	0	0	0	1	0	0	0	0	0	0.082077	0	0
pseudogen	-	3	0	1	1	0	5	0.198777	0	0.087313	0.05732	0	0.329249
pseudogen	fatty_acid_	3	1	0	0	0	0	0.419058	0.164611	0	0	0	0
antisense	-	4	12	10	2	5	23	0.100267	0.354476	0.330319	0.04337	0.140805	0.572975
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.028984	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.642983	0
pseudogen	-	3	0	1	0	0	1	0.193451	0	0.084974	0	0	0.064085
lincRNA	-	0	0	0	0	3	0	0	0	0	0	0.325005	0
lincRNA	-	0	0	0	1	2	1	0	0	0	0.055989	0.145418	0.06432
protein_co	transmemb	0	0	0	1	1	0	0	0	0	0.100879	0.131004	0
antisense	-	0	0	2	0	0	0	0	0	0.16093	0	0	0
protein_co	chromoson	714	581	590	4212	2660	3387	27.67194	26.53534	30.13202	141.2189	115.8169	130.4567
processed_	-	6	8	0	9	9	10	0.444882	0.699022	0	0.577297	0.749696	0.736891
protein_co	small_integ	9	15	8	8	11	40	0.872654	1.713949	1.022173	0.671046	1.198233	3.854509
processed_	-	0	0	0	4	2	1	0	0	0	0.186364	0.121009	0.053524
protein_co	family_with	50	41	32	143	106	95	1.045851	1.010627	0.882033	2.587611	2.490892	1.974846
pseudogen	ribosomal_	86	87	78	53	44	132	29.18542	34.79316	34.88164	15.55988	16.77526	44.51958

lincRNA	long_interg	14	7	6	0	1	0	0.634567	0.373899	0.358373	0	0.050921	0
pseudogen	-	0	0	1	3	1	0	0	0	0.213343	0.420173	0.181884	0
antisense	-	0	2	0	0	0	0	0	0.60278	0	0	0	0
antisense	-	1	0	0	0	0	0	0.100648	0	0	0	0	0
antisense	NUCB1_ant	0	3	0	0	4	1	0	0.432248	0	0	0.549431	0.121511
lincRNA	-	0	2	0	0	0	0	0	0.160174	0	0	0	0
protein_co	protein_ph	101	89	80	94	83	90	1.184808	1.230336	1.236664	0.953932	1.09384	1.04925
pseudogen	TBC1_dom	2	0	0	0	0	0	0.098039	0	0	0	0	0
antisense	-	25	16	21	1	10	5	4.297159	3.240921	4.756587	0.148698	1.931036	0.854124
pseudogen	TatD_DNas	0	0	0	0	0	2	0	0	0	0	0	0.028712
lincRNA	-	1	6	3	0	0	0	0.078084	0.552104	0.308687	0	0	0
pseudogen	olfactory_r	1	0	0	0	0	1	0.057358	0	0	0	0	0.057003
antisense	FAM83C_ar	1	0	0	4	1	0	0.150401	0	0	0.520442	0.168966	0
lincRNA	-	1	0	0	0	0	0	0.167006	0	0	0	0	0
pseudogen	testis_speci	137	105	78	78	73	108	1.867383	1.686589	1.401013	0.919751	1.117853	1.463007
IG_V_pseu	immunoglo	0	0	2	1	0	0	0	0	0.394143	0.129375	0	0
antisense	-	3	0	0	2	3	4	0.286168	0	0	0.165041	0.321491	0.3792
pseudogen	SMT3_supp	9	3	3	12	3	15	1.677708	0.659025	0.736936	1.935165	0.628267	2.778911
pseudogen	-	6	0	4	0	2	2	0.625287	0	0.549317	0	0.234157	0.207142
processed_	-	8	5	13	3	5	5	0.173222	0.127582	0.37093	0.056195	0.121628	0.107595
antisense	-	28	23	11	9	26	24	2.367968	2.292201	1.225872	0.658451	2.470246	2.017152
processed_	-	0	2	0	0	3	3	0	0.420119	0	0	0.600767	0.531455
pseudogen	-	0	3	0	0	0	0	0	0.199747	0	0	0	0
pseudogen	-	1	7	11	11	10	9	0.043934	0.362418	0.636843	0.418081	0.493576	0.392968
pseudogen	transmemb	2	0	0	2	0	0	0.193923	0	0	0.167762	0	0
processed_	-	12	29	18	37	45	39	0.202387	0.576376	0.400044	0.539841	0.852633	0.653695
pseudogen	-	1	3	4	1	0	0	0.144648	0.511375	0.76244	0.125134	0	0
sense_intro	KDM5C_int	0	0	0	4	1	1	0	0	0	0.242643	0.078776	0.069687
pseudogen	-	3	3	1	0	0	2	0.400058	0.471444	0.175726	0	0	0.265058
protein_co	lysine_(K)-s	0	0	0	4	1	1	0	0	0	0.078322	0.025428	0.022494
lincRNA	-	0	0	0	0	2	2	0	0	0	0	0.197594	0.174798
lincRNA	-	0	0	0	1	0	0	0	0	0	0.088586	0	0
pseudogen	family_with	0	7	1	5	1	5	0	1.233656	0.197071	0.646877	0.168011	0.743136
antisense	-	0	0	1	0	1	3	0	0	0.089326	0	0.076154	0.202103
pseudogen	zinc_finger	0	0	0	0	4	0	0	0	0	0	0.181745	0
antisense	MCF2L_ant	0	0	1	8	6	6	0	0	0.097982	0.514594	0.501202	0.443377
sense_intro	-	0	0	5	0	2	6	0	0	4.056005	0	1.383161	3.670748
pseudogen	-	4	4	3	2	1	1	0.146145	0.172223	0.144437	0.063215	0.041046	0.036311
pseudogen	major_hist	6	0	5	0	2	2	0.411992	0	0.452421	0	0.154283	0.136483
antisense	-	0	5	4	0	0	0	0	0.451431	0.40384	0	0	0
pseudogen	FBR-MuSV-	1	2	1	3	1	1	0.127877	0.30139	0.16851	0.331876	0.143662	0.127087
antisense	-	0	4	0	0	0	1	0	0.639874	0	0	0	0.134908
pseudogen	mitochond	4	1	1	0	0	0	0.663837	0.195573	0.218694	0	0	0
pseudogen	-	1	4	1	4	7	7	0.111455	0.52537	0.14687	0.385675	0.876487	0.775365

sense_intrc	HM13_intr	19	13	21	11	15	25	2.825502	2.278204	4.11525	1.415135	2.506008	3.694807
processed_	-	12	3	4	5	1	1	0.245286	0.072264	0.107743	0.088415	0.022964	0.020314
pseudogen	dual_specif	53	42	50	30	48	40	1.545935	1.443683	1.921853	0.757007	1.572917	1.159538
lincRNA	-	0	0	2	0	0	6	0	0	0.207013	0	0	0.468374
lincRNA	-	1	4	0	0	0	0	0.098587	0.464713	0	0	0	0
pseudogen	-	0	1	1	1	0	0	0	0.190206	0.212693	0.139631	0	0
pseudogen	-	0	0	2	0	6	1	0	0	0.207013	0	0.529459	0.078062
antisense	-	0	1	0	0	3	0	0	0.097026	0	0	0.277493	0
lincRNA	-	3	0	0	0	0	0	0.457703	0	0	0	0	0
pseudogen	-	1	0	2	1	1	0	0.04343	0	0.11446	0.037571	0.048791	0
antisense	-	5	0	2	0	3	7	0.453262	0	0.238915	0	0.305527	0.630648
lincRNA	-	0	0	0	0	1	3	0	0	0	0	0.083887	0.222626
pseudogen	small_nucl	52	53	41	195	156	124	12.23525	14.69578	12.71242	39.69238	41.23664	28.99619
pseudogen	ribosomal_	2	1	2	0	1	3	0.398053	0.23454	0.524536	0	0.223594	0.593392
processed_	chondroiti	13	7	5	0	0	0	0.078637	0.049899	0.039856	0	0	0
pseudogen	-	0	0	2	0	0	0	0	0	0.060401	0	0	0
lincRNA	-	27	22	12	13	29	26	0.294117	0.282414	0.172255	0.122507	0.354897	0.281474
pseudogen	signal_sequ	8	5	6	10	14	9	0.437981	0.322584	0.432864	0.473618	0.861078	0.489686
pseudogen	-	0	0	0	0	3	1	0	0	0	0	0.083769	0.024701
pseudogen	mitochond	4	3	0	2	0	2	1.628954	1.439717	0	0.704599	0	0.809447
antisense	-	18	19	9	61	29	44	0.308594	0.383862	0.203326	0.904706	0.55855	0.749682
lincRNA	-	12	10	8	4	6	7	0.424377	0.416752	0.372816	0.122375	0.23838	0.246024
pseudogen	-	1	2	0	2	2	4	0.5042	1.188338	0	0.87236	1.132875	2.004345
processed_	-	3	0	4	2	6	0	0.098525	0	0.17311	0.056822	0.221374	0
sense_intrc	-	0	3	0	0	0	0	0	0.385109	0	0	0	0
antisense	EPN2_antis	14	14	13	6	12	18	0.622835	0.733973	0.76212	0.230919	0.599757	0.795843
lincRNA	long_interg	3	0	4	7	7	11	0.076211	0	0.133903	0.153835	0.199775	0.277713
lincRNA	-	7	8	9	13	13	16	2.724904	3.669866	4.616688	4.377837	5.685198	6.189888
antisense	-	0	0	0	2	1	0	0	0	0	0.115947	0.075286	0
pseudogen	-	0	2	1	0	0	1	0	0.108031	0.060401	0	0	0.045553
pseudogen	-	0	1	4	0	4	2	0	0.063726	0.285039	0	0.243007	0.107485
processed_	-	4	0	1	0	2	0	0.370865	0	0.122177	0	0.208322	0
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.173644
3prime_ov	-	33	44	35	49	53	52	1.573921	2.473027	2.199743	2.021753	2.839841	2.464802
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.206514	0
antisense	-	20	17	12	1	8	2	2.072055	2.075521	1.638277	0.089626	0.93113	0.205926
antisense	-	4	0	1	3	3	0	0.548611	0	0.180734	0.35595	0.462248	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.059384
pseudogen	-	0	0	2	0	0	0	0	0	0.34451	0	0	0
pseudogen	dpy-19-like	0	0	0	4	0	3	0	0	0	0.078456	0	0.067598
processed_	-	47	31	57	73	73	73	4.703642	3.655992	7.517027	6.320076	8.207452	7.26054
pseudogen	-	1	3	3	3	3	5	0.064562	0.228248	0.255232	0.167557	0.217595	0.320817
sense_intrc	-	0	0	1	2	7	2	0	0	0.19325	0.253734	1.153273	0.291491
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.274083	0

pseudogen	-	0	0	0	1	0	0	0	0	0	0.043125	0	0
processed_	-	2	5	3	0	0	0	0.132518	0.390411	0.26194	0	0	0
pseudogen	-	0	0	4	0	1	0	0	0	1.468701	0	0.313031	0
lincRNA	-	0	0	2	0	0	0	0	0	0.690726	0	0	0
processed_	TOPORS_an	2	4	6	9	9	20	0.105882	0.249551	0.41858	0.41219	0.535283	1.052281
pseudogen	-	7	0	2	1	7	17	0.334767	0	0.12604	0.041372	0.37609	0.807985
lincRNA	-	0	0	0	3	2	0	0	0	0	0.121054	0.104803	0
pseudogen	TGF-beta_a	0	0	0	0	1	4	0	0	0	0	0.036399	0.128798
pseudogen	-	0	0	0	0	1	1	0	0	0	0	0.093811	0.082987
pseudogen	eukaryotic_	0	1	0	0	0	0	0	0.051137	0	0	0	0
lincRNA	-	8	12	9	7	9	16	0.86611	1.530987	1.283987	0.655608	1.094649	1.721523
antisense	-	146	124	117	150	108	140	4.279837	4.283543	4.519548	3.803896	3.556699	4.078609
protein_co	Uncharacte	3	1	0	0	1	3	0.135168	0.053096	0	0	0.050618	0.134334
antisense	-	2	2	4	1	9	1	0.163651	0.192852	0.431303	0.070787	0.827331	0.08132
pseudogen	ribosomal_	1	0	0	1	3	1	0.066929	0	0	0.0579	0.225572	0.066516
antisense	GYG2_antis	0	2	0	0	0	0	0	0.242282	0	0	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.083951	0	0	0
antisense	JARID2_ant	3	5	5	3	3	12	0.349061	0.685579	0.766629	0.301971	0.392149	1.387623
pseudogen	DBF4_hom	0	0	0	0	1	1	0	0	0	0	0.031435	0.027809
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.157527
lincRNA	-	0	0	0	3	0	9	0	0	0	0.181982	0	0.627187
lincRNA	-	0	0	0	5	4	0	0	0	0	0.814927	0.846632	0
lincRNA	-	5	5	12	2	35	5	0.678731	0.799843	2.146563	0.234866	5.337582	0.674539
antisense	-	37	42	26	23	24	28	2.057581	2.7524	1.9053	1.106486	1.499393	1.547472
pseudogen	-	10	10	3	0	0	0	0.149974	0.176736	0.059289	0	0	0
pseudogen	ribosomal_	5	2	3	13	13	4	0.299102	0.140989	0.236486	0.672752	0.873658	0.237804
antisense	-	9	7	20	6	2	4	0.190588	0.174686	0.558106	0.109917	0.047581	0.084182
lincRNA	-	0	0	0	0	5	0	0	0	0	0	0.499798	0
antisense	-	5	9	3	0	5	1	0.297421	0.630887	0.235157	0	0.334134	0.059117
antisense	-	0	0	0	2	0	0	0	0	0	0.180311	0	0
processed_	-	8	1	0	2	2	6	0.20006	0.02947	0	0.043268	0.056189	0.149119
sense_intro	AGAP1_int	11	6	1	4	21	24	0.877035	0.563745	0.105065	0.275897	1.881015	1.901713
antisense	-	4	8	5	16	27	30	0.183823	0.433248	0.302792	0.636096	1.393967	1.370158
protein_co	Protein_LO	5	9	8	2	0	0	0.062726	0.133054	0.132253	0.021706	0	0
processed_	long_interg	2	0	0	2	0	1	0.031701	0	0	0.027424	0	0.015753
pseudogen	ferrochelat	0	0	0	1	0	0	0	0	0	0.037726	0	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.22069	0
pseudogen	ribosomal_	0	0	0	0	0	3	0	0	0	0	0	0.333704
antisense	-	5	1	4	7	9	8	0.215558	0.050804	0.227242	0.261069	0.435898	0.342763
pseudogen	ribosomal_	138	199	140	188	154	280	8.426594	14.31967	11.26512	9.93102	10.56435	16.99185
pseudogen	-	3	1	5	0	1	3	0.153601	0.060336	0.337347	0	0.05752	0.152652
pseudogen	-	0	0	2	4	2	1	0	0	0.375071	0.492461	0.319763	0.141436
antisense	-	3	12	2	26	29	20	0.109912	0.518099	0.096558	0.824063	1.193634	0.728222
lincRNA	-	1	0	0	0	0	0	0.068048	0	0	0	0	0

lincRNA	-	1	3	0	1	1	5	0.023301	0.082378	0	0.020158	0.026178	0.115788
protein_co	NFAT_activ	0	0	1	2	4	8	0	0	0.012453	0.016351	0.042468	0.075136
pseudogen	-	0	1	0	0	0	0	0	0.164178	0	0	0	0
antisense	-	0	0	1	0	0	0	0	0	0.189574	0	0	0
pseudogen	-	0	0	0	1	3	1	0	0	0	0.232482	0.905725	0.267076
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.126008	0
antisense	-	9	3	3	18	19	14	2.044931	0.803275	0.89824	3.538113	4.849968	3.161359
pseudogen	glyceraldeh	1	4	1	8	1	6	0.052625	0.248063	0.069347	0.364206	0.059121	0.313801
antisense	GNAS_antis	15	16	6	21	34	32	0.686951	0.863498	0.362093	0.831987	1.749292	1.456444
antisense	RBMS3_ant	2	0	0	0	1	0	0.191123	0	0	0	0.107357	0
lincRNA	-	4	0	2	0	0	0	0.056052	0	0.036931	0	0	0
pseudogen	POU_class_	5	6	5	1	2	1	0.395082	0.558696	0.520622	0.068357	0.17754	0.078528
lincRNA	-	60	52	67	19	24	26	1.590616	1.624518	2.340581	0.435743	0.714783	0.68501
lincRNA	-	0	1	0	0	0	0	0	0.085346	0	0	0	0
pseudogen	nuclear_sp	1	0	5	6	1	8	0.031271	0	0.206035	0.162312	0.03513	0.248619
lincRNA	-	0	0	0	1	1	0	0	0	0	0.020733	0.026924	0
pseudogen	-	3	10	8	10	9	6	0.573368	2.252265	2.014824	1.65339	1.932431	1.139655
processed_	-	6	1	4	1	0	1	0.14591	0.028658	0.128182	0.021038	0	0.024168
pseudogen	-	8	0	4	0	2	0	1.366219	0	0.900171	0	0.383716	0
pseudogen	small_nucl	0	0	3	9	2	5	0	0	0.864834	1.703265	0.491537	1.087067
antisense	-	0	4	1	3	5	0	0	0.575002	0.160745	0.316582	0.685206	0
pseudogen	nuclear_un	3	2	3	3	7	0	0.180071	0.141469	0.23729	0.155779	0.472031	0
lincRNA	long_interg	4	2	1	2	0	1	0.077145	0.045456	0.025415	0.033369	0	0.019167
pseudogen	matrix-rem	0	0	1	0	0	0	0	0	0.00872	0	0	0
pseudogen	-	4	1	3	3	5	8	0.151476	0.044626	0.149707	0.098281	0.212718	0.301082
antisense	-	7	8	6	0	8	0	0.518303	0.698045	0.585426	0	0.665465	0
pseudogen	H3_histone	396	375	249	966	597	784	20.51334	22.89178	16.99712	43.28938	34.74278	40.36146
lincRNA	long_interg	0	0	0	0	0	1	0	0	0	0	0	0.184611
antisense	SAPCD1_an	0	0	0	0	0	1	0	0	0	0	0	0.11413
lincRNA	-	0	2	0	9	3	2	0	0.184853	0	0.610652	0.264337	0.155893
lincRNA	-	1	3	2	0	0	1	0.146651	0.518458	0.3865	0	0	0.145745
antisense	-	0	1	0	5	7	4	0	0.07818	0	0.286961	0.521719	0.26373
pseudogen	-	4	0	0	6	2	1	0.360756	0	0	0.468132	0.202644	0.089632
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.172144	0
pseudogen	nucleopho	2	2	7	4	5	5	0.143472	0.169072	0.661711	0.248233	0.402953	0.356464
pseudogen	-	20	5	19	20	10	19	4.856972	1.430911	6.080286	4.201734	2.728253	4.585628
pseudogen	-	1	8	0	0	1	0	0.025687	0.242165	0	0	0.028858	0
antisense	-	0	0	4	1	3	9	0	0	0.524536	0.086088	0.335391	0.890087
pseudogen	-	1	0	1	7	4	4	0.17133	0	0.225771	1.037516	0.769915	0.681088
pseudogen	cytochrom	4	1	2	2	1	0	0.68311	0.201251	0.450086	0.295477	0.191858	0
pseudogen	poly(rC)_bi	6	7	2	0	3	0	0.325124	0.446995	0.142811	0	0.182628	0
processed_	-	105	112	62	39	90	53	1.628238	2.046698	1.266937	0.523186	1.567906	0.816797
lincRNA	-	1	0	0	1	0	2	0.062064	0	0	0.053692	0	0.123362
processed_	DICER1_an	25	28	10	46	33	43	0.569748	0.751983	0.300315	0.906909	0.844901	0.973915

pseudogen	-	0	0	0	1	0	0	0	0	0	0.041485	0	0
antisense	-	0	0	1	0	0	0	0	0	0.030424	0	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.038801
antisense	-	1	7	0	0	0	0	0.049385	0.407383	0	0	0	0
processed_	-	2	4	5	0	5	2	0.064093	0.15106	0.211148	0	0.180012	0.063697
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.153394
pseudogen	olfactory_r	0	0	0	1	0	0	0	0	0	0.051517	0	0
pseudogen	high_mobil	2	8	3	13	11	12	0.349446	1.647201	0.690726	1.96497	2.159192	2.083725
antisense	-	1	0	0	1	3	0	0.03116	0	0	0.026956	0.105019	0
pseudogen	C-terminal_	0	0	0	1	0	0	0	0	0	0.034332	0	0
pseudogen	-	1	2	2	7	1	0	0.094537	0.222813	0.249155	0.572486	0.106207	0
protein_co	KIAA0040	0	0	0	16	5	12	0	0	0	0.160557	0.065158	0.138337
sense_intrc	MAGI2_int	1	0	0	0	0	0	0.092232	0	0	0	0	0
antisense	-	3	1	1	0	3	7	0.365952	0.143751	0.160745	0	0.411124	0.848614
pseudogen	small_nucl	1	0	0	1	0	0	0.240641	0	0	0.208177	0	0
processed_	long_interg	91	97	110	0	0	0	1.305591	1.640003	2.079664	0	0	0
antisense	-	0	5	2	1	6	4	0	0.542502	0.242655	0.07965	0.620618	0.366011
pseudogen	-	1	0	0	2	2	2	0.066094	0	0	0.114354	0.148504	0.131371
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.099127	0
antisense	-	0	0	0	1	0	0	0	0	0	0.053818	0	0
pseudogen	heterogene	1	6	1	3	0	0	0.060229	0.425855	0.079367	0.15631	0	0
sense_intrc	ZNRF3_intr	1	5	1	7	4	0	0.078547	0.462817	0.103506	0.475656	0.352973	0
antisense	-	8	9	5	5	15	1	0.485697	0.64391	0.400019	0.262608	1.023095	0.060337
antisense	-	9	1	5	3	0	3	0.710088	0.092977	0.519846	0.204764	0	0.235234
antisense	HCFC1_ant	3	2	3	0	0	8	0.45378	0.356501	0.597971	0	0	1.202607
lincRNA	-	1	0	1	1	5	0	0.044865	0	0.059121	0.038813	0.252017	0
pseudogen	myosin_ligl	0	0	0	0	3	0	0	0	0	0	0.411124	0
pseudogen	ADAM_met	3	0	0	0	0	1	0.07319	0	0	0	0	0.024246
lincRNA	-	3	6	2	0	0	0	0.169321	0.399069	0.148749	0	0	0
pseudogen	PRELI_dom	8	2	0	1	0	4	0.644639	0.189917	0	0.069709	0	0.320329
processed_	long_interg	56	47	46	97	84	88	1.16217	1.149441	1.257982	1.741472	1.958439	1.814989
pseudogen	tubulin_fol	2	0	1	0	1	1	0.324791	0	0.213998	0	0.182441	0.161393
antisense	BHLHE40_a	5	1	1	26	7	1	0.112354	0.02648	0.029611	0.505421	0.176711	0.022332
sense_intrc	-	3	0	1	0	0	0	0.102203	0	0.044893	0	0	0
antisense	-	10	1	1	6	13	1	0.816991	0.096277	0.107659	0.424064	1.19319	0.081195
processed_	-	8	10	4	13	18	9	0.413198	0.608661	0.272247	0.580864	1.044455	0.461977
antisense	-	2	0	0	3	0	2	0.218313	0	0	0.283292	0	0.216965
antisense	RMDN2_an	1	7	0	3	1	3	0.061631	0.508398	0	0.15995	0.069239	0.183751
antisense	HS6ST2_an	3	1	0	0	0	0	0.288769	0.113432	0	0	0	0
antisense	-	2	0	0	0	5	8	0.115214	0	0	0	0.32359	0.458011
pseudogen	-	5	4	4	80	39	56	0.21451	0.202229	0.226137	2.969135	1.879709	2.387672
protein_co	UDP-Gal:be	17	6	9	27	37	25	0.533806	0.22202	0.372402	0.733434	1.305225	0.780161
pseudogen	heat_shock	0	0	0	0	1	0	0	0	0	0	0.038322	0
antisense	GSN_antise	296	234	186	23	65	73	3.290055	3.065028	2.724327	0.221158	0.81166	0.806388

pseudogen	-	0	0	0	1	0	1	0	0	0	0.137122	0	0.157527
antisense	-	2	0	0	3	1	0	0.13627	0	0	0.17683	0.076546	0
processed_	ARHGEF7_a	0	0	0	0	0	1	0	0	0	0	0	0.067714
protein_co	Protein_LO	17	11	19	4	4	4	1.119399	0.853563	1.648635	0.227855	0.2959	0.261761
antisense	-	0	0	0	0	1	0	0	0	0	0	0.146492	0
processed_	-	81	68	74	124	83	117	2.606821	2.578946	3.138287	3.452319	3.000913	3.742154
lincRNA	-	2	0	0	0	0	0	0.098587	0	0	0	0	0
lincRNA	-	2	1	0	0	0	0	0.074987	0.044184	0	0	0	0
antisense	TSPEAR_ant	14	13	6	3	12	12	0.533987	0.584323	0.30157	0.098989	0.514201	0.454877
pseudogen	-	2	3	0	0	0	0	0.195715	0.345958	0	0	0	0
antisense	TM4SF19_a	4	1	5	2	5	1	0.115781	0.03411	0.190714	0.050081	0.162591	0.028767
antisense	-	0	0	0	1	1	2	0	0	0	0.074108	0.096239	0.170272
processed_	CPB2_antis	5	1	7	5	11	12	0.354357	0.083518	0.653739	0.306552	0.875817	0.845206
antisense	RBMS3_ant	1	1	6	8	11	10	0.086364	0.101774	0.682838	0.597702	1.067268	0.858304
pseudogen	-	0	2	0	1	5	0	0	0.169532	0	0.062227	0.404048	0
sense_intro	RHOA_intro	8	4	2	5	1	15	0.819203	0.48269	0.269877	0.442929	0.11504	1.52652
antisense	-	3	3	0	0	1	1	0.282101	0.332439	0	0	0.105641	0.093453
pseudogen	-	1	2	0	1	1	3	0.275734	0.649872	0	0.238536	0.30977	0.822095
pseudogen	-	6	1	0	1	0	0	0.467126	0.091747	0	0.067351	0	0
processed_	ASH1L_anti	28	19	24	72	25	52	0.758234	0.606326	0.856429	1.686712	0.760562	1.399453
pseudogen	-	1	0	0	0	2	0	0.054132	0	0	0	0.121628	0
antisense	NEXN_antis	10	12	3	2	4	6	0.230982	0.326637	0.091313	0.039964	0.103797	0.137733
pseudogen	-	0	2	2	0	0	0	0	0.302853	0.338657	0	0	0
pseudogen	MT-ND1_ps	2	0	1	0	1	0	0.371516	0	0.244783	0	0.208687	0
pseudogen	zinc_finger_	19	24	21	20	21	28	0.365774	0.544475	0.532738	0.333083	0.45418	0.535707
pseudogen	-	4	1	0	0	2	6	0.108375	0.031928	0	0	0.060876	0.161558
pseudogen	-	9	10	7	7	11	5	0.960623	1.257817	0.984562	0.646356	1.319022	0.530384
processed_	TTC28_anti	162	175	115	172	104	173	1.463806	1.863433	1.369308	1.344498	1.055725	1.553547
pseudogen	-	2	0	0	0	0	0	0.037801	0	0	0	0	0
pseudogen	cytochrom	0	0	0	1	4	0	0	0	0	0.238536	1.239082	0
processed_	UBOX5_ant	8	2	2	6	4	17	0.236344	0.069629	0.077861	0.153345	0.132759	0.499129
pseudogen	-	1	1	1	0	0	0	0.124861	0.147141	0.164536	0	0	0
protein_co	paraneopla	7	1	2	2	0	1	0.16434	0.027666	0.061874	0.04062	0	0.023332
pseudogen	cytochrom	0	0	1	0	0	1	0	0	0.190091	0	0	0.143363
pseudogen	vomeronas	0	5	0	0	1	1	0	0.29652	0	0	0.056536	0.050013
pseudogen	-	2	1	2	0	0	0	0.205996	0.121377	0.271452	0	0	0
antisense	GPC5_antis	0	0	1	0	1	0	0	0	0.177515	0	0.151338	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.138365	0	0
antisense	MORC2_an	89	120	101	178	122	110	2.171313	3.450013	3.247047	3.756777	3.343807	2.667072
pseudogen	-	0	1	1	9	0	4	0	0.148189	0.165709	0.979074	0	0.499896
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.051785
pseudogen	ubiquitin-c	0	0	0	0	3	0	0	0	0	0	0.422815	0
antisense	-	0	0	0	0	2	0	0	0	0	0	0.325005	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.015515	0	0

processed_	-	38	25	13	102	30	43	1.01297	0.785344	0.456658	2.35221	0.898428	1.139176
pseudogen	-	7	7	6	6	9	4	0.42892	0.505456	0.484467	0.318048	0.619541	0.243584
antisense	-	1	2	0	0	2	2	0.081198	0.191373	0	0	0.182441	0.161393
lincRNA	-	0	0	0	4	0	0	0	0	0	0.020726	0	0
lincRNA	-	0	0	4	1	5	0	0	0	0.222886	0.036581	0.237524	0
pseudogen	-	17	6	7	15	4	7	1.093556	0.454832	0.593369	0.834731	0.289069	0.447507
antisense	-	5	7	5	12	18	1	0.288979	0.476762	0.380804	0.599986	1.168741	0.057439
antisense	ASMTL_ant	77	56	23	48	67	90	4.852924	4.159182	1.910185	2.61708	4.743912	5.63722
pseudogen	-	8	7	5	7	3	5	0.552909	0.570123	0.455374	0.418528	0.232934	0.343434
antisense	-	1	2	1	2	3	4	0.091435	0.215502	0.120489	0.1582	0.308165	0.363482
antisense	-	5	3	4	0	0	0	0.617028	0.436278	0.650473	0	0	0
protein_co	prostate_ar	0	0	0	0	4	0	0	0	0	0	0.178072	0
protein_co	-	0	0	0	0	0	1	0	0	0	0	0	0.011633
lincRNA	-	1	0	4	8	0	0	0.061703	0	0.325237	0.427029	0	0
antisense	-	0	0	2	0	0	0	0	0	0.185788	0	0	0
pseudogen	-	0	4	5	5	0	3	0	0.31509	0.440425	0.289135	0	0.199296
lincRNA	-	8	2	1	7	0	1	0.719063	0.211843	0.118444	0.544299	0	0.089328
pseudogen	chitinase_a	0	0	0	0	0	1	0	0	0	0	0	0.052878
pseudogen	fatty_acid_	1	0	1	1	0	2	0.129757	0	0.170988	0.112252	0	0.257912
antisense	-	6	4	0	0	0	0	0.436927	0.343261	0	0	0	0
pseudogen	-	1	1	1	0	1	3	0.089883	0.105921	0.118444	0	0.100978	0.267983
pseudogen	-	0	3	0	0	0	0	0	0.156753	0	0	0	0
lincRNA	-	0	0	0	3	1	0	0	0	0	0.05435	0.023527	0
antisense	MYCBP2_ar	0	0	0	0	1	0	0	0	0	0	0.071314	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.100297	0
pseudogen	glyceraldeh	0	0	0	0	0	1	0	0	0	0	0	0.056152
pseudogen	-	1	0	3	1	0	0	0.096432	0	0.38122	0.083422	0	0
pseudogen	heat_shock	0	1	2	1	2	2	0	0.243702	0.545026	0.178902	0.464656	0.411047
processed_	-	0	1	0	0	0	0	0	0.029851	0	0	0	0
antisense	-	1	0	1	0	2	3	0.031512	0	0.041526	0	0.070805	0.093954
lincRNA	-	2	2	4	4	6	5	0.242849	0.286182	0.64003	0.420173	0.818476	0.603372
lincRNA	-	18	10	16	4	0	2	1.393184	0.912101	1.63189	0.26783	0	0.153842
pseudogen	-	0	0	0	0	3	0	0	0	0	0	0.240145	0
lincRNA	-	3	0	10	2	3	1	0.24933	0	1.095185	0.143796	0.280106	0.082597
antisense	-	0	0	0	0	1	0	0	0	0	0	0.399167	0
pseudogen	olfactory_r	7	6	3	0	1	0	0.401938	0.405994	0.226995	0	0.064508	0
processed_	COX10_ant	155	152	130	115	98	106	2.737109	3.163087	3.025092	1.756796	1.944176	1.86027
pseudogen	lactate_deh	1	0	1	0	0	0	0.052521	0	0.06921	0	0	0
lincRNA	-	0	2	2	0	2	0	0	0.129839	0.145189	0	0.123779	0
sense_intro	-	2	1	0	1	0	3	0.13592	0.080087	0	0.058792	0	0.202622
lincRNA	-	2	0	6	1	2	3	0.178855	0	0.70706	0.077363	0.200932	0.266625
protein_co	zinc_finger_	573	546	443	298	271	395	11.44292	12.84938	11.65792	5.148274	6.07996	7.839513
lincRNA	-	0	0	0	5	5	2	0	0	0	0.131154	0.17032	0.060268
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.022826

pseudogen	-	0	1	0	0	0	0	0	0.20455	0	0	0	0
pseudogen	-	3	0	3	0	0	2	0.08095	0	0.106672	0	0	0.053633
antisense	-	0	3	0	1	0	0	0	0.562052	0	0.137534	0	0
sense_intrc	-	1	0	0	0	0	0	0.098039	0	0	0	0	0
lincRNA	-	0	0	2	3	0	0	0	0	0.16224	0.159764	0	0
pseudogen	-	5	1	0	3	6	1	0.554937	0.130792	0	0.288043	0.748125	0.110302
pseudogen	-	0	0	1	0	0	1	0	0	0.082854	0	0	0.062487
antisense	-	1	0	3	4	6	19	0.029185	0	0.115375	0.10099	0.196723	0.551084
pseudogen	-	10	18	11	2	4	3	0.421841	0.894804	0.611471	0.072986	0.189565	0.125771
lincRNA	-	0	4	0	4	0	5	0	0.654989	0	0.480828	0	0.690473
antisense	-	32	30	39	180	150	212	0.433166	0.478556	0.695671	2.10785	2.281101	2.852002
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.35508	0
pseudogen	mitochond	1	0	0	0	0	0	0.172446	0	0	0	0	0
antisense	-	0	0	0	1	0	0	0	0	0	0.172826	0	0
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.209201
pseudogen	-	1	0	0	0	0	0	0.025114	0	0	0	0	0
pseudogen	coiled-coil-	14	6	5	6	6	18	1.807741	0.912991	0.850772	0.670228	0.870379	2.309885
pseudogen	-	0	2	0	0	0	0	0	0.213291	0	0	0	0
pseudogen	-	0	0	1	1	1	0	0	0	0.129431	0.08497	0.110345	0
pseudogen	protease-as	1	0	2	1	0	13	0.10084	0	0.265765	0.087236	0	1.302824
lincRNA	-	1	3	2	0	0	0	0.095908	0.339064	0.252766	0	0	0
lincRNA	-	0	2	1	0	0	0	0	0.179792	0.100523	0	0	0
pseudogen	SSU72_RNA	0	0	2	0	0	0	0	0	0.285915	0	0	0
pseudogen	-	0	1	0	0	4	0	0	0.082742	0	0	0.315522	0
pseudogen	transcriptic	2	10	5	14	9	8	0.125453	0.739191	0.41329	0.759697	0.634222	0.498711
pseudogen	gap_junctic	2	0	0	0	0	0	0.101614	0	0	0	0	0
antisense	PRKX_antis	0	0	3	0	4	2	0	0	0.4056	0	0.461054	0.20393
sense_intrc	-	3	1	2	1	3	6	0.185758	0.072968	0.163189	0.053566	0.208687	0.369221
antisense	-	1	0	0	0	4	0	0.020608	0	0	0	0.092606	0
antisense	-	12	2	9	2	3	2	1.5126	0.297084	1.494927	0.21809	0.424828	0.250543
antisense	KDM4A_an	12	16	15	26	17	20	0.762655	1.198324	1.256242	1.429498	1.213794	1.263243
antisense	GRM7_anti	2	0	0	0	0	0	0.246237	0	0	0	0	0
lincRNA	-	8	2	4	8	3	7	0.217305	0.06402	0.143178	0.187989	0.091548	0.188968
processed_	-	1	0	0	0	0	0	0.078431	0	0	0	0	0
lincRNA	-	0	1	0	0	0	0	0	0.075897	0	0	0	0
pseudogen	-	5	4	2	1	3	1	0.106607	0.100504	0.056193	0.018445	0.07186	0.02119
antisense	-	16	9	1	3	0	6	1.101503	0.730155	0.090719	0.178669	0	0.410513
pseudogen	-	0	0	0	2	0	2	0	0	0	0.260221	0	0.298943
sense_intrc	GPC5_intrc	0	0	0	5	4	3	0	0	0	0.348016	0.361556	0.239882
antisense	MYO16_ant	0	0	0	3	0	0	0	0	0	0.236891	0	0
pseudogen	-	1	0	0	0	0	0	0.041917	0	0	0	0	0
lincRNA	-	54	36	37	57	44	55	0.925182	0.726847	0.835353	0.844834	0.846906	0.936496
antisense	DIAPH2_an	2	1	3	13	6	5	0.093867	0.055308	0.185541	0.527824	0.316361	0.233218
antisense	SHANK2_ar	0	0	0	0	0	3	0	0	0	0	0	0.443377

pseudogen	ribosomal_	4	3	1	9	1	2	0.328316	0.290175	0.10816	0.639054	0.092211	0.163144
lincRNA	-	0	0	0	2	1	1	0	0	0	0.060025	0.038975	0.034478
sense_intrc	ENO1_intrc	25	41	10	2	8	12	1.778931	3.438033	0.937679	0.123115	0.639526	0.848614
pseudogen	-	2	0	2	0	1	6	0.105565	0	0.139109	0	0.059298	0.31474
pseudogen	-	0	0	0	0	1	1	0	0	0	0	0.11731	0.103775
protein_co	zinc_finger_	555	499	548	940	654	668	7.990822	8.466543	10.39714	11.70818	10.57853	9.558386
pseudogen	eukaryotic_	0	0	0	0	0	1	0	0	0	0	0	0.074842
pseudogen	glucuronid	8	8	7	16	11	21	0.212935	0.250931	0.245522	0.368418	0.328927	0.555503
pseudogen	-	0	0	1	0	0	0	0	0	0.094916	0	0	0
antisense	-	19	9	9	0	3	0	0.705385	0.393751	0.440301	0	0.125125	0
antisense	-	18	3	4	7	5	18	2.582488	0.507217	0.756242	0.868814	0.805907	2.566539
lincRNA	-	0	0	0	1	0	2	0	0	0	0.098918	0	0.227275
pseudogen	-	0	2	2	10	5	7	0	0.290175	0.32448	1.065091	0.69158	0.856508
antisense	-	1	2	7	10	5	13	0.091593	0.215874	0.844884	0.792369	0.514498	1.183361
processed_	-	0	1	2	0	0	0	0	0.161626	0.361468	0	0	0
pseudogen	-	1	0	0	0	0	0	0.275734	0	0	0	0	0
lincRNA	-	33	21	11	0	0	0	2.087279	1.565284	0.916841	0	0	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.177805	0
antisense	-	4	0	0	0	0	0	0.569258	0	0	0	0	0
pseudogen	-	0	1	0	2	1	0	0	0.230213	0	0.337999	0.219468	0
processed_	TRHDE_ant	24	20	19	241	259	328	0.268452	0.263629	0.280055	2.332038	3.254651	3.646188
sense_intrc	FMR1_intrc	0	3	3	14	16	20	0	0.545665	0.610174	1.869343	2.774387	3.067875
antisense	-	15	15	16	4	2	4	0.546159	0.643615	0.767684	0.125994	0.08181	0.144743
lincRNA	-	1	0	1	0	0	0	0.088678	0	0.116856	0	0	0
pseudogen	proteasom	1	0	1	0	0	0	0.039895	0	0.052572	0	0	0
pseudogen	succinate-C	0	0	3	0	0	0	0	0	0.161489	0	0	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.0579	0	0
antisense	-	2	1	0	6	10	6	0.305135	0.179792	0	0.791912	1.714003	0.909753
lincRNA	-	0	0	0	1	0	0	0	0	0	0.019973	0	0
lincRNA	-	0	0	0	0	3	0	0	0	0	0	0.07962	0
pseudogen	POU_class_	3	3	2	0	0	7	0.379959	0.447759	0.333796	0	0	0.881097
lincRNA	-	0	0	0	1	0	0	0	0	0	0.089451	0	0
processed_	long_interg	73	41	37	6	9	18	3.943564	2.610099	2.63392	0.280401	0.546207	0.966381
lincRNA	long_interg	0	0	0	0	5	2	0	0	0	0	0.146276	0.05176
lincRNA	-	8	0	1	0	0	0	0.585792	0	0.096491	0	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.235083	0
antisense	ITCH_antise	2	0	3	0	0	0	0.35412	0	0.699966	0	0	0
antisense	-	4	2	4	3	3	5	0.365741	0.215502	0.481957	0.2373	0.308165	0.454353
processed_	-	0	2	0	0	0	1	0	0.371356	0	0	0	0.156589
lincRNA	-	1	0	3	4	9	1	0.017647	0	0.069763	0.061065	0.178428	0.017538
pseudogen	DEAD/H_(A	43	16	40	126	88	86	1.378839	0.604605	1.690207	3.495253	3.170128	2.740647
processed_	-	21	13	16	85	75	64	0.351045	0.256091	0.352451	1.22921	1.408492	1.063246
pseudogen	neurotroph	0	3	0	5	3	1	0	0.270858	0	0.331396	0.258217	0.076142
pseudogen	NADH_dehy	0	1	2	1	2	0	0	0.118834	0.265765	0.087236	0.226575	0

pseudogen	cathepsin_l	0	0	3	0	0	0	0	0	0.208872	0	0	0
lincRNA	-	26	17	14	43	39	55	0.449972	0.346712	0.319283	0.64379	0.758274	0.945987
pseudogen	-	0	0	0	2	0	0	0	0	0	0.250267	0	0
antisense	-	3	0	1	1	0	4	0.224962	0	0.098815	0.064871	0	0.298097
antisense	-	0	0	0	5	1	2	0	0	0	0.576812	0.149813	0.265058
pseudogen	keratin_8_p	0	1	1	5	2	7	0	0.045505	0.050885	0.167027	0.086763	0.268635
antisense	-	24	12	11	20	9	11	0.494776	0.291531	0.29883	0.356689	0.208444	0.225372
antisense	-	2	0	0	0	0	0	0.243407	0	0	0	0	0
lincRNA	family_with	45	32	43	41	70	72	1.098867	0.920852	1.383681	0.866123	1.920348	1.74733
pseudogen	-	17	18	18	16	11	16	2.795021	3.487513	3.899811	2.275722	2.031786	2.614363
pseudogen	ubiquitin-c	1	0	0	0	0	0	0.092393	0	0	0	0	0
sense_intrc	ATG10_intr	2	0	1	0	2	1	0.217417	0	0.143251	0	0.244254	0.108037
lincRNA	-	11	28	11	2	3	2	0.242646	0.727857	0.319748	0.038166	0.074345	0.043845
lincRNA	-	0	0	4	0	0	0	0	0	0.135331	0	0	0
lincRNA	-	0	2	1	0	0	0	0	0.167935	0.093894	0	0	0
antisense	-	5	11	8	2	4	1	0.188402	0.488445	0.397229	0.065194	0.169326	0.037448
sense_intrc	-	1	3	0	0	0	0	0.163904	0.579453	0	0	0	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.030032	0	0
lincRNA	long_interg	2	1	0	0	1	2	0.246237	0.145088	0	0	0.138316	0.244717
antisense	-	21	13	16	6	17	6	0.311767	0.227437	0.313015	0.077059	0.283536	0.088526
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.078823
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.133354	0
antisense	-	1	0	1	0	0	0	0.113122	0	0.149067	0	0	0
pseudogen	glucosamin	0	1	0	0	6	0	0	0.048176	0	0	0.275564	0
pseudogen	tripartite_r	2	0	2	0	0	0	0.140614	0	0.185294	0	0	0
pseudogen	-	11	8	4	17	24	30	0.512182	0.438964	0.245429	0.684768	1.255428	1.388234
pseudogen	pyruvate_k	0	0	0	1	0	2	0	0	0	0.030072	0	0.069093
pseudogen	-	1	0	1	4	2	2	0.06295	0	0.082953	0.217831	0.141441	0.125123
pseudogen	-	0	0	1	0	5	0	0	0	0.233322	0	0.994581	0
pseudogen	-	0	0	1	0	0	0	0	0	0.095566	0	0	0
pseudogen	eukaryotic_	0	1	0	0	0	0	0	0.06245	0	0	0	0
lincRNA	-	3	4	5	4	7	7	0.099952	0.157049	0.219519	0.11529	0.262008	0.23178
pseudogen	-	0	1	0	0	0	0	0	0.063274	0	0	0	0
antisense	-	15	9	2	10	12	10	0.990168	0.700112	0.173973	0.571059	0.889914	0.656036
protein_co	Em:AC0065	1	1	3	0	0	0	0.087217	0.10278	0.344794	0	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.553677	0	0	0
pseudogen	ribosomal_	1	0	6	0	0	0	0.111221	0	0.879369	0	0	0
antisense	-	0	0	0	3	12	3	0	0	0	0.16051	0.833775	0.184395
pseudogen	-	1	0	1	2	2	2	0.115845	0	0.152655	0.200433	0.260288	0.230258
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.127395
antisense	-	1	1	0	2	9	10	0.051349	0.060512	0	0.088844	0.519188	0.510321
antisense	GPC6_antis	0	1	1	0	0	0	0	0.089381	0.099947	0	0	0
antisense	-	0	0	0	0	2	0	0	0	0	0	0.222756	0
antisense	-	5	15	10	3	10	7	0.144569	0.511096	0.381012	0.075039	0.324828	0.201146

pseudogen	ADP-ribosy	1	2	1	0	1	1	0.100648	0.237216	0.13263	0	0.113072	0.100027
antisense	-	0	0	0	0	1	0	0	0	0	0	0.070054	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.154483	0
pseudogen	-	1	0	0	0	0	0	0.033275	0	0	0	0	0
lincRNA	-	0	0	0	0	5	0	0	0	0	0	0.066291	0
pseudogen	-	0	2	0	0	0	0	0	0.31272	0	0	0	0
pseudogen	H3_histone	0	1	0	1	0	0	0	0.154808	0	0.113645	0	0
sense_intro	RC3H1_int	3	4	1	4	1	4	0.354516	0.557033	0.155722	0.408919	0.132759	0.469768
antisense	-	4	1	4	3	5	5	0.306017	0.090156	0.403256	0.19855	0.429739	0.380159
lincRNA	-	23	32	34	13	28	28	2.871799	4.708508	5.594225	1.404212	3.927655	3.474513
pseudogen	-	0	1	0	0	0	1	0	0.006422	0	0	0	0.005416
antisense	-	47	46	31	49	45	59	2.675513	3.085845	2.325443	2.413061	2.877867	3.337881
pseudogen	mediator_c	4	0	0	0	0	0	0.399555	0	0	0	0	0
antisense	-	0	1	3	2	3	3	0	0.106282	0.356541	0.156044	0.303966	0.268896
antisense	-	0	0	0	0	0	3	0	0	0	0	0	0.201073
processed_	-	8	11	8	3	7	5	0.093971	0.152266	0.123831	0.030485	0.092374	0.058369
pseudogen	-	1	1	0	5	1	1	0.116354	0.137116	0	0.503285	0.130716	0.115635
pseudogen	ribosomal_	345	341	217	255	157	316	29.84419	34.76179	24.73633	19.08288	15.25771	27.16673
pseudogen	asparagine_	0	3	4	2	0	0	0	0.14331	0.21367	0.070136	0	0
pseudogen	-	0	2	0	0	0	0	0	0.503127	0	0	0	0
antisense	-	2	0	0	0	0	0	0.315125	0	0	0	0	0
antisense	-	0	0	0	0	1	9	0	0	0	0	0.029634	0.235937
antisense	-	7	0	2	8	3	11	0.990874	0	0.373066	0.979656	0.47708	1.547472
pseudogen	-	1	0	0	0	0	0	0.132684	0	0	0	0	0
pseudogen	heterogene	16	10	14	12	27	17	1.016874	0.748952	1.172492	0.659768	1.927791	1.073756
pseudogen	-	1	0	2	0	3	2	0.027331	0	0.072032	0	0.092116	0.054325
pseudogen	-	2	4	5	2	6	0	0.096344	0.227071	0.317394	0.083347	0.324709	0
pseudogen	small_nucl	2	0	2	0	1	1	0.483479	0	0.637108	0	0.27158	0.240247
pseudogen	-	2	2	0	0	0	0	0.33507	0.394859	0	0	0	0
antisense	STARD13_a	5	5	10	9	3	2	0.294117	0.346598	0.775148	0.457989	0.198253	0.11692
pseudogen	PRP38_dor	0	0	0	0	2	0	0	0	0	0	0.139779	0
pseudogen	-	1	6	6	1	0	0	0.037494	0.265104	0.296445	0.032435	0	0
antisense	-	10	4	8	2	0	1	4.072384	1.919622	4.293125	0.704599	0	0.404723
pseudogen	RAN_memb	1	0	2	8	6	10	0.081323	0	0.214327	0.562813	0.548165	0.808204
protein_co	zinc_finger_	49	35	35	110	64	78	0.672572	0.566132	0.633061	1.306165	0.986896	1.064012
lincRNA	-	0	1	0	0	0	0	0	0.180311	0	0	0	0
antisense	-	4	0	1	0	5	6	0.381557	0	0.1257	0	0.535819	0.568801
antisense	PITPNA_ant	6	1	0	7	2	7	0.586063	0.115107	0	0.591499	0.219468	0.679517
protein_co	coiled-coil_	40	43	36	93	37	60	0.95004	1.203532	1.126729	1.910856	0.987263	1.41626
pseudogen	-	0	2	1	0	0	0	0	0.288832	0.161489	0	0	0
lincRNA	-	0	0	0	1	0	1	0	0	0	0.095018	0	0.109158
antisense	-	0	3	1	5	0	6	0	0.303344	0.113069	0.371142	0	0.511644
lincRNA	-	0	1	2	4	18	9	0	0.065671	0.14687	0.192837	1.126912	0.498449
pseudogen	-	0	2	0	3	2	0	0	0.60278	0	0.663752	0.574647	0

antisense	-	3	0	2	2	0	0	0.376358	0	0.330632	0.217056	0	0
antisense	-	0	1	0	0	0	5	0	0.029072	0	0	0	0.122586
pseudogen	keratin_18_	9	10	2	11	4	14	0.36907	0.483251	0.108076	0.390231	0.184279	0.570563
processed_	PRKG1_ant	0	0	0	0	4	1	0	0	0	0	0.214135	0.047357
processed_	-	0	0	0	0	1	0	0	0	0	0	0.025803	0
pseudogen	metaxin_1_	134	119	93	33	39	83	8.465505	8.859355	7.742226	1.803537	2.767972	5.211177
pseudogen	-	1	0	0	0	0	0	0.042763	0	0	0	0	0
processed_	-	5	4	6	5	3	5	0.098403	0.09277	0.155606	0.085128	0.06633	0.097796
pseudogen	basic_leuci	0	0	3	0	0	0	0	0	0.168782	0	0	0
pseudogen	eukaryotic_	10	3	4	14	23	28	1.217034	0.43026	0.641501	1.473988	3.144704	3.386652
protein_co	Rho_guanir	1	0	1	7	6	4	0.009707	0	0.012791	0.058781	0.06543	0.038587
antisense	-	0	0	0	6	12	14	0	0	0	0.27983	0.726793	0.750098
sense_intro	DAPK1_intr	3	2	0	7	1	2	0.226244	0.177743	0	0.456684	0.084724	0.149898
pseudogen	-	0	5	2	0	1	2	0	0.427313	0.191132	0	0.081474	0.144148
antisense	SMAD9_ant	9	7	5	0	3	1	0.945375	0.866496	0.692096	0	0.354023	0.104393
lincRNA	-	2	8	4	1	0	0	0.047332	0.223112	0.124744	0.020473	0	0
lincRNA	-	0	1	0	0	0	0	0	0.297084	0	0	0	0
pseudogen	-	3	1	0	0	0	0	0.43276	0.169994	0	0	0	0
antisense	-	3	0	3	0	0	0	0.653593	0	0.861275	0	0	0
pseudogen	-	0	0	5	0	0	0	0	0	0.739018	0	0	0
processed_	galectin-rel	2	1	0	0	0	0	0.163398	0.096277	0	0	0	0
pseudogen	ribosomal_	0	3	0	0	0	0	0	0.479906	0	0	0	0
pseudogen	-	2	0	5	0	3	0	0.19791	0	0.651993	0	0.33351	0
pseudogen	-	0	0	0	2	0	0	0	0	0	0.203099	0	0
lincRNA	-	4	0	0	0	0	0	0.482378	0	0	0	0	0
pseudogen	yrdC_doma	0	1	0	4	2	10	0	0.097177	0	0.285351	0.185283	0.819533
pseudogen	-	0	1	5	0	0	0	0	0.179792	1.005235	0	0	0
lincRNA	-	0	1	0	10	17	7	0	0.099661	0	0.731612	1.615161	0.588336
processed_	-	41	43	21	32	28	13	1.062448	1.313104	0.717097	0.717359	0.815137	0.334793
antisense	-	0	0	0	1	5	4	0	0	0	0.024918	0.161795	0.114503
protein_co	DNAJC9_an	0	4	0	0	2	2	0	0.08217	0	0	0.039168	0.034649
lincRNA	-	0	0	0	1	0	1	0	0	0	0.064688	0	0.074314
protein_co	CTAGE_fam	0	0	0	0	0	2	0	0	0	0	0	0.040072
pseudogen	tRNA_meth	0	0	0	1	0	0	0	0	0	0.120841	0	0
pseudogen	-	0	0	1	0	0	1	0	0	0.127538	0	0	0.096187
antisense	-	6	12	6	3	2	2	0.322156	0.759283	0.424523	0.139348	0.120641	0.106722
pseudogen	-	5	0	0	0	0	0	1.145909	0	0	0	0	0
pseudogen	-	2	2	2	0	0	0	0.230178	0.271251	0.303319	0	0	0
processed_	INTS6_antis	14	21	9	11	19	17	0.818073	1.446073	0.693013	0.556057	1.247287	0.987239
pseudogen	-	0	0	0	0	5	0	0	0	0	0	0.350683	0
lincRNA	long_interg	0	1	1	4	1	0	0	0.026639	0.029788	0.078222	0.025395	0
pseudogen	-	0	0	0	3	0	0	0	0	0	0.116045	0	0
pseudogen	sperm_auto	0	1	0	0	0	0	0	0.138026	0	0	0	0
lincRNA	-	1	0	3	0	0	4	0.153898	0	0.608401	0	0	0.611791

pseudogen	-	16	3	7	12	17	8	1.787038	0.394859	1.030259	1.159466	2.133103	0.888001
pseudogen	ribosomal_	2	0	0	0	2	0	0.140614	0	0	0	0.157971	0
pseudogen	sorting_nex	0	0	1	10	3	11	0	0	0.083649	0.549148	0.213942	0.69395
antisense	-	10	22	4	15	20	10	0.492933	1.277961	0.259826	0.63965	1.107559	0.489889
pseudogen	glyceraldeh	1	3	7	3	2	4	0.053047	0.187538	0.489322	0.137672	0.11919	0.210878
pseudogen	-	6	1	1	8	1	13	0.271492	0.053323	0.059627	0.313155	0.050834	0.584601
pseudogen	ankyrin_rep	0	0	0	0	2	0	0	0	0	0	0.049276	0
pseudogen	ADP-ribosy	0	0	0	1	0	0	0	0	0	0.085927	0	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.26791	0
lincRNA	brain_cyto	70	44	57	90	67	50	0.275366	0.203972	0.295475	0.306279	0.296098	0.195475
processed_	-	3	0	5	4	2	3	0.092608	0	0.203391	0.10682	0.06936	0.092036
processed_	CBR3_antis	4	0	2	18	17	36	0.045531	0	0.029999	0.177248	0.217392	0.407247
processed_	-	0	0	0	0	0	2	0	0	0	0	0	0.071535
antisense	-	0	2	1	0	0	0	0	0.30885	0.172681	0	0	0
antisense	-	24	24	21	0	3	0	0.343959	0.405334	0.396597	0	0.048302	0
pseudogen	-	0	0	0	5	3	0	0	0	0	0.483111	0.37643	0
pseudogen	-	1	0	0	0	0	0	0.199777	0	0	0	0	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.08378
pseudogen	-	359	307	227	407	356	372	10.70147	10.78437	8.916816	10.49558	11.92197	11.02051
pseudogen	-	6	6	4	0	0	0	0.574405	0.676901	0.504617	0	0	0
processed_	-	73	43	36	76	75	74	3.035894	2.107362	1.972882	2.734263	3.50408	3.058476
antisense	-	2	8	8	7	4	2	0.188067	0.886504	0.991308	0.569436	0.422564	0.186906
pseudogen	ribosomal_	2	0	2	0	3	2	0.224803	0	0.296235	0	0.378827	0.223414
pseudogen	-	6	7	8	1	1	6	0.68311	0.93917	1.200229	0.098492	0.127905	0.678891
antisense	-	2	2	6	1	7	2	0.232197	0.27363	0.917938	0.100436	0.913008	0.230763
lincRNA	long_interg	86	82	38	41	42	73	12.3052	13.82647	7.164878	5.075014	6.75132	10.38061
pseudogen	DEAD/H_(A	0	3	0	0	0	0	0	0.125782	0	0	0	0
pseudogen	thymosin_b	2	1	1	2	0	0	0.551469	0.324936	0.36335	0.477072	0	0
pseudogen	-	0	5	3	1	3	4	0	0.471206	0.316148	0.069183	0.269528	0.31791
protein_co	chromosom	2	0	4	1	6	4	0.051599	0	0.135991	0.022319	0.173906	0.102562
pseudogen	-	0	0	2	0	7	2	0	0	0.664412	0	1.982531	0.501086
lincRNA	-	0	0	1	0	0	0	0	0	0.16224	0	0	0
antisense	-	1	9	0	1	22	7	0.131694	1.39674	0	0.113928	3.254901	0.916165
pseudogen	translocase	0	0	0	0	3	2	0	0	0	0	0.696983	0.411047
sense_intrc	MIR600_ho	65	41	51	120	222	163	0.575061	0.427456	0.594573	0.918427	2.206493	1.43317
pseudogen	-	0	4	1	0	0	0	0	0.520983	0.145644	0	0	0
lincRNA	-	0	0	0	0	1	4	0	0	0	0	0.019799	0.070059
processed_	-	6	15	7	14	14	15	0.328486	0.967752	0.505008	0.663066	0.861078	0.816143
lincRNA	-	1	0	0	0	0	0	0.119506	0	0	0	0	0
processed_	-	0	0	0	2	3	1	0	0	0	0.17414	0.339216	0.100027
pseudogen	-	1	2	0	2	0	0	0.101614	0.239492	0	0.175812	0	0
antisense	-	0	4	5	0	2	2	0	0.330969	0.462621	0	0.157761	0.13956
antisense	-	0	0	1	1	0	0	0	0	0.103814	0.068153	0	0
antisense	-	2	4	1	3	0	0	0.146448	0.34516	0.096491	0.190037	0	0

pseudogen	prostaglan	1	0	3	0	1	0	0.148711	0	0.587893	0	0.167067	0
lincRNA	-	0	1	0	0	0	0	0	0.139883	0	0	0	0
protein_co	chromoson	9	5	7	0	0	0	0.960623	0.628909	0.984562	0	0	0
pseudogen	-	0	0	0	3	0	0	0	0	0	0.297395	0	0
pseudogen	-	1	0	1	1	0	2	0.038927	0	0.051297	0.033676	0	0.077374
pseudogen	-	0	1	0	0	2	1	0	0.176736	0	0	0.336974	0.149048
antisense	-	7	9	9	14	16	21	0.178768	0.270858	0.30288	0.309303	0.459052	0.532993
lincRNA	-	4	2	0	0	3	2	0.313724	0.184853	0	0	0.264337	0.155893
sense_intrc	ZDHHC20_i	3	4	4	1	6	1	0.360961	0.567161	0.634212	0.104088	0.811035	0.119577
sense_intrc	-	0	0	0	0	3	0	0	0	0	0	0.86197	0
lincRNA	-	0	3	0	0	0	0	0	0.537825	0	0	0	0
lincRNA	-	2	0	1	0	0	0	0.035377	0	0.023309	0	0	0
lincRNA	-	0	0	0	4	0	0	0	0	0	0.30686	0	0
pseudogen	gamma-glu	0	0	2	0	0	0	0	0	0.262268	0	0	0
pseudogen	glyceraldeh	0	0	0	3	0	1	0	0	0	0.137397	0	0.052614
lincRNA	-	0	0	0	8	6	4	0	0	0	0.611672	0.595752	0.351346
sense_intrc	ANKRD44_i	1	0	2	1	0	1	0.049524	0	0.130521	0.042843	0	0.049218
lincRNA	long_interg	9	0	2	0	4	0	0.738712	0	0.21632	0	0.368843	0
antisense	-	11	3	4	6	5	8	0.625511	0.201035	0.299735	0.295159	0.31942	0.452108
pseudogen	-	0	0	0	1	0	0	0	0	0	0.132367	0	0
antisense	-	4	11	8	5	2	10	0.297421	0.963855	0.783857	0.321622	0.167067	0.738961
pseudogen	-	1	3	3	0	0	1	0.105671	0.373579	0.417744	0	0	0.105018
pseudogen	glyceraldeh	0	0	0	0	5	5	0	0	0	0	0.294435	0.260466
pseudogen	-	2	1	0	2	0	0	0.084841	0.04999	0	0.073396	0	0
antisense	WASF3_ant	4	0	0	0	1	0	0.288507	0	0	0	0.08103	0
pseudogen	-	3	0	0	4	0	0	0.494776	0	0	0.570703	0	0
pseudogen	zinc_and_ri	9	13	14	46	41	35	1.075551	1.830791	2.204709	4.755643	5.504543	4.156866
pseudogen	keratin_18_	0	0	1	0	3	0	0	0	0.082463	0	0.210908	0
antisense	GLIS3_antis	2	7	4	0	0	0	0.144253	0.594978	0.380181	0	0	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.072571
antisense	-	6	5	0	19	21	22	0.825054	0.81023	0	2.260206	3.244141	3.006517
antisense	-	7	15	7	4	5	26	0.089126	0.225064	0.117447	0.044059	0.07152	0.328996
lincRNA	-	1	3	1	3	6	0	0.02544	0.089939	0.033524	0.066024	0.171483	0
pseudogen	-	0	6	0	4	2	2	0	0.529457	0	0.259117	0.168249	0.148837
pseudogen	-	0	0	0	1	2	0	0	0	0	0.146791	0.381256	0
antisense	-	0	3	0	0	1	0	0	0.230781	0	0	0.073337	0
processed_	-	1	1	0	1	1	0	0.121703	0.14342	0	0.105285	0.136726	0
antisense	ZEB1_antis	46	28	43	7	14	7	4.162882	2.986079	5.127899	0.548021	1.423355	0.62957
antisense	NDUFA6_ar	27	27	35	13	10	3	0.508505	0.599242	0.868629	0.211806	0.211583	0.056152
pseudogen	-	2	7	5	4	0	8	0.5042	2.079591	1.661031	0.87236	0	2.004345
pseudogen	-	1	0	0	0	1	0	0.127877	0	0	0	0.143662	0
pseudogen	ribosomal_	0	0	1	0	0	0	0	0	0.197071	0	0	0
antisense	PRMT5_ant	4	1	2	1	4	5	0.100648	0.029652	0.066315	0.021768	0.113072	0.125033
sense_intrc	-	0	0	0	0	6	19	0	0	0	0	0.743449	2.082639

pseudogen	Nanog_hon	0	0	0	4	3	0	0	0	0	0.203325	0.198033	0
antisense	-	6	5	7	0	0	0	0.084864	0.083339	0.130468	0	0	0
antisense	-	2	0	0	0	5	1	0.268056	0	0	0	0.75286	0.1332
pseudogen	-	0	0	8	0	6	0	0	0	0.158059	0	0.101064	0
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	1.252715
antisense	EHMT2_ant	0	1	2	0	0	3	0	0.279766	0.62568	0	0	0.707812
pseudogen	cytochrom	0	0	4	17	23	21	0	0	1.322527	3.689959	6.483157	5.236469
lincRNA	-	0	0	0	3	2	1	0	0	0	0.238536	0.206514	0.091344
pseudogen	-	0	6	0	0	2	0	0	0.475033	0	0	0.150954	0
pseudogen	PEST_conta	0	0	0	0	0	3	0	0	0	0	0	0.305304
lincRNA	-	29	29	14	47	24	29	0.576959	0.679911	0.367037	0.808925	0.536423	0.573396
antisense	-	2	0	3	7	5	6	0.080032	0	0.158193	0.242322	0.224777	0.238612
lincRNA	-	2	0	0	0	0	0	0.05635	0	0	0	0	0
pseudogen	-	2	0	1	1	5	0	0.043519	0	0.028674	0.018824	0.122228	0
pseudogen	cytochrom	24	34	14	2	4	0	1.203204	2.008696	0.924892	0.08674	0.225288	0
pseudogen	piezo-type_	4	0	0	0	0	0	0.097139	0	0	0	0	0
pseudogen	MT-ND2_ps	0	0	0	1	7	1	0	0	0	0.070677	0.642487	0.081195
antisense	-	655	562	585	29	35	28	6.569979	6.643028	7.732383	0.251642	0.394403	0.27912
antisense	-	18	6	13	8	13	18	0.766027	0.300905	0.729038	0.294527	0.621533	0.761297
lincRNA	-	0	0	0	1	0	0	0	0	0	0.167762	0	0
pseudogen	mitochond	0	0	0	0	1	4	0	0	0	0	0.160746	0.568801
antisense	-	3	3	0	0	0	2	0.46989	0.553737	0	0	0	0.311326
pseudogen	DEAD_(Asp	0	0	3	0	0	0	0	0	0.108272	0	0	0
protein_co	chromoson	1	2	1	0	2	4	0.062578	0.147489	0.082463	0	0.140605	0.248766
antisense	-	0	0	2	3	0	2	0	0	0.226504	0.223047	0	0.170825
pseudogen	-	0	3	0	0	0	5	0	0.659025	0	0	0	0.926304
processed_	ZNF503_an	138	110	93	54	38	63	3.609613	3.390637	3.205526	1.221908	1.116643	1.63769
antisense	DLEU7_ant	3	0	1	0	0	0	0.166307	0	0.073051	0	0	0
pseudogen	-	0	0	0	0	4	6	0	0	0	0	0.460162	0.610608
antisense	-	1	0	2	0	0	1	0.059351	0	0.15642	0	0	0.058984
pseudogen	-	6	4	14	8	17	10	0.205065	0.161105	0.630527	0.236534	0.652738	0.339665
pseudogen	-	0	3	1	0	0	0	0	0.509981	0.190091	0	0	0
lincRNA	-	1	0	0	0	3	0	0.08457	0	0	0	0.285028	0
pseudogen	-	0	3	0	0	7	1	0	0.320485	0	0	0.712896	0.090093
protein_co	UDP-GlcNA	448	393	293	51	25	30	8.130807	8.40534	7.007419	0.800735	0.509735	0.541111
pseudogen	-	0	0	2	0	0	2	0	0	0.354128	0	0	0.267076
lincRNA	-	0	0	0	1	0	0	0	0	0	0.059868	0	0
antisense	-	0	0	1	0	1	0	0	0	0.095435	0	0.081362	0
pseudogen	-	0	0	1	0	0	1	0	0	0.11198	0	0	0.084453
processed_	-	267	255	211	23	37	34	4.928607	5.547026	5.132515	0.367286	0.767297	0.623737
processed_	-	45	19	31	36	25	35	2.253874	1.121445	2.046038	1.559849	1.406715	1.742187
protein_co	CDKN2A_in	415	417	273	1195	872	1186	17.96444	21.27202	15.57267	44.75036	42.40638	51.02229
protein_co	family_witl	0	0	0	2	1	5	0	0	0	0.068306	0.044352	0.196175
sense_intrc	ZBTB40_int	1	1	4	3	2	0	0.193923	0.228526	1.022173	0.503285	0.435721	0

pseudogen	IMP_(inosi	1	8	6	6	7	2	0.034512	0.32536	0.272868	0.179135	0.271402	0.068597
pseudogen	-	0	0	0	3	0	2	0	0	0	0.234866	0	0.179877
pseudogen	-	0	3	0	0	0	0	0	0.436278	0	0	0	0
antisense	PPEF1_anti	0	0	0	0	1	0	0	0	0	0	0.138316	0
pseudogen	sulfotransfe	0	1	0	0	0	0	0	0.033273	0	0	0	0
pseudogen	olfactory_r	0	2	1	0	2	2	0	0.127975	0.071552	0	0.122002	0.107926
pseudogen	ribosomal_	0	1	0	0	0	0	0	0.0805	0	0	0	0
pseudogen	-	0	0	0	8	13	10	0	0	0	1.193457	2.518524	1.713813
pseudogen	keratin_ass	0	3	0	0	0	0	0	0.472634	0	0	0	0
lincRNA	ZNF295_an	2	0	4	4	1	0	0.036906	0	0.097265	0.063853	0.020731	0
antisense	-	13	4	7	0	0	0	0.885757	0.321172	0.628498	0	0	0
pseudogen	-	106	112	83	60	54	74	5.010487	6.238773	5.169958	2.453513	2.867589	3.476285
antisense	-	6	10	11	0	3	0	0.550513	1.081243	1.329976	0	0.309234	0
lincRNA	-	0	0	0	4	0	0	0	0	0	0.0745	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.176616	0	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.068241
pseudogen	-	3	0	0	0	1	1	0.344518	0	0	0	0.129015	0.11413
lincRNA	-	0	0	1	0	0	0	0	0	0.191132	0	0	0
TR_V_gene	T_cell_rece	0	0	0	1	0	0	0	0	0	0.102458	0	0
pseudogen	MT-ND2_ps	0	0	0	0	1	0	0	0	0	0	0.058025	0
pseudogen	-	1	0	0	0	1	0	0.120048	0	0	0	0.134866	0
pseudogen	mitogen-ac	1	3	0	4	4	1	0.024487	0.086569	0	0.084734	0.110039	0.024336
pseudogen	ferritin_hea	9	5	9	4	0	0	0.864735	0.566132	1.139509	0.332478	0	0
processed_	-	6	0	0	0	0	0	0.455733	0	0	0	0	0
pseudogen	RNA_bindi	0	1	0	0	0	0	0	0.065879	0	0	0	0
pseudogen	ribosomal_	3	0	0	0	0	0	0.322811	0	0	0	0	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.045616	0	0
pseudogen	anoctamin_	14	9	9	6	4	7	0.430915	0.326447	0.36504	0.159764	0.138316	0.214127
pseudogen	-	0	0	1	0	0	0	0	0	0.176616	0	0	0
sense_intrc	-	7	1	6	0	4	5	0.538644	0.09068	0.608401	0	0.34579	0.38237
antisense	-	0	0	0	2	0	2	0	0	0	0.171211	0	0.196688
antisense	long_interg	1	0	0	0	0	0	0.072821	0	0	0	0	0
lincRNA	-	0	0	0	4	0	0	0	0	0	0.249926	0	0
protein_co	creatine_ki	0	0	0	45	30	41	0	0	0	0.860163	0.74469	0.900324
lincRNA	-	0	2	1	1	6	2	0	0.20624	0.115311	0.075701	0.589844	0.173931
lincRNA	-	0	0	1	0	0	0	0	0	0.128715	0	0	0
pseudogen	smg-1_hom	9	4	23	7	9	6	0.112827	0.059093	0.379956	0.075916	0.126754	0.074754
antisense	TTN_antise	23	16	18	36	31	33	0.265166	0.217379	0.273462	0.359051	0.401514	0.378106
pseudogen	-	4	0	2	0	0	2	0.423528	0	0.279053	0	0	0.210456
processed_	-	0	2	6	0	0	6	0	0.043858	0.147128	0	0	0.110961
pseudogen	-	4	0	2	0	1	0	0.647596	0	0.426687	0	0.181884	0
pseudogen	serine/argi	2	0	10	1	5	11	0.039538	0	0.260505	0.017102	0.111045	0.216114
lincRNA	-	13	11	11	23	12	16	1.274505	1.270861	1.421104	1.950694	1.321687	1.558935
pseudogen	-	3	1	0	5	2	3	0.209529	0.082306	0	0.302104	0.156929	0.208235

antisense	RAI1_antise	2	5	6	3	14	4	0.146246	0.430854	0.578149	0.189774	1.150087	0.290685
pseudogen	-	2	9	2	0	4	3	0.20884	1.107474	0.2752	0	0.469238	0.311326
protein_co	ring_finger_	0	0	0	3	0	0	0	0	0	0.122457	0	0
antisense	XIAP_antise	5	6	5	4	1	0	0.54918	0.776611	0.723685	0.380074	0.123394	0
antisense	-	7	0	2	2	0	0	0.513278	0	0.19325	0.126867	0	0
antisense	FTCD_antis	1	2	1	0	2	0	0.105882	0.249551	0.139527	0	0.237904	0
pseudogen	-	4	0	0	0	0	2	0.525469	0	0	0	0	0.261112
pseudogen	-	0	1	0	0	0	0	0	0.220451	0	0	0	0
pseudogen	cell_divisio	1	3	2	4	6	17	0.091911	0.324936	0.242234	0.318048	0.619541	1.552845
pseudogen	-	8	5	9	3	4	16	0.339365	0.249951	0.503101	0.110094	0.190628	0.674539
protein_co	prostate_ar	0	0	0	0	4	2	0	0	0	0	0.119972	0.053065
lincRNA	-	1	12	1	4	4	15	0.093535	1.322708	0.123257	0.323667	0.420325	1.394365
lincRNA	-	0	1	0	10	2	1	0	0.024191	0	0.177584	0.046123	0.020401
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.081698	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.085824	0
antisense	-	1	0	2	0	0	0	0.281601	0	0.742163	0	0	0
processed_	BRWD1_int	1	0	1	0	3	0	0.108264	0	0.142665	0	0.364883	0
lincRNA	-	0	0	1	0	0	0	0	0	0.203391	0	0	0
pseudogen	chromobox	0	0	1	0	0	0	0	0	0.132378	0	0	0
antisense	HOXD_clus	110	112	112	0	0	0	5.829339	6.99442	7.821309	0	0	0
pseudogen	ribosomal_	2	1	0	3	7	3	0.227703	0.134167	0	0.295477	0.895336	0.339445
antisense	-	0	0	0	0	0	4	0	0	0	0	0	0.318873
lincRNA	-	1	0	0	0	0	0	0.12881	0	0	0	0	0
pseudogen	major_hist	0	0	0	0	1	0	0	0	0	0	0.25972	0
processed_	PITRM1_an	32	32	13	21	23	17	0.443137	0.52221	0.237228	0.251577	0.35782	0.233963
pseudogen	NADH_dehy	4	1	1	1	2	3	0.186576	0.054967	0.061465	0.040351	0.104803	0.139068
pseudogen	-	0	0	2	0	0	0	0	0	0.325997	0	0	0
antisense	-	0	0	1	0	0	0	0	0	0.148749	0	0	0
processed_	-	10	11	12	0	0	0	0.265635	0.344338	0.42005	0	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.086573	0
processed_	-	0	1	1	0	5	9	0	0.089509	0.100091	0	0.426657	0.679378
pseudogen	X-ray_repai	1	0	0	0	0	0	0.02933	0	0	0	0	0
pseudogen	-	4	2	12	9	13	7	1.366219	0.805003	5.401028	2.659291	4.988303	2.376118
antisense	FOXD2_ant	12	14	4	17	31	18	0.253205	0.348118	0.111221	0.310315	0.734856	0.377462
antisense	-	2	4	2	1	2	0	0.374141	0.881805	0.493027	0.161834	0.420325	0
pseudogen	-	0	0	1	0	0	0	0	0	0.08385	0	0	0
protein_co	Uncharacte	0	0	0	0	0	1	0	0	0	0	0	0.055794
antisense	-	1	0	1	16	14	19	0.127569	0	0.168104	1.765741	2.006416	2.408836
pseudogen	argininosuc	31	12	12	6	6	12	1.337548	0.610149	0.682281	0.223956	0.290836	0.514563
lincRNA	cat_eye_syn	0	0	0	4	4	0	0	0	0	0.067203	0.087272	0
protein_co	zinc_finger_	133	116	111	170	184	171	2.45593	2.524233	2.700985	2.715666	3.81708	3.138124
protein_co	ral_guanine	430	376	335	934	814	976	6.94467	7.156128	7.129561	13.04947	14.76919	15.66544
pseudogen	-	0	0	0	2	0	0	0	0	0	0.095614	0	0
pseudogen	cyclin-depe	1	0	0	0	0	0	0.144253	0	0	0	0	0

protein_co	Uncharacte	0	0	0	1	1	0	0	0	0	0.01666	0.021635	0
pseudogen	-	1	4	1	0	0	0	0.130719	0.616175	0.172255	0	0	0
processed_	-	0	0	0	0	0	1	0	0	0	0	0	0.100027
processed_	-	0	0	0	0	1	0	0	0	0	0	0.038521	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.021923
lincRNA	-	1	0	2	0	0	1	0.095389	0	0.251399	0	0	0.0948
lincRNA	-	0	0	1	10	5	6	0	0	0.101993	0.669575	0.434765	0.461527
antisense	-	2	0	0	0	1	1	0.165441	0	0	0	0.092931	0.082209
pseudogen	-	1	0	2	1	0	0	0.118969	0	0.313543	0.102919	0	0
antisense	SGOL1_ant	0	1	0	0	6	2	0	0.076175	0	0	0.435721	0.128484
lincRNA	-	12	15	7	7	13	10	0.223458	0.329165	0.17177	0.112766	0.271962	0.185065
lincRNA	-	38	13	18	27	19	21	1.074083	0.433017	0.670443	0.660208	0.603333	0.589907
pseudogen	-	15	13	11	4	12	7	1.31476	1.342782	1.270523	0.303304	1.181641	0.609765
processed_	-	6	0	2	38	13	18	0.32985	0	0.144887	1.807226	0.802894	0.98344
antisense	-	6	1	7	4	0	0	0.481282	0.094527	0.739914	0.277569	0	0
processed_	-	0	1	1	5	5	1	0	0.017614	0.019696	0.064651	0.083958	0.014854
pseudogen	ribosomal_	51	40	40	95	50	80	2.618808	2.420474	2.706626	4.220074	2.88438	4.082565
antisense	UNC5B_ant	8	18	25	8	7	24	0.654603	1.735671	2.695645	0.566292	0.64348	1.95168
processed_	-	7	6	11	0	0	0	0.415923	0.420119	0.861275	0	0	0
protein_co	shisa_homo	80	53	61	845	638	715	0.629688	0.491607	0.632703	5.753802	5.641635	5.593078
antisense	DiGeorge_s	6	9	8	15	17	39	0.057838	0.102238	0.101622	0.125088	0.184102	0.373625
pseudogen	non-POU_d	5	11	6	1	3	2	0.215032	0.557486	0.340032	0.037205	0.144945	0.085482
processed_	long_interg	7	16	18	210	158	153	0.171489	0.461917	0.581092	4.450611	4.34854	3.725104
lincRNA	-	8	7	1	0	0	0	0.257934	0.265965	0.042487	0	0	0
antisense	-	0	2	0	0	1	1	0	0.236766	0	0	0.112858	0.099837
lincRNA	-	0	0	0	3	0	0	0	0	0	0.290479	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.114179	0	0	0
processed_	-	3	2	1	0	0	0	0.23322	0.183224	0.102442	0	0	0
processed_	TTLL11_int	0	11	3	0	0	3	0	0.652343	0.198945	0	0	0.15004
pseudogen	-	0	0	0	2	0	0	0	0	0	0.132176	0	0
pseudogen	ribosomal_	2	1	0	4	0	2	0.157328	0.092701	0	0.272207	0	0.156357
pseudogen	peptide_YY	4	6	3	10	6	26	0.196807	0.347887	0.194507	0.42564	0.33165	1.271343
pseudogen	-	2	1	0	0	0	0	0.332962	0.196188	0	0	0	0
lincRNA	-	0	2	0	0	0	0	0	0.422968	0	0	0	0
pseudogen	-	1	5	3	0	0	0	0.108043	0.636609	0.427122	0	0	0
lincRNA	-	3	0	1	2	0	3	0.038549	0	0.016933	0.022232	0	0.038311
pseudogen	immunoglo	5	1	0	0	0	0	0.804574	0.189628	0	0	0	0
lincRNA	-	7	0	12	20	33	32	0.439605	0	0.993072	1.08657	2.328239	1.997212
lincRNA	-	8	2	1	1	2	3	0.577801	0.170226	0.095175	0.062481	0.162281	0.215337
antisense	-	6	4	12	0	0	0	0.385493	0.302853	1.01597	0	0	0
antisense	-	0	4	0	1	0	5	0	0.69707	0	0.12793	0	0.734833
pseudogen	-	16	14	10	21	16	30	3.321788	3.425209	2.735815	3.771675	3.731822	6.189888
pseudogen	3-oxoacid_	0	0	0	2	3	3	0	0	0	0.059673	0.11624	0.102829
pseudogen	-	5	0	0	0	0	2	0.44265	0	0	0	0	0.175967

pseudogen	ubiquinol-c	2	0	0	0	0	0	0.367646	0	0	0	0	0
pseudogen	-	3	0	4	2	0	1	0.279127	0	0.490427	0.16098	0	0.092468
processed_	FRY_antiser	0	0	0	0	1	0	0	0	0	0	0.053342	0
pseudogen	-	4	2	1	1	0	1	0.520305	0.306574	0.171409	0.112528	0	0.129273
sense_intrc	HLCS_intro	2	1	4	2	0	2	0.199401	0.117491	0.525524	0.172501	0	0.19817
protein_co	kinesin_fan	486	378	335	2765	2225	2615	9.508249	8.714916	8.636622	46.79748	48.90389	50.84469
pseudogen	ribonuclea	0	1	0	0	0	0	0	0.124278	0	0	0	0
pseudogen	-	0	0	0	0	1	4	0	0	0	0	0.08272	0.292707
pseudogen	DnaJ_(Hsp4	0	1	0	1	2	0	0	0.18136	0	0.133136	0.34579	0
lincRNA	long_interg	2	0	0	0	0	0	0.232708	0	0	0	0	0
pseudogen	HLA_compl	1	3	0	0	0	2	0.053154	0.187915	0	0	0	0.105651
pseudogen	KRR1_smal	22	19	10	7	4	11	1.450438	1.476173	0.868783	0.399243	0.296269	0.72074
pseudogen	glutathione	0	0	0	0	0	4	0	0	0	0	0	0.469768
pseudogen	-	0	0	4	0	2	0	0	0	0.327527	0	0.139615	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.058721
protein_co	cDNA_FLJ5	62	54	36	291	197	168	1.233499	1.266042	0.94381	5.008448	4.40314	3.321744
processed_	-	0	0	0	2	0	2	0	0	0	0.0621	0	0.071341
processed_	-	3	6	2	0	0	5	0.071157	0.167709	0.062512	0	0	0.117863
lincRNA	-	1	3	0	0	0	0	0.105882	0.374326	0	0	0	0
protein_co	immunity-r	0	0	0	2	0	0	0	0	0	0.055213	0	0
lincRNA	long_interg	2	1	0	4	2	0	0.050564	0.029794	0	0.087486	0.056806	0
pseudogen	-	0	2	0	0	0	1	0	0.085639	0	0	0	0.036111
antisense	-	0	1	3	1	1	3	0	0.100788	0.33811	0.073989	0.096084	0.254995
pseudogen	-	4	0	3	0	1	3	0.274306	0	0.271101	0	0.077041	0.204459
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.153685	0
lincRNA	-	2	0	4	0	0	2	0.125751	0	0.331417	0	0	0.124974
antisense	P4HA2_ant	1	3	1	0	0	0	0.0631	0.223079	0.083151	0	0	0
lincRNA	-	0	1	0	0	0	0	0	0.23454	0	0	0	0
antisense	-	5	0	3	0	3	15	0.507098	0	0.400938	0	0.341816	1.511898
pseudogen	-	11	1	6	8	10	10	0.88773	0.095103	0.638079	0.558523	0.906645	0.802043
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.114818	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.236016	0
pseudogen	RNA_guany	0	0	1	0	0	0	0	0	0.095829	0	0	0
pseudogen	-	6	0	4	18	13	28	0.236168	0	0.207474	0.612922	0.57486	1.095311
antisense	-	0	0	0	0	4	3	0	0	0	0	0.336022	0.222941
processed_	DCTN1_ant	5	3	0	9	5	3	0.123406	0.087256	0	0.192163	0.138639	0.073586
sense_intrc	RNF216_in	3	0	1	0	0	2	0.471285	0	0.207013	0	0	0.31225
antisense	-	1	1	0	0	1	0	0.136446	0.160793	0	0	0.153288	0
processed_	-	0	0	0	4	1	1	0	0	0	0.258751	0.084006	0.074314
pseudogen	ubiquinol-c	4	0	1	0	0	1	0.63025	0	0.207629	0	0	0.156589
antisense	-	0	0	0	2	4	7	0	0	0	0.030543	0.079328	0.122807
lincRNA	-	0	1	0	0	0	0	0	0.09982	0	0	0	0
processed_	-	24	25	10	12	12	18	0.62838	0.771362	0.345021	0.271804	0.352973	0.468374
lincRNA	-	0	1	0	0	0	1	0	0.133023	0	0	0	0.112183

pseudogen	eukaryotic_	0	0	0	2	0	2	0	0	0	0.068613	0	0.078823
pseudogen	barrier_to_	4	8	3	0	8	16	0.811356	1.912268	0.801877	0	1.823017	3.225382
processed_	-	0	0	1	0	2	2	0	0	0.048013	0	0.081866	0.072421
protein_co	family_witl	360	330	298	1090	722	779	6.434422	6.950692	7.018723	16.85375	14.49751	13.83739
pseudogen	-	0	2	1	3	3	7	0	0.110912	0.062012	0.12213	0.158602	0.327376
antisense	-	6	1	0	1	2	3	1.091567	0.214391	0	0.157385	0.408769	0.542413
lincRNA	-	0	0	0	1	0	6	0	0	0	0.067351	0	0.464242
antisense	-	1	1	0	0	2	0	0.073529	0.08665	0	0	0.165211	0
pseudogen	-	2	3	3	0	0	1	0.168067	0.297084	0.332206	0	0	0.083514
antisense	-	8	6	0	5	2	2	0.638805	0.564595	0	0.345391	0.179415	0.158715
antisense	GFOD1_ant	3	0	0	1	0	0	0.478382	0	0	0.137949	0	0
pseudogen	-	1	3	2	4	0	1	0.032027	0.113226	0.084408	0.110826	0	0.031829
lincRNA	-	0	0	0	1	0	0	0	0	0	0.131985	0	0
antisense	-	0	0	1	0	0	0	0	0	0.152655	0	0	0
pseudogen	adenosylm	2	0	0	0	0	0	0.106736	0	0	0	0	0
lincRNA	long_interg	0	0	1	1	0	0	0	0	0.036278	0.023816	0	0
antisense	-	2	0	2	0	2	1	0.159943	0	0.210765	0	0.179686	0.079477
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.024917	0
antisense	-	0	0	0	3	2	3	0	0	0	0.196562	0.170174	0.225811
pseudogen	-	2	8	1	0	2	3	0.784311	3.697051	0.516765	0	0.881125	1.169201
pseudogen	ribosomal_	2	0	0	0	0	0	0.137688	0	0	0	0	0
antisense	-	5	6	2	3	3	3	0.502286	0.710297	0.264756	0.260715	0.338573	0.299511
pseudogen	-	1	0	3	1	2	1	0.048172	0	0.190437	0.041673	0.108236	0.047874
pseudogen	-	8	0	0	0	1	0	1.05882	0	0	0	0.14869	0
antisense	PHKA2_ant	6	3	1	8	0	2	0.484216	0.28531	0.106346	0.558523	0	0.160409
lincRNA	-	8	0	3	7	1	8	0.725219	0	0.358373	0.548959	0.101842	0.72074
pseudogen	family_witl	13	8	16	4	2	1	0.608517	0.441293	0.986925	0.161977	0.105174	0.04652
pseudogen	-	1	0	0	0	0	0	0.034579	0	0	0	0	0
lincRNA	-	2	0	1	0	2	0	0.143084	0	0.094275	0	0.160746	0
pseudogen	-	139	150	107	98	60	136	10.42323	13.25518	10.57319	6.357355	5.054611	10.13528
pseudogen	-	0	0	0	3	0	0	0	0	0	0.587165	0	0
lincRNA	-	3	0	0	0	0	0	0.357709	0	0	0	0	0
sense_intrc	-	0	0	3	2	2	2	0	0	0.494775	0.216543	0.28121	0.248766
pseudogen	long_interg	37	27	20	32	65	68	2.88911	2.484467	2.057914	2.1616	5.701968	5.276925
lincRNA	-	8	7	5	35	24	42	0.301658	0.31105	0.248445	1.141711	1.016682	1.573925
pseudogen	-	0	3	0	0	0	0	0	0.181009	0	0	0	0
processed_	-	3	3	1	0	0	0	0.139074	0.163891	0.061089	0	0	0
processed_	-	7	3	4	0	0	0	0.189268	0.095589	0.142519	0	0	0
pseudogen	POU_class_	8	1	2	3	0	0	0.390348	0.0575	0.128596	0.126633	0	0
lincRNA	-	5	2	9	9	3	6	0.245324	0.11564	0.581899	0.382011	0.165364	0.292571
antisense	DGUOK_an	11	9	6	17	24	8	0.96897	0.934259	0.696472	1.295477	2.375078	0.700353
antisense	-	7	10	8	9	8	14	0.50215	0.845362	0.756242	0.558523	0.644725	0.998099
pseudogen	-	4	3	0	12	6	2	0.461359	0.407763	0	1.197357	0.777463	0.229255
sense_intrc	KLF7_intro	8	5	1	3	6	4	0.646608	0.476242	0.106509	0.209766	0.544818	0.321307

lincRNA	-	7	0	4	14	7	10	0.786809	0	0.592469	1.361326	0.883931	1.117071
sense_intrc	-	5	5	8	4	5	7	0.611328	0.720413	1.288929	0.423085	0.686789	0.850574
pseudogen	signal_reco	1	1	0	9	0	0	0.153898	0.18136	0	1.198227	0	0
pseudogen	-	2	2	4	1	0	1	0.340457	0.401207	0.897277	0.147263	0	0.169177
pseudogen	poly_(ADP-	0	0	0	0	1	0	0	0	0	0	0.02545	0
pseudogen	-	0	0	0	0	4	0	0	0	0	0	0.292265	0
lincRNA	-	4	0	0	0	0	0	0.105776	0	0	0	0	0
antisense	-	1	4	5	0	0	0	0.041522	0.195726	0.273581	0	0	0
antisense	-	7	0	0	3	4	2	0.646749	0	0	0.239785	0.41519	0.183644
antisense	-	7	11	3	1	0	7	0.574553	1.063977	0.32448	0.071006	0	0.571005
pseudogen	-	0	0	0	0	1	6	0	0	0	0	0.091221	0.484178
processed_	-	29	33	17	6	6	6	0.707506	0.948753	0.546533	0.126633	0.16445	0.145477
lincRNA	PRKCQ_ant	1	2	1	124	57	72	0.046726	0.110128	0.061574	5.012413	2.992169	3.343523
antisense	long_interg	4	1	20	47	43	49	0.02321	0.006838	0.152923	0.235922	0.280301	0.282561
antisense	-	0	6	6	1	8	6	0	0.757746	0.847327	0.09271	0.963173	0.639037
pseudogen	peptidylpr	0	2	0	0	0	0	0	0.250051	0	0	0	0
pseudogen	ribosomal_	0	0	1	1	0	0	0	0	0.19763	0.129742	0	0
pseudogen	-	2	0	0	0	0	0	0.138408	0	0	0	0	0
pseudogen	-	0	0	0	0	1	2	0	0	0	0	0.043668	0.07726
pseudogen	tubulin_ga	1	2	0	5	3	1	0.038985	0.091882	0	0.168626	0.13139	0.038744
pseudogen	hsa-mir-67	566	458	479	804	509	664	19.4197	18.5182	21.65691	23.86411	19.61973	22.64143
processed_	FLG_antise	0	0	0	67	56	76	0	0	0	1.02455	1.112071	1.335114
antisense	-	0	0	2	1	0	0	0	0	0.225771	0.074108	0	0
pseudogen	-	10	6	6	31	14	26	0.940337	0.664878	0.743481	2.521787	1.478975	2.429779
processed_	-	6	3	7	7	18	14	0.329508	0.194153	0.50658	0.332565	1.110546	0.764104
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.066348
lincRNA	-	1	2	5	0	0	2	0.111926	0.263796	0.737455	0	0	0.22247
pseudogen	-	0	1	0	0	0	0	0	0.128634	0	0	0	0
pseudogen	phosphatas	2	3	4	3	3	4	0.026497	0.046838	0.069833	0.034384	0.044652	0.052667
antisense	CELF2_anti	0	0	0	0	3	6	0	0	0	0	0.209177	0.370087
processed_	-	0	0	1	0	0	0	0	0	0.024933	0	0	0
antisense	-	2	9	5	0	2	1	0.119776	0.635169	0.394589	0	0.134561	0.059518
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.170825
lincRNA	-	2	1	1	0	0	6	0.119102	0.070177	0.078474	0	0	0.3551
lincRNA	-	4	0	0	0	1	0	0.077061	0	0	0	0.021643	0
antisense	-	16	11	15	8	13	7	1.40707	1.139975	1.738288	0.608623	1.284364	0.611791
antisense	-	0	3	1	0	0	0	0	1.308833	0.487855	0	0	0
pseudogen	DEAD_(Asp	5	0	0	0	0	0	1.025988	0	0	0	0	0
pseudogen	zinc_finger_	1	0	1	0	0	0	0.051151	0	0.067404	0	0	0
lincRNA	-	74	77	49	69	79	95	1.472241	1.805282	1.28463	1.18757	1.765726	1.878367
processed_	-	1	0	2	0	1	0	0.080826	0	0.213018	0	0.090803	0
pseudogen	-	0	4	0	0	0	0	0	0.963517	0	0	0	0
lincRNA	-	4	2	2	2	0	0	0.294117	0.173299	0.193787	0.127219	0	0
antisense	-	3	3	0	2	1	6	0.065091	0.076706	0	0.03754	0.024375	0.129379

pseudogen	-	0	0	0	2	1	0	0	0	0	0.341783	0.221925	0
lincRNA	-	0	0	2	0	0	0	0	0	0.237694	0	0	0
pseudogen	-	5	0	3	0	1	4	0.811978	0	0.641993	0	0.182441	0.645571
antisense	ZEB2_antis	0	11	4	0	0	3	0	0.359678	0.146254	0	0	0.082726
antisense	-	30	13	28	35	14	45	5.106848	2.607847	6.280939	5.154218	2.677372	7.612965
pseudogen	-	2	0	1	0	0	0	0.10882	0	0.071699	0	0	0
processed_	-	0	0	1	2	0	4	0	0	0.019887	0.026111	0	0.059993
antisense	ZNF630_an	0	0	1	0	0	0	0	0	0.17617	0	0	0
pseudogen	-	0	3	2	2	3	8	0	0.725439	0.540801	0.35503	0.69158	1.631443
pseudogen	mitochond	0	0	0	0	1	0	0	0	0	0	0.093516	0
pseudogen	-	0	1	0	0	0	0	0	0.070256	0	0	0	0
lincRNA	-	1	2	0	0	0	0	0.055032	0.129704	0	0	0	0
pseudogen	-	1	0	1	0	5	11	0.074251	0	0.097845	0	0.417082	0.811717
protein_co	leucine_ric	95	47	61	63	68	51	0.887175	0.517238	0.750672	0.508966	0.713417	0.473332
pseudogen	protein_ph	3	8	2	5	5	1	0.043959	0.138141	0.038618	0.063381	0.082308	0.014562
pseudogen	-	0	0	1	0	0	0	0	0	0.075583	0	0	0
protein_co	HDCMB45F	0	0	0	2	0	0	0	0	0	0.209127	0	0
pseudogen	ATP-bindin	4	2	5	3	3	7	0.050564	0.029794	0.083289	0.032807	0.042605	0.087941
lincRNA	-	1	0	0	1	0	0	0.108043	0	0	0.093467	0	0
pseudogen	ribosomal_	16	6	9	10	0	3	1.323525	0.584885	0.981046	0.715608	0	0.246628
pseudogen	-	3	2	1	127	72	118	0.03016	0.023695	0.013248	1.104531	0.813191	1.17897
lincRNA	-	0	0	0	2	0	2	0	0	0	0.047757	0	0.054863
pseudogen	-	4	1	3	2	1	6	0.15202	0.044787	0.150244	0.065756	0.042696	0.226622
pseudogen	-	2	0	1	0	0	0	0.141553	0	0.093266	0	0	0
processed_	-	64	66	74	99	97	78	1.177693	1.43121	1.794398	1.575979	2.005271	1.42645
antisense	-	4	2	3	0	0	0	0.416039	0.245138	0.411178	0	0	0
antisense	-	5	6	5	0	0	0	0.483038	0.683077	0.636526	0	0	0
lincRNA	long_interg	1	1	1	0	1	2	0.033317	0.039262	0.043904	0	0.03743	0.066223
antisense	MID1IP1_a	29	22	19	1	9	13	4.083215	3.650346	3.525272	0.121806	1.423626	1.819103
pseudogen	cancer_sus	0	0	0	0	2	0	0	0	0	0	0.090665	0
antisense	MLK7_anti	0	1	3	6	5	6	0	0.024581	0.082463	0.108272	0.117171	0.124383
pseudogen	actin_relat	0	0	0	0	1	1	0	0	0	0	0.111587	0.098713
antisense	-	1	0	1	1	0	1	0.078084	0	0.102896	0.06755	0	0.077602
antisense	BRWD1_an	0	0	3	0	0	1	0	0	0.30288	0	0	0.076142
lincRNA	-	5	0	7	7	7	13	0.651983	0	1.202815	0.789636	1.025447	1.684686
pseudogen	-	0	0	1	0	0	0	0	0	0.178423	0	0	0
pseudogen	myeloid/ly	0	1	1	5	0	3	0	0.238121	0.266272	0.874025	0	0.602451
antisense	-	0	2	0	0	1	0	0	0.16268	0	0	0.077544	0
pseudogen	olfactory_r	0	0	0	0	0	1	0	0	0	0	0	0.047315
processed_	-	0	0	0	0	0	2	0	0	0	0	0	0.029165
pseudogen	-	5	1	3	4	2	8	0.617028	0.145426	0.487855	0.427029	0.277277	0.981148
lincRNA	-	0	0	0	4	0	0	0	0	0	0.219923	0	0
pseudogen	ribosomal_	0	0	0	0	0	4	0	0	0	0	0	0.234622
pseudogen	ribosomal_	1	0	0	1	0	0	0.35294	0	0	0.305326	0	0

antisense	-	0	0	0	13	18	21	0	0	0	0.574142	1.032369	1.065473
processed_	-	0	0	0	2	4	0	0	0	0	0.085605	0.22234	0
pseudogen	adenosylhc	0	0	0	1	0	0	0	0	0	0.03523	0	0
processed_	-	5	6	3	8	7	5	0.181305	0.256388	0.143349	0.250953	0.285159	0.180185
antisense	-	2	1	3	17	16	16	0.193923	0.114263	0.383315	1.425973	1.742884	1.541804
pseudogen	-	2	1	1	0	0	0	0.175592	0.103462	0.115694	0	0	0
lincRNA	ENOX1_ant	0	0	2	0	1	0	0	0	0.562607	0	0.239822	0
pseudogen	high_mobil	0	0	0	0	0	2	0	0	0	0	0	0.241904
lincRNA	-	0	0	2	0	0	0	0	0	0.453008	0	0	0
processed_	PAXBP1_an	14	4	23	23	17	18	0.210381	0.070835	0.455451	0.298999	0.286997	0.26882
processed_	-	8	12	12	11	3	12	0.172236	0.304454	0.340447	0.204875	0.072561	0.256758
pseudogen	ubiquitin-c	6	0	0	4	6	5	0.726879	0	0	0.419212	0.816603	0.601991
lincRNA	-	73	56	63	27	16	32	6.356402	5.746238	7.228761	2.033833	1.565156	2.769161
antisense	-	0	1	1	0	1	0	0	0.105385	0.117843	0	0.100466	0
lincRNA	-	0	2	0	0	0	0	0	0.222813	0	0	0	0
pseudogen	polymerase	0	0	1	2	0	0	0	0	0.373066	0.489828	0	0
pseudogen	TAR_DNA_b	0	0	0	0	6	0	0	0	0	0	0.289891	0
pseudogen	-	0	0	1	0	0	0	0	0	0.17888	0	0	0
antisense	-	0	2	0	0	2	2	0	0.249551	0	0	0.237904	0.210456
antisense	-	3	6	1	4	0	0	0.586063	1.381278	0.257429	0.675999	0	0
protein_co	chromoson	1412	1140	925	1759	1579	1882	26.28435	25.00774	22.69024	28.3264	33.02126	34.81703
pseudogen	-	11	22	3	13	11	8	0.575446	1.356255	0.206808	0.588326	0.646477	0.415921
pseudogen	-	3	0	0	1	2	0	0.43276	0	0	0.124793	0.324119	0
lincRNA	-	5	0	2	0	0	0	1.454423	0	0.766629	0	0	0
protein_co	olfactory_r	0	0	0	84	35	82	0	0	0	2.116121	1.145026	2.373131
protein_co	GABA(A)_re	0	0	0	0	0	2	0	0	0	0	0	0.056849
pseudogen	myosin_VB	0	5	3	19	0	11	0	0.244275	0.163892	0.681425	0	0.453214
antisense	-	0	0	0	1	2	1	0	0	0	0.091781	0.23838	0.105439
sense_intrc	ST6GAL2_ir	0	7	0	2	1	4	0	1.125552	0	0.236077	0.153288	0.542413
pseudogen	-	0	0	0	0	8	2	0	0	0	0	0.925695	0.204724
antisense	-	12	2	10	1	0	0	0.813434	0.159764	0.893256	0.058641	0	0
pseudogen	-	7	0	2	0	0	0	1.23529	0	0.465089	0	0	0
antisense	-	4	0	3	0	4	9	0.340457	0	0.336479	0	0.382482	0.761297
lincRNA	-	24	18	17	28	26	31	0.509252	0.450092	0.475341	0.513976	0.619789	0.653722
processed_	long_interg	0	0	1	0	0	0	0	0	0.022724	0	0	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.221067
processed_	-	0	0	1	0	0	0	0	0	0.101696	0	0	0
pseudogen	interferon_	0	6	0	0	1	4	0	0.661354	0	0	0.105081	0.371831
antisense	-	21	13	5	5	15	14	0.553666	0.403905	0.173713	0.114041	0.444292	0.366831
lincRNA	long_interg	6	3	2	11	9	9	0.971394	0.572364	0.426687	1.540636	1.636952	1.448093
pseudogen	asparagine-	132	111	91	115	102	96	9.219276	9.135934	8.375275	6.948383	8.003356	6.663521
antisense	-	0	7	0	0	0	1	0	0.822437	0	0	0	0.099085
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.152948
lincRNA	-	0	2	0	0	0	0	0	0.742711	0	0	0	0

pseudogen	mitochond	0	0	0	0	2	2	0	0	0	0	0.246788	0.218316
pseudogen	solute_carr	5	0	3	0	4	0	0.306371	0	0.242234	0	0.275351	0
antisense	-	17	18	19	14	12	13	1.487598	1.856164	2.190913	1.059809	1.179688	1.13055
pseudogen	-	3	0	0	3	0	0	0.457703	0	0	0.395956	0	0
lincRNA	-	3	0	3	0	6	3	0.077702	0	0.102392	0	0.174587	0.077222
pseudogen	glyceraldeh	0	0	1	0	0	2	0	0	0.07126	0	0	0.107485
antisense	-	7	20	19	10	16	15	0.310374	1.045021	1.110136	0.383575	0.796997	0.660981
pseudogen	ribosomal_	0	0	0	0	1	1	0	0	0	0	0.150954	0.133538
pseudogen	ribosomal_	24	16	12	40	40	39	0.964024	0.757362	0.635174	1.389952	1.805035	1.556865
pseudogen	-	1	0	0	0	2	0	0.317012	0	0	0	0.712286	0
antisense	-	16	21	13	12	26	15	0.636884	0.985069	0.681897	0.413223	1.162687	0.593392
pseudogen	-	4	2	0	3	2	2	0.473745	0.27914	0	0.307375	0.266111	0.23541
pseudogen	-	3	3	1	0	0	1	0.090704	0.106889	0.039842	0	0	0.030048
pseudogen	RNA_bindir	0	0	0	0	0	2	0	0	0	0	0	0.097343
protein_co	thioredoxir	186	133	190	69	98	51	3.322208	2.799449	4.472005	1.066169	1.966478	0.905302
antisense	CLRN1_ant	0	0	0	1	0	0	0	0	0	0.020602	0	0
processed_	-	9	1	6	1	5	4	0.860052	0.112613	0.755559	0.08267	0.536786	0.379885
pseudogen	ribosomal_	0	0	0	0	0	1	0	0	0	0	0	0.05925
pseudogen	ribosomal_	0	3	7	2	3	2	0	0.381966	0.996618	0.186934	0.364138	0.214751
pseudogen	-	5	4	5	5	1	5	0.612743	0.577664	0.807445	0.53008	0.137676	0.608959
pseudogen	ribosomal_	2	0	0	1	1	5	0.778544	0	0	0.336757	0.437323	1.93434
protein_co	GATS_prote	17	22	7	1	3	3	0.554527	0.845675	0.300889	0.028219	0.109937	0.097253
pseudogen	-	12	13	3	2	9	2	0.791148	1.010013	0.260635	0.11407	0.666604	0.131044
antisense	-	5	3	10	0	9	12	0.539114	0.381188	1.420841	0	1.09019	1.285883
protein_co	ring_finger_	142	107	118	80	105	90	1.648601	1.463923	1.805278	0.80349	1.369511	1.038435
protein_co	RNA_bindir	1047	769	631	2679	1818	2056	19.60015	16.9647	15.56599	43.38588	38.23452	38.25123
pseudogen	-	0	1	1	0	1	0	0	0.262133	0.293123	0	0.249899	0
antisense	-	0	0	0	5	1	0	0	0	0	0.20283	0.05268	0
protein_co	Protein_LO	13	7	6	2	3	6	0.31907	0.202464	0.194056	0.042465	0.08272	0.146353
antisense	-	9	2	1	12	20	10	0.764798	0.200282	0.11198	0.882162	1.909339	0.844527
pseudogen	-	0	0	0	0	3	0	0	0	0	0	0.238221	0
pseudogen	nucleophos	2	1	13	10	4	10	0.131858	0.077693	1.129418	0.570348	0.296269	0.655219
lincRNA	-	3	2	1	0	2	2	0.415767	0.326637	0.182626	0	0.311392	0.275466
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.123908	0
antisense	-	9	5	6	2	4	15	1.13445	0.742711	0.996618	0.21809	0.566437	1.879073
protein_co	alkB_alkyla	25	14	22	38	34	56	0.397933	0.262606	0.461453	0.523259	0.607992	0.885865
protein_co	ankyrin_rep	10	13	8	7	9	14	0.166533	0.255124	0.17556	0.100847	0.168381	0.231707
protein_co	protocadhe	7	7	11	2	4	4	0.070454	0.083025	0.145893	0.017414	0.045229	0.040011
pseudogen	-	0	0	0	3	0	0	0	0	0	0.089219	0	0
pseudogen	-	0	0	1	0	1	0	0	0	0.197071	0	0.168011	0
pseudogen	transmemb	0	0	0	3	3	3	0	0	0	0.224504	0.291549	0.257912
processed_	-	22	17	16	4	7	2	1.02798	0.936091	0.985183	0.161691	0.367459	0.092876
processed_	-	34	55	47	48	41	62	0.893741	1.703736	1.628041	1.091533	1.210781	1.619698
pseudogen	poly(A)_bin	5	3	1	0	0	0	0.694764	0.491242	0.183106	0	0	0

antisense	ST3GAL6_a	1	0	3	2	3	3	0.068844	0	0.272158	0.119113	0.232026	0.205256
pseudogen	-	0	0	0	6	13	14	0	0	0	0.154726	0.435353	0.41475
antisense	-	8	1	0	0	1	0	1.072223	0.157944	0	0	0.150572	0
pseudogen	-	3	3	2	2	0	3	0.32747	0.385903	0.287684	0.188861	0	0.325448
lincRNA	-	6	0	1	16	18	20	0.481282	0	0.105702	1.110276	1.62207	1.594365
pseudogen	-	1	2	0	0	0	0	0.094876	0.223612	0	0	0	0
protein_co	kelch-like_f	62	46	47	1	0	0	1.332119	1.164706	1.330712	0.018587	0	0
pseudogen	HYDIN2_ax	0	0	0	1	0	1	0	0	0	0.025658	0	0.029476
antisense	-	4	1	4	8	7	8	0.391431	0.115319	0.51581	0.677248	0.769559	0.778027
processed_	-	0	0	0	0	2	0	0	0	0	0	0.108434	0
pseudogen	ribosomal_	2	3	0	1	3	1	0.293302	0.518458	0	0.126867	0.49426	0.145745
pseudogen	-	22	17	21	29	19	22	3.445864	3.137844	4.334405	3.929492	3.343321	3.424583
processed_	-	0	0	0	0	0	4	0	0	0	0	0	0.338899
pseudogen	MAP/micro	8	1	6	0	1	12	0.444882	0.065533	0.439685	0	0.062475	0.663202
antisense	PLCH1_ant	1	0	0	0	0	0	0.040475	0	0	0	0	0
pseudogen	ribosomal_	0	0	1	0	5	0	0	0	0.148117	0	0.631379	0
protein_co	POM121_t	0	1	0	0	0	0	0	0.025952	0	0	0	0
lincRNA	-	0	0	0	14	6	1	0	0	0	0.497814	0.277062	0.040849
antisense	CADM2_an	0	0	0	0	0	1	0	0	0	0	0	0.01981
pseudogen	GATS_stron	82	100	79	64	41	40	1.232584	1.771372	1.564821	0.832235	0.692366	0.597547
antisense	MYLK_antis	5	8	6	9	13	15	0.348296	0.656713	0.550763	0.542355	1.017351	1.038435
pseudogen	ribosomal_	1	3	5	0	0	0	0.132352	0.467908	0.872041	0	0	0
pseudogen	-	0	3	0	0	6	3	0	0.507217	0	0	0.967088	0.427757
pseudogen	-	0	0	1	0	1	0	0	0	0.191657	0	0.163395	0
antisense	HOXB_clust	18	12	10	0	10	9	1.127737	0.88598	0.825601	0	0.703857	0.560386
pseudogen	-	10	12	6	18	8	14	0.67355	0.952484	0.532544	1.04883	0.605353	0.937146
pseudogen	-	5	5	6	5	1	3	0.215032	0.253403	0.340032	0.186023	0.048315	0.128223
antisense	-	24	46	29	39	26	72	1.726337	3.899233	2.748825	2.426844	2.101051	5.147027
pseudogen	SET_pseudo	0	0	0	0	3	4	0	0	0	0	0.258591	0.305009
lincRNA	-	0	0	0	1	1	4	0	0	0	0.05979	0.077645	0.274747
pseudogen	-	0	0	0	0	0	4	0	0	0	0	0	1.209518
pseudogen	-	1	4	3	1	5	6	0.065038	0.306574	0.257113	0.056264	0.365331	0.387819
pseudogen	MT-ND1_ps	0	0	0	0	5	8	0	0	0	0	0.331158	0.468722
processed_	-	3	1	3	0	3	1	0.189526	0.074448	0.249749	0	0.212921	0.062785
pseudogen	-	0	1	3	1	2	0	0	0.194354	0.651993	0.142676	0.370566	0
protein_co	chromoson	0	0	2	2	0	1	0	0	0.086074	0.056507	0	0.032458
antisense	RUVBL1_an	0	0	1	0	0	4	0	0	0.118645	0	0	0.357919
pseudogen	high_mobil	0	0	2	0	0	1	0	0	0.445772	0	0	0.168096
pseudogen	-	2	0	0	4	0	0	0.267379	0	0	0.462615	0	0
pseudogen	ribosomal_	0	0	0	4	1	0	0	0	0	0.213018	0.069158	0
lincRNA	-	0	0	0	0	0	3	0	0	0	0	0	0.33655
pseudogen	-	0	0	0	4	2	0	0	0	0	0.663752	0.430985	0
antisense	-	5	4	3	4	3	1	0.310687	0.2929	0.245645	0.215018	0.209422	0.061754
pseudogen	MT-ND1_ps	2	1	0	0	2	9	0.111221	0.065533	0	0	0.124949	0.497402

pseudogen	glucuronid	15	3	6	4	0	11	1.181719	0.278517	0.622886	0.272613	0	0.861242
antisense	PSMD6_ant	14	16	1	9	11	11	0.301781	0.406435	0.028405	0.16783	0.266382	0.235649
protein_co	Uncharacte	123	83	101	109	84	97	4.50328	3.581038	4.872816	3.452338	3.455033	3.529435
pseudogen	-	2	1	3	3	3	1	0.122691	0.072292	0.242514	0.159208	0.206753	0.060966
protein_co	NME/NM23	170	181	175	623	299	442	5.471106	6.864547	7.421626	17.34512	10.81052	14.13703
antisense	PDZRN3_ar	8	11	12	0	0	0	0.857344	1.3892	1.694655	0	0	0
pseudogen	prostaglan	0	0	0	0	1	0	0	0	0	0	0.236016	0
processed_	-	1	0	0	0	0	0	0.054918	0	0	0	0	0
pseudogen	-	0	3	1	0	0	2	0	0.537825	0.200469	0	0	0.30238
pseudogen	ribosomal_	0	0	0	4	0	0	0	0	0	0.336757	0	0
protein_co	tumor_nec	30	37	13	34	22	18	0.89832	1.305626	0.512965	0.880748	0.740085	0.535663
protein_co	CMT1A_du	30	22	12	8	19	17	0.636565	0.550112	0.335535	0.14685	0.452923	0.358493
antisense	-	0	0	4	1	3	0	0	0	0.507369	0.083271	0.324414	0
protein_co	apolipopro	13	8	8	11	3	6	0.248012	0.179857	0.201119	0.181545	0.064298	0.11376
pseudogen	-	0	0	1	1	2	0	0	0	0.385432	0.253033	0.657192	0
protein_co	toll-like_re	4	0	0	5	0	0	0.051287	0	0	0.05546	0	0
lincRNA	-	1	6	2	0	0	0	0.201297	1.423294	0.530519	0	0	0
pseudogen	-	14	14	12	13	5	9	1.566964	1.846571	1.769893	1.258744	0.628709	1.001113
pseudogen	family_witl	0	2	0	2	3	0	0	0.126676	0	0.092993	0.181145	0
processed_	-	1	0	0	0	0	0	0.094034	0	0	0	0	0
protein_co	WW_doma	178	145	100	89	64	124	4.603565	4.419258	3.408074	1.991257	1.85953	3.187173
protein_co	mitochond	65	58	27	170	85	138	1.867154	1.963369	1.022034	4.224533	2.743056	3.93963
antisense	-	0	0	0	4	0	2	0	0	0	0.123115	0	0.070718
pseudogen	ribosomal_	0	0	1	2	0	0	0	0	0.144437	0.189644	0	0
antisense	-	0	0	2	0	0	0	0	0	0.383315	0	0	0
pseudogen	-	0	1	0	0	0	0	0	0.240879	0	0	0	0
lincRNA	-	12	17	11	0	2	0	1.473995	2.460769	1.780501	0	0.27599	0
pseudogen	suppressor_	1	4	0	1	3	4	0.050372	0.237441	0	0.043577	0.16977	0.200244
lincRNA	-	6	4	13	8	6	4	0.366797	0.288165	1.047255	0.423085	0.412073	0.243021
pseudogen	ribosomal_	2	4	0	0	0	0	0.135746	0.319937	0	0	0	0
pseudogen	ring_finger_	0	0	0	4	0	0	0	0	0	0.53566	0	0
pseudogen	-	0	0	0	0	3	4	0	0	0	0	0.158041	0.186409
pseudogen	ribosomal_	0	1	0	0	0	0	0	0.14342	0	0	0	0
protein_co	golgi_to_EF	94	56	67	187	187	217	1.142437	0.802046	1.073035	1.966115	2.553259	2.62104
pseudogen	glyceraldeh	2	0	1	0	0	0	0.103806	0	0.068395	0	0	0
antisense	IGSF11_ant	0	0	0	0	4	0	0	0	0	0	0.148319	0
pseudogen	ribosomal_	0	0	0	0	0	1	0	0	0	0	0	0.108707
lincRNA	-	9	13	14	3	4	1	0.597079	1.016341	1.223917	0.172176	0.298125	0.065932
protein_co	chromoson	65	38	36	128	88	154	0.83564	0.5757	0.609878	1.42357	1.270976	1.967597
pseudogen	zinc_finger_	30	9	14	3	0	2	1.18084	0.417464	0.726161	0.102154	0	0.078237
protein_co	adenylosuc	1495	1263	1000	3057	1905	2113	31.34526	31.20622	27.62902	55.44842	44.87193	44.0291
antisense	-	9	0	3	4	10	8	1.475136	0	0.647956	0.567169	1.84136	1.303134
antisense	PRKAG2_ar	1	1	0	0	4	2	0.050181	0.059135	0	0	0.225501	0.099742
pseudogen	ribosomal_	10	2	7	7	0	6	3.393653	0.799843	3.130404	2.055079	0	2.023617

pseudogen	small_nucl	0	2	0	0	0	0	0	0.549672	0	0	0	0
processed_	-	0	0	2	0	0	0	0	0	0.260797	0	0	0
lincRNA	-	0	0	0	0	5	2	0	0	0	0	0.115757	0.040961
pseudogen	peroxiredo	14	4	8	2	12	3	0.992201	0.334071	0.74713	0.122621	0.955436	0.211301
processed_	-	5	0	1	0	0	0	0.165131	0	0.04352	0	0	0
pseudogen	-	4	0	0	3	3	6	0.224564	0	0	0.145702	0.189213	0.334766
pseudogen	-	0	1	0	11	5	2	0	0.103634	0	0.836857	0.493986	0.174798
pseudogen	ribosomal_	0	0	2	2	0	2	0	0	0.380181	0.249585	0	0.286725
pseudogen	FCF1_small	0	0	0	0	10	3	0	0	0	0	1.008066	0.267529
pseudogen	-	1	2	2	2	0	6	0.0704	0.165925	0.185541	0.121806	0	0.419793
antisense	-	2	1	0	1	0	3	0.219672	0.129435	0	0.095018	0	0.327473
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.357919
pseudogen	-	1	0	0	0	0	0	0.031419	0	0	0	0	0
antisense	SLC9A9_an	4	1	1	0	0	0	0.408811	0.12044	0.134678	0	0	0
antisense	-	4	0	0	3	0	0	0.341005	0	0	0.221251	0	0
protein_co	testis_expr	1	0	1	0	1	1	0.021591	0	0.028452	0	0.024256	0.021458
pseudogen	-	68	70	65	150	108	192	2.416099	2.930967	3.043365	4.610628	4.311006	6.779797
pseudogen	olfactory_r	1	0	0	0	0	0	0.060297	0	0	0	0	0
antisense	-	10	8	10	3	5	4	0.746699	0.703952	0.983967	0.193789	0.419435	0.296835
pseudogen	-	1	1	2	4	2	4	0.140801	0.165925	0.371081	0.487222	0.316361	0.559724
protein_co	amylase_al	6	17	10	16	9	10	0.067355	0.224892	0.147929	0.155382	0.113504	0.111565
lincRNA	-	6	4	2	0	0	0	0.363856	0.285854	0.159824	0	0	0
pseudogen	DEAD/H_(A	0	0	0	0	0	1	0	0	0	0	0	0.023992
processed_	-	4	2	5	7	5	5	0.132684	0.07818	0.218557	0.200872	0.186328	0.164831
pseudogen	ribosomal_	1	0	0	0	0	3	0.113607	0	0	0	0	0.338717
protein_co	lymphocyt	40	38	10	59	34	48	0.797905	0.893268	0.262861	1.018137	0.761937	0.951573
antisense	-	1	0	1	0	0	0	0.183823	0	0.242234	0	0	0
antisense	-	1	3	4	6	4	2	0.069294	0.244978	0.365253	0.359677	0.311392	0.137733
antisense	-	0	2	0	4	1	0	0	0.066476	0	0.0976	0.031687	0
protein_co	proteasom	1	1	1	10	7	8	0.019784	0.023314	0.02607	0.171147	0.15558	0.157292
pseudogen	ribosomal_	0	4	0	0	0	1	0	0.434758	0	0	0	0.091662
processed_	-	0	3	0	7	12	5	0	0.226316	0	0.387657	0.863012	0.318102
pseudogen	-	11	9	3	26	11	18	0.655801	0.632308	0.235687	1.340959	0.736751	1.066501
lincRNA	-	2	0	0	0	0	0	0.186084	0	0	0	0	0
pseudogen	-	0	0	0	0	6	0	0	0	0	0	0.658405	0
pseudogen	-	0	0	1	0	0	0	0	0	0.055456	0	0	0
processed_	-	0	0	1	0	0	0	0	0	0.160008	0	0	0
pseudogen	eukaryotic_	4	0	6	10	10	6	0.133521	0	0.263922	0.28877	0.375006	0.199044
antisense	-	5	9	8	22	16	11	0.426256	0.90417	0.898722	1.622506	1.532391	0.931972
processed_	-	0	4	2	0	4	3	0	0.765494	0.427996	0	0.729766	0.484178
pseudogen	-	3	2	0	3	6	4	0.509048	0.399921	0	0.440374	1.143768	0.674539
pseudogen	ribosomal_	0	0	0	0	0	2	0	0	0	0	0	0.184287
antisense	MAGI1_ant	2	1	4	3	3	1	0.179157	0.105563	0.472171	0.232482	0.301908	0.089025
protein_co	protocadhe	2547	2004	2191	644	1146	960	28.62252	26.53895	32.44563	6.260772	14.46814	10.72161

antisense	ARHGEF3_a	0	0	0	0	0	2	0	0	0	0	0	0.21519
protein_co	small_lysin	0	1	0	14	5	6	0	0.060278	0	0.619502	0.287323	0.305009
processed_	-	1	3	3	2	2	5	0.048704	0.172183	0.192539	0.084267	0.109431	0.242015
pseudogen	-	0	3	2	0	3	0	0	0.233662	0.17419	0	0.222756	0
antisense	-	0	0	2	1	1	3	0	0	0.460484	0.151152	0.19629	0.520931
lincRNA	-	1	0	2	12	5	6	0.023858	0	0.062878	0.247673	0.134015	0.142264
protein_co	UDP_glucu	0	0	0	0	1	0	0	0	0	0	0.025363	0
pseudogen	zinc_finger_	149	162	113	573	276	383	2.293084	2.938027	2.291643	7.628713	4.771905	5.857902
protein_co	cytochrom	255	275	204	400	281	370	3.682475	4.679931	3.882081	4.997153	4.558847	5.310201
lincRNA	-	0	0	0	627	389	538	0	0	0	49.85402	40.1669	49.14298
pseudogen	glyceraldeh	0	0	0	0	0	2	0	0	0	0	0	0.103878
antisense	B4GALT4_a	0	0	1	1	1	0	0	0	0.128241	0.084189	0.109331	0
processed_	MAGI1_intr	4	0	0	0	9	2	0.082495	0	0	0	0.208525	0.040993
pseudogen	ribosomal_	0	0	0	0	0	4	0	0	0	0	0	0.425164
pseudogen	testicular_c	0	0	0	0	0	2	0	0	0	0	0	0.031724
processed_	-	0	0	0	0	6	21	0	0	0	0	0.608968	1.885486
antisense	ghrelin_op	10	10	12	20	11	15	0.450179	0.530508	0.71187	0.778893	0.556322	0.671098
processed_	-	16	19	15	60	19	28	0.823984	1.153081	1.017947	2.673088	1.099263	1.433068
lincRNA	-	0	0	1	0	0	0	0	0	0.105542	0	0	0
processed_	-	0	0	3	0	0	4	0	0	0.375745	0	0	0.377839
pseudogen	ribosomal_	0	0	0	0	1	0	0	0	0	0	0.161181	0
protein_co	acyl-CoA_d	1	0	1	0	0	2	0.012782	0	0.016843	0	0	0.025405
pseudogen	-	0	1	1	7	0	3	0	0.074448	0.08325	0.382568	0	0.188356
pseudogen	-	1	2	1	0	0	1	0.154798	0.364841	0.203986	0	0	0.153842
pseudogen	-	3	9	13	7	6	28	0.126855	0.448474	0.724379	0.256064	0.285028	1.176672
pseudogen	ribosomal_	1937	1754	1222	1446	1079	2227	110.1468	117.5382	91.56899	71.13342	68.93074	125.8555
protein_co	peptidylpr	318	282	219	569	340	401	12.28849	12.84185	11.15194	19.02159	14.76045	15.40017
lincRNA	-	5	0	2	0	0	0	0.349676	0	0.184315	0	0	0
lincRNA	-	0	1	0	0	0	0	0	0.129167	0	0	0	0
pseudogen	ribosomal_	217	156	164	210	231	246	5.528487	4.683583	5.505861	4.628378	6.611615	6.228612
pseudogen	ribosomal_	0	0	1	0	0	0	0	0	0.219381	0	0	0
processed_	-	5	3	2	1	3	1	0.501335	0.354476	0.264255	0.08674	0.337931	0.099648
pseudogen	ribosomal_	17	16	13	16	4	12	0.625867	0.694161	0.630683	0.509584	0.165441	0.43906
antisense	SEC62_anti	5	5	3	4	1	5	0.765043	0.901557	0.604884	0.529467	0.171896	0.760319
pseudogen	-	7	0	1	1	2	2	0.589168	0	0.110911	0.072812	0.189113	0.167294
pseudogen	ribosomal_	0	0	0	0	0	2	0	0	0	0	0	0.183005
pseudogen	-	0	0	0	2	0	2	0	0	0	0.11407	0	0.131044
pseudogen	-	0	11	1	2	0	2	0	0.790628	0.080372	0.105527	0	0.121231
pseudogen	-	6	5	4	15	3	31	0.407761	0.400435	0.35822	0.881879	0.229047	2.093756
antisense	-	6	3	8	4	6	1	0.286168	0.168615	0.502798	0.165041	0.321491	0.0474
pseudogen	-	1	0	0	0	0	0	0.187071	0	0	0	0	0
lincRNA	-	0	2	0	0	0	0	0	0.061045	0	0	0	0
pseudogen	mitochond	0	0	0	0	1	0	0	0	0	0	0.287323	0
pseudogen	-	1	0	0	0	0	0	0.067014	0	0	0	0	0

pseudogen	-	1	3	2	1	3	1	0.059284	0.209589	0.156245	0.051287	0.199807	0.058918
lincRNA	long_interg	0	5	0	0	1	0	0	0.246787	0	0	0.047054	0
pseudogen	ribosomal_	0	0	0	0	2	0	0	0	0	0	0.340836	0
protein_co	LIM_and_se	0	1	0	0	0	0	0	0.025299	0	0	0	0
pseudogen	leucine_ric	10	23	13	7	9	10	0.235712	0.638877	0.403795	0.142739	0.238327	0.234257
pseudogen	ribosomal_	1	1	0	1	2	3	0.157095	0.185127	0	0.135902	0.352973	0.468374
pseudogen	-	0	3	0	1	1	0	0	0.583063	0	0.142676	0.185283	0
pseudogen	-	4	0	4	0	3	0	0.395821	0	0.521595	0	0.33351	0
pseudogen	forkhead_b	73	53	51	55	70	72	2.004509	1.715015	1.845398	1.306504	2.159395	1.96484
antisense	-	3	6	1	8	12	19	0.275256	0.648746	0.120907	0.634993	1.236934	1.732525
pseudogen	-	0	2	0	0	0	0	0	0.433248	0	0	0	0
pseudogen	ribosomal_	2	1	2	0	0	1	0.670139	0.394859	0.88308	0	0	0.333
pseudogen	ribosomal_	9	3	6	0	4	11	1.080428	0.424406	0.94916	0	0.539464	1.312369
lincRNA	-	25	33	13	11	0	0	1.375805	2.14012	0.942747	0.523688	0	0
pseudogen	SET_pseudo	2	3	1	12	7	8	0.121285	0.214391	0.079912	0.629538	0.476897	0.482145
lincRNA	-	0	0	0	7	2	1	0	0	0	1.399967	0.51944	0.229756
antisense	CDKN2B_ar	22	7	10	0	1	5	0.303703	0.113876	0.181912	0	0.015509	0.068597
antisense	-	0	0	0	0	2	0	0	0	0	0	0.160097	0
pseudogen	-	0	0	4	0	3	0	0	0	0.788286	0	0.504033	0
pseudogen	urate_oxid	3	4	6	3	0	0	0.176666	0.277587	0.465606	0.152833	0	0
pseudogen	ribosomal_	9	12	6	11	14	6	0.602363	0.946464	0.529178	0.6369	1.052671	0.399095
processed_	-	52	24	28	42	39	45	4.611276	2.508049	3.27198	3.222034	3.885361	3.965883
pseudogen	ribosomal_	4	0	2	0	0	1	0.520305	0	0.342817	0	0	0.129273
antisense	TM4SF1_ar	0	2	0	0	1	0	0	0.165485	0	0	0.078881	0
antisense	THOC7_ant	1	3	1	9	7	9	0.078664	0.278103	0.10366	0.612467	0.61862	0.703605
processed_	-	6	2	2	12	1	0	0.476946	0.187351	0.209499	0.825206	0.089303	0
protein_co	LINE-1_typ	22	5	8	2910	2667	2695	0.302599	0.081044	0.145	34.62583	41.21129	36.8394
lincRNA	-	0	0	1	0	0	0	0	0	0.024521	0	0	0
antisense	-	2	1	1	2	7	0	0.184143	0.1085	0.121327	0.159301	0.724055	0
pseudogen	-	3	1	2	0	1	0	0.24933	0.09794	0.219037	0	0.093369	0
protein_co	aquaporin_	117	85	93	11	10	4	2.250762	1.926947	2.357553	0.183062	0.216119	0.076474
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.059183
antisense	-	1	0	0	2	0	0	0.086083	0	0	0.14894	0	0
antisense	KCNAB1_ar	0	0	2	0	0	0	0	0	0.259343	0	0	0
pseudogen	-	1	2	0	8	9	9	0.070777	0.166812	0	0.489828	0.715619	0.633057
lincRNA	-	1	1	2	0	0	9	0.179461	0.211484	0.472971	0	0	1.605174
pseudogen	-	3	0	0	0	0	0	0.223066	0	0	0	0	0
pseudogen	-	0	0	0	2	5	0	0	0	0	0.131985	0.428501	0
protein_co	C1q_and_t	0	2	0	1	0	3	0	0.067301	0	0.024703	0	0.085136
antisense	-	0	6	0	0	1	0	0	0.460426	0	0	0.073156	0
pseudogen	lymphocyt	2	0	0	0	0	0	0.796105	0	0	0	0	0
antisense	MME_antis	0	6	6	2	5	7	0	0.819095	0.915929	0.200433	0.650721	0.805904
pseudogen	keratin_8_p	0	1	1	2	6	2	0	0.043325	0.048447	0.06361	0.247816	0.073075
pseudogen	-	1	0	0	0	0	0	0.105671	0	0	0	0	0

pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.123908	0
pseudogen	myosin_lig	3	0	0	0	0	0	0.350603	0	0	0	0	0
protein_co	ISY1_splicir	204	195	158	274	192	267	2.811026	3.166478	2.868974	3.266242	2.972248	3.656416
protein_co	paraneopla	116	104	100	73	83	73	1.236889	1.306812	1.405101	0.673378	0.99426	0.77358
pseudogen	-	4	0	1	1	1	6	0.290088	0	0.095566	0.062738	0.081474	0.432444
pseudogen	ribosomal_	2	0	1	0	0	1	0.158506	0	0.104436	0	0	0.078764
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.032843
pseudogen	-	0	4	0	0	0	0	0	0.567161	0	0	0	0
protein_co	leucine-rich	6	1	0	0	2	0	0.090472	0.017769	0	0	0.03388	0
pseudogen	-	1	0	0	0	1	0	0.111221	0	0	0	0.124949	0
sense_intro	-	46	54	29	54	46	77	6.30903	8.727817	5.241283	6.407101	7.087804	10.49555
pseudogen	-	0	0	0	1	7	0	0	0	0	0.145393	1.321687	0
processed_	-	2	7	4	4	3	7	0.264705	1.091785	0.697633	0.457989	0.446069	0.920746
protein_co	KRAB_box_	0	0	0	1	0	0	0	0	0	0.017848	0	0
pseudogen	-	1	3	0	2	0	0	0.050276	0.177743	0	0.086987	0	0
pseudogen	-	4	0	0	0	0	3	0.52809	0	0	0	0	0.393621
pseudogen	-	90	103	76	106	73	75	7.197416	9.706852	8.009078	7.333359	6.558523	5.960806
pseudogen	-	0	0	1	2	0	1	0	0	0.207629	0.272613	0	0.156589
protein_co	protocadhe	489	411	342	8	27	26	5.57814	5.524964	5.140927	0.078947	0.346014	0.294757
antisense	PLCXD2_an	0	0	0	0	3	0	0	0	0	0	0.363397	0
processed_	C21orf91_(	0	1	1	1	0	0	0	0.087012	0.097299	0.063876	0	0
protein_co	Rho_guanir	285	257	163	3	24	29	5.912298	6.282777	4.455884	0.053839	0.559335	0.597887
pseudogen	-	1	0	0	0	0	0	0.163904	0	0	0	0	0
antisense	-	0	2	2	0	2	0	0	0.252072	0.281872	0	0.240307	0
pseudogen	-	0	1	0	0	0	0	0	0.212203	0	0	0	0
pseudogen	ubiquitin_/	4	1	1	1	0	6	0.551469	0.162468	0.181675	0.119268	0	0.822095
pseudogen	MT-ND2_ps	0	0	0	2	3	0	0	0	0	0.260962	0.508341	0
pseudogen	-	8	8	10	3	7	3	1.460441	1.721041	2.40563	0.473782	1.435626	0.544283
pseudogen	-	1	0	6	1	2	5	0.03752	0	0.296655	0.032458	0.084303	0.186442
pseudogen	-	1	4	3	0	0	0	0.111221	0.524267	0.439685	0	0	0
pseudogen	ribosomal_	0	2	0	0	0	0	0	0.260492	0	0	0	0
protein_co	transmemb	635	525	433	1752	1201	1379	11.52865	11.23236	10.35923	27.51704	24.49608	24.88161
protein_co	retinol_deh	224	187	143	343	232	316	7.472453	7.351295	6.286168	9.898566	8.694652	10.4764
processed_	-	1	0	1	14	6	4	0.010571	0	0.01393	0.128032	0.071257	0.042024
pseudogen	ribosomal_	0	0	2	0	0	0	0	0	0.243078	0	0	0
protein_co	keratin_ass	0	0	1	1	0	0	0	0	0.074375	0.048826	0	0
pseudogen	ribosomal_	0	0	0	0	3	1	0	0	0	0	1.06207	0.313179
processed_	-	25	5	23	36	28	25	0.40034	0.094355	0.485346	0.498718	0.503728	0.397868
pseudogen	-	0	0	2	0	0	0	0	0	0.113714	0	0	0
sense_intro	-	0	1	0	0	0	0	0	0.141469	0	0	0	0
antisense	NDUFB2_an	2	1	0	3	10	3	0.064249	0.037857	0	0.083372	0.360898	0.095778
protein_co	phosphatid	3	2	7	2	15	6	0.076986	0.060483	0.236715	0.0444	0.432447	0.153022
lincRNA	-	0	4	1	0	0	0	0	0.123418	0.034502	0	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.074252	0

pseudogen	-	12	3	11	8	10	8	1.315304	0.387501	1.588812	0.758574	1.231385	0.871454
pseudogen	-	1	1	0	2	1	0	0.096082	0.113226	0	0.166239	0.107942	0
pseudogen	ribosomal_	7	1	2	16	5	7	0.60258	0.101443	0.226872	1.191516	0.483544	0.598859
antisense	-	1	0	0	0	0	0	0.096256	0	0	0	0	0
antisense	LSAMP_ant	5	5	8	5	6	4	0.478671	0.564084	1.009234	0.414095	0.645308	0.380572
pseudogen	ribosomal_	2	0	0	2	9	4	0.318922	0	0	0.275897	1.612299	0.633904
pseudogen	plasminoge	1	0	3	0	0	0	0.017501	0	0.069187	0	0	0
pseudogen	-	3	4	0	0	0	0	0.250905	0.394235	0	0	0	0
pseudogen	-	0	0	2	0	0	0	0	0	0.203688	0	0	0
pseudogen	ribosomal_	0	0	0	0	0	4	0	0	0	0	0	0.164676
pseudogen	ribosomal_	25	16	9	31	33	58	3.042586	2.294721	1.443378	3.26383	4.511966	7.015207
protein_co	macrophag	1	10	1	15	0	2	0.05638	0.664406	0.074295	0.731612	0	0.112064
pseudogen	-	0	2	0	0	1	2	0	0.599882	0	0	0.285942	0.505904
antisense	HOXA11_ar	199	206	149	5	0	0	6.114485	7.459009	6.032925	0.132905	0	0
pseudogen	ribosomal_	1	3	0	0	0	0	0.11169	0.394859	0	0	0	0
pseudogen	-	1	2	1	0	0	0	0.125156	0.294977	0.164925	0	0	0
lincRNA	-	2	1	2	5	2	3	0.158744	0.093535	0.209185	0.34332	0.178339	0.236645
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.137373
pseudogen	septin_7_p	1	0	1	3	2	0	0.046318	0	0.061035	0.120207	0.10407	0
pseudogen	-	0	0	0	0	4	6	0	0	0	0	0.334604	0.444
pseudogen	-	0	0	0	2	0	3	0	0	0	0.256577	0	0.442135
processed_	-	58	43	53	14	15	25	0.97078	0.848142	1.168971	0.202714	0.282055	0.415856
pseudogen	tropomyos	152	109	132	180	204	277	2.755833	2.328857	3.153683	2.82322	4.155167	4.991127
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.217864
pseudogen	ribosomal_	5	0	0	0	7	3	0.584338	0	0	0	0.919054	0.348437
pseudogen	-	2	0	0	2	0	0	0.29576	0	0	0.25586	0	0
protein_co	GVQW_mo	26	9	18	39	18	49	0.750936	0.306323	0.685073	0.974445	0.584052	1.406486
pseudogen	-	4	0	0	2	1	2	0.460356	0	0	0.199126	0.129295	0.228757
pseudogen	-	0	2	0	4	1	6	0	0.106646	0	0.156577	0.050834	0.269816
protein_co	NOP2/Sun_	105	101	57	150	143	148	2.525581	2.862863	1.806682	3.121234	3.864178	3.537883
pseudogen	-	0	2	0	9	0	5	0	0.13957	0	0.461063	0	0.294262
pseudogen	ribosomal_	1	0	0	0	4	2	0.128186	0	0	0	0.576038	0.25479
processed_	-	0	1	0	0	1	0	0	0.162468	0	0	0.154885	0
pseudogen	-	6	5	1	3	0	1	0.849321	0.834061	0.186533	0.367371	0	0.140679
pseudogen	ribosomal_	0	0	0	0	3	0	0	0	0	0	0.324414	0
pseudogen	-	2	0	1	0	0	0	0.07026	0	0.046293	0	0	0
antisense	PRICKLE2_a	3	0	3	0	1	0	0.320208	0	0.421955	0	0.119911	0
pseudogen	carcinoemb	0	0	0	3	2	1	0	0	0	0.079835	0.069118	0.030572
protein_co	major_hist	0	1	0	0	1	0	0	0.041207	0	0	0.039284	0
antisense	-	3	5	11	6	3	7	0.024416	0.047954	0.11797	0.042243	0.027429	0.056618
pseudogen	ribosomal_	8	5	7	9	3	11	0.989551	0.728829	1.140988	0.963061	0.416887	1.35223
pseudogen	high_mobil	3	0	4	1	7	13	0.551469	0	0.968934	0.159024	1.445595	2.37494
protein_co	Yae1_doma	117	115	125	256	131	209	6.39886	7.411765	9.008688	12.11211	8.04891	11.35985
pseudogen	ribosomal_	3	2	3	0	3	0	0.360143	0.282938	0.47458	0	0.404598	0

lincRNA	-	1	0	0	0	0	0	0.066929	0	0	0	0	0
pseudogen	-	1	0	0	8	2	0	0.047227	0	0	0.326843	0.106112	0
lincRNA	-	6	7	8	0	0	0	0.547665	0.752955	0.962252	0	0	0
antisense	ARHGAP31	10	10	7	8	5	5	0.848413	0.999803	0.782601	0.587165	0.47657	0.421587
pseudogen	-	3	0	4	2	0	1	0.441175	0	0.775148	0.254438	0	0.14615
antisense	ADAMTS9_	4	5	5	4	2	5	0.12262	0.180625	0.201978	0.106077	0.068878	0.152328
lincRNA	-	9	21	13	10	3	4	0.190131	0.522802	0.361901	0.182757	0.0712	0.083981
processed_	-	22	19	14	1	0	0	0.635061	0.646329	0.532544	0.024972	0	0
lincRNA	-	1	0	0	0	0	0	0.123694	0	0	0	0	0
pseudogen	-	3	5	6	26	7	14	0.219672	0.43145	0.578948	1.646987	0.575839	1.018806
pseudogen	-	0	2	1	0	1	0	0	0.35148	0.196516	0	0.167538	0
antisense	-	1	0	2	0	0	0	0.119506	0	0.314958	0	0	0
processed_	-	10	10	7	1	1	3	0.238044	0.28052	0.219579	0.020593	0.026743	0.070972
pseudogen	ribosomal_	0	0	2	0	2	1	0	0	0.262762	0	0.224015	0.099085
protein_co	teratocarci	0	1	0	377	305	338	0	0.024826	0	6.870747	7.218526	7.076621
pseudogen	-	0	3	0	1	0	0	0	0.403369	0	0.098705	0	0
antisense	IQCJ-SCHIP	0	0	0	3	1	1	0	0	0	0.270466	0.117079	0.103571
processed_	-	0	2	1	1	0	0	0	0.255165	0.142665	0.093658	0	0
pseudogen	-	15	2	7	2	6	1	0.580493	0.09121	0.356976	0.066957	0.260859	0.038461
lincRNA	-	2	1	0	1	0	0	0.084503	0.049791	0	0.036551	0	0
lincRNA	-	4	0	0	0	0	0	0.334013	0	0	0	0	0
pseudogen	-	1	0	4	0	0	2	0.117647	0	0.620118	0	0	0.23384
protein_co	keratin_ass	2	3	0	0	0	1	0.089503	0.158211	0	0	0	0.044475
processed_	-	4	5	3	0	0	0	0.619193	0.912101	0.611959	0	0	0
protein_co	keratin_ass	0	0	1	2	0	0	0	0	0.098536	0.129375	0	0
processed_	-	0	0	3	0	1	0	0	0	0.666528	0	0.189414	0
protein_co	CGRP_rece	596	591	423	1316	784	1046	10.05187	11.74614	9.401041	19.20082	14.85477	17.53243
antisense	-	5	14	9	14	18	36	0.454039	1.498162	1.076963	1.099802	1.836306	3.248895
pseudogen	-	17	21	16	10	2	8	0.828726	1.206393	1.02782	0.421721	0.109532	0.38758
lincRNA	-	83	80	47	31	31	39	2.201454	2.50051	1.642723	0.711306	0.923724	1.02803
pseudogen	phosphorib	1	0	0	0	0	0	0.034222	0	0	0	0	0
pseudogen	-	0	4	0	0	0	0	0	0.415226	0	0	0	0
antisense	WWTR1_ar	8	8	3	4	7	11	0.249134	0.293589	0.123112	0.107762	0.244901	0.340444
processed_	-	6	8	14	38	22	33	0.142698	0.224215	0.438763	0.781832	0.587812	0.779993
pseudogen	SET_pseudo	0	0	3	0	0	0	0	0	0.368468	0	0	0
protein_co	CMT1A_du	0	2	1	2	0	0	0	0.048532	0.027135	0.035627	0	0
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.079658
lincRNA	-	0	0	1	0	0	0	0	0	0.077086	0	0	0
protein_co	ribosomal_	86	97	49	194	163	138	2.032556	2.701611	1.526072	3.966512	4.327935	3.241401
pseudogen	-	0	1	0	0	1	0	0	0.30433	0	0	0.290126	0
pseudogen	-	0	0	0	1	4	6	0	0	0	0.060341	0.313444	0.415921
pseudogen	-	1	0	6	0	0	0	0.1024	0	0.809632	0	0	0
antisense	SYNPR_anti	0	0	0	3	0	0	0	0	0	0.246231	0	0
protein_co	pyridoxal_(	44	34	30	73	85	63	1.158907	1.055315	1.041243	1.663343	2.515151	1.649097

pseudogen	ribosomal_	5	10	6	1	2	3	0.862231	2.032174	1.363452	0.149182	0.387465	0.514144
lincRNA	cancer/test	4	1	3	0	0	0	0.13941	0.041072	0.137781	0	0	0
protein_co	ribonuclea	9	3	5	10	8	20	0.319349	0.125444	0.233791	0.306963	0.318906	0.705282
processed_	HNF1A_ant	0	0	0	2	0	0	0	0	0	0.037311	0	0
protein_co	CD302_mo	231	271	213	68	28	50	3.185561	4.404031	3.87069	0.811234	0.433792	0.685257
pseudogen	-	0	2	0	0	0	0	0	0.344684	0	0	0	0
protein_co	EGF-like-do	29	26	16	16	25	31	0.628959	0.664515	0.457277	0.300198	0.609135	0.668183
pseudogen	keratin_8_p	2	0	3	0	0	0	0.104834	0	0.207218	0	0	0
pseudogen	-	0	3	1	11	2	3	0	0.366268	0.136523	0.985886	0.232782	0.308889
pseudogen	eukaryotic_	0	5	0	2	0	0	0	0.246203	0	0.072295	0	0
pseudogen	teratocarci	1	1	3	0	1	0	0.118172	0.139258	0.467165	0	0.132759	0
antisense	-	0	5	0	0	1	0	0	0.553083	0	0	0.105454	0
antisense	PLSCR5_an	0	0	0	4	0	0	0	0	0	0.407101	0	0
pseudogen	-	0	1	0	0	0	1	0	0.100951	0	0	0	0.085136
pseudogen	-	0	0	0	1	0	1	0	0	0	0.119579	0	0.137373
protein_co	ATP_syntha	130	144	126	236	187	322	8.891898	11.60702	11.35681	13.96452	14.3695	21.88853
processed_	-	0	0	2	0	0	0	0	0	0.332206	0	0	0
processed_	PTPRG_ant	11	12	16	33	37	58	0.218847	0.281343	0.419471	0.567968	0.826986	1.146793
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.06125
protein_co	Rho_GTPas	0	1	0	58	62	57	0	0.021476	0	0.914402	1.269366	1.032358
processed_	-	11	27	16	2	9	17	0.557807	1.613476	1.069169	0.087737	0.512723	0.856742
pseudogen	-	6	7	9	8	4	4	2.406409	3.30844	4.756587	2.775691	1.802301	1.594365
pseudogen	-	0	1	1	2	3	1	0	0.198687	0.222176	0.291713	0.568241	0.167561
pseudogen	proteasom	19	19	16	35	18	55	0.762029	0.898005	0.845616	1.214365	0.811035	2.192252
pseudogen	ribosomal_	2	1	0	0	4	0	0.267379	0.157545	0	0	0.600767	0
antisense	-	2	0	2	5	0	0	0.108486	0	0.142958	0.234626	0	0
pseudogen	carbonic_a	3	0	3	1	6	0	0.175495	0	0.231259	0.050607	0.394315	0
processed_	-	10	2	3	10	9	5	0.366881	0.086469	0.145038	0.317387	0.370952	0.182308
pseudogen	angiogenic_	0	1	0	1	0	0	0	0.051433	0	0.037757	0	0
pseudogen	chromobo	0	4	1	0	0	0	0	0.444832	0.124355	0	0	0
pseudogen	-	1	0	0	0	0	0	0.056743	0	0	0	0	0
processed_	-	1	1	3	0	0	0	0.035365	0.041675	0.139806	0	0	0
pseudogen	-	0	0	2	0	0	3	0	0	0.400938	0	0	0.453569
pseudogen	-	6	10	5	9	7	8	0.678731	1.333071	0.745334	0.880748	0.889597	0.899385
pseudogen	glucuronid	49	26	31	36	13	26	1.780445	1.113302	1.484325	1.131613	0.530671	0.938892
protein_co	actin_relat	2143	1735	1556	3450	2406	3543	43.93979	41.92204	42.0417	61.19528	55.42179	72.19658
pseudogen	-	16	9	11	13	6	9	1.821626	1.207504	1.650314	1.2804	0.767431	1.018336
antisense	ZBTB20_an	4	0	4	0	0	1	0.125527	0	0.165414	0	0	0.031188
protein_co	cortistatin	16	12	11	11	13	9	0.749607	0.662525	0.679112	0.44583	0.684236	0.41905
antisense	-	1	0	1	0	0	0	0.058049	0	0.076495	0	0	0
lincRNA	-	0	0	1	1	0	0	0	0	0.0688	0.045167	0	0
sense_intrc	-	0	0	0	0	0	1	0	0	0	0	0	0.093619
pseudogen	-	0	0	0	4	2	4	0	0	0	0.3164	0.205444	0.363482
lincRNA	-	3	4	0	0	8	6	0.347534	0.546063	0	0	1.041154	0.690775

pseudogen	-	1	0	2	0	1	0	0.109609	0	0.288875	0	0.123139	0
pseudogen	-	0	5	5	0	3	6	0	0.648521	0.72519	0	0.370952	0.656308
pseudogen	ubiquilin_4	1	2	1	0	4	0	0.029395	0.069281	0.038736	0	0.132095	0
pseudogen	-	13	6	7	25	44	19	1.352128	0.735415	0.959416	2.249455	5.141337	1.963982
protein_co	UDP_glucu	1	0	0	0	0	3	0.015621	0	0	0	0	0.046575
lincRNA	-	0	0	1	0	0	0	0	0	0.121117	0	0	0
pseudogen	-	1	2	0	0	0	0	0.113364	0.267185	0	0	0	0
pseudogen	ribosomal_	0	1	1	3	0	0	0	0.144751	0.161864	0.318786	0	0
protein_co	indolethyla	0	1	2	0	0	0	0	0.02438	0.054524	0	0	0
pseudogen	-	0	0	5	0	0	0	0	0	0.582331	0	0	0
pseudogen	protein_ph	0	1	0	0	0	2	0	0.106102	0	0	0	0.178959
pseudogen	-	0	0	0	3	5	3	0	0	0	0.286841	0.620834	0.329524
lincRNA	-	14	10	14	1	0	0	1.401085	1.179352	1.846287	0.086576	0	0
pseudogen	ribosomal_	0	5	1	2	0	0	0	0.831836	0.186035	0.244261	0	0
processed_	ADAMTS9_a	7	11	26	8	9	14	0.100403	0.185929	0.491424	0.099266	0.145024	0.199566
protein_co	actin_relat	3386	2760	2314	5085	3176	3624	105.3221	101.1693	94.84855	136.8316	110.9844	112.029
protein_co	transmemb	26	7	20	25	46	36	0.52718	0.167259	0.53438	0.438519	1.047833	0.725433
processed_	-	2	0	0	0	0	0	0.131042	0	0	0	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.097024	0
lincRNA	-	2	1	0	94	92	102	0.05165	0.030433	0	2.100047	2.669163	2.61787
pseudogen	fatty_acid_	1	3	0	1	5	0	0.051549	0.182243	0	0.044595	0.289561	0
pseudogen	zinc_finger_	6	0	5	4	5	5	0.162812	0	0.178789	0.093898	0.152424	0.134839
pseudogen	ribosomal_	9	13	11	2	5	9	0.598579	1.018895	0.964065	0.115073	0.373592	0.594882
lincRNA	-	0	0	0	0	4	5	0	0	0	0	0.478679	0.529316
pseudogen	ribosomal_	46	67	64	14	31	17	2.128746	3.653827	3.902841	0.560476	1.611673	0.781852
processed_	-	9	5	6	24	18	31	0.725219	0.474792	0.637108	1.673019	1.629477	2.48255
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.154747
processed_	-	23	22	20	4	9	12	1.087181	1.225473	1.245773	0.163568	0.477931	0.563722
antisense	-	2	1	1	0	2	1	0.330881	0.194962	0.21801	0	0.371724	0.164419
processed_	-	0	1	0	1	3	4	0	0.116831	0	0.085766	0.334134	0.394113
pseudogen	-	5	0	2	6	0	10	0.558449	0	0.29436	0.579733	0	1.110001
antisense	-	1	5	0	3	0	1	0.084435	0.49751	0	0.219134	0	0.083914
pseudogen	MT-ND4_ps	0	0	0	2	4	0	0	0	0	0.067006	0.174033	0
pseudogen	cytochrom	0	0	1	0	0	0	0	0	0.303319	0	0	0
antisense	-	4	0	0	1	0	2	0.459358	0	0	0.099347	0	0.228261
pseudogen	-	0	2	0	0	1	0	0	0.183764	0	0	0.087593	0
pseudogen	-	0	0	0	4	2	3	0	0	0	0.558523	0.362658	0.481226
pseudogen	ribosomal_	3	0	1	0	0	0	0.342291	0	0.150352	0	0	0
protein_co	ATP_syntha	77	86	80	149	76	101	1.435878	1.889871	1.965855	2.403676	1.59217	1.871793
protein_co	pleckstrin_	274	324	246	252	167	248	3.899417	5.43377	4.613378	3.102506	2.670021	3.507603
pseudogen	-	3	1	1	5	1	0	0.186193	0.073139	0.081786	0.268458	0.069726	0
protein_co	chromoson	173	172	149	604	407	411	4.531812	5.309594	5.143359	13.68755	11.97758	10.69984
pseudogen	-	0	0	0	1	0	0	0	0	0	0.117735	0	0
pseudogen	Kallmann_s	1	3	0	31	20	14	0.029153	0.103063	0	0.78181	0.655021	0.405615

processed_	-	32	44	16	33	34	51	0.348583	0.564827	0.229673	0.31098	0.416087	0.552123
pseudogen	translocase	0	2	1	0	0	0	0	0.305074	0.17057	0	0	0
protein_co	phosphatid	287	296	247	982	760	853	5.692793	6.918984	6.456175	16.8507	16.93582	16.81521
lincRNA	-	1	0	3	0	1	1	0.025404	0	0.100427	0	0.028539	0.025247
processed_	-	2	1	4	0	9	5	0.188402	0.11101	0.496536	0	0.952461	0.468097
pseudogen	-	6	4	4	1	5	1	0.43276	0.339988	0.380181	0.062396	0.405149	0.071681
pseudogen	ribosomal_	4	0	0	0	5	0	0.376804	0	0	0	0.529145	0
pseudogen	-	5	7	7	3	2	1	0.745648	1.230181	1.375614	0.387033	0.335076	0.148209
lincRNA	-	1	0	0	4	0	0	0.138589	0	0	0.47957	0	0
pseudogen	-	0	2	0	0	0	0	0	0.733973	0	0	0	0
pseudogen	raftlin_lipi	3	0	1	0	0	0	0.159461	0	0.070043	0	0	0
pseudogen	-	0	0	0	0	0	6	0	0	0	0	0	0.507531
pseudogen	-	3	0	0	0	1	2	0.213185	0	0	0	0.079833	0.141246
processed_	-	0	0	0	0	1	1	0	0	0	0	0.020375	0.018025
protein_co	4-hydroxy-	0	0	1	0	0	0	0	0	0.02703	0	0	0
pseudogen	ribosomal_	1	0	0	2	7	1	0.131367	0	0	0.22729	1.03308	0.130556
protein_co	PWP2_peri	473	409	342	1324	1006	1234	5.486654	5.590837	5.22766	13.2861	13.10972	14.22562
antisense	-	0	1	1	0	2	3	0	0.140513	0.157125	0	0.26791	0.3555
antisense	-	8	8	2	0	0	0	0.26176	0.308468	0.086234	0	0	0
protein_co	chromoson	12	5	7	113	69	87	0.247292	0.121424	0.190091	2.01451	1.597446	1.781792
protein_co	phosphatid	1325	1054	944	1463	1329	1401	10.38904	9.738843	9.753634	9.923548	11.70668	10.9171
pseudogen	transcriptic	6	2	0	0	1	0	0.998887	0.392376	0	0	0.187031	0
protein_co	A_kinase_(I	0	3	0	7	13	5	0	0.027259	0	0.046693	0.112611	0.038315
pseudogen	-	0	3	1	0	5	1	0	0.40424	0.150677	0	0.642289	0.113637
pseudogen	-	5	1	1	4	2	0	0.357709	0.084308	0.094275	0.247562	0.160746	0
sense_intrc	WWTR1_in	9	8	1	8	8	7	1.056472	1.106656	0.154686	0.812397	1.055005	0.816626
processed_	-	0	1	6	0	0	0	0	0.071138	0.477286	0	0	0
pseudogen	-	0	0	0	1	0	1	0	0	0	0.12793	0	0.146967
processed_	-	0	0	0	2	2	1	0	0	0	0.159024	0.206514	0.091344
protein_co	ubiquitin_s	79	77	58	118	90	121	1.550737	1.781185	1.500286	2.003808	1.984736	2.360512
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.088576
protein_co	huntingtin	30	16	16	24	22	8	0.332474	0.20896	0.233664	0.230097	0.27391	0.088112
pseudogen	-	0	0	0	2	0	0	0	0	0	0.246231	0	0
pseudogen	-	0	8	0	6	0	0	0	0.798563	0	0.439669	0	0
pseudogen	MAP/micro	0	0	1	0	0	0	0	0	0.077774	0	0	0
pseudogen	ribosomal_	228	222	129	127	107	200	14.84692	17.03576	11.06945	7.154319	7.827704	12.94319
lincRNA	-	0	0	0	0	2	1	0	0	0	0	0.390006	0.172505
processed_	-	0	0	0	0	0	1	0	0	0	0	0	0.060062
pseudogen	ribosomal_	4	2	1	4	1	0	0.265368	0.15636	0.087423	0.229568	0.074531	0
pseudogen	ribosomal_	7	5	4	2	2	14	1.046856	0.881183	0.788286	0.258751	0.336022	2.080782
lincRNA	-	315	270	170	482	272	413	3.963026	4.003015	2.818384	5.245977	3.844451	5.163879
pseudogen	ribosomal_	3	0	0	0	1	0	0.519029	0	0	0	0.194366	0
pseudogen	-	1	0	0	0	3	4	0.210083	0	0	0	0.708047	0.835144
sense_intrc	FOXP1_intr	6	21	4	0	1	2	0.089756	0.370201	0.078851	0	0.016806	0.029734

pseudogen	ribosomal_	0	0	0	0	2	0	0	0	0	0	0.191858	0
protein_co	alpha-meth	1	5	11	1	7	4	0.012748	0.075112	0.184781	0.011028	0.100248	0.050676
protein_co	mitochond	6	4	4	13	13	10	0.231015	0.181492	0.202948	0.433008	0.562318	0.382648
processed_	small_nucl	816	691	594	3136	1759	2266	16.52634	16.49194	15.85287	54.94467	40.02224	45.60958
pseudogen	ribosomal_	0	0	4	0	0	0	0	0	0.393587	0	0	0
processed_	-	0	0	0	1	1	1	0	0	0	0.083727	0.108731	0.096187
lincRNA	-	7	2	8	3	8	7	0.531689	0.179018	0.800726	0.197126	0.68265	0.528405
antisense	-	0	0	4	0	1	0	0	0	0.511086	0	0.10893	0
pseudogen	-	0	0	0	2	2	1	0	0	0	0.228423	0.296638	0.131207
protein_co	Rho_GDP_(	6	2	2	3	4	2	0.249722	0.098094	0.109691	0.108016	0.187031	0.082726
lincRNA	-	1	1	1	0	1	0	0.140801	0.165925	0.185541	0	0.158181	0
pseudogen	-	11	27	13	40	30	24	0.199367	0.576675	0.310484	0.627167	0.610845	0.432296
pseudogen	-	0	0	1	0	0	0	0	0	0.238915	0	0	0
pseudogen	-	14	9	4	4	10	11	2.135948	1.618126	0.804188	0.527941	1.714003	1.667881
pseudogen	-	2	1	0	0	2	1	0.31419	0.185127	0	0	0.352973	0.156125
antisense	HOXB_clust	0	0	0	0	3	0	0	0	0	0	0.315243	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.113084	0	0
pseudogen	MT-ND3_ps	0	0	0	1	0	0	0	0	0	0.1351	0	0
protein_co	t-complex_	0	0	0	1	0	2	0	0	0	0.046544	0	0.106939
protein_co	pregnancy_	0	0	0	17	11	2	0	0	0	0.50623	0.42538	0.068419
pseudogen	ribosomal_	1	0	0	0	0	0	0.067873	0	0	0	0	0
antisense	PVRL3_anti	15	18	17	13	10	23	1.00267	1.417903	1.497444	0.75175	0.750959	1.527933
pseudogen	ATP_syntha	2	0	0	0	0	0	0.258249	0	0	0	0	0
protein_co	ADP-ribosy	836	797	819	432	294	314	15.49131	17.40393	19.99864	6.925141	6.120378	5.782573
protein_co	bone_gamr	0	2	1	2	3	10	0	0.134023	0.074934	0.098386	0.191652	0.565135
processed_	-	0	0	0	4	4	1	0	0	0	0.08967	0.116448	0.025753
protein_co	chromoson	135	126	80	264	212	213	2.399139	2.638756	1.873468	4.058715	4.232593	3.761931
pseudogen	-	54	46	26	92	71	96	2.775547	2.786248	1.761015	4.090776	4.099796	4.903834
pseudogen	-	0	0	1	1	0	0	0	0	0.113252	0.074349	0	0
protein_co	paternally_	2699	2325	2842	19493	22411	18407	21.59077	21.91772	29.95879	134.8985	201.4075	146.3383
lincRNA	-	0	4	1	0	1	0	0	0.35148	0.098258	0	0.083769	0
processed_	-	23	12	11	34	16	23	1.332213	0.819095	0.839602	1.703679	1.041154	1.323986
pseudogen	ribosomal_	1	0	0	0	0	0	0.062801	0	0	0	0	0
processed_	-	25	37	31	45	36	44	0.347382	0.605865	0.567628	0.540932	0.561977	0.607616
lincRNA	-	1	0	1	0	0	0	0.085114	0	0.11216	0	0	0
pseudogen	-	6	2	5	8	10	22	0.465075	0.182687	0.510712	0.536444	0.870804	1.694742
pseudogen	-	4	0	0	0	0	0	0.622835	0	0	0	0	0
pseudogen	-	51	43	33	43	40	46	5.882333	5.844602	5.015661	4.290529	5.183086	5.272868
pseudogen	ribosomal_	0	0	0	2	4	0	0	0	0	0.263212	0.683631	0
pseudogen	-	0	0	1	0	0	0	0	0	0.438763	0	0	0
pseudogen	-	1	0	0	0	0	0	0.107168	0	0	0	0	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.096622	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.134908
pseudogen	ribosomal_	8	5	5	4	0	2	1.064141	0.783765	0.876423	0.460291	0	0.264392

pseudogen	-	3	0	0	2	0	1	0.575446	0	0	0.331876	0	0.190631
pseudogen	transferrin_	7	9	7	1	1	5	0.235592	0.356955	0.310453	0.029116	0.037811	0.167241
pseudogen	BMS1_pseu	15	5	15	10	7	17	0.462771	0.181782	0.609819	0.266893	0.242617	0.521235
antisense	NPPA_antis	3	5	2	13	12	14	0.153898	0.302266	0.1352	0.576924	0.69158	0.713756
pseudogen	-	1	0	0	0	0	0	0.02081	0	0	0	0	0
processed_	-	8	1	5	0	11	0	0.770051	0.113432	0.634212	0	1.189518	0
protein_co	eukaryotic_	1291	1137	913	1462	1181	1537	53.02314	55.03091	49.4134	51.94569	54.49268	62.73685
processed_	-	3	2	0	3	2	2	0.33507	0.263239	0	0.289866	0.250953	0.222
protein_co	TBC1_dom	0	0	0	1	0	0	0	0	0	0.013514	0	0
protein_co	RNA_bindi	0	2	0	0	0	0	0	0.064953	0	0	0	0
pseudogen	-	0	0	2	0	0	1	0	0	0.162429	0	0	0.06125
antisense	-	0	0	0	0	1	0	0	0	0	0	0.156516	0
antisense	-	0	0	0	2	0	0	0	0	0	0.159301	0	0
pseudogen	-	0	0	2	2	0	0	0	0	0.273046	0.179252	0	0
lincRNA	-	10	1	8	0	0	0	0.995131	0.11727	1.049072	0	0	0
pseudogen	diazepam_b	2	0	0	0	1	1	0.062578	0	0	0	0.035151	0.031096
protein_co	protocadhe	102	66	60	172	171	200	1.168069	0.890675	0.905429	1.703961	2.199953	2.276186
pseudogen	-	1	0	3	0	3	2	0.101032	0	0.399408	0	0.340511	0.200817
pseudogen	-	0	0	0	1	0	0	0	0	0	0.109567	0	0
pseudogen	-	2	0	0	0	0	0	0.190778	0	0	0	0	0
pseudogen	ribosomal_	3	3	1	4	3	6	0.198777	0.234247	0.087313	0.229281	0.223314	0.395099
pseudogen	retinoblast	1	0	2	4	1	3	0.041884	0	0.110385	0.144933	0.047054	0.124875
lincRNA	-	9	5	5	32	22	27	0.719742	0.471206	0.526913	2.213844	1.976541	2.14589
pseudogen	-	1	1	3	4	1	4	0.081323	0.095834	0.32149	0.281406	0.091361	0.323281
protein_co	mitochond	869	692	570	1872	1323	1735	27.17408	25.50048	23.48793	50.6412	46.47764	53.9193
pseudogen	-	7	4	1	1	2	1	0.386834	0.260492	0.072822	0.047807	0.124167	0.054921
protein_co	chromoson	117	137	102	166	175	218	2.319886	3.201168	2.665114	2.847423	3.898234	4.295829
pseudogen	-	2	0	1	0	0	0	0.050734	0	0.033428	0	0	0
pseudogen	NADH_deh	0	0	0	0	3	0	0	0	0	0	0.468314	0
lincRNA	-	83	47	59	42	49	31	2.06684	1.379221	1.936046	0.904776	1.3708	0.767185
pseudogen	-	1	0	0	0	0	0	0.189753	0	0	0	0	0
pseudogen	-	1	0	3	0	1	4	0.40413	0	1.597632	0	0.454015	1.606536
lincRNA	-	0	0	0	0	4	0	0	0	0	0	0.332268	0
antisense	-	160	123	152	147	118	113	4.99149	4.521916	6.248685	3.967259	4.135627	3.503469
processed_	-	8	1	7	19	14	8	0.555083	0.081766	0.64003	1.140471	1.091301	0.551655
protein_co	serpin_pep	0	0	1	0	0	0	0	0	0.032876	0	0	0
pseudogen	POU_class_	0	3	5	0	0	0	0	0.189054	0.35234	0	0	0
lincRNA	-	7	6	7	1	12	13	0.712667	0.719858	0.939121	0.088075	1.372521	1.315351
processed_	-	4	0	1	3	3	2	0.363856	0	0.119868	0.236077	0.306577	0.180804
pseudogen	DDB1_and_	0	0	0	5	1	0	0	0	0	0.172176	0.044719	0
lincRNA	-	0	0	0	2	0	0	0	0	0	0.035108	0	0
pseudogen	ribosomal_	0	0	0	4	0	0	0	0	0	0.379287	0	0
protein_co	major_hist	1	0	0	0	0	0	0.011587	0	0	0	0	0
pseudogen	-	0	0	0	17	6	3	0	0	0	0.607792	0.278576	0.123218

lincRNA	-	0	0	1	2	2	0	0	0	0.105065	0.137949	0.179144	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.064688	0	0
pseudogen	-	290	257	261	159	252	264	8.106066	8.465494	9.613631	3.844787	7.913374	7.333743
antisense	-	0	7	2	2	0	0	0	0.101326	0.032373	0.021252	0	0
pseudogen	-	4	3	0	2	1	4	0.487935	0.431252	0	0.211055	0.137041	0.484922
pseudogen	mannose-b	4	0	2	9	10	6	0.148711	0	0.097982	0.289459	0.417668	0.221688
pseudogen	-	0	5	8	1	11	8	0	0.980939	1.755051	0.144022	2.057343	1.323624
pseudogen	ribosomal_	0	0	6	10	17	8	0	0	0.535954	0.586414	1.29461	0.53894
pseudogen	-	2	0	0	0	0	0	0.126351	0	0	0	0	0
pseudogen	olfactory_r	0	0	1	0	0	1	0	0	0.075912	0	0	0.057251
protein_co	24-dienoyl_	185	154	151	173	100	125	4.749798	4.659413	5.108756	3.842488	2.88438	3.189504
pseudogen	-	14	5	1	19	32	26	0.488579	0.205629	0.045988	0.573618	1.254601	0.901757
protein_co	guanine_nu	8	1	3	4	9	7	0.284056	0.041843	0.140369	0.122868	0.35901	0.247014
processed_	-	27	19	19	36	35	40	1.455608	1.207095	1.349799	1.678982	2.119814	2.143138
antisense	-	1	0	3	0	0	0	0.122549	0	0.484467	0	0	0
sense_intro	USP6NL_in	19	10	32	69	66	72	0.403805	0.250453	0.896196	1.268617	1.575837	1.520759
pseudogen	-	0	0	1	1	7	0	0	0	0.177968	0.116834	1.06207	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.106397	0
lincRNA	-	0	2	0	0	2	2	0	0.4118	0	0	0.39258	0.347287
processed_	-	2	0	0	0	0	0	0.23068	0	0	0	0	0
lincRNA	-	1	0	0	0	0	0	0.028945	0	0	0	0	0
pseudogen	ankyrin_rep	0	0	0	3	0	0	0	0	0	0.057416	0	0
pseudogen	-	1	0	0	0	0	0	0.102203	0	0	0	0	0
antisense	-	0	0	0	0	1	1	0	0	0	0	0.04285	0.037906
antisense	-	41	40	44	47	47	56	0.638782	0.734405	0.90335	0.633475	0.822651	0.867094
protein_co	ciliary_neu	8	8	3	18	22	8	0.224564	0.264635	0.11097	0.437105	0.693781	0.223177
pseudogen	chaperonin	2	0	0	0	0	0	0.06796	0	0	0	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.120123
protein_co	coiled-coil_	24	21	16	34	25	8	0.778544	0.802783	0.683954	0.954144	0.911089	0.257912
protein_co	retrotransp	533	411	465	166	208	213	6.4734	5.882394	7.442057	1.74412	2.838034	2.570955
pseudogen	-	2	1	1	6	3	0	0.294936	0.173782	0.194327	0.765441	0.497013	0
lincRNA	-	0	1	0	0	0	0	0	0.07978	0	0	0	0
pseudogen	-	0	0	0	0	5	0	0	0	0	0	0.624747	0
pseudogen	-	3	0	4	4	1	0	0.340092	0	0.597544	0.392282	0.127357	0
processed_	-	0	0	0	0	1	0	0	0	0	0	0.0867	0
lincRNA	-	18	12	11	114	73	104	0.350603	0.275443	0.282339	1.920925	1.597403	2.013194
processed_	-	0	0	0	1	0	0	0	0	0	0.080208	0	0
pseudogen	zinc_finger_	10	9	13	192	201	188	0.17706	0.187789	0.303319	2.940933	3.998214	3.308174
lincRNA	-	1	3	2	0	0	0	0.119236	0.421539	0.314249	0	0	0
lincRNA	-	0	0	3	15	6	11	0	0	0.307779	1.01027	0.524788	0.85111
processed_	GLYCTK_an	14	0	4	1	3	3	1.063377	0	0.400363	0.065709	0.255994	0.226459
processed_	-	20	13	6	6	12	22	1.851084	1.417903	0.731783	0.480408	1.247747	2.023617
protein_co	adaptor-rel	1200	1031	781	1134	786	1024	11.22424	11.36427	9.626347	9.175964	8.259376	9.518867
processed_	SOX2_overl	0	2	0	9	4	1	0	0.034892	0	0.115266	0.066528	0.014713

pseudogen	mitochond	2	0	0	0	0	0	0.285396	0	0	0	0	0
pseudogen	ribosomal_	0	0	2	2	1	0	0	0	0.400938	0.263212	0.170908	0
pseudogen	-	0	0	0	2	1	0	0	0	0	0.117283	0.076154	0
protein_co	zinc_finger_	1	2	3	3	1	4	0.010782	0.025413	0.042625	0.027983	0.012113	0.042863
processed_	-	22	16	16	15	20	28	3.346844	2.868401	3.207507	1.974091	3.418156	4.233314
protein_co	stereocilin	1	2	0	0	0	2	0.009321	0.021968	0	0	0	0.018526
processed_	-	0	0	2	7	0	0	0	0	0.367175	0.843664	0	0
processed_	-	0	0	1	0	0	0	0	0	0.130888	0	0	0
pseudogen	-	8	1	3	0	0	0	0.474275	0.069863	0.234367	0	0	0
pseudogen	-	0	0	0	3	0	1	0	0	0	0.168792	0	0.064636
processed_	-	2	3	3	7	1	2	0.189413	0.334818	0.3744	0.57351	0.106397	0.188243
processed_	-	0	0	1	0	4	3	0	0	0.111088	0	0.378827	0.251341
pseudogen	-	1	0	0	0	1	1	0.074775	0	0	0	0.084006	0.074314
pseudogen	-	0	0	0	4	0	0	0	0	0	0.53566	0	0
protein_co	endogenou	9	10	16	26	35	27	0.142145	0.186121	0.332999	0.355242	0.621019	0.423801
pseudogen	-	3	2	4	0	1	4	0.395082	0.310387	0.694162	0	0.14795	0.523523
pseudogen	-	0	1	0	0	0	0	0	0.469081	0	0	0	0
pseudogen	-	0	2	0	3	1	0	0	0.394859	0	0.4348	0.188215	0
pseudogen	ferritin_hea	8	15	19	8	0	5	0.770051	1.701484	2.410004	0.666166	0	0.47831
pseudogen	-	0	1	0	0	2	0	0	0.180834	0	0	0.344788	0
pseudogen	ribosomal_	0	0	0	1	0	0	0	0	0	0.116834	0	0
pseudogen	-	1	0	0	1	3	2	0.125156	0	0	0.108272	0.421815	0.248766
pseudogen	ferritin_hea	4	1	7	6	3	0	0.382937	0.112817	0.88308	0.496914	0.322654	0
pseudogen	-	1	0	0	0	0	0	0.154347	0	0	0	0	0
processed_	-	0	2	2	6	4	2	0	0.155193	0.173541	0.341783	0.2959	0.130881
antisense	-	1	0	3	0	0	2	0.245097	0	0.968934	0	0	0.487167
pseudogen	-	0	0	0	4	0	0	0	0	0	0.246231	0	0
pseudogen	ubiquitin_/	4	0	0	0	0	0	0.554356	0	0	0	0	0
pseudogen	ribosomal_	4	0	1	0	2	0	0.155025	0	0.051071	0	0.08708	0
pseudogen	ribosomal_	0	1	2	0	2	0	0	0.164611	0.368144	0	0.313857	0
antisense	GK_antisen	5	1	2	5	1	1	0.406613	0.095834	0.214327	0.351758	0.091361	0.08082
protein_co	eukaryotic_	8	3	3	9	1	10	0.61292	0.270858	0.30288	0.596513	0.086072	0.761419
IG_V_gene	immunoglo	0	0	0	0	1	0	0	0	0	0	0.133654	0
pseudogen	ATP-bindin	0	0	0	0	1	0	0	0	0	0	0.014577	0
antisense	ARHGEF26_	0	0	0	0	0	1	0	0	0	0	0	0.020252
pseudogen	-	1	1	0	2	0	2	0.110294	0.129974	0	0.190829	0	0.219225
processed_	-	4	2	1	6	2	3	0.601602	0.354476	0.198191	0.780663	0.337931	0.448415
lincRNA	long_interg	4	2	1	0	0	0	0.078635	0.046333	0.025905	0	0	0
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.226297
pseudogen	-	0	1	0	0	3	1	0	0.154425	0	0	0.441653	0.130233
pseudogen	ribosomal_	2	0	0	0	0	0	0.090964	0	0	0	0	0
pseudogen	ribosomal_	1	0	0	0	0	0	0.072921	0	0	0	0	0
processed_	-	12	15	16	23	27	16	0.399806	0.588934	0.702462	0.662917	1.010604	0.529783
pseudogen	-	0	0	0	0	2	2	0	0	0	0	0.13548	0.11985

pseudogen	-	0	0	0	0	4	0	0	0	0	0	0.685601	0
protein_co	pregnancy_	0	0	0	6	2	0	0	0	0	0.1415	0.061252	0
protein_co	pregnancy_	0	0	0	163	127	85	0	0	0	3.254238	3.292695	1.949518
pseudogen	-	0	0	0	1	0	0	0	0	0	0.095614	0	0
lincRNA	-	0	2	0	0	1	0	0	0.183224	0	0	0.087336	0
protein_co	mitochond	539	505	347	952	743	1046	39.14293	43.21784	33.20694	59.80872	60.61812	75.49286
processed_	-	0	1	0	0	0	0	0	0.038041	0	0	0	0
antisense	-	0	2	2	1	3	3	0	0.242754	0.271452	0.089103	0.347136	0.307086
processed_	-	3	7	1	13	9	8	0.065521	0.180163	0.02878	0.245621	0.220826	0.173644
protein_co	microtubul	526	429	506	317	743	591	2.948329	2.833704	3.737451	1.537136	4.67873	3.292208
pseudogen	-	1	3	6	9	5	0	0.041983	0.148424	0.331943	0.326876	0.235828	0
processed_	-	10	5	3	7	15	10	0.933704	0.550156	0.369118	0.565419	1.573437	0.927937
lincRNA	-	1	0	0	0	0	0	0.064958	0	0	0	0	0
pseudogen	-	3	1	0	4	1	1	0.334364	0.131343	0	0.385675	0.125212	0.110766
antisense	CCDC39_ar	0	0	0	0	1	0	0	0	0	0	0.210162	0
pseudogen	-	82	62	52	77	56	116	4.989841	4.446022	4.169759	4.053466	3.828335	7.015207
antisense	-	0	0	0	1	0	3	0	0	0	0.066183	0	0.228096
processed_	-	13	3	8	8	3	6	0.625098	0.169994	0.506908	0.33278	0.16206	0.286725
pseudogen	-	0	1	0	20	18	7	0	0.134747	0	1.978354	2.312239	0.795461
antisense	-	1	6	5	14	2	8	0.098955	0.699675	0.651993	1.198476	0.22234	0.786752
protein_co	protocadhe	32	20	30	25	56	33	0.283771	0.209004	0.350569	0.191788	0.557898	0.290831
pseudogen	-	0	1	2	0	0	0	0	0.103634	0.231772	0	0	0
antisense	-	1	7	10	14	6	20	0.062875	0.518663	0.828543	0.761502	0.423819	1.24974
protein_co	stonin_1	179	132	108	66	66	43	1.633305	1.419369	1.298593	0.52098	0.676562	0.389935
pseudogen	ribosomal_	0	1	1	1	5	0	0	0.095248	0.106509	0.069922	0.454015	0
protein_co	piggyBac_t	0	0	0	0	1	0	0	0	0	0	0.017437	0
pseudogen	-	2	0	0	0	0	1	0.234252	0	0	0	0	0.116403
antisense	-	0	0	0	0	1	0	0	0	0	0	0.105267	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.066854
protein_co	PRA1_dom	383	328	308	171	115	137	15.17695	15.31675	16.08315	5.861986	5.119559	5.395303
pseudogen	-	0	0	0	4	3	1	0	0	0	0.58529	0.570057	0.168096
protein_co	V-set_and_i	10	0	3	0	0	0	0.291205	0	0.115121	0	0	0
pseudogen	ribosomal_	0	0	0	0	0	2	0	0	0	0	0	0.279862
pseudogen	-	266	255	205	255	281	237	12.24548	13.8338	12.43606	10.15541	14.53281	10.84307
pseudogen	-	7	8	0	4	12	1	0.465562	0.627012	0	0.230145	0.896622	0.066098
pseudogen	-	1	4	0	0	0	1	0.141553	0.667248	0	0	0	0.140679
protein_co	chromoson	858	793	680	1626	1123	1323	22.66635	24.68736	23.67217	37.16019	33.32907	34.73472
lincRNA	-	0	0	1	10	5	4	0	0	0.035467	0.232836	0.151184	0.106993
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.244757	0
pseudogen	protein_tyr	1	0	0	1	0	0	0.010448	0	0	0.009039	0	0
protein_co	potassium_	359	314	296	297	279	324	3.900229	4.020059	4.237622	2.791355	3.40525	3.498246
pseudogen	-	0	0	1	0	0	4	0	0	0.407972	0	0	1.230738
protein_co	ephrin-A4	191	151	102	194	179	228	8.00612	7.458866	5.634089	7.034828	8.429287	9.498023
antisense	MCCC1_ant	1	5	2	3	6	3	0.069204	0.407763	0.182388	0.179604	0.466478	0.20633

pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.203685	0
processed_	-	2	2	3	2	1	0	0.249134	0.293589	0.492447	0.215524	0.139943	0
pseudogen	-	1	0	0	0	0	0	0.131694	0	0	0	0	0
pseudogen	-	2	0	1	0	0	0	0.304259	0	0.200469	0	0	0
pseudogen	ribosomal_	6	2	11	7	4	9	0.983424	0.386302	2.375839	0.992546	0.736544	1.466026
protein_co	toll-like_re	1	0	2	7	0	0	0.015087	0	0.039762	0.091363	0	0
antisense	-	5	3	7	1	2	2	0.476946	0.337231	0.879897	0.082521	0.214328	0.1896
processed_	-	6	4	0	0	0	0	0.56824	0.446424	0	0	0	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.058943	0	0
pseudogen	-	11	12	13	20	20	23	1.24434	1.599685	1.937869	1.957218	2.541706	2.585733
pseudogen	-	2	0	0	0	2	3	0.390708	0	0	0	0.438937	0.582443
pseudogen	ribosomal_	21	24	10	9	6	6	1.247768	1.680478	0.782977	0.462615	0.400511	0.354303
antisense	-	7	8	1	2	1	3	0.725219	0.976716	0.136523	0.179252	0.116391	0.308889
protein_co	paralemmi	35	38	41	57	55	62	0.199412	0.255137	0.307823	0.280945	0.352042	0.351062
protein_co	chromoson	476	323	260	478	273	439	52.83001	42.24578	38.02611	45.89492	34.03968	48.42257
protein_co	neuroblast	516	442	435	464	374	466	5.803602	5.858376	6.447212	4.5147	4.725726	5.208869
processed_	-	0	2	3	0	1	1	0	0.382747	0.641993	0	0.182441	0.161393
protein_co	N-acetyltra	125	122	71	78	61	44	3.636057	4.182035	2.721535	1.96281	1.993424	1.271988
pseudogen	aldehyde_c	0	0	0	2	0	0	0	0	0	0.028813	0	0
lincRNA	-	2	0	0	0	0	0	0.150614	0	0	0	0	0
lincRNA	-	0	0	1	0	0	0	0	0	0.035831	0	0	0
pseudogen	ubiquitin_	3	3	0	0	0	1	0.752716	0.887029	0	0	0	0.249356
pseudogen	-	1	0	0	0	1	3	0.074251	0	0	0	0.083416	0.221377
pseudogen	ribosomal_	3	0	0	0	0	0	0.403104	0	0	0	0	0
pseudogen	-	0	0	0	3	0	0	0	0	0	0.226727	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.062636
IG_V_pseu	immunoglo	0	1	0	0	0	0	0	0.189054	0	0	0	0
processed_	-	2	3	4	0	5	5	0.31419	0.55538	0.828051	0	0.882432	0.780624
pseudogen	heterogene	2	1	0	0	1	0	0.076394	0.045013	0	0	0.042912	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.136713	0	0
pseudogen	-	81	94	64	115	78	140	9.593334	13.11957	9.988479	11.78272	10.37835	16.47867
processed_	-	0	1	2	0	0	0	0	0.107565	0.240563	0	0	0
protein_co	uroplakin_	3	2	1	48	33	34	0.098771	0.077597	0.043385	1.367132	1.220588	1.112486
pseudogen	-	0	0	0	6	0	0	0	0	0	0.345218	0	0
lincRNA	-	0	0	0	4	0	0	0	0	0	0.386489	0	0
polymorph	chromoson	6	4	13	7	8	4	0.128654	0.101074	0.367324	0.129847	0.192713	0.085239
pseudogen	ribosomal_	0	0	0	0	0	2	0	0	0	0	0	0.190286
pseudogen	-	0	2	0	0	0	0	0	0.25674	0	0	0	0
pseudogen	ribosomal_	0	0	0	0	0	1	0	0	0	0	0	0.163907
pseudogen	ribosomal_	5	3	1	0	2	5	0.31289	0.221233	0.082463	0	0.140605	0.310958
antisense	-	0	4	0	0	0	0	0	0.437809	0	0	0	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.622651
protein_co	-	0	0	1	0	2	1	0	0	0.066441	0	0.113287	0.050109
lincRNA	-	0	1	2	3	1	4	0	0.08629	0.192983	0.190037	0.082263	0.291087

lincRNA	-	0	0	0	0	2	1	0	0	0	0	0.058945	0.026072
pseudogen	-	0	0	1	0	0	0	0	0	0.123039	0	0	0
processed_	-	0	0	1	2	0	1	0	0	0.11198	0.147027	0	0.084453
protein_co	interleukin	204	223	175	166	98	138	5.424391	6.987676	6.131881	3.818492	2.927494	3.64678
pseudogen	-	0	0	1	0	0	0	0	0	0.140087	0	0	0
protein_co	complemer	0	0	3	0	0	0	0	0	0.054024	0	0	0
pseudogen	MT-ND5_ps	0	1	0	0	4	1	0	0.036634	0	0	0.139697	0.030895
pseudogen	-	5	0	2	0	0	3	0.93867	0	0.494775	0	0	0.559724
protein_co	zinc_finger_	37	50	39	39	37	37	0.713594	1.136389	0.991172	0.650695	0.801679	0.709188
pseudogen	-	1	2	2	0	0	0	0.067786	0.159764	0.178651	0	0	0
protein_co	WD_repeat	82	59	49	265	137	177	1.653146	1.401705	1.301752	4.621748	3.102894	3.546339
pseudogen	-	0	1	0	1	0	0	0	0.193151	0	0.141792	0	0
protein_co	NME1-NME	22	8	9	31	53	21	1.344921	0.57633	0.725023	1.639453	3.639981	1.27586
pseudogen	-	220	196	106	356	241	219	15.44697	16.2175	9.80757	21.62389	19.01021	15.2818
pseudogen	ribosomal_	0	4	0	0	0	0	0	0.848813	0	0	0	0
pseudogen	-	0	0	0	1	1	0	0	0	0	0.138365	0.179686	0
protein_co	musculoske	2	1	0	2	9	4	0.018773	0.011062	0	0.016241	0.094908	0.037315
pseudogen	-	5	3	2	5	3	0	0.332544	0.23513	0.175285	0.287682	0.224155	0
processed_	-	1	0	3	0	0	1	0.097139	0	0.384018	0	0	0.09654
processed_	-	200	168	163	1361	1266	1154	3.868542	3.829426	4.1547	22.77395	27.5106	22.18364
protein_co	phospholip	5	8	0	1	6	14	0.087217	0.164449	0	0.01509	0.11758	0.242701
protein_co	left-right_d	1	2	0	5	0	0	0.032559	0.076738	0	0.140833	0	0
protein_co	WD_repeat	0	5	4	14	3	6	0	0.073501	0.065752	0.15108	0.042042	0.074384
antisense	CACNA2D3	1	0	0	4	0	0	0.025477	0	0	0.08816	0	0
protein_co	Putative_N	158	135	126	595	278	327	1.46543	1.475533	1.539974	4.774062	2.89669	3.014155
pseudogen	-	1	0	1	3	0	0	0.112401	0	0.148117	0.291713	0	0
protein_co	tetratricop	10	5	6	16	1	10	0.221048	0.130246	0.174772	0.305963	0.024833	0.219683
processed_	-	0	2	1	3	0	0	0	0.268913	0.150352	0.296114	0	0
pseudogen	ribosomal_	85	55	59	0	3	3	1.276591	0.973426	1.167669	0	0.050618	0.044778
pseudogen	eukaryotic_	0	2	0	1	0	0	0	0.089767	0	0.032949	0	0
pseudogen	major_hist	54	35	27	10	10	10	0.623243	0.476035	0.410641	0.099845	0.129662	0.114703
processed_	-	0	0	3	17	4	10	0	0	0.111443	0.41458	0.126679	0.28016
pseudogen	suppressior	5	2	1	0	4	1	0.239119	0.112715	0.06302	0	0.214908	0.047529
antisense	HOXA_dista	11	14	15	2	0	0	0.129096	0.193622	0.231977	0.020305	0	0
pseudogen	-	0	2	0	0	2	0	0	0.261584	0	0	0.249375	0
processed_	-	1	0	0	3	2	1	0.144253	0	0	0.374378	0.324119	0.143363
protein_co	jumonji_dc	3	4	2	0	2	2	0.112163	0.176237	0.098536	0	0.084006	0.074314
pseudogen	-	0	0	0	0	2	3	0	0	0	0	0.566437	0.751629
lincRNA	-	1	8	3	0	2	0	0.021159	0.199481	0.083649	0	0.047543	0
pseudogen	-	0	0	0	2	0	0	0	0	0	0.253033	0	0
pseudogen	-	2	7	4	0	0	9	0.144253	0.594978	0.380181	0	0	0.645131
protein_co	apolipopro	11	14	15	22	12	24	0.232661	0.348953	0.418078	0.402547	0.285142	0.504489
pseudogen	-	7	4	2	9	5	1	0.744151	0.501106	0.280174	0.827691	0.597148	0.105651
pseudogen	-	5	0	1	0	0	0	0.453262	0	0.119458	0	0	0

processed_	WDR86_an	7	6	1	35	41	78	0.493458	0.498437	0.092894	2.134436	3.247021	5.464575
processed_	-	22	14	17	14	13	6	1.491296	1.118346	1.518535	0.820979	0.989996	0.404205
antisense	WDR52_an	2	1	0	0	0	0	0.154347	0.090944	0	0	0	0
protein_co	olfactory_r	1	4	4	6	8	13	0.047438	0.223612	0.250048	0.246231	0.426351	0.612888
pseudogen	BMS1_pseu	2	0	0	0	0	0	0.080335	0	0	0	0	0
processed_	-	1	2	0	0	0	0	0.026874	0.063338	0	0	0	0
pseudogen	-	3	0	0	0	0	0	0.179664	0	0	0	0	0
pseudogen	tubulin_alp	0	2	0	0	0	0	0	0.090417	0	0	0	0
pseudogen	protein-kin	0	0	0	0	2	0	0	0	0	0	0.052471	0
antisense	TIPARP_ant	0	0	3	3	2	3	0	0	0.284748	0.186934	0.161839	0.214751
protein_co	mitochond	550	459	435	757	547	660	7.401512	7.279097	7.714039	8.812855	8.269783	8.826963
protein_co	zinc_finger_	441	406	342	713	398	510	6.822612	7.401934	6.972251	9.542554	6.917421	7.841369
processed_	-	2	0	1	2	0	0	0.190093	0	0.125248	0.164448	0	0
lincRNA	-	5	3	2	0	0	2	0.508071	0.359238	0.267805	0	0	0.201973
protein_co	glutathione	0	1	0	3	4	7	0	0.061224	0	0.134835	0.233468	0.361431
processed_	-	6	8	4	7	8	7	0.439344	0.690321	0.385966	0.44342	0.658101	0.509403
processed_	-	0	1	0	0	0	0	0	0.06022	0	0	0	0
lincRNA	-	8	0	0	0	0	0	1.206632	0	0	0	0	0
pseudogen	peptidylpro	7	1	2	6	2	4	0.455827	0.076738	0.171619	0.337999	0.146312	0.258864
pseudogen	-	2	0	0	0	0	1	0.149762	0	0	0	0	0.074419
protein_co	retrotransp	20	6	2	3	0	3	0.195138	0.068988	0.025714	0.025322	0	0.02909
pseudogen	-	0	0	0	1	0	0	0	0	0	0.082077	0	0
pseudogen	enolase_1_	1	0	3	6	3	8	0.043252	0	0.170988	0.224504	0.145774	0.343883
protein_co	aminoacyla	4	3	8	8	3	19	0.11534	0.101941	0.303979	0.19956	0.097183	0.544481
protein_co	NFS1_nitro	288	337	253	394	341	368	5.062087	6.9803	5.85993	5.990959	6.733495	6.428277
pseudogen	-	0	0	1	1	0	9	0	0	0.086555	0.056822	0	0.587502
pseudogen	ribosomal_	0	0	1	0	0	0	0	0	0.187536	0	0	0
pseudogen	metallothio	0	0	0	0	2	0	0	0	0	0	0.464656	0
pseudogen	-	0	1	0	0	0	0	0	0.071057	0	0	0	0
pseudogen	family_with	208	178	187	338	233	270	4.540918	4.579388	5.379684	6.383518	5.714593	5.858059
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.063238
protein_co	dolichyl-di	6848	6054	4797	8131	4990	5924	174.3819	181.6716	160.969	179.1202	142.7536	149.9209
processed_	-	10	7	15	15	11	15	0.188805	0.155747	0.373199	0.245001	0.233322	0.281459
protein_co	transmemb	36	42	28	178	111	153	0.605424	0.832365	0.620512	2.589646	2.09715	2.557163
pseudogen	-	2	0	1	0	0	0	0.20802	0	0.137059	0	0	0
pseudogen	ribosomal_	0	0	0	0	0	2	0	0	0	0	0	0.198544
processed_	long_interg	3	1	7	4	3	1	0.457703	0.179792	1.407328	0.527941	0.514201	0.151626
processed_	-	3	7	4	5	1	5	0.247003	0.679182	0.433986	0.356135	0.092498	0.409129
pseudogen	ribosomal_	2	3	1	0	6	0	0.175592	0.310387	0.115694	0	0.5918	0
pseudogen	-	0	1	0	0	0	0	0	0.10398	0	0	0	0
lincRNA	-	0	0	2	5	0	0	0	0	0.3354	0.550468	0	0
pseudogen	-	0	3	2	0	0	1	0	0.222548	0.165906	0	0	0.062561
protein_co	glutathione	0	0	0	0	2	1	0	0	0	0	0.091291	0.040379
pseudogen	-	6	0	0	0	4	5	0.398552	0	0	0	0.298499	0.330076

pseudogen	ribosomal_	0	0	3	4	0	0	0	0	0.586246	0.513153	0	0
pseudogen	ribosomal_	0	0	0	3	6	0	0	0	0	0.182224	0.473283	0
pseudogen	-	3	0	2	2	0	1	0.270107	0	0.23729	0.155779	0	0.08948
pseudogen	phosducin-	4	1	0	9	6	8	0.294117	0.08665	0	0.572486	0.495633	0.584601
antisense	ATP1B3_an	19	24	7	11	28	37	2.67521	3.982195	1.298785	1.339862	4.429058	5.177446
lincRNA	-	0	0	0	1	0	0	0	0	0	0.042604	0	0
pseudogen	ribosomal_	2	0	2	0	0	1	0.164158	0	0.21632	0	0	0.081572
pseudogen	ribosomal_	1	2	1	0	0	3	0.139318	0.328356	0.183588	0	0	0.415374
processed_	-	0	7	0	0	0	2	0	0.513781	0	0	0	0.123798
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.304127
processed_	-	0	1	0	0	0	2	0	0.144083	0	0	0	0.243021
antisense	-	0	0	1	0	2	2	0	0	0.056718	0	0.096709	0.085551
pseudogen	cytochrom	0	0	0	2	0	0	0	0	0	0.190432	0	0
pseudogen	-	0	0	0	6	8	1	0	0	0	1.159466	2.007626	0.222
antisense	FLNB_antis	5	4	6	35	45	31	0.071368	0.067283	0.112855	0.432182	0.721601	0.439751
protein_co	purinergic_	130	120	58	112	117	183	3.542115	3.853076	2.082486	2.639978	3.581411	4.955415
pseudogen	-	4	1	2	0	0	0	0.567732	0.167259	0.374066	0	0	0
pseudogen	pre-B-cell_l	3	2	1	3	3	7	0.072821	0.05721	0.031987	0.062997	0.08181	0.168867
processed_	-	5	0	0	0	0	6	0.840333	0	0	0	0	1.002172
antisense	-	0	0	0	0	0	5	0	0	0	0	0	0.557352
protein_co	transmemb	410	293	211	415	373	477	25.87105	21.78737	17.54476	22.65381	26.44162	29.91287
antisense	-	11	4	8	15	16	13	0.680317	0.291531	0.651993	0.802551	1.111699	0.799045
processed_	FOXP1_ant	2	0	0	0	0	0	0.15126	0	0	0	0	0
pseudogen	-	0	2	0	1	1	0	0	0.170691	0	0.062652	0.081362	0
processed_	-	4	1	1	0	0	1	0.16116	0.047479	0.053092	0	0	0.040041
pseudogen	ribosomal_	2	4	1	0	11	4	0.230178	0.542502	0.151659	0	1.42225	0.457513
protein_co	interferon_	191	131	107	16	22	19	2.656089	2.14678	1.960775	0.192483	0.343701	0.262587
pseudogen	-	0	2	0	0	0	0	0	0.347564	0	0	0	0
pseudogen	-	1	0	2	0	0	0	0.077286	0	0.203688	0	0	0
pseudogen	polycystic_	5	14	0	0	0	12	0.038899	0.128351	0	0	0	0.09278
antisense	SIAH2_anti	1	2	2	0	10	6	0.120048	0.282938	0.316387	0	1.34866	0.715837
pseudogen	-	0	0	2	0	0	0	0	0	0.438763	0	0	0
antisense	-	2	2	4	4	5	1	0.327808	0.386302	0.863942	0.567169	0.92068	0.162892
protein_co	dysbindin_	3	10	3	15	19	21	0.103333	0.405906	0.136168	0.446964	0.735226	0.718865
pseudogen	endothelin	0	2	0	11	0	13	0	0.096352	0	0.389025	0	0.528172
pseudogen	-	0	0	3	1	0	0	0	0	0.2028	0.044379	0	0
antisense	ITGB5_anti	2	0	0	3	10	1	0.230178	0	0	0.298689	1.292955	0.114378
protein_co	chromoson	45	24	18	53	28	58	1.039417	0.653275	0.547879	1.05905	0.726582	1.33142
pseudogen	-	0	0	0	1	1	0	0	0	0	0.095216	0.123651	0
processed_	-	0	2	3	359	294	270	0	0.079072	0.13263	10.4194	11.08106	9.002404
lincRNA	-	16	19	17	0	0	2	0.198653	0.277994	0.278137	0	0	0.024678
pseudogen	-	35	43	42	71	41	74	3.720753	5.386892	5.88365	6.529563	4.896612	7.818152
processed_	-	0	0	1	1	1	0	0	0	0.091194	0.059868	0.077746	0
processed_	-	3	4	3	6	3	6	0.246237	0.386901	0.32448	0.426036	0.276632	0.489433

pseudogen	-	0	1	7	5	7	0	0	0.114895	0.899342	0.421721	0.766725	0
antisense	HLA_compl	0	8	0	15	6	20	0	1.574454	0	2.167141	1.125727	3.319498
processed_	-	0	0	1	0	5	0	0	0	0.084767	0	0.361336	0
pseudogen	-	16	9	6	7	9	6	1.041889	0.690639	0.514858	0.394333	0.658405	0.388296
pseudogen	profilin_1_	0	3	1	1	4	0	0	0.344684	0.128477	0.084344	0.438128	0
pseudogen	ribosomal_	5	1	0	0	0	2	0.128685	0.030329	0	0	0	0.051156
processed_	-	0	8	1	0	2	0	0	0.563957	0.078829	0	0.134409	0
processed_	-	0	0	1	0	1	1	0	0	0.071187	0	0.06069	0.053688
pseudogen	-	253	280	170	206	174	349	41.72608	54.4192	36.94629	29.3912	32.23928	57.20344
protein_co	ets_variant	1066	866	948	836	868	695	13.72783	13.14225	16.08747	9.313521	12.5578	8.894859
protein_co	keratin_ass	0	2	0	0	0	0	0	0.138948	0	0	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.327527	0	0	0
pseudogen	piggyBac_t	0	0	0	0	2	0	0	0	0	0	0.194366	0
processed_	-	22	23	19	19	19	30	1.842883	2.27044	2.097314	1.376866	1.788042	2.497502
pseudogen	-	1	0	0	0	0	0	0.156168	0	0	0	0	0
pseudogen	ribosomal_	0	0	2	1	1	0	0	0	0.486155	0.159578	0.207233	0
lincRNA	-	20	17	13	1	2	3	1.828704	1.831764	1.56636	0.0791	0.205444	0.272612
protein_co	RNA_bindi	849	701	695	2349	2011	1885	6.746758	6.564665	7.277917	16.14855	17.95348	14.88704
lincRNA	-	0	0	1	0	0	0	0	0	0.030266	0	0	0
antisense	-	0	0	0	4	4	4	0	0	0	0.332478	0.431767	0.381953
protein_co	endogenou	1	0	5	15	10	10	0.016554	0	0.109073	0.214817	0.185978	0.164522
antisense	-	34	14	17	38	57	39	1.419553	0.688824	0.935312	1.372522	2.673602	1.618255
pseudogen	-	13	7	18	1	5	0	0.494065	0.313506	0.901464	0.032878	0.213481	0
protein_co	leukocyte_i	10	7	5	5	20	6	0.236555	0.195136	0.155861	0.102321	0.53151	0.141056
protein_co	scavenger_	1762	1398	990	768	465	537	26.96012	25.20753	19.96117	10.16577	7.993151	8.165822
pseudogen	RWD_dom	8	2	1	2	3	0	0.749607	0.220842	0.123475	0.16212	0.315801	0
protein_co	apolipopro	826	701	461	545	518	642	33.40662	33.41008	24.56904	19.0683	23.53592	25.8046
pseudogen	-	0	0	1	2	0	0	0	0	0.462008	0.606608	0	0
antisense	-	17	21	11	16	16	16	0.935548	1.361894	0.797709	0.761728	0.989204	0.875078
pseudogen	keratin_18_	3	5	2	2	2	9	0.125057	0.245621	0.109863	0.072124	0.093663	0.372855
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.303251
lincRNA	-	0	0	0	1	3	0	0	0	0	0.087236	0.339862	0
pseudogen	-	0	4	3	0	4	13	0	0.152258	0.127694	0	0.145152	0.417317
pseudogen	-	23	18	18	1	2	4	0.434252	0.400492	0.447838	0.016333	0.042422	0.075056
lincRNA	-	0	0	1	0	0	0	0	0	0.123475	0	0	0
lincRNA	-	33	47	24	45	11	33	1.384352	2.323473	1.326719	1.633083	0.518411	1.375803
pseudogen	-	1	0	0	2	0	1	0.14788	0	0	0.25586	0	0.146967
processed_	-	8	6	5	5	3	2	0.119708	0.105802	0.098591	0.064724	0.050432	0.029742
pseudogen	ribosomal_	0	0	0	3	0	0	0	0	0	0.273699	0	0
antisense	WNT5A_an	243	146	252	20	41	30	25.72932	18.21722	35.16069	1.831956	4.877025	3.156843
protein_co	RAD21-like	0	0	0	1	0	3	0	0	0	0.025331	0	0.087302
pseudogen	-	0	0	1	1	0	0	0	0	0.201047	0.131985	0	0
protein_co	coiled-coil_	5	7	0	3	9	5	0.089944	0.148391	0	0.046686	0.181884	0.089388
protein_co	aspartic_pe	10	5	10	14	3	12	0.243743	0.143618	0.321194	0.295205	0.082149	0.290685

protein_co	olfactory_r	0	0	2	0	0	0	0	0	0.130277	0	0	0
processed_	-	32	25	18	47	40	32	1.684008	1.550391	1.24825	2.13971	2.364848	1.673608
pseudogen	-	140	117	79	196	150	185	7.609588	7.494214	5.658418	9.216207	9.159536	9.993428
pseudogen	-	0	1	0	0	0	0	0	0.185127	0	0	0	0
lincRNA	-	6	0	0	39	10	11	0.221202	0	0	1.243842	0.414178	0.403032
pseudogen	-	1	0	1	0	4	3	0.111221	0	0.146562	0	0.499798	0.331601
pseudogen	ribosomal_	0	0	0	2	2	0	0	0	0	0.117283	0.152307	0
processed_	-	2	7	0	0	1	1	0.035747	0.147439	0	0	0.02008	0.017763
processed_	-	4	4	2	0	1	0	0.50181	0.591353	0.330632	0	0.140938	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.04055
polymorph	Fc_fragmen	0	0	0	1	7	0	0	0	0	0.028063	0.255105	0
protein_co	ubiquitin-c	41	53	45	45	55	43	0.855907	1.303845	1.237913	0.812678	1.289896	0.892115
pseudogen	-	0	2	2	1	4	0	0	0.194052	0.216993	0.071227	0.36999	0
protein_co	CTAGE_fam	2	1	0	20	11	9	0.040913	0.024107	0	0.353933	0.252796	0.18297
protein_co	patched_d	385	300	280	212	174	210	6.306399	5.79094	6.043849	3.004136	3.201983	3.418611
processed_	-	1	2	4	0	10	2	0.040661	0.095834	0.214327	0	0.456804	0.08082
pseudogen	-	1	2	1	0	0	0	0.143472	0.338145	0.18906	0	0	0
processed_	-	1	5	0	3	11	14	0.068755	0.405115	0	0.178437	0.849656	0.956619
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.113392
pseudogen	-	68	68	47	73	32	79	5.882333	6.93197	5.357638	5.462941	3.109852	6.791683
pseudogen	-	3	0	0	3	3	1	0.182765	0	0	0.158109	0.205325	0.060546
pseudogen	argininosu	10	7	5	3	2	2	0.831099	0.685579	0.547592	0.215693	0.186738	0.165193
pseudogen	-	2	1	0	0	2	2	0.320855	0.189054	0	0	0.36046	0.318873
protein_co	complemer	16	18	13	4	4	9	0.155138	0.205674	0.166103	0.033552	0.043572	0.086726
lincRNA	-	3	1	5	3	0	0	0.168781	0.066299	0.370687	0.146011	0	0
pseudogen	-	0	0	2	8	0	0	0	0	0.44154	1.159466	0	0
protein_co	NEDD4_bin	1127	1161	1000	1178	830	981	11.22146	13.62275	13.1208	10.14691	9.284373	9.707426
pseudogen	-	1	1	0	0	0	0	0.183823	0.216624	0	0	0	0
antisense	-	4	4	2	0	2	0	0.290885	0.34279	0.191657	0	0.163395	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.037
processed_	GABPB1_ar	107	144	112	219	144	202	2.452245	3.889105	3.382462	4.341974	3.70759	4.600882
pseudogen	-	0	3	1	8	11	21	0	0.250553	0.093391	0.490484	0.875817	1.47911
antisense	-	7	0	8	0	5	1	0.194432	0	0.292815	0	0.156023	0.027604
pseudogen	-	27	29	33	33	33	36	2.76481	3.499505	4.452975	2.923334	3.796335	3.663648
antisense	-	8	3	13	21	23	20	0.215426	0.0952	0.461303	0.489205	0.695802	0.53524
lincRNA	-	1	4	3	4	2	6	0.072324	0.340917	0.285915	0.250267	0.162503	0.431263
lincRNA	-	0	5	0	0	0	0	0	0.152537	0	0	0	0
processed_	LIFR_antise	11	7	14	5	14	4	0.153129	0.114834	0.25682	0.060214	0.218949	0.05534
processed_	-	0	0	0	1	0	1	0	0	0	0.033188	0	0.038126
protein_co	Uncharacte	1	6	0	5	4	0	0.029009	0.20511	0	0.125476	0.130358	0
processed_	-	2	1	3	2	3	3	0.054438	0.032076	0.107604	0.047094	0.091737	0.081153
lincRNA	-	0	1	1	0	2	7	0	0.057342	0.064121	0	0.109331	0.33851
processed_	long_interg	186	157	152	212	175	180	5.262974	5.235101	5.667568	5.1894	5.562953	5.061747
antisense	-	5	6	5	4	0	0	0.190572	0.269493	0.251128	0.13189	0	0

processed_	-	0	0	6	0	1	0	0	0	0.159035	0	0.022597	0
processed_	A2M_antise	5	4	3	4	8	7	0.121036	0.114107	0.095697	0.083766	0.217562	0.168403
antisense	SMARCA5_	1	0	0	1	0	0	0.056022	0	0	0.048464	0	0
processed_	-	6	9	5	16	6	20	0.114715	0.202777	0.125972	0.264638	0.128875	0.380022
antisense	ARAP1_ant	9	14	3	0	1	10	0.261222	0.478853	0.114742	0	0.032607	0.288454
processed_	-	33	35	28	43	47	50	0.308994	0.386199	0.345485	0.348311	0.494405	0.465282
lincRNA	-	12	7	6	19	8	11	0.22754	0.156416	0.149921	0.311669	0.170418	0.20729
processed_	long_interg	0	0	0	2	0	0	0	0	0	0.017185	0	0
pseudogen	eukaryotic_	8	7	12	8	6	6	0.301443	0.310829	0.595843	0.260777	0.25399	0.224686
processed_	-	6	15	4	22	8	14	0.156015	0.459635	0.137059	0.49488	0.233697	0.361786
antisense	-	5	2	4	11	16	5	0.106478	0.050191	0.11225	0.20265	0.382789	0.105821
processed_	-	14	18	13	10	15	26	0.713353	1.080827	0.87288	0.440798	0.858651	1.316617
processed_	-	1	3	2	14	3	8	0.050324	0.177912	0.13263	0.609491	0.169608	0.400107
antisense	-	0	0	0	0	3	1	0	0	0	0	0.063497	0.018724
antisense	-	1	0	0	0	0	0	0.065847	0	0	0	0	0
protein_co	Uncharacte	11	26	16	12	9	10	0.400516	1.115599	0.767684	0.377983	0.368145	0.361857
antisense	-	2	0	1	0	3	3	0.137688	0	0.090719	0	0.232026	0.205256
processed_	-	0	1	0	0	1	1	0	0.029072	0	0	0.027715	0.024517
sense_over	-	0	0	2	1	2	0	0	0	0.107743	0.035366	0.091855	0
antisense	-	5	4	2	2	15	10	0.09172	0.086469	0.048346	0.031739	0.309126	0.182308
processed_	-	24	18	24	16	45	29	0.549798	0.485928	0.7245	0.317085	1.15812	0.660237
lincRNA	long_interg	0	0	0	3	0	0	0	0	0	0.038616	0	0
lincRNA	nuclear_pa	11929	13420	9866	894	2001	2131	27.76824	36.81323	30.26358	1.8003	5.232877	4.929892
antisense	-	0	10	3	1	3	2	0	0.717926	0.24084	0.052703	0.205325	0.121091
antisense	-	15	16	14	23	50	37	0.412313	0.518278	0.507106	0.546924	1.544027	1.010758
lincRNA	-	86	29	51	75	56	64	3.078381	1.223289	2.40563	2.32246	2.251962	2.276741
processed_	-	3	0	0	0	4	0	0.105882	0	0	0	0.158602	0
lincRNA	-	11	8	11	45	54	25	0.275996	0.236541	0.363695	0.976754	1.522132	0.623389
antisense	BDNF_antis	29	17	35	20	17	34	0.660623	0.456365	1.050652	0.394139	0.435065	0.769741
antisense	DACT3_ant	7	3	4	17	13	7	0.284192	0.14353	0.213998	0.597072	0.592935	0.282437
processed_	DDX11_ant	11	13	9	29	43	27	0.286731	0.399331	0.309143	0.653948	1.259214	0.699448
antisense	-	0	0	0	0	1	0	0	0	0	0	0.021016	0
lincRNA	-	11	11	8	0	0	0	0.166054	0.195684	0.159141	0	0	0
lincRNA	-	0	0	0	2	0	0	0	0	0	0.097756	0	0
antisense	-	6	2	5	1	5	8	0.567225	0.222813	0.622886	0.081784	0.531035	0.751629
protein_co	zinc_finger_	131	116	121	91	95	87	1.116791	1.165375	1.359317	0.671127	0.909857	0.737105
lincRNA	-	4	5	3	7	15	4	0.216306	0.31863	0.213779	0.327469	0.911276	0.214971
antisense	colorectal_	184	158	149	131	138	121	13.25326	13.41124	14.14249	8.162798	11.16691	8.661633
antisense	NADKD1_a	9	11	22	1	4	1	0.661762	0.953146	2.131656	0.06361	0.330422	0.073075
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.026492
antisense	-	9	0	6	3	11	5	0.110807	0	0.097344	0.031953	0.152148	0.061179
lincRNA	-	2	2	2	0	1	3	0.077969	0.091882	0.102744	0	0.043797	0.116231
processed_	-	61	44	50	2	0	0	1.212237	1.030428	1.309371	0.034384	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.042574	0

protein_co	CCAAT/enh	0	0	0	0	0	1	0	0	0	0	0	0.019998
processed_	-	110	88	62	107	64	98	5.059522	4.76987	3.757883	4.257587	3.307088	4.479737
processed_	-	0	0	4	4	8	9	0	0	0.251399	0.165041	0.428655	0.4266
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.06393
protein_co	HCG18159	1	4	0	3	0	0	0.020409	0.096203	0	0.052967	0	0
antisense	-	7	20	3	3	2	0	0.065027	0.218943	0.036724	0.024109	0.020872	0
processed_	small_nucl	896	796	581	853	754	1010	73.20236	76.63678	62.5501	60.28776	69.205	82.00647
antisense	-	2	0	2	0	0	0	0.062838	0	0.082805	0	0	0
processed_	-	185	136	143	242	176	175	3.289917	2.850094	3.351075	3.722988	3.516211	3.092865
processed_	-	0	0	0	0	0	2	0	0	0	0	0	0.066098
pseudogen	-	94	29	56	103	109	86	2.094467	0.761466	1.644252	1.98539	2.728483	1.904381
antisense	-	6	13	16	29	16	43	0.159701	0.407763	0.561193	0.667757	0.478439	1.137458
processed_	-	3	1	0	12	13	22	0.11377	0.04469	0	0.393687	0.553859	0.829161
lincRNA	-	18	25	48	61	72	58	1.108067	1.813597	3.893765	3.248527	4.979379	3.548389
pseudogen	-	3	9	1	10	0	1	0.071931	0.254298	0.031596	0.207423	0	0.023829
processed_	-	113	75	73	172	92	175	2.479209	1.939113	2.110534	3.264572	2.267627	3.815772
processed_	-	57	53	41	114	68	90	0.625417	0.685295	0.592807	1.082088	0.83821	0.981402
lincRNA	-	0	0	0	5	0	2	0	0	0	0.18131	0	0.083316
lincRNA	-	7	7	8	5	10	2	0.111555	0.131461	0.168003	0.068933	0.179036	0.031676
processed_	-	13	16	11	19	24	30	0.26109	0.378681	0.291121	0.330114	0.541511	0.598794
processed_	-	1	1	5	10	24	40	0.012126	0.014289	0.079894	0.104899	0.32694	0.482034
processed_	-	58	30	28	113	61	103	1.716365	1.046189	1.091879	2.892832	2.027966	3.029205
pseudogen	-	34	42	33	6	14	15	0.71856	1.046022	0.919037	0.109698	0.3324	0.315054
processed_	-	0	0	0	0	1	4	0	0	0	0	0.035529	0.125721
antisense	-	2	0	0	0	0	0	0.052184	0	0	0	0	0
antisense	-	3	3	1	16	7	9	0.111847	0.131805	0.049129	0.516044	0.293191	0.333469
antisense	-	15	10	5	0	13	7	0.36261	0.284875	0.159277	0	0.353053	0.168173
antisense	-	26	27	42	61	35	47	0.672102	0.822494	1.430692	1.364128	1.016434	1.207451
processed_	SBF2_antis	12	13	16	129	79	87	0.234512	0.299387	0.412039	2.1809	1.73444	1.689709
processed_	-	2	3	5	13	11	12	0.045346	0.080156	0.149386	0.254983	0.280186	0.270393
processed_	-	0	1	0	0	0	1	0	0.049791	0	0	0	0.04199
processed_	-	0	1	1	0	4	4	0	0.040198	0.044951	0	0.153288	0.135603
processed_	PRR7_antis	63	43	38	41	34	61	4.501056	3.620341	3.577604	2.534082	2.728989	4.331251
processed_	EXTL3_anti	14	18	8	15	12	20	0.200969	0.304495	0.15133	0.186275	0.193523	0.285326
processed_	-	1	0	0	0	0	0	0.018421	0	0	0	0	0
lincRNA	-	5	4	4	0	2	2	0.090005	0.084852	0.094884	0	0.040446	0.03578
protein_co	Uncharacte	13	5	8	5	4	1	0.185208	0.083945	0.15019	0.061624	0.064021	0.014159
processed_	-	0	0	3	0	0	0	0	0	0.126536	0	0	0
processed_	-	0	0	0	2	0	1	0	0	0	0.034204	0	0.019647
lincRNA	-	7	0	0	3	0	3	0.32197	0	0	0.119372	0	0.137135
antisense	-	0	2	0	0	5	0	0	0.050313	0	0	0.119911	0
lincRNA	-	3	3	4	0	0	0	0.067127	0.079105	0.117943	0	0	0
antisense	-	2	2	1	0	0	0	0.187071	0.220451	0.123257	0	0	0
antisense	-	151	113	103	101	129	201	5.693796	5.021235	5.117962	3.294651	5.464668	7.532353

lincRNA	-	8	8	3	45	33	40	0.170709	0.20117	0.084357	0.830694	0.791094	0.848272
antisense	-	15	10	11	15	12	12	0.135746	0.106646	0.131179	0.117433	0.122002	0.107926
processed_	-	5	1	1	1	6	16	0.216439	0.051012	0.057043	0.037448	0.291787	0.688328
processed_	-	1	0	0	1	4	6	0.029072	0	0	0.02515	0.130645	0.173358
processed_	-	0	0	1	0	0	0	0	0	0.084255	0	0	0
lincRNA	-	0	1	2	0	3	0	0	0.021336	0.047718	0	0.061022	0
antisense	-	15	12	8	41	16	18	0.899337	0.847851	0.632057	2.126563	1.077706	1.07254
pseudogen	-	18	21	14	19	11	24	1.353605	1.860998	1.387338	1.23605	0.929311	1.793661
processed_	-	15	14	17	29	29	34	0.403104	0.443365	0.602018	0.674197	0.875534	0.90806
pseudogen	-	32	23	31	3	12	1	1.986063	1.682201	2.53536	0.161075	0.836707	0.061681
antisense	CACNA1C_a	0	3	8	0	3	2	0	0.085424	0.254727	0	0.081437	0.048027
processed_	-	2	0	1	3	0	2	0.041801	0	0.027542	0.054243	0	0.041543
processed_	long_interg	5	7	8	16	5	5	0.138299	0.228168	0.291592	0.382854	0.155371	0.137445
antisense	-	194	190	170	150	130	95	3.935078	4.541635	4.543969	2.632121	2.962402	1.915071
protein_co	H2A_histor	1048	814	619	1194	1085	1584	15.13838	13.85637	11.78267	14.92057	17.60747	22.73961
antisense	-	15	10	0	6	3	8	0.317519	0.249451	0	0.109873	0.071343	0.168298
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.042108
antisense	-	13	15	20	2	6	4	0.338364	0.460086	0.685971	0.045033	0.175445	0.103469
lincRNA	-	3	1	0	0	0	0	0.081406	0.031977	0	0	0	0
lincRNA	-	10	5	5	21	10	23	0.182934	0.107788	0.120531	0.332335	0.205515	0.418149
processed_	-	9	2	10	6	0	4	0.137192	0.035927	0.200873	0.079123	0	0.060598
antisense	-	3	7	9	8	1	6	0.051499	0.141606	0.203589	0.118804	0.019285	0.102362
processed_	STARD4_an	233	149	236	42	53	46	2.232625	1.682493	2.979934	0.348155	0.570538	0.438054
processed_	-	0	0	0	2	0	0	0	0	0	0.019039	0	0
antisense	DNM1_pse	4	11	4	4	0	6	0.066425	0.215265	0.087532	0.057464	0	0.099023
antisense	-	10	12	13	29	28	40	0.203463	0.287722	0.348548	0.510441	0.640018	0.808825
lincRNA	-	11	6	8	30	27	20	0.271239	0.174349	0.259947	0.639947	0.747951	0.490117
protein_co	ubiquitin_a	91	105	79	72	72	92	0.653061	0.887991	0.747092	0.447	0.580489	0.65616
processed_	-	7	7	3	3	4	2	0.30129	0.355052	0.170154	0.111705	0.193418	0.085551
processed_	SOCS2_anti	21	26	12	47	27	59	0.334364	0.487844	0.251777	0.647383	0.482962	0.933603
lincRNA	-	0	0	0	2	0	0	0	0	0	0.044595	0	0
protein_co	phosphogly	223	154	169	1809	1221	1692	4.305559	3.503906	4.299779	30.21525	26.48435	32.46644
processed_	-	111	129	88	39	45	54	4.343274	5.948276	4.537449	1.320146	1.978135	2.099896
antisense	small_nucl	66	46	46	212	167	217	2.282237	1.874484	2.096088	6.341847	6.487576	7.45738
processed_	MIR210_hc	226	245	135	32	41	36	6.088888	7.778623	4.792897	0.745835	1.240973	0.963922
protein_co	Uncharacte	2	7	2	12	6	10	0.047163	0.194527	0.06215	0.244805	0.158956	0.234361
antisense	-	0	0	1	0	2	0	0	0	0.027488	0	0.046868	0
processed_	-	128	133	102	253	128	168	9.194637	11.25857	9.655163	15.72201	10.3296	11.99343
processed_	-	52	41	52	42	42	41	1.199535	1.114552	1.580693	0.83815	1.088448	0.939946
antisense	CSTF3_anti	2	3	2	0	2	5	0.052133	0.092153	0.068698	0	0.058568	0.129527
processed_	-	2	9	4	1	0	2	0.028827	0.152869	0.075974	0.012469	0	0.028649
processed_	-	3	0	4	4	1	10	0.078122	0	0.137262	0.090111	0.029255	0.2588
processed_	-	0	0	0	2	0	0	0	0	0	0.030696	0	0
antisense	-	98	92	56	252	144	197	2.314102	2.560067	1.742526	5.147781	3.820041	4.62309

antisense	-	10	15	7	59	58	64	0.328418	0.580531	0.302942	1.676263	2.139952	2.088895
processed_	-	40	42	25	80	92	91	1.977255	2.446578	1.628461	3.42102	5.109042	4.470475
processed_	-	0	4	0	13	10	15	0	0.055468	0	0.132337	0.132198	0.175419
antisense	-	2	1	0	0	0	0	0.144845	0.085346	0	0	0	0
processed_	-	2	0	0	8	2	1	0.059451	0	0	0.205722	0.066789	0.029542
antisense	-	0	1	2	1	0	1	0	0.022337	0.049956	0.016398	0	0.018838
antisense	-	1	5	1	1	1	3	0.072621	0.427899	0.095697	0.062824	0.081586	0.216519
lincRNA	-	2	0	0	1	1	3	0.061098	0	0	0.026428	0.03432	0.09108
antisense	-	0	0	1	0	0	1	0	0	0.132378	0	0	0.099837
lincRNA	-	23	26	22	21	23	34	0.624432	0.831836	0.787073	0.493219	0.701511	0.917373
processed_	DNAJC3_an	18	24	20	40	29	25	0.327695	0.514892	0.479802	0.629971	0.593123	0.452322
lincRNA	-	0	2	0	5	8	2	0	0.319119	0	0.585664	1.216899	0.269126
antisense	-	1	0	0	7	0	3	0.027374	0	0	0.165766	0	0.081614
antisense	CARS_antis	9	8	6	0	1	9	0.178855	0.187351	0.157125	0	0.022326	0.17775
antisense	-	3	10	7	7	17	14	0.090964	0.357318	0.279692	0.183615	0.57909	0.421877
processed_	OIP5_antis	2628	2424	2364	2931	2280	2774	15.75818	17.12854	18.6794	15.20405	15.35905	16.53091
processed_	-	33	29	25	65	72	98	0.709319	0.734569	0.708113	1.20866	1.738638	2.093454
processed_	SPTY2D1_a	21	26	15	29	13	25	0.764622	1.115599	0.719704	0.913458	0.531765	0.904643
protein_co	twinfilin_a	491	367	307	519	353	555	16.05561	14.14225	13.22874	14.68168	12.96788	18.03632
processed_	-	6	3	3	1	2	1	0.175884	0.103634	0.115886	0.025359	0.065865	0.029133
protein_co	methionyl-	97	73	85	413	388	356	1.69649	1.50456	1.958995	6.248744	7.623606	6.187843
pseudogen	MT-ND4_ps	1	3	3	4	2	13	0.038447	0.135921	0.15199	0.13304	0.086385	0.496719
processed_	LRP4_antis	1	4	3	5	5	8	0.0352	0.165925	0.139155	0.152257	0.197726	0.279862
antisense	-	55	43	54	20	39	44	1.66291	1.53208	2.151466	0.523117	1.324706	1.322112
processed_	-	16	4	4	10	5	13	1.169967	0.344684	0.385432	0.632582	0.410745	0.944727
antisense	-	2	3	0	0	0	2	0.109157	0.192952	0	0	0	0.108483
antisense	-	16	17	9	35	13	19	0.480735	0.601925	0.356339	0.90974	0.438812	0.567348
protein_co	ubiquitin_s	44	52	60	145	116	127	0.528569	0.736138	0.949806	1.506885	1.565511	1.516221
pseudogen	-	0	2	0	0	0	0	0	0.091612	0	0	0	0
lincRNA	-	9	9	6	1	11	6	0.220485	0.259829	0.193697	0.021193	0.302746	0.146083
processed_	PCED1B_an	0	0	0	6	0	2	0	0	0	0.110182	0	0.042193
processed_	-	0	2	0	0	2	0	0	0.047156	0	0	0.044955	0
processed_	-	28	14	24	36	10	27	0.472537	0.278428	0.533732	0.525585	0.189595	0.452846
antisense	NR2F2_ant	223	211	242	57	82	129	6.117016	6.820627	8.74752	1.35261	2.526956	3.51669
processed_	TMEM161E	80	57	69	63	74	63	3.846757	3.229882	4.372086	2.620646	3.997473	3.010613
processed_	colon_canc	0	0	0	0	3	1	0	0	0	0	0.08373	0.02469
antisense	-	14	7	11	19	12	18	0.337511	0.198868	0.349452	0.396256	0.325005	0.431263
pseudogen	signal_pept	0	0	0	1	0	0	0	0	0	0.069815	0	0
processed_	-	1	4	1	6	2	4	0.033742	0.159051	0.044464	0.175139	0.075814	0.134134
antisense	-	52	75	56	485	382	473	1.080005	1.835653	1.532657	8.71419	8.913221	9.763219
pseudogen	high_mobil	0	0	6	0	2	0	0	0	2.146563	0	0.610009	0
antisense	-	0	0	1	1	0	2	0	0	0.099096	0.065055	0	0.149472
antisense	-	2	6	2	9	3	6	0.143277	0.506531	0.188805	0.557767	0.241445	0.427178
processed_	SEC24B_an	43	28	13	21	21	19	1.588599	1.219021	0.632884	0.671163	0.871594	0.697604

lincRNA	-	4	1	0	0	0	6	0.203815	0.060046	0	0	0	0.303835
lincRNA	-	40	18	26	49	21	21	0.837012	0.443865	0.716935	0.887014	0.493674	0.436717
antisense	-	169	145	108	304	241	239	4.706485	4.758664	3.963406	7.32397	7.540082	6.614812
antisense	-	7	8	3	0	13	26	0.103777	0.139765	0.058608	0	0.216518	0.383076
antisense	FAM13A_ar	16	10	18	8	2	8	0.26388	0.194354	0.391196	0.114141	0.037057	0.131125
processed_	-	2	3	5	1	14	8	0.056773	0.100356	0.187033	0.024557	0.446468	0.22569
processed_	-	63	39	51	53	45	62	1.288251	0.939792	1.374248	0.93756	1.033764	1.259973
processed_	-	97	94	51	209	120	151	1.532004	1.749537	1.061434	2.8556	2.129209	2.370144
protein_co	Uncharacte	0	0	0	13	14	3	0	0	0	0.193621	0.270785	0.051331
lincRNA	ATPBD4_ar	4	0	1	1	8	6	0.143374	0	0.047233	0.031008	0.322144	0.213733
processed_	-	55	42	35	31	31	23	2.799764	2.519504	2.347803	1.36516	1.77284	1.16358
protein_co	branched_(	0	0	1	2	0	3	0	0	0.033173	0.043556	0	0.075056
protein_co	insulin-like	1	0	1	0	0	0	0.058889	0	0.077601	0	0	0
lincRNA	-	16	5	18	2	20	8	0.320976	0.118203	0.475839	0.034709	0.450746	0.159497
lincRNA	-	117	73	102	18	119	85	11.28251	8.295636	12.96148	1.501603	12.89187	8.146073
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.197594	0
lincRNA	-	0	3	1	7	3	1	0	0.251226	0.093642	0.430325	0.2395	0.070623
antisense	-	5	1	4	1	1	0	0.105167	0.024787	0.110867	0.018196	0.02363	0
pseudogen	-	0	1	0	0	0	0	0	0.240879	0	0	0	0
pseudogen	SMAD_spec	24	15	13	27	27	27	2.229094	1.641782	1.591092	2.169422	2.81728	2.492244
pseudogen	RNA_polym	178	182	132	169	151	160	3.613304	4.353745	3.530964	2.967797	3.443583	3.227856
lincRNA	-	10	1	8	0	0	0	0.809495	0.095394	0.853373	0	0	0
pseudogen	-	0	0	0	3	0	6	0	0	0	1.13551	0	2.608961
lincRNA	-	0	0	0	1	0	2	0	0	0	0.066279	0	0.152284
polymorph	alcohol_de	3	0	1	0	0	0	0.091278	0	0.040094	0	0	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.056109	0
antisense	-	0	0	1	0	2	0	0	0	0.059323	0	0.10115	0
pseudogen	-	0	0	1	0	3	0	0	0	0.251853	0	0.644144	0
pseudogen	heat_shock	0	0	1	0	6	0	0	0	0.036756	0	0.188017	0
processed_	-	10	5	2	21	10	11	0.786642	0.463505	0.20732	1.429089	0.883743	0.859962
processed_	-	2	11	8	0	2	0	0.07973	0.516766	0.420261	0	0.089572	0
lincRNA	-	57	61	55	59	41	70	1.352594	1.705805	1.719848	1.211177	1.093013	1.650822
pseudogen	glyceraldeh	4	0	1	1	1	1	0.212828	0	0.070114	0.046029	0.059775	0.052878
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.198253	0
lincRNA	-	7	4	2	30	19	24	0.228335	0.153759	0.085968	0.84656	0.696268	0.778027
antisense	ATG10_ant	0	4	0	0	0	0	0	0.385109	0	0	0	0
pseudogen	-	0	1	1	1	0	0	0	0.07002	0.078298	0.051402	0	0
pseudogen	-	0	0	2	0	0	2	0	0	0.244355	0	0	0.184287
processed_	-	12	5	10	1	0	1	0.43543	0.213803	0.478158	0.031391	0	0.036062
lincRNA	-	3	3	3	0	0	0	0.225281	0.26548	0.296865	0	0	0
sense_intro	-	0	0	1	0	0	0	0	0	0.11216	0	0	0
antisense	TRPC7_anti	0	0	0	5	1	0	0	0	0	0.497814	0.129295	0
pseudogen	capicua_tra	61	75	52	27	44	51	1.148027	1.663377	1.289616	0.439591	0.930302	0.953899
lincRNA	-	0	3	4	6	0	3	0	0.237517	0.354128	0.348723	0	0.200307

pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.050834	0
sense_intrc	STX18_intr	0	4	2	0	0	0	0	0.460426	0.257429	0	0	0
antisense	-	0	1	0	0	7	3	0	0.041899	0	0	0.279605	0.106005
lincRNA	-	0	0	2	0	0	0	0	0	0.279053	0	0	0
sense_intrc	SLIT2_intrc	0	1	5	0	1	2	0	0.103807	0.580393	0	0.098962	0.175088
pseudogen	keratin_8_p	0	2	1	0	1	0	0	0.085815	0.04798	0	0.040905	0
pseudogen	-	1	0	0	0	0	0	0.196807	0	0	0	0	0
antisense	-	1	5	2	0	0	2	0.1034	0.609255	0.272513	0	0	0.205524
processed_	-	0	0	0	0	0	3	0	0	0	0	0	0.274508
lincRNA	-	0	0	0	0	2	2	0	0	0	0	0.166833	0.147585
antisense	-	4	8	8	6	0	1	0.352353	0.830452	0.928629	0.457227	0	0.087544
antisense	OCIAD1_an	7	10	5	13	9	8	1.398441	2.354254	1.316288	2.246739	2.019937	1.588349
lincRNA	-	0	2	1	2	3	0	0	0.031653	0.017697	0.023236	0.045263	0
sense_intrc	-	0	2	0	0	0	0	0	0.436278	0	0	0	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.105267	0
antisense	-	133	104	54	223	105	144	8.725096	8.040054	4.668175	12.65571	7.738502	9.388381
pseudogen	-	14	19	3	26	15	12	1.004301	1.606188	0.283591	1.613512	1.20886	0.855513
pseudogen	-	8	8	1	12	20	18	1.189685	1.401971	0.195964	1.543783	3.341344	2.660261
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.054297
processed_	-	0	0	0	0	2	0	0	0	0	0	0.543159	0
pseudogen	-	0	0	0	0	1	2	0	0	0	0	0.0807	0.142779
pseudogen	tenascin_X	0	1	0	0	0	0	0	0.030612	0	0	0	0
lincRNA	-	0	0	0	3	0	0	0	0	0	0.172392	0	0
lincRNA	-	3	2	0	0	0	0	0.24174	0.189917	0	0	0	0
processed_	-	2	9	11	14	12	13	0.060366	0.320119	0.437512	0.365556	0.406905	0.389956
antisense	-	8	10	11	0	12	0	0.214662	0.316207	0.388949	0	0.361739	0
processed_	-	9	4	5	23	18	13	0.178319	0.093395	0.130545	0.394227	0.400661	0.255982
processed_	-	38	16	14	0	0	0	0.773158	0.383629	0.37536	0	0	0
protein_co	cyclin-depe	460	331	294	1150	698	862	10.21512	8.662055	8.603358	22.09259	17.41367	19.02404
pseudogen	WAS_prote	76	45	40	21	18	36	1.358378	0.947822	0.94211	0.324705	0.361434	0.639469
antisense	-	0	0	0	0	1	5	0	0	0	0	0.14795	0.654404
pseudogen	-	0	0	0	4	0	0	0	0	0	0.246562	0	0
lincRNA	-	1	7	7	0	1	1	0.102203	0.843077	0.942747	0	0.114818	0.101572
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.249356
antisense	-	4	1	1	0	1	0	0.284247	0.083742	0.093642	0	0.079833	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.066348
antisense	-	1	3	2	10	11	8	0.13471	0.476242	0.355029	1.165367	1.66472	1.071024
lincRNA	-	12	18	9	0	0	0	1.069515	1.890537	1.057019	0	0	0
pseudogen	-	1	0	0	0	0	0	0.077399	0	0	0	0	0
pseudogen	-	9	1	1	19	13	20	0.634446	0.083073	0.092894	1.158694	1.029543	1.401173
protein_co	protocadhe	38	16	18	51	94	81	0.379649	0.188376	0.236977	0.44079	1.055055	0.804253
antisense	-	0	3	0	0	0	0	0	0.563745	0	0	0	0
pseudogen	FOS-like_an	0	0	0	3	0	0	0	0	0	0.168378	0	0
lincRNA	long_interg	1	0	0	0	0	0	0.116354	0	0	0	0	0

pseudogen	-	0	0	0	0	1	1	0	0	0	0	0.057856	0.051181
protein_co	PRR5-ARHG	0	0	0	0	0	3	0	0	0	0	0	0.07726
pseudogen	-	0	0	0	26	37	47	0	0	0	1.893119	3.498583	3.931416
pseudogen	glyceraldeh	5	1	4	7	4	6	0.263388	0.062077	0.277665	0.318997	0.23672	0.314114
antisense	-	8	15	3	0	2	2	0.744337	1.644668	0.36782	0	0.209054	0.184935
pseudogen	-	1	4	0	0	4	1	0.081573	0.384516	0	0	0.36657	0.081069
processed_	-	45	44	70	59	43	43	0.816711	0.941056	1.674127	0.926341	0.876745	0.775593
lincRNA	-	0	0	0	5	2	4	0	0	0	0.763315	0.396506	0.701521
lincRNA	-	0	0	0	7	4	3	0	0	0	0.231642	0.171896	0.114048
antisense	-	5	7	3	13	69	27	0.307082	0.506629	0.242796	0.690703	4.760833	1.648004
pseudogen	protocadhe	22	9	15	16	6	16	0.492058	0.237216	0.442099	0.309583	0.150763	0.355651
pseudogen	-	0	0	1	0	0	0	0	0	0.042358	0	0	0
pseudogen	-	0	0	0	36	12	11	0	0	0	2.8476	1.232661	0.999576
protein_co	Uncharacte	2	1	8	0	2	0	0.091593	0.053969	0.482791	0	0.1029	0
pseudogen	-	0	0	1	0	0	0	0	0	0.171831	0	0	0
processed_	-	0	1	0	0	0	0	0	0.024247	0	0	0	0
antisense	-	3	0	4	1	0	1	0.276214	0	0.48531	0.07965	0	0.091503
pseudogen	DEAD/H_(A	0	0	1	2	2	0	0	0	0.042204	0.055413	0.071961	0
sense_intrc	BACH1_int	17	21	12	18	23	14	1.09622	1.595788	1.019683	1.004117	1.666195	0.897195
pseudogen	-	2	8	3	2	3	13	0.098678	0.465146	0.195051	0.085366	0.166289	0.637449
lincRNA	-	27	25	24	0	0	0	3.712745	4.051151	4.34888	0	0	0
protein_co	POU_doma	1	0	3	0	1	0	0.039686	0	0.156889	0	0.044585	0
protein_co	Purkinje_ce	0	0	0	11	4	3	0	0	0	0.353784	0.167067	0.110844
protein_co	abhydrolas	113	98	57	62	35	58	5.622493	5.746238	3.737319	2.668733	1.956445	2.868059
processed_	-	3	5	2	2	4	13	0.332266	0.652591	0.291897	0.191627	0.497706	1.430926
lincRNA	-	1	0	1	2	1	0	0.082079	0	0.10816	0.142012	0.092211	0
sense_intrc	LNX1_antis	5	0	0	6	1	0	0.421505	0	0	0.437569	0.094707	0
pseudogen	-	6	1	3	0	6	3	0.134425	0.026402	0.08857	0	0.151018	0.066797
processed_	-	68	46	42	81	44	45	1.553728	1.2386	1.264591	1.601084	1.129452	1.021853
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.059595	0
pseudogen	SET_bindin	0	0	0	0	10	0	0	0	0	0	0.105622	0
pseudogen	mitochond	1820	1723	1542	4586	2475	3471	141.4869	157.8474	157.9662	308.4196	216.157	268.1694
pseudogen	-	0	1	0	4	0	0	0	0.085113	0	0.249926	0	0
antisense	-	4	0	1	0	1	0	0.541596	0	0.178423	0	0.152112	0
lincRNA	-	0	2	1	35	11	14	0	0.178506	0.099804	2.293221	0.935959	1.053786
protein_co	HCG20047	4	6	2	32	27	35	0.072423	0.128019	0.047718	0.501219	0.549196	0.629785
antisense	-	4	2	1	8	13	16	0.109609	0.064584	0.036109	0.189644	0.4002	0.435727
pseudogen	MT-ND4_ps	0	0	0	0	1	0	0	0	0	0	0.043668	0
antisense	-	1	7	1	7	1	11	0.092554	0.763486	0.121964	0.560476	0.103979	1.011809
processed_	-	0	0	0	0	0	2	0	0	0	0	0	0.187572
pseudogen	-	4	2	3	5	11	1	0.401068	0.236317	0.396382	0.433702	1.239082	0.099648
antisense	-	6	7	1	27	19	31	0.610858	0.839835	0.13416	2.37802	2.173159	3.136607
pseudogen	-	0	2	2	1	6	2	0	0.256212	0.286502	0.094043	0.732763	0.216074
pseudogen	trans-23-en	0	0	0	0	1	0	0	0	0	0	0.06409	0

pseudogen	-	0	4	1	0	0	0	0	0.20455	0.057183	0	0	0
pseudogen	-	0	0	0	2	1	2	0	0	0	0.097861	0.063543	0.112423
antisense	EGFLAM_ar	6	0	2	0	0	0	0.589325	0	0.258862	0	0	0
antisense	-	4	0	2	0	9	0	0.525469	0	0.34622	0	1.328246	0
pseudogen	-	2	2	6	0	1	0	0.158033	0.186232	0.624746	0	0.08877	0
pseudogen	-	2	2	2	0	0	0	0.133858	0.157744	0.176393	0	0	0
pseudogen	-	0	0	3	0	1	0	0	0	0.102997	0	0.02927	0
lincRNA	GDNF_anti	12	15	8	32	65	64	0.218089	0.321255	0.191592	0.503112	1.327132	1.155956
protein_co	TMEM110-I	2	6	1	1	5	10	0.020053	0.070895	0.013213	0.008674	0.056322	0.099648
pseudogen	destrin_(ac	53	55	49	53	38	42	2.539251	3.105272	3.093575	2.19669	2.045326	1.99981
processed_	-	9	12	10	2	2	5	0.131186	0.206127	0.19208	0.02522	0.032751	0.072431
lincRNA	-	0	0	0	2	1	0	0	0	0	0.047021	0.030532	0
processed_	-	49	64	41	36	20	41	0.994674	1.530987	1.096739	0.632193	0.456104	0.827138
lincRNA	-	0	0	0	34	19	15	0	0	0	2.440694	1.771226	1.237007
pseudogen	-	0	0	2	0	0	0	0	0	0.083101	0	0	0
pseudogen	heat_shock	0	5	0	4	0	0	0	0.162468	0	0.095414	0	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.084006	0
sense_intrc	-	0	0	0	1	0	0	0	0	0	0.099132	0	0
pseudogen	-	1	0	1	0	0	0	0.070588	0	0.093018	0	0	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.065898	0	0
pseudogen	high_mobil	6	4	12	4	10	3	0.980389	0.770219	2.583825	0.565419	1.835676	0.487167
pseudogen	-	0	2	4	5	1	5	0	0.505164	1.12977	0.927103	0.240793	1.065062
lincRNA	-	0	0	0	0	4	0	0	0	0	0	0.390006	0
pseudogen	-	0	0	0	1	0	2	0	0	0	0.096622	0	0.222
lincRNA	-	0	0	1	3	22	10	0	0	0.113069	0.222685	2.120697	0.85274
antisense	-	4	1	9	8	1	5	0.223852	0.065949	0.66371	0.387306	0.062871	0.278087
processed_	-	1	2	2	2	0	0	0.069751	0.164395	0.183829	0.120682	0	0
processed_	OXCT1_ant	0	4	1	0	2	2	0	0.500102	0.139806	0	0.23838	0.210878
processed_	-	3	2	3	1	5	2	0.073359	0.057633	0.09667	0.021154	0.137358	0.048604
lincRNA	-	0	0	0	3	6	9	0	0	0	0.241896	0.628267	0.833673
processed_	-	6	10	2	0	3	3	0.094425	0.185457	0.041476	0	0.05304	0.046921
lincRNA	-	0	1	0	0	0	0	0	0.114263	0	0	0	0
antisense	HAS2_antis	10	14	8	6	9	6	0.319692	0.527432	0.337021	0.165938	0.323239	0.190631
processed_	-	0	0	3	0	0	0	0	0	0.345363	0	0	0
antisense	-	1	1	1	0	0	0	0.119236	0.140513	0.157125	0	0	0
pseudogen	-	3	0	2	0	0	4	0.429251	0	0.377099	0	0	0.568801
processed_	-	5	9	8	0	0	0	0.13342	0.283009	0.281304	0	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.100466	0
pseudogen	-	2	0	2	0	0	0	0.071542	0	0.094275	0	0	0
protein_co	coiled-coil_	6	9	1	16	7	17	0.186741	0.330094	0.041013	0.430795	0.244757	0.525831
protein_co	Protein_LO	0	0	0	0	1	0	0	0	0	0	0.005897	0
lincRNA	-	11	1	6	2	3	2	0.96897	0.103807	0.696472	0.152409	0.296885	0.175088
antisense	-	0	1	0	0	0	0	0	0.110226	0	0	0	0
processed_	-	3	0	0	0	0	1	0.34303	0	0	0	0	0.113637

pseudogen	adenylate_	1	0	0	0	0	0	0.090808	0	0	0	0	0
processed_	NPHP3_ant	3	0	0	0	1	0	0.05344	0	0	0	0.020012	0
protein_co	Uncharacte	0	1	0	0	0	0	0	0.095103	0	0	0	0
pseudogen	-	0	1	0	0	0	0	0	0.107565	0	0	0	0
pseudogen	-	2	2	6	0	0	0	0.040031	0.047174	0.158253	0	0	0
antisense	-	7	1	3	20	14	21	0.373199	0.062828	0.210765	0.922435	0.838533	1.112684
pseudogen	R3H_doma	0	0	0	0	4	0	0	0	0	0	0.121379	0
lincRNA	-	0	0	1	8	5	10	0	0	0.132378	0.69524	0.564288	0.998369
polymorph	actinin_alp	15	8	14	2	11	0	0.257495	0.161836	0.316695	0.029701	0.212138	0
pseudogen	MT-ND5_ps	0	0	0	4	0	0	0	0	0	0.104385	0	0
lincRNA	-	1	0	0	0	0	0	0.075415	0	0	0	0	0
lincRNA	-	2	0	2	0	0	0	0.193569	0	0.255076	0	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.111797	0
antisense	-	0	2	0	6	0	0	0	0.646505	0	1.4238	0	0
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.111826
lincRNA	-	0	1	0	0	0	0	0	0.117713	0	0	0	0
pseudogen	-	0	1	0	0	0	0	0	0.30139	0	0	0	0
sense_intrc	-	11	1	0	5	3	1	1.481809	0.158747	0	0.582683	0.454015	0.133878
antisense	-	1	0	3	13	9	15	0.101614	0	0.401708	1.142775	1.027415	1.5148
lincRNA	-	3	0	1	0	0	0	0.268736	0	0.118043	0	0	0
pseudogen	-	0	0	0	9	3	2	0	0	0	0.685841	0.296885	0.175088
pseudogen	HIG1_hypo	1	0	2	2	2	2	0.187734	0	0.494775	0.324815	0.421815	0.373149
lincRNA	-	18	6	9	3	7	7	2.231705	0.876643	1.47042	0.321772	0.975015	0.862525
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.08132
pseudogen	-	1	0	3	8	7	0	0.196078	0	0.775148	1.357005	1.541968	0
pseudogen	-	0	2	0	0	2	2	0	0.100788	0	0	0.096084	0.084998
protein_co	HCG17875	0	0	0	4	2	8	0	0	0	0.114497	0.074345	0.26307
lincRNA	-	12	0	8	0	0	3	0.223773	0	0.196586	0	0	0.055598
antisense	-	0	0	1	0	2	1	0	0	0.134678	0	0.229637	0.101572
pseudogen	zinc_finger_	0	0	0	0	1	0	0	0	0	0	0.034842	0
pseudogen	-	0	0	1	0	0	0	0	0	0.080558	0	0	0
processed_	-	21	3	2	96	67	83	0.2987	0.050286	0.037487	1.181272	1.07063	1.173285
protein_co	CDNA:_FLJ2	64	46	27	126	76	84	1.271378	1.076861	0.706795	2.165352	1.696124	1.658379
pseudogen	-	4	8	5	0	6	3	0.653593	1.540438	1.076594	0	1.101406	0.487167
pseudogen	-	2	4	2	0	0	0	0.13471	0.317495	0.177515	0	0	0
processed_	-	7	9	11	2	3	0	0.086545	0.131128	0.179214	0.021391	0.041669	0
pseudogen	-	4	0	5	7	5	3	0.212401	0	0.349866	0.321557	0.298274	0.158317
processed_	-	0	0	1	0	0	0	0	0	0.160008	0	0	0
antisense	USP46_ant	20	7	17	29	21	32	1.010324	0.416712	1.131656	1.267336	1.191788	1.606536
lincRNA	-	3	6	5	11	1	3	0.095218	0.224416	0.209123	0.302031	0.035657	0.09463
pseudogen	SERPINE1_r	0	2	1	0	1	1	0	0.133879	0.074853	0	0.063815	0.056453
processed_	HHIP_antis	41	50	46	40	38	10	1.984077	2.851359	2.933374	1.674549	2.065891	0.480933
processed_	-	0	0	2	20	27	23	0	0	0.169947	1.115686	1.955968	1.473962
antisense	-	2	5	4	0	0	1	0.178553	0.526035	0.470579	0	0	0.088725

lincRNA	-	0	3	0	0	0	0	0	0.287501	0	0	0	0
protein_co	formin_1	52	77	91	87	158	105	0.222819	0.388819	0.513837	0.322501	0.760599	0.447145
pseudogen	MT-ND2_ps	0	0	0	6	0	0	0	0	0	0.266531	0	0
pseudogen	high_mobil	5	7	0	8	9	2	0.455602	0.751659	0	0.630622	0.921314	0.181115
pseudogen	nucleopori	0	0	0	0	1	0	0	0	0	0	0.153288	0
protein_co	ATP5J2-PTC	0	4	2	0	1	1	0	0.100181	0.056012	0	0.023876	0.021122
pseudogen	MT-ND5_ps	4	9	3	4	22	40	0.116868	0.309873	0.115502	0.101101	0.722114	1.161458
antisense	-	3	8	4	12	0	6	0.304259	0.956134	0.534585	1.052848	0	0.604759
pseudogen	-	0	0	0	0	2	2	0	0	0	0	0.152307	0.134735
lincRNA	-	2	2	7	1	0	0	0.095047	0.112007	0.438369	0.041112	0	0
pseudogen	-	4	0	0	0	1	0	0.186576	0	0	0	0.052402	0
processed_	-	34	27	42	62	57	58	2.990023	2.798121	4.867206	4.716831	5.631441	5.069128
antisense	-	0	1	1	3	2	1	0	0.116831	0.130643	0.257297	0.222756	0.098528
lincRNA	-	0	0	0	1	0	0	0	0	0	0.08193	0	0
pseudogen	high_mobil	0	1	0	3	0	0	0	0.109069	0	0.240204	0	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.212794	0
lincRNA	-	0	3	3	3	5	3	0	0.100248	0.1121	0.073592	0.159282	0.084543
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.144148
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.218769
antisense	-	3	1	0	0	3	1	0.230847	0.09068	0	0	0.259343	0.076474
antisense	-	2	4	0	0	0	0	0.196078	0.462131	0	0	0	0
pseudogen	keratin_8_p	4	5	0	5	23	4	0.148502	0.218751	0	0.160585	0.959289	0.147585
lincRNA	-	0	0	0	4	0	0	0	0	0	0.254085	0	0
pseudogen	late_endos	0	0	0	2	2	0	0	0	0	0.394818	0.512723	0
pseudogen	-	1	0	0	1	0	0	0.073837	0	0	0.063876	0	0
lincRNA	-	0	1	0	0	0	0	0	0.127844	0	0	0	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.063787	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.133056	0
antisense	-	3	5	6	0	10	21	0.365952	0.718753	0.964469	0	1.370413	2.545841
antisense	-	0	0	0	0	1	2	0	0	0	0	0.072443	0.128171
processed_	-	0	0	0	0	5	0	0	0	0	0	0.301296	0
pseudogen	-	1	0	0	0	2	3	0.108932	0	0	0	0.244757	0.324778
pseudogen	high_mobil	0	0	0	1	1	1	0	0	0	0.120207	0.156105	0.138095
antisense	-	0	0	2	0	0	0	0	0	0.264756	0	0	0
pseudogen	-	0	0	1	2	0	1	0	0	0.243078	0.319156	0	0.183324
sense_intrc	-	2	2	2	0	1	4	0.772861	0.91077	1.018442	0	0.434131	1.536177
pseudogen	-	1	0	2	0	0	0	0.019407	0	0.051146	0	0	0
antisense	-	1	2	1	0	2	1	0.025355	0.059758	0.033412	0	0.056969	0.025198
protein_co	Uncharacte	7	5	7	18	21	16	0.128498	0.108162	0.169328	0.285846	0.433077	0.291895
processed_	-	52	52	39	0	22	16	1.395302	1.644279	1.379001	0	0.663188	0.426672
antisense	-	36	57	37	133	97	105	1.655843	3.089575	2.242608	5.292141	5.012306	4.799718
processed_	-	43	42	41	37	58	56	4.154129	4.781541	5.219516	3.092262	6.294896	5.376618
pseudogen	cytochrom	0	1	0	1	2	4	0	0.250553	0	0.183931	0.477718	0.845206
pseudogen	tubulin_fol	1	0	0	0	0	0	0.169683	0	0	0	0	0

sense_intrc	MAST4_intr	0	0	0	0	1	0	0	0	0	0	0.090389	0
pseudogen	keratin_18_	0	1	0	0	0	0	0	0.048817	0	0	0	0
pseudogen	-	1	3	0	0	0	2	0.093701	0.331262	0	0	0	0.186244
lincRNA	-	0	2	0	0	0	0	0	0.169763	0	0	0	0
pseudogen	-	8	0	1	0	0	0	0.687545	0	0.113252	0	0	0
antisense	-	1	4	0	2	5	4	0.070307	0.331409	0	0.121644	0.394926	0.27949
processed_	-	0	0	3	0	0	0	0	0	0.634212	0	0	0
protein_co	chromosor	44	57	36	39	44	83	0.914568	1.396192	0.986053	0.701279	1.02746	1.714553
pseudogen	-	0	0	0	0	2	2	0	0	0	0	0.23838	0.210878
lincRNA	-	2	0	0	0	0	0	0.145442	0	0	0	0	0
lincRNA	-	4	2	0	0	2	3	0.103806	0.061164	0	0	0.05831	0.077374
pseudogen	-	1	3	3	0	3	3	0.092554	0.327208	0.365891	0	0.311937	0.275948
lincRNA	-	1	0	0	0	0	0	0.088382	0	0	0	0	0
lincRNA	-	2	2	1	4	3	0	0.127262	0.149971	0.08385	0.220187	0.214456	0
protein_co	HAUS_augn	192	178	157	653	604	669	2.278053	2.488798	2.454692	6.702529	8.050976	7.88857
antisense	-	0	0	0	8	1	1	0	0	0	0.862097	0.139943	0.123798
pseudogen	MT-ND6_ps	1	2	0	0	4	1	0.10142	0.239033	0	0	0.455754	0.100793
antisense	-	0	1	0	0	0	0	0	0.111208	0	0	0	0
lincRNA	-	0	0	0	0	1	3	0	0	0	0	0.110345	0.292843
pseudogen	suppressor_	7	4	10	6	5	12	0.38363	0.258334	0.722187	0.284465	0.307846	0.653591
lincRNA	-	0	2	2	0	0	1	0	0.302853	0.338657	0	0	0.127704
pseudogen	-	3	0	0	0	0	0	0.211482	0	0	0	0	0
pseudogen	peroxiredo	1	2	3	5	0	1	0.090343	0.212927	0.35715	0.390776	0	0.089785
pseudogen	-	1	0	0	0	0	0	0.047781	0	0	0	0	0
pseudogen	-	0	0	0	1	1	0	0	0	0	0.097032	0.126008	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.215103	0
protein_co	protocadhe	150	112	183	71	108	98	1.510586	1.329166	2.428511	0.618551	1.221875	0.980821
lincRNA	-	0	0	0	2	2	2	0	0	0	0.190037	0.246788	0.218316
antisense	-	4	4	1	0	1	0	0.109157	0.128634	0.03596	0	0.030658	0
pseudogen	MT-ND4_ps	0	0	0	3	0	0	0	0	0	0.100143	0	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.105267	0
pseudogen	-	0	0	0	0	2	1	0	0	0	0	0.119071	0.052667
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.881125	0
pseudogen	heat_shock	1	0	0	1	0	0	0.03078	0	0	0.026627	0	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.160698	0	0
antisense	-	5	3	3	9	7	3	0.279815	0.197847	0.221237	0.435719	0.440097	0.166852
pseudogen	ATPase_Na-	1	4	6	0	0	2	0.057859	0.272733	0.457464	0	0	0.115003
pseudogen	-	0	0	0	0	2	4	0	0	0	0	0.90115	1.594365
antisense	-	0	0	0	0	0	3	0	0	0	0	0	0.362856
protein_co	ATP_synthe	3	0	0	0	2	1	0.198777	0	0	0	0.148876	0.06585
pseudogen	-	0	0	1	0	0	0	0	0	0.062568	0	0	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.143662	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.046447	0
lincRNA	-	1	0	0	0	0	0	0.05532	0	0	0	0	0

protein_co	transmemb	1	10	9	31	7	23	0.026604	0.313506	0.315512	0.71345	0.209212	0.608102
pseudogen	-	4	2	3	0	0	2	0.060418	0.035599	0.059712	0	0	0.030022
pseudogen	-	0	0	1	0	0	0	0	0	0.037167	0	0	0
antisense	-	4	2	5	3	2	4	0.276816	0.163105	0.455969	0.179604	0.155493	0.275106
antisense	-	2	15	10	2	6	0	0.168067	1.485422	1.107354	0.145393	0.566437	0
pseudogen	phosphogly	0	0	0	0	4	0	0	0	0	0	0.315104	0
lincRNA	-	15	8	19	11	4	7	0.346472	0.217758	0.578317	0.219803	0.103797	0.160689
pseudogen	eukaryotic_	9	3	7	1	2	5	0.344518	0.135331	0.353104	0.033116	0.08601	0.190217
lincRNA	-	0	0	0	7	5	1	0	0	0	0.06448	0.059811	0.010582
lincRNA	-	0	0	0	2	0	0	0	0	0	0.209606	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.079367	0	0	0
pseudogen	-	0	0	0	0	3	0	0	0	0	0	0.177364	0
pseudogen	-	0	0	0	0	1	5	0	0	0	0	0.136413	0.603372
pseudogen	-	8	5	8	4	7	0	0.426084	0.313822	0.561475	0.184301	0.418844	0
antisense	-	0	0	2	0	1	0	0	0	0.250947	0	0.106971	0
processed_	-	0	0	0	0	0	2	0	0	0	0	0	0.322786
pseudogen	ferritin_hea	8	3	1	1	5	0	0.916727	0.405115	0.151003	0.099132	0.643679	0
antisense	-	4	7	6	4	13	4	0.48019	0.990281	0.94916	0.41541	1.753258	0.477225
processed_	-	0	0	0	13	7	5	0	0	0	0.705433	0.493284	0.311695
antisense	-	12	6	14	9	10	10	0.652921	0.384714	1.003788	0.423628	0.611263	0.54074
antisense	-	0	0	1	0	1	0	0	0	0.133903	0	0.114157	0
pseudogen	olfactory_r	0	0	0	30	14	24	0	0	0	1.480568	0.897266	1.360708
antisense	-	0	0	0	0	1	2	0	0	0	0	0.036377	0.06436
lincRNA	-	9	6	5	0	15	3	0.224115	0.176071	0.164072	0	0.419633	0.074244
sense_intro	-	0	0	2	0	0	2	0	0	0.086341	0	0	0.065116
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.164298	0
lincRNA	-	0	5	0	0	0	0	0	0.098997	0	0	0	0
antisense	UGDH_anti	41	18	26	29	32	25	0.778823	0.402935	0.650824	0.476558	0.682895	0.47196
pseudogen	nucleophos	228	204	172	418	250	402	14.54283	15.33385	14.45697	23.06499	17.91443	25.48295
pseudogen	-	3	0	0	0	2	0	0.255754	0	0	0	0.191549	0
processed_	-	1	0	0	0	0	0	0.103806	0	0	0	0	0
lincRNA	-	0	0	1	0	0	0	0	0	0.012791	0	0	0
pseudogen	-	13	2	8	0	1	1	0.785654	0.142438	0.637108	0	0.067895	0.060062
processed_	-	5	9	12	0	0	3	0.170119	0.360854	0.53802	0	0	0.101441
lincRNA	-	0	0	0	1	0	0	0	0	0	0.10155	0	0
processed_	-	0	0	0	1	2	0	0	0	0	0.013874	0.036035	0
processed_	-	42	41	25	24	18	19	0.913151	1.050471	0.716255	0.451406	0.439658	0.410541
antisense	-	1	3	0	0	4	2	0.096784	0.342163	0	0	0.434924	0.192373
lincRNA	-	0	0	1	0	0	0	0	0	0.040489	0	0	0
processed_	-	2	0	0	0	0	0	0.11422	0	0	0	0	0
lincRNA	-	118	109	105	55	66	66	5.366871	5.84215	6.29308	2.164038	3.372346	2.983271
lincRNA	-	2	2	1	0	0	0	0.04971	0.05858	0.032753	0	0	0
lincRNA	-	11	2	1	2	3	0	0.694101	0.148719	0.083151	0.109175	0.212667	0
antisense	-	0	3	0	0	0	0	0	0.328934	0	0	0	0

processed_	-	1	0	0	0	0	0	0.070214	0	0	0	0	0
processed_	-	2	0	4	0	1	0	0.250905	0	0.661263	0	0.140938	0
pseudogen	-	1	0	0	0	0	0	0.122549	0	0	0	0	0
antisense	-	0	0	1	0	0	0	0	0	0.063134	0	0	0
antisense	-	2	1	0	20	25	24	0.13471	0.079374	0	1.165367	1.891728	1.606536
lincRNA	-	3	0	2	0	0	0	0.319563	0	0.280738	0	0	0
protein_co	Uncharacte	4	3	1	0	0	0	0.151476	0.133879	0.049902	0	0	0
lincRNA	-	121	93	81	128	213	206	9.086327	8.229871	8.015356	8.315262	17.96932	15.37375
protein_co	NLR_family	16	27	14	43	22	23	0.138317	0.27506	0.159485	0.32158	0.213663	0.197603
lincRNA	-	3	0	0	0	0	0	0.45508	0	0	0	0	0
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.238073
processed_	-	17	5	7	5	23	5	1.621616	0.562052	0.879897	0.412603	2.464768	0.474
protein_co	zinc_finger_	297	239	232	229	184	207	2.951103	2.798549	3.037741	1.968459	2.053973	2.044127
processed_	-	2	3	1	4	0	0	0.020122	0.035569	0.013258	0.034815	0	0
pseudogen	RNA_bindi	9	12	5	7	4	3	0.420167	0.660188	0.307598	0.282709	0.209792	0.139191
protein_co	zinc_finger_	123	88	90	144	103	157	1.727253	1.456265	1.665436	1.749348	1.624939	2.191089
lincRNA	-	26	25	12	9	19	11	0.251593	0.285084	0.153018	0.075341	0.206551	0.105786
protein_co	spermatoge	1	0	0	0	0	0	0.0391	0	0	0	0	0
lincRNA	-	0	0	3	0	0	0	0	0	0.095435	0	0	0
pseudogen	retinoblast	0	4	0	0	1	1	0	0.195573	0	0	0.046611	0.041234
lincRNA	-	1	0	2	0	2	0	0.028851	0	0.076036	0	0.064824	0
processed_	-	5	8	9	5	8	4	0.54918	1.035481	1.302634	0.475092	0.987152	0.436631
pseudogen	ankyrin_rep	3	0	4	13	15	14	0.322811	0	0.567181	1.210134	1.81329	1.497148
antisense	-	1	0	0	0	0	0	0.065198	0	0	0	0	0
lincRNA	-	7	8	4	0	2	0	0.17133	0.230745	0.129012	0	0.054994	0
antisense	-	3	2	3	0	7	1	0.211764	0.166367	0.279053	0	0.555109	0.070152
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.227766
pseudogen	-	1	0	0	0	0	0	0.092716	0	0	0	0	0
lincRNA	-	4	4	3	3	4	0	0.372824	0.43935	0.368468	0.241896	0.418844	0
antisense	-	1	0	2	1	1	1	0.08272	0	0.21801	0.071561	0.092931	0.082209
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.051106
pseudogen	-	0	2	0	0	0	0	0	0.113535	0	0	0	0
antisense	-	0	3	1	0	0	0	0	0.355148	0.132378	0	0	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.021934	0	0
pseudogen	-	0	0	0	2	0	1	0	0	0	0.341783	0	0.196321
pseudogen	SERPINE1_r	7	3	3	13	12	14	0.313791	0.158479	0.177214	0.504137	0.604328	0.623706
antisense	-	0	2	2	1	0	0	0	0.043935	0.049129	0.016126	0	0
antisense	-	10	8	5	5	12	17	0.985866	0.929426	0.649565	0.426433	1.329071	1.665622
pseudogen	-	4	0	0	0	0	0	0.71301	0	0	0	0	0
lincRNA	-	2	0	0	0	1	0	0.026022	0	0	0	0.014617	0
lincRNA	-	0	0	1	0	0	0	0	0	0.118847	0	0	0
processed_	-	107	103	57	44	86	99	9.166159	10.39795	6.434477	3.260763	8.276584	8.428464
antisense	-	3	8	5	0	3	11	0.14885	0.467762	0.326913	0	0.167224	0.542413
lincRNA	-	0	1	0	0	0	0	0	0.122089	0	0	0	0

processed_	-	2	0	0	5	3	12	0.277178	0	0	0.599462	0.467088	1.652797
antisense	-	0	5	1	0	0	0	0	0.099123	0.022168	0	0	0
sense_intrc	-	0	0	1	0	0	0	0	0	0.148749	0	0	0
antisense	-	4	7	11	3	9	5	0.38363	0.791149	1.39021	0.248907	0.969716	0.476577
antisense	-	0	0	1	0	0	0	0	0	0.162998	0	0	0
lincRNA	-	2	0	0	0	0	0	0.130397	0	0	0	0	0
pseudogen	high_mobil	0	2	0	0	0	0	0	0.90417	0	0	0	0
pseudogen	-	1	0	0	5	0	0	0.130397	0	0	0.564026	0	0
lincRNA	-	0	0	3	0	0	0	0	0	0.358988	0	0	0
antisense	-	7	3	1	0	0	2	0.827203	0.417775	0.155722	0	0	0.234884
protein_co	Uncharacte	2	2	5	0	0	2	0.077683	0.091545	0.255918	0	0	0.077203
pseudogen	-	1	1	2	20	10	34	0.035365	0.041675	0.093204	0.611876	0.397301	1.194975
lincRNA	-	3	7	4	6	4	2	0.065711	0.180684	0.115454	0.113692	0.098429	0.043537
lincRNA	-	0	0	1	0	0	0	0	0	0.093391	0	0	0
pseudogen	olfactory_r	1	0	2	0	0	0	0.058954	0	0.155375	0	0	0
antisense	-	8	1	1	0	0	0	0.120116	0.017694	0.019785	0	0	0
antisense	-	2	0	0	18	13	17	0.192863	0	0	1.501603	1.408355	1.629215
antisense	HOXC_clust	0	0	0	0	5	1	0	0	0	0	0.211207	0.037368
antisense	-	0	0	0	0	1	0	0	0	0	0	0.097983	0
processed_	-	0	0	1	0	0	0	0	0	0.032268	0	0	0
pseudogen	mitochond	0	0	0	0	2	0	0	0	0	0	0.369416	0
antisense	-	0	2	1	1	0	0	0	0.211126	0.118043	0.077494	0	0
antisense	-	0	1	6	13	12	22	0	0.113639	0.76244	1.084491	1.30002	2.108395
pseudogen	TNRC18P1	12	3	5	7	34	23	0.174053	0.051278	0.095566	0.087834	0.554022	0.331541
lincRNA	-	2	0	0	1	0	0	0.128342	0	0	0.055514	0	0
pseudogen	-	0	0	2	0	0	0	0	0	0.234105	0	0	0
processed_	MIR143_ho	253	253	196	11	22	28	1.594912	1.879506	1.628198	0.059989	0.155807	0.175422
processed_	NOP14_ant	236	179	206	233	226	253	3.236807	2.89311	3.723118	2.764545	3.482269	3.448537
antisense	-	0	0	0	6	12	6	0	0	0	1.52663	3.965061	1.753802
protein_co	Uncharacte	0	0	0	0	2	0	0	0	0	0	0.301908	0
antisense	-	18	14	14	12	6	13	1.554548	1.424842	1.593289	0.896553	0.582146	1.115796
lincRNA	-	10	4	9	11	2	12	1.163538	0.548464	1.379933	1.107226	0.261433	1.387623
processed_	-	1	0	1	2	3	2	0.023966	0	0.031581	0.041466	0.080773	0.047636
protein_co	theg_sperm	0	0	2	0	2	1	0	0	0.084562	0	0.072092	0.031887
processed_	-	0	0	0	6	0	0	0	0	0	0.161169	0	0
antisense	-	0	1	0	6	2	2	0	0.012698	0	0.055932	0.024212	0.021418
antisense	SRD5A3_an	16	38	27	13	3	7	0.523844	1.466131	1.164879	0.368204	0.110345	0.227766
processed_	-	0	1	0	0	0	0	0	0.123785	0	0	0	0
protein_co	zinc_finger_	2	2	7	5	4	11	0.036076	0.042513	0.166386	0.078022	0.081057	0.197191
antisense	-	0	0	0	2	0	2	0	0	0	0.057681	0	0.066265
pseudogen	fer-1-like_5	6	12	3	5	4	1	0.049042	0.115586	0.032313	0.035355	0.036731	0.008123
processed_	-	1	3	2	0	0	3	0.094201	0.333031	0.248268	0	0	0.280858
pseudogen	-	1	0	0	3	0	2	0.136095	0	0	0.353205	0	0.270509
processed_	-	38	27	48	2	4	3	2.403534	2.012507	4.000762	0.109436	0.284234	0.188581

pseudogen	-	4	1	0	2	0	3	0.392156	0.115533	0	0.169626	0	0.2923
lincRNA	-	0	0	4	0	0	0	0	0	0.29655	0	0	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.182441	0
protein_co	endothelial	31	22	29	6	0	7	3.647046	3.050067	4.495856	0.610652	0	0.818441
processed_	-	3	5	0	5	6	6	0.577538	1.134322	0	0.832707	1.297656	1.147943
pseudogen	-	4	2	1	0	0	0	0.32232	0.189917	0.106185	0	0	0
pseudogen	-	1	0	0	0	0	0	0.289295	0	0	0	0	0
pseudogen	-	2	0	0	3	1	2	0.113486	0	0	0.147263	0.063747	0.112785
antisense	-	0	0	0	1	0	0	0	0	0	0.082521	0	0
pseudogen	-	0	2	1	0	5	0	0	0.113124	0.063249	0	0.26961	0
processed_	-	2	2	3	0	0	1	0.057326	0.067556	0.113313	0	0	0.028486
sense_intrc	small_Cajal	0	0	0	0	1	0	0	0	0	0	0.475807	0
antisense	EAF1_antis	3	3	3	0	0	6	0.167182	0.197014	0.220305	0	0	0.332299
lincRNA	-	4	0	0	0	1	0	0.376135	0	0	0	0.105641	0
processed_	-	175	151	148	873	630	807	4.698111	4.777154	5.235784	20.27507	19.00093	21.53121
antisense	-	0	0	1	0	0	0	0	0	0.188549	0	0	0
pseudogen	hydroxy-de	0	0	0	0	1	0	0	0	0	0	0.059835	0
lincRNA	-	0	0	3	0	0	0	0	0	0.22194	0	0	0
lincRNA	-	0	4	0	35	49	27	0	0.428046	0	2.749505	4.998834	2.436671
processed_	-	2	1	0	2	6	4	0.142314	0.083854	0	0.123115	0.479644	0.282871
antisense	-	1	4	0	3	12	10	0.019572	0.092255	0	0.050794	0.263849	0.194507
antisense	VCAN_antis	2	2	7	0	4	1	0.233735	0.275443	1.07802	0	0.525174	0.116146
lincRNA	-	0	7	0	0	0	0	0	1.015614	0	0	0	0
pseudogen	-	1	1	0	0	2	1	0.016365	0.019285	0	0	0.03677	0.016264
processed_	-	8	10	13	24	23	19	0.263388	0.387983	0.564007	0.683566	0.850713	0.621683
pseudogen	-	2	0	7	0	4	2	0.081952	0	0.377974	0	0.184136	0.081446
protein_co	Uncharacte	6	7	4	0	0	0	0.158506	0.217921	0.139248	0	0	0
protein_co	heparan_su	11	8	11	124	75	76	0.149282	0.127942	0.196718	1.455797	1.143474	1.025037
pseudogen	eukaryotic_	14	10	22	16	19	17	0.536305	0.451431	1.110559	0.530233	0.817686	0.647206
processed_	-	0	0	0	1	2	2	0	0	0	0.054136	0.140605	0.124383
processed_	Pvt1_onco	295	266	226	360	277	335	9.192227	9.76759	9.279872	9.7043	9.69678	10.37417
protein_co	MT-RNR2-li	0	0	0	0	0	1	0	0	0	0	0	0.030255
protein_co	lectin_gala	0	0	0	0	2	2	0	0	0	0	0.181884	0.160899
pseudogen	-	9	4	14	32	29	26	0.450349	0.23587	0.923144	1.385222	1.630247	1.292973
processed_	-	1	0	0	0	0	0	0.119506	0	0	0	0	0
lincRNA	-	1	0	0	0	0	0	0.065684	0	0	0	0	0
processed_	-	2	0	7	16	6	7	0.12032	0	0.554935	0.832707	0.405518	0.418521
antisense	-	0	0	1	0	0	0	0	0	0.21013	0	0	0
pseudogen	-	2	0	2	0	0	0	0.15663	0	0.2064	0	0	0
lincRNA	-	0	3	0	0	0	0	0	0.43935	0	0	0	0
pseudogen	-	0	1	0	0	0	0	0	0.202558	0	0	0	0
pseudogen	asparagine-	0	0	0	0	6	1	0	0	0	0	0.793012	0.11692
lincRNA	-	0	0	0	3	1	1	0	0	0	0.053945	0.023351	0.020657
antisense	-	29	13	25	28	27	25	0.715086	0.377755	0.812334	0.597284	0.747951	0.612646

antisense	-	0	1	0	2	1	3	0	0.104853	0	0.153946	0.09996	0.265281
antisense	-	0	0	0	0	2	0	0	0	0	0	0.097422	0
pseudogen	tripartite_r	0	0	0	2	0	0	0	0	0	0.0675	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.074345	0
antisense	-	2	0	0	1	0	5	0.163904	0	0	0.070896	0	0.407229
protein_co	programme	1238	1098	929	1468	990	1262	17.41721	18.20402	17.22298	17.86681	15.6474	17.64521
antisense	-	0	0	1	0	0	0	0	0	0.123913	0	0	0
lincRNA	long_interg	0	1	1	3	3	0	0	0.023175	0.025915	0.051039	0.066281	0
pseudogen	-	0	2	0	0	0	1	0	0.13162	0	0	0	0.0555
protein_co	golgin_A8_	3	0	1	2	0	2	0.083856	0	0.036834	0.048362	0	0.055559
pseudogen	ras-related_	14	10	11	11	11	25	0.889765	0.748952	0.921244	0.604787	0.785396	1.579053
lincRNA	-	4	10	3	0	0	0	0.271145	0.798819	0.267977	0	0	0
antisense	-	0	0	0	1	4	4	0	0	0	0.062567	0.325005	0.287508
pseudogen	X-box_bind	1	13	3	10	9	14	0.081198	1.243927	0.320997	0.702437	0.820987	1.12975
protein_co	coiled-coil_	1	0	5	0	0	0	0.020835	0	0.137275	0	0	0
pseudogen	cell_divisio	1	0	3	0	1	1	0.094034	0	0.37174	0	0.105641	0.093453
pseudogen	coiled-coil-	0	0	0	4	1	7	0	0	0	0.4053	0.131584	0.814819
pseudogen	olfactory_r	0	0	0	8	0	1	0	0	0	0.398685	0	0.057251
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.195228
pseudogen	-	5	0	0	4	0	0	0.689336	0	0	0.477072	0	0
lincRNA	-	0	0	1	0	0	0	0	0	0.095566	0	0	0
pseudogen	YWHAQ_ps	2	0	2	0	2	0	0.348296	0	0.458969	0	0.391289	0
pseudogen	ribosomal_	0	0	0	4	0	0	0	0	0	0.2373	0	0
protein_co	transmemb	220	196	160	200	150	119	6.424169	6.744619	6.156715	5.052279	4.920787	3.453432
antisense	-	0	0	0	22	12	10	0	0	0	1.127042	0.798334	0.588524
antisense	-	2	2	0	0	2	1	0.188738	0.222416	0	0	0.212035	0.093786
sense_intrc	-	0	0	3	0	4	0	0	0	0.385432	0	0.438128	0
processed_	-	0	0	0	5	0	1	0	0	0	0.083973	0	0.019294
pseudogen	high_mobil	2	0	0	0	0	0	0.171886	0	0	0	0	0
antisense	-	2	0	0	0	2	5	0.238473	0	0	0	0.26791	0.592501
lincRNA	-	2	0	0	0	1	0	0.51399	0	0	0	0.288718	0
pseudogen	-	1	2	0	1	5	0	0.073734	0.173782	0	0.063787	0.414178	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.090402
antisense	-	3	2	2	4	3	2	0.204405	0.160586	0.179571	0.235773	0.229637	0.135429
pseudogen	-	0	2	0	0	1	0	0	0.405115	0	0	0.193104	0
pseudogen	-	1	1	2	0	10	3	0.029759	0.035069	0.07843	0	0.334322	0.088725
processed_	SLC7A11_a	2	4	5	5	16	2	0.022751	0.053621	0.07495	0.049204	0.204472	0.02261
antisense	-	0	2	2	0	0	2	0	0.066582	0.074454	0	0	0.056152
processed_	-	29	20	29	7	3	15	2.756353	2.240134	3.6322	0.57557	0.320337	1.416895
lincRNA	-	0	0	0	2	0	0	0	0	0	0.183931	0	0
pseudogen	chromobo	5	0	2	0	0	3	0.497566	0	0.262268	0	0	0.296696
processed_	-	0	0	0	0	0	2	0	0	0	0	0	0.1422
lincRNA	-	1	2	1	0	0	2	0.017904	0.042197	0.023593	0	0	0.035586
pseudogen	MT-ND4_ps	4	0	0	1	0	0	0.157328	0	0	0.034026	0	0

processed_	-	0	4	0	4	4	0	0	0.082197	0	0.060341	0.078361	0
antisense	-	1	0	1	0	0	3	0.084033	0	0.110735	0	0	0.250543
protein_co	YjeF_N-tern	76	76	38	109	92	180	1.453057	1.712339	0.957387	1.802846	1.976087	3.420198
pseudogen	-	1	0	0	1	0	2	0.203619	0	0	0.17615	0	0.404723
sense_intrc	-	0	3	0	4	0	1	0	0.061872	0	0.060561	0	0.017393
pseudogen	-	0	0	0	7	3	2	0	0	0	0.289605	0.161181	0.095057
processed_	-	0	0	0	6	2	0	0	0	0	0.088901	0.038483	0
processed_	-	4	4	2	13	6	2	0.141838	0.167147	0.093454	0.398785	0.239019	0.070481
lincRNA	-	3	0	0	8	6	3	0.07977	0	0	0.184024	0.179234	0.079278
pseudogen	-	0	0	0	1	0	0	0	0	0	0.05732	0	0
lincRNA	-	1	1	0	26	16	15	0.145044	0.170925	0	3.262388	2.607163	2.162221
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.237
protein_co	dynein_axc	111	87	85	40	24	43	1.165962	1.076931	1.176563	0.363483	0.283219	0.44889
processed_	-	1	0	0	0	0	3	0.332962	0	0	0	0	0.992718
antisense	NREP_antis	1	0	0	0	0	1	0.086789	0	0	0	0	0.086253
antisense	-	2	5	4	0	2	2	0.193569	0.570272	0.510152	0	0.217462	0.192373
processed_	-	4	3	6	0	0	0	0.404902	0.357865	0.800344	0	0	0
lincRNA	-	3	0	0	38	16	46	0.322156	0	0	3.530139	1.930253	4.909222
antisense	ANKRD33B	8	7	2	0	2	1	0.811356	0.836617	0.267292	0	0.227877	0.100793
antisense	CACNA1G_	4	9	3	0	0	0	0.147777	0.391828	0.14605	0	0	0
pseudogen	-	1	4	0	2	0	1	0.040724	0.191962	0	0.07046	0	0.040472
pseudogen	-	0	0	2	0	0	0	0	0	0.674041	0	0	0
antisense	-	8	7	5	4	9	3	0.27882	0.287501	0.229636	0.120603	0.352392	0.103912
protein_co	protocadhe	8	7	15	99	66	58	0.080611	0.08312	0.199172	0.862979	0.747128	0.580817
lincRNA	-	0	1	0	0	0	0	0	0.157545	0	0	0	0
antisense	-	6	6	5	1	0	4	0.473392	0.557863	0.519846	0.068255	0	0.313646
pseudogen	-	6	1	0	2	1	0	0.317012	0.062263	0	0.091415	0.059357	0
antisense	-	3	5	2	119	82	123	0.073495	0.144349	0.064566	2.522013	2.256837	2.994691
processed_	-	45	24	28	42	42	37	1.166672	0.733254	0.956597	0.941995	1.223305	0.95334
antisense	HOXC_clust	16	3	7	0	0	0	0.40529	0.089552	0.233657	0	0	0
pseudogen	-	26	14	22	6	30	5	0.310224	0.196851	0.345908	0.061932	0.402136	0.05929
pseudogen	-	0	1	0	0	0	1	0	0.146795	0	0	0	0.123798
pseudogen	keratin_8_p	0	0	0	1	2	2	0	0	0	0.032528	0.084483	0.074736
antisense	-	8	19	26	1	13	4	0.621921	1.740627	2.663503	0.067252	1.13537	0.30904
lincRNA	-	2	0	0	0	0	0	0.139135	0	0	0	0	0
antisense	-	0	0	0	2	0	0	0	0	0	0.079789	0	0
pseudogen	casein_kina	0	1	0	0	0	0	0	0.189054	0	0	0	0
processed_	-	0	4	5	3	1	1	0	0.129704	0.181298	0.071412	0.030913	0.027346
antisense	-	0	0	0	6	5	2	0	0	0	0.433428	0.469053	0.165975
sense_intrc	RASA2_intr	1	0	2	0	1	9	0.086505	0	0.227985	0	0.097183	0.773736
antisense	MYLK_antis	0	0	4	0	1	0	0	0	0.370097	0	0.078881	0
pseudogen	eukaryotic_	52	31	45	53	22	33	1.981952	1.392383	2.26015	1.747546	0.942023	1.25001
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.093954
antisense	-	2	0	0	1	0	0	0.251501	0	0	0.108786	0	0

pseudogen	high_mobil	0	9	0	0	0	0	0	1.903354	0	0	0	0
lincRNA	-	5	1	3	0	0	0	0.097966	0.023089	0.077457	0	0	0
antisense	-	4	1	2	0	10	2	0.376135	0.110813	0.247827	0	1.056411	0.186906
processed_	-	0	1	1	43	34	41	0	0.015001	0.016774	0.473516	0.486218	0.518677
pseudogen	-	0	0	1	2	0	3	0	0	0.234893	0.30841	0	0.531455
pseudogen	corepresso	0	0	0	0	0	4	0	0	0	0	0	0.156823
antisense	-	12	15	10	2	25	10	0.927433	1.366155	1.018442	0.133719	2.170654	0.768088
antisense	-	5	0	1	0	1	1	0.675268	0	0.177968	0	0.151724	0.13422
pseudogen	-	0	1	1	0	0	0	0	0.402501	0.450086	0	0	0
lincRNA	-	0	0	0	6	6	9	0	0	0	0.116983	0.151918	0.201586
antisense	-	5	1	2	0	0	2	0.650381	0.153287	0.342817	0	0	0.258546
antisense	-	1	1	0	11	3	4	0.06544	0.077117	0	0.622729	0.220553	0.260144
processed_	-	7	6	7	9	19	13	0.131414	0.13274	0.173171	0.146167	0.400724	0.242547
antisense	-	0	1	0	0	0	0	0	0.16038	0	0	0	0
pseudogen	selenophos	0	1	0	0	0	0	0	0.05369	0	0	0	0
antisense	-	0	2	1	0	0	0	0	0.344684	0.192716	0	0	0
pseudogen	polycystic_	346	345	272	123	178	229	3.84097	4.513266	3.97895	1.181226	2.219902	2.526445
lincRNA	-	0	0	0	0	3	2	0	0	0	0	0.270755	0.159678
antisense	-	1	3	1	10	5	3	0.115089	0.406876	0.151659	0.995628	0.646477	0.343135
lincRNA	-	0	0	1	0	0	0	0	0	0.256483	0	0	0
lincRNA	-	0	0	0	2	0	3	0	0	0	0.141792	0	0.244338
pseudogen	-	0	0	5	0	3	1	0	0	0.310611	0	0.158885	0.046851
lincRNA	-	1	0	0	0	0	0	0.112881	0	0	0	0	0
antisense	-	0	2	0	3	6	2	0	0.075944	0	0.083626	0.217198	0.064046
pseudogen	proteasom	0	0	0	2	1	0	0	0	0	0.517502	0.336022	0
sense_intro	-	12	6	13	3	7	7	0.18377	0.108281	0.262344	0.039744	0.120431	0.106537
antisense	-	0	2	0	0	0	0	0	0.290175	0	0	0	0
processed_	-	0	0	0	0	0	2	0	0	0	0	0	0.146762
pseudogen	-	2	3	0	0	3	0	0.058369	0.103177	0	0	0.098361	0
antisense	-	2	0	2	2	3	8	0.032469	0	0.042786	0.028089	0.054716	0.129075
pseudogen	mitochond	1	0	0	0	0	0	0.057607	0	0	0	0	0
processed_	-	35	38	33	16	12	29	0.67404	0.862399	0.837464	0.266563	0.259626	0.555041
protein_co	KIAA1456	30	40	29	399	319	334	0.165665	0.260301	0.211029	1.906098	1.979015	1.833013
pseudogen	-	1	0	0	0	0	0	0.169141	0	0	0	0	0
lincRNA	zinc_finger_	89	84	100	320	270	298	1.466008	1.630544	2.170606	4.559941	4.996421	4.878341
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.089979	0
protein_co	small_integ	409	329	274	372	314	391	23.15815	21.95247	20.444	18.2216	19.97373	22.00224
pseudogen	-	28	20	5	9	3	4	2.422137	2.038815	0.569961	0.673513	0.291549	0.343883
antisense	-	21	17	18	18	33	23	1.403738	1.339131	1.585529	1.040884	2.478163	1.527933
pseudogen	-	0	0	1	0	0	0	0	0	0.410372	0	0	0
pseudogen	mitochond	1	0	1	0	1	0	0.085943	0	0.113252	0	0.096552	0
pseudogen	immunoglo	0	0	2	2	0	1	0	0	0.158733	0.104207	0	0.059857
antisense	-	19	5	6	1	9	6	1.325269	0.410986	0.551488	0.060341	0.705248	0.415921
pseudogen	-	3	5	5	0	4	1	0.183823	0.36104	0.403723	0	0.275351	0.060896

antisense	-	2	1	0	0	0	0	0.074355	0.043812	0	0	0	0
pseudogen	KDEL_(Lys-	0	2	0	0	0	2	0	0.082688	0	0	0	0.069734
pseudogen	-	0	0	1	0	0	0	0	0	0.194327	0	0	0
lincRNA	-	0	1	0	0	0	0	0	0.086171	0	0	0	0
processed_	-	163	148	187	407	385	464	5.359865	5.735021	8.10294	11.57774	14.2225	15.1633
lincRNA	-	0	0	1	0	0	0	0	0	0.044266	0	0	0
lincRNA	-	5	0	1	0	0	1	0.426256	0	0.11234	0	0	0.084725
pseudogen	-	0	1	0	0	0	0	0	0.053277	0	0	0	0
pseudogen	-	0	1	0	0	1	0	0	0.148897	0	0	0.141947	0
antisense	-	0	0	0	0	0	6	0	0	0	0	0	0.417572
pseudogen	-	0	2	0	0	3	0	0	0.765494	0	0	1.094649	0
lincRNA	-	0	0	1	1	0	4	0	0	0.113436	0.07447	0	0.342205
antisense	-	18	23	9	16	6	6	0.785604	1.18295	0.517617	0.604108	0.294193	0.260251
lincRNA	long_interg	2	0	0	19	5	16	0.033119	0	0	0.272186	0.093018	0.263317
lincRNA	-	0	0	0	1	1	0	0	0	0	0.017	0.022077	0
pseudogen	-	0	0	0	5	0	0	0	0	0	0.162754	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.097708	0	0	0
lincRNA	-	0	0	0	1	8	0	0	0	0	0.121483	1.262088	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.089939
pseudogen	unc-93_ho	0	0	0	0	0	2	0	0	0	0	0	0.140868
antisense	-	0	0	0	0	3	1	0	0	0	0	0.448311	0.132196
pseudogen	ubiquitin-c	3	4	3	1	2	4	0.35294	0.554558	0.465089	0.101775	0.264337	0.46768
pseudogen	-	5	1	0	12	13	8	0.6472	0.152537	0	1.343733	1.890433	1.029126
lincRNA	-	0	0	0	1	0	0	0	0	0	0.080349	0	0
antisense	-	55	58	37	28	22	59	1.412787	1.755695	1.252422	0.622207	0.634872	1.506176
lincRNA	-	14	5	18	0	0	0	0.637295	0.268219	1.079741	0	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.094147	0	0	0
processed_	-	30	36	14	32	32	36	0.558646	0.789996	0.343541	0.515499	0.669444	0.666235
lincRNA	-	0	0	0	4	0	0	0	0	0	0.065264	0	0
antisense	-	4	14	3	0	0	0	0.30646	1.264006	0.30288	0	0	0
antisense	-	6	5	2	9	7	11	0.541135	0.531412	0.237694	0.702198	0.709253	0.985953
pseudogen	kelch-like_f	0	2	4	5	4	2	0	0.239492	0.535611	0.439529	0.456629	0.201973
pseudogen	acetoacetyl	0	0	0	14	7	11	0	0	0	0.227209	0.147531	0.205087
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.089328
processed_	-	5	0	0	1	0	0	0.368157	0	0	0.063698	0	0
antisense	-	0	0	0	4	0	0	0	0	0	0.068027	0	0
pseudogen	-	0	0	2	0	1	0	0	0	0.494775	0	0.210908	0
pseudogen	-	3	1	1	1	10	4	0.092608	0.036378	0.040678	0.026705	0.346798	0.122715
pseudogen	chaperonin	1	2	0	0	0	0	0.03272	0.077117	0	0	0	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.091233	0	0
antisense	HOXC_clus	9	23	16	0	1	0	0.869469	2.618463	2.036884	0	0.108533	0
pseudogen	-	3	0	0	0	0	0	0.491712	0	0	0	0	0
pseudogen	-	10	7	6	17	9	8	0.711572	0.586981	0.562607	1.04648	0.719467	0.565742
pseudogen	guanine_m	0	0	0	5	2	3	0	0	0	0.3955	0.205444	0.272612

pseudogen	deoxyuridi	1	1	1	0	4	0	0.108932	0.12837	0.143546	0	0.489514	0
pseudogen	WW_doma	3	3	0	6	6	2	0.167889	0.197847	0	0.290479	0.377226	0.111235
pseudogen	-	0	1	0	1	1	0	0	0.070099	0	0.051459	0.066827	0
protein_co	coiled-coil-	343	272	209	462	351	449	15.50705	14.49143	12.45135	18.06925	17.82754	20.17396
pseudogen	protein_ph	0	5	5	10	4	10	0	0.274836	0.307327	0.403515	0.209607	0.46356
protein_co	family_witl	15	4	6	6	2	20	0.365278	0.114789	0.192539	0.1264	0.054716	0.48403
lincRNA	-	0	2	0	4	3	0	0	0.051581	0	0.075732	0.073761	0
pseudogen	integrator_	0	0	2	0	0	0	0	0	0.055149	0	0	0
antisense	-	1	5	1	0	1	0	0.008385	0.049404	0.011049	0	0.00942	0
pseudogen	-	0	0	0	2	0	0	0	0	0	0.06775	0	0
protein_co	cyclin-depe	9	1	2	4	0	5	0.301181	0.039436	0.088196	0.1158	0	0.16629
lincRNA	-	9	6	2	0	2	0	0.146516	0.115107	0.042905	0	0.036578	0
protein_co	G_protein-	134	117	85	51	37	57	2.562895	2.637054	2.142297	0.843838	0.795018	1.083454
antisense	-	0	0	0	4	0	2	0	0	0	0.126604	0	0.072722
lincRNA	-	4	0	1	4	0	8	0.371516	0	0.122392	0.321396	0	0.738443
antisense	-	0	5	0	0	0	0	0	0.545347	0	0	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.156589
pseudogen	abhydrolas	0	0	1	0	4	8	0	0	0.061357	0	0.209238	0.370196
antisense	-	0	0	0	2	0	1	0	0	0	0.058417	0	0.033555
pseudogen	keratin_8_p	19	10	18	18	37	19	0.706872	0.438424	0.882459	0.579326	1.546457	0.702507
antisense	-	6	3	2	0	3	1	0.657652	0.387501	0.288875	0	0.369416	0.108932
lincRNA	-	0	0	0	3	2	2	0	0	0	0.065614	0.056806	0.050252
processed_	-	0	0	0	1	0	0	0	0	0	0.016386	0	0
lincRNA	-	8	4	10	0	0	4	0.082996	0.048903	0.13671	0	0	0.041242
lincRNA	-	0	0	0	0	1	2	0	0	0	0	0.084483	0.149472
pseudogen	coiled-coil_	0	0	0	1	4	3	0	0	0	0.088586	0.460162	0.305304
processed_	-	2	5	2	2	5	8	0.286168	0.843077	0.377099	0.247562	0.803729	1.137601
lincRNA	-	0	1	0	0	0	0	0	0.093255	0	0	0	0
protein_co	ATPase_H+_	37	58	36	95	67	83	0.839253	1.550338	1.07604	1.864137	1.707321	1.871022
pseudogen	-	0	0	1	0	2	1	0	0	0.221471	0	0.377625	0.167029
pseudogen	N-terminal_	17	12	14	2	7	1	0.957444	0.796439	1.039028	0.097444	0.442906	0.055972
protein_co	GLI_family_	228	239	145	238	187	217	5.173831	6.391199	4.335909	4.672156	4.767251	4.893806
pseudogen	-	1	0	0	0	0	0	0.076284	0	0	0	0	0
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.127395
antisense	-	4	5	4	0	0	2	0.238205	0.350887	0.313896	0	0	0.118367
antisense	-	5	1	13	0	2	0	0.242849	0.057236	0.832039	0	0.10913	0
lincRNA	-	1	2	1	1	0	0	0.057733	0.136069	0.076078	0.049944	0	0
lincRNA	-	0	0	0	1	0	1	0	0	0	0.028341	0	0.032558
lincRNA	long_interg	0	2	0	0	0	0	0	0.250051	0	0	0	0
protein_co	IQCJ-SCHIP	33	19	48	168	188	164	0.663522	0.450196	1.271795	2.922224	4.246666	3.277138
processed_	-	5	2	1	0	1	3	0.778544	0.366987	0.205186	0	0.174929	0.464242
processed_	-	0	0	0	2	4	0	0	0	0	0.041598	0.10804	0
pseudogen	-	0	5	0	0	0	0	0	0.273871	0	0	0	0
antisense	ROPN1L_ar	0	0	0	0	1	0	0	0	0	0	0.314687	0

antisense	-	6	3	3	1	2	2	0.425229	0.250553	0.280174	0.06131	0.159239	0.140868
processed_	-	11	6	15	15	2	15	0.266035	0.171003	0.478049	0.313834	0.054341	0.360535
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.154444
processed_	-	3	4	3	1	2	1	0.153749	0.241579	0.202604	0.044336	0.115152	0.050933
pseudogen	-	1	0	0	0	0	1	0.160915	0	0	0	0	0.159921
antisense	-	2	0	2	0	0	0	0.233735	0	0.308006	0	0	0
antisense	-	2	2	3	8	1	8	0.064171	0.075621	0.126842	0.222055	0.036046	0.255098
antisense	-	7	0	0	0	0	0	0.460356	0	0	0	0	0
lincRNA	-	0	0	0	0	3	0	0	0	0	0	0.332888	0
antisense	-	2	0	0	2	0	0	0.182241	0	0	0.157655	0	0
pseudogen	-	0	0	0	0	12	6	0	0	0	0	0.964474	0.4266
lincRNA	-	0	0	1	0	0	0	0	0	0.035039	0	0	0
antisense	-	1	0	2	0	0	0	0.093701	0	0.24695	0	0	0
lincRNA	-	0	0	1	0	1	0	0	0	0.031312	0	0.026695	0
lincRNA	-	12	13	10	0	4	4	1.101026	1.405616	1.209069	0	0.412311	0.364742
protein_co	HCG43720	0	0	0	0	3	0	0	0	0	0	0.140938	0
pseudogen	-	23	14	18	1	0	0	2.991752	2.146015	3.085354	0.112528	0	0
processed_	-	0	0	2	0	0	0	0	0	0.306652	0	0	0
pseudogen	poly(A)_bin	2	1	0	0	0	2	0.069981	0.041234	0	0	0	0.069549
pseudogen	-	0	1	0	0	0	0	0	0.110617	0	0	0	0
pseudogen	ST3_beta-g	0	1	1	1	0	0	0	0.061526	0.0688	0.045167	0	0
processed_	-	17	14	2	0	0	0	1.378249	1.337562	0.21367	0	0	0
lincRNA	-	0	0	6	8	18	17	0	0	0.198004	0.173317	0.506417	0.423103
antisense	-	13	10	8	19	28	27	2.606943	2.363172	2.114039	3.296133	6.308052	5.380982
processed_	-	2	3	1	1	5	5	0.218764	0.386701	0.144139	0.094626	0.614421	0.543534
pseudogen	heterogene	0	2	0	0	0	0	0	0.493184	0	0	0	0
lincRNA	-	0	0	0	2	0	0	0	0	0	0.154726	0	0
pseudogen	-	0	0	1	0	8	0	0	0	0.172255	0	1.174833	0
protein_co	Uncharacte	0	0	0	0	1	0	0	0	0	0	0.149813	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.741043
pseudogen	-	0	0	1	0	0	0	0	0	0.144437	0	0	0
lincRNA	long_interg	11	5	18	16	24	22	0.616897	0.330443	1.330232	0.776253	1.5121	1.226175
pseudogen	-	0	2	0	0	0	0	0	0.290852	0	0	0	0
pseudogen	-	2	0	0	0	0	0	0.098678	0	0	0	0	0
lincRNA	-	0	0	0	7	3	3	0	0	0	0.6583	0.366381	0.324111
processed_	-	6	7	3	0	0	0	0.51316	0.705516	0.33811	0	0	0
antisense	-	2	1	0	0	1	0	0.16116	0.094958	0	0	0.090527	0
antisense	-	0	3	0	0	0	2	0	0.383531	0	0	0	0.215631
lincRNA	-	0	1	0	0	0	0	0	0.122089	0	0	0	0
protein_co	selenoprot	37	34	34	75	70	65	0.469178	0.508068	0.568132	0.822735	0.997201	0.819141
pseudogen	tropomyos	21	6	11	22	12	36	1.49833	0.504483	1.034227	1.357919	0.961875	2.552703
processed_	-	2	3	4	0	7	13	0.19791	0.349838	0.521595	0	0.77819	1.278472
antisense	-	0	0	0	2	0	0	0	0	0	0.189644	0	0
lincRNA	-	28	14	12	101	78	81	1.082796	0.638005	0.611512	3.378882	3.388694	3.11303

pseudogen	-	1	1	0	3	0	2	0.025737	0.030329	0	0.066795	0	0.051156
lincRNA	-	64	59	63	3	0	0	3.160656	3.433653	4.099894	0.128169	0	0
pseudogen	-	0	0	1	0	0	1	0	0	0.15199	0	0	0.114628
pseudogen	-	0	0	0	1	0	0	0	0	0	0.420173	0	0
antisense	-	0	0	3	0	0	0	0	0	0.400938	0	0	0
pseudogen	-	3	0	0	3	2	0	0.597079	0	0	0.516529	0.447187	0
processed_	-	8	7	19	20	6	11	0.112551	0.116055	0.352246	0.243417	0.094833	0.153801
antisense	-	12	8	2	5	2	2	0.761741	0.598443	0.167298	0.274574	0.142628	0.126173
lincRNA	-	6	9	3	2	2	1	0.137927	0.243808	0.090877	0.039773	0.051651	0.022846
lincRNA	-	9	2	3	0	0	0	1.063547	0.278517	0.467165	0	0	0
pseudogen	-	1	0	0	0	0	0	0.089126	0	0	0	0	0
processed_	-	2	3	3	4	4	8	0.114097	0.201684	0.225528	0.197409	0.256362	0.453569
lincRNA	-	699	618	508	239	179	251	20.57018	21.43169	19.69969	6.084457	5.917837	7.340815
lincRNA	-	2	7	3	3	4	6	0.094707	0.390621	0.1872	0.122895	0.212794	0.282365
pseudogen	asparagine-	0	0	0	0	4	2	0	0	0	0	0.548165	0.242461
pseudogen	-	2	0	0	0	0	0	0.32183	0	0	0	0	0
protein_co	proline_del	0	1	0	0	0	0	0	0.031896	0	0	0	0
processed_	ZBED3_anti	30	30	31	32	26	29	0.79931	0.941939	1.088406	0.737577	0.778246	0.767895
lincRNA	-	0	0	1	0	0	0	0	0	0.139806	0	0	0
processed_	-	0	2	1	0	1	0	0	0.219675	0.122823	0	0.104711	0
lincRNA	-	0	0	0	0	0	3	0	0	0	0	0	0.839586
lincRNA	-	1	1	0	0	0	0	0.209253	0.246592	0	0	0	0
pseudogen	LSM3_hom	0	1	0	0	0	0	0	0.201902	0	0	0	0
antisense	-	1	2	1	6	14	15	0.123694	0.291531	0.162998	0.642041	1.945474	1.84395
lincRNA	-	3	4	6	0	0	0	0.299666	0.470851	0.789773	0	0	0
processed_	-	43	49	68	0	0	0	1.934123	2.59728	4.030504	0	0	0
pseudogen	-	9	10	6	4	17	5	0.396067	0.518601	0.347947	0.152282	0.840474	0.218679
pseudogen	ring_finger_	2	3	3	0	0	0	0.193923	0.34279	0.383315	0	0	0
lincRNA	-	0	1	0	2	0	5	0	0.129704	0	0.190432	0	0.546924
pseudogen	-	0	0	1	0	0	0	0	0	0.049548	0	0	0
pseudogen	-	3	2	3	2	4	6	0.067355	0.052916	0.088757	0.038846	0.100892	0.133878
pseudogen	methyltran	0	7	2	0	3	1	0	0.18889	0.060349	0	0.077175	0.022757
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.115129
pseudogen	-	1	1	0	2	0	3	0.116099	0.136815	0	0.200872	0	0.346145
lincRNA	-	0	6	8	21	21	29	0	0.700986	1.045143	1.801081	2.338941	2.857317
lincRNA	-	0	1	2	1	2	5	0	0.022257	0.049778	0.016339	0.042437	0.093853
pseudogen	-	1	0	2	8	8	4	0.055727	0	0.14687	0.385675	0.50085	0.221533
antisense	-	0	0	0	0	0	3	0	0	0	0	0	0.183112
pseudogen	RNA_bindi	1	1	2	4	2	9	0.05767	0.06796	0.15199	0.19956	0.129577	0.515824
processed_	-	96	68	66	197	303	377	1.446311	1.207275	1.310295	2.567554	5.128402	5.644706
antisense	-	0	0	2	3	0	3	0	0	0.18906	0.186174	0	0.213878
processed_	-	45	39	23	20	9	21	0.289929	0.296108	0.195273	0.111474	0.065143	0.134465
antisense	-	0	4	0	0	3	1	0	0.523168	0	0	0.374062	0.110302
antisense	-	11	4	10	2	4	7	1.155458	0.495141	1.384192	0.181742	0.472031	0.730751

antisense	-	1	0	2	5	1	1	0.063025	0	0.166103	0.272613	0.070805	0.062636
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.051944	0
processed_	-	0	3	0	0	0	0	0	0.391555	0	0	0	0
pseudogen	-	2	11	2	3	2	0	0.08973	0.581581	0.118243	0.116438	0.100807	0
lincRNA	-	1	0	0	0	0	1	0.063784	0	0	0	0	0.06339
antisense	-	1	1	5	0	0	0	0.095218	0.112208	0.627368	0	0	0
antisense	LNX1_antis	3	0	0	0	0	0	0.288769	0	0	0	0	0
pseudogen	glyceraldeh	2	0	0	0	1	1	0.109495	0	0	0	0.061506	0.05441
lincRNA	-	8	0	0	6	1	4	0.845365	0	0	0.54849	0.118714	0.420072
processed_	-	1	1	0	2	3	3	0.022634	0.026673	0	0.039161	0.076284	0.067483
pseudogen	-	0	0	0	0	2	1	0	0	0	0	0.189716	0.083914
lincRNA	-	0	1	0	0	0	0	0	0.096277	0	0	0	0
antisense	-	5	2	1	0	2	0	1.080428	0.509288	0.284748	0	0.485518	0
processed_	-	4	9	7	10	25	12	0.369571	0.979912	0.852256	0.799283	2.594935	1.101865
lincRNA	-	0	2	1	2	0	0	0	0.051903	0.02902	0.038102	0	0
lincRNA	-	3	0	1	0	0	0	0.138831	0	0.060982	0	0	0
lincRNA	long_interg	0	0	0	0	0	1	0	0	0	0	0	0.088725
pseudogen	glutamate_	74	36	52	38	39	75	4.372359	2.50665	4.048762	1.942364	2.588796	4.404078
processed_	-	0	0	0	4	3	0	0	0	0	0.204231	0.198916	0
processed_	-	1	0	0	0	10	0	0.093206	0	0	0	1.047111	0
pseudogen	-	1	5	0	0	2	1	0.12881	0.758975	0	0	0.289421	0.128015
lincRNA	-	6	1	5	0	0	1	0.509048	0.09998	0.559001	0	0	0.084317
pseudogen	CDC28_prc	2	0	0	0	0	0	0.387846	0	0	0	0	0
antisense	-	0	0	1	0	0	0	0	0	0.447201	0	0	0
processed_	-	1	0	1	0	0	1	0.077286	0	0.101844	0	0	0.076809
pseudogen	-	0	2	1	0	4	0	0	0.040937	0.022888	0	0.078052	0
pseudogen	-	1	1	1	0	2	0	0.068844	0.081128	0.090719	0	0.154684	0
antisense	-	0	2	0	0	0	0	0	0.176237	0	0	0	0
processed_	-	0	3	6	1	12	14	0	0.041362	0.092504	0.010121	0.157726	0.162784
antisense	-	35	52	27	47	37	67	2.345487	4.106534	2.384315	2.724745	2.785581	4.462204
antisense	-	7	4	0	0	3	0	0.650153	0.437809	0	0	0.313031	0
pseudogen	MHC_class_	4	1	3	0	1	0	0.183029	0.053922	0.18089	0	0.051405	0
lincRNA	-	0	1	0	2	0	2	0	0.115747	0	0.16994	0	0.195228
antisense	-	6	5	4	12	23	11	0.65494	0.643172	0.575367	1.133169	2.820507	1.193308
pseudogen	-	4	2	0	2	6	7	0.506612	0.298506	0	0.219134	0.853721	0.881097
pseudogen	-	0	0	0	1	3	1	0	0	0	0.085446	0.332888	0.098161
processed_	-	180	166	170	2	1	2	11.89685	12.92929	14.80619	0.114354	0.074252	0.131371
pseudogen	oral_cance	0	0	0	2	0	1	0	0	0	0.231893	0	0.1332
lincRNA	-	1	1	0	2	1	0	0.069476	0.081874	0	0.120207	0.078052	0
antisense	-	0	0	1	0	0	0	0	0	0.095305	0	0	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.021679
pseudogen	glyceraldeh	3	0	1	3	0	0	0.160427	0	0.070468	0.138785	0	0
lincRNA	SLC25A30_	3	1	0	3	0	0	0.226566	0.088998	0	0.196001	0	0
antisense	-	0	0	0	0	0	4	0	0	0	0	0	0.26307

pseudogen	HIG1_hypo	0	0	3	0	0	0	0	0	0.724186	0	0	0
processed_	THAP9_ant	186	228	149	590	347	432	3.809294	5.50267	4.021172	10.45314	7.983808	8.792754
sense_intrc	-	3	1	3	2	0	7	0.050308	0.019762	0.066294	0.029014	0	0.116661
lincRNA	-	0	1	0	0	0	2	0	0.126547	0	0	0	0.213444
antisense	-	7	16	7	16	10	6	0.090919	0.244898	0.119809	0.17978	0.145917	0.07745
processed_	-	2	1	1	5	6	4	0.23322	0.137418	0.153664	0.504393	0.786025	0.46356
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.191324
lincRNA	-	0	0	0	0	0	3	0	0	0	0	0	0.073724
pseudogen	zinc_finger_	1	11	0	3	1	1	0.022615	0.29315	0	0.058691	0.025406	0.022475
pseudogen	-	10	15	4	16	0	16	1.696827	2.99941	0.894401	2.348662	0	2.698156
lincRNA	-	0	1	0	3	1	3	0	0.150695	0	0.331876	0.143662	0.381261
pseudogen	ankyrin_rep	0	0	0	0	0	1	0	0	0	0	0	0.039559
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.33727
pseudogen	BMS1_pseu	0	2	1	1	1	1	0	0.093746	0.052414	0.034409	0.044685	0.03953
lincRNA	-	0	0	0	4	0	0	0	0	0	0.200433	0	0
pseudogen	nudix_(nuc	5	0	0	2	1	0	0.465211	0	0	0.16098	0.104527	0
antisense	HTT_antise	0	0	0	2	1	5	0	0	0	0.17786	0.115487	0.510816
antisense	-	5	6	1	0	1	5	0.3723	0.526479	0.09812	0	0.083651	0.37
pseudogen	BMS1_pseu	2	1	1	1	1	5	0.056987	0.033578	0.037548	0.02465	0.032011	0.141588
lincRNA	-	0	0	0	3	1	0	0	0	0	0.246673	0.106779	0
lincRNA	-	0	0	1	0	0	0	0	0	0.153326	0	0	0
lincRNA	-	1	0	0	0	0	0	0.088678	0	0	0	0	0
antisense	-	7	5	6	208	108	136	0.204068	0.171772	0.230495	5.24569	3.537114	3.940259
pseudogen	C-terminal_	0	0	0	0	1	0	0	0	0	0	0.064648	0
pseudogen	FCF1_small	0	5	1	0	0	0	0	0.52251	0.116856	0	0	0
lincRNA	-	0	1	0	0	0	0	0	0.022686	0	0	0	0
antisense	WWC2_ant	5	0	0	0	1	1	0.65521	0	0	0	0.147218	0.130233
lincRNA	-	1	0	0	2	9	3	0.072127	0	0	0.124793	0.729269	0.215044
antisense	-	7	6	4	2	4	2	0.785142	0.793064	0.591214	0.194063	0.504033	0.222941
processed_	-	106	75	61	106	125	101	1.475998	1.230689	1.119295	1.276876	1.955415	1.39769
protein_co	Uncharacte	2	0	3	0	0	0	0.171608	0	0.339206	0	0	0
antisense	-	27	18	17	3	9	3	1.844396	1.449005	1.530291	0.177286	0.690688	0.203667
antisense	-	29	22	3	6	8	8	0.362695	0.324245	0.049442	0.064917	0.112404	0.099436
lincRNA	-	19	12	19	1	0	2	3.504804	2.608546	4.618475	0.159578	0	0.366648
antisense	-	6	5	4	0	1	0	0.564202	0.554065	0.495654	0	0.105641	0
antisense	HOXC_clust	0	1	0	0	0	0	0	0.022155	0	0	0	0
pseudogen	-	7	14	6	7	11	4	1.992403	4.695851	2.250428	1.723615	3.517393	1.131485
processed_	-	0	0	0	2	1	2	0	0	0	0.04652	0.030206	0.053442
lincRNA	-	1	14	10	14	9	20	0.089883	1.4829	1.184436	1.088599	0.9088	1.786555
lincRNA	highly_up-r	0	0	0	1	0	7	0	0	0	0.082372	0	0.662407
processed_	-	2	0	0	0	0	0	0.070028	0	0	0	0	0
pseudogen	olfactory_r	0	0	0	0	1	0	0	0	0	0	0.066528	0
antisense	-	1	0	1	1	0	1	0.08311	0	0.109518	0.071898	0	0.082597
antisense	UCHL1_ant	2	0	0	0	0	0	0.178855	0	0	0	0	0

antisense	-	2	3	4	4	3	4	0.220129	0.389113	0.580152	0.380864	0.370952	0.437539
antisense	-	18	17	19	4	0	0	1.270584	1.414122	1.767336	0.244261	0	0
antisense	-	0	1	0	0	2	1	0	0.093957	0	0	0.179144	0.079238
antisense	-	0	0	0	2	3	7	0	0	0	0.155779	0.303449	0.626358
pseudogen	-	12	12	1	69	56	89	1.155076	1.361187	0.126842	5.745681	6.05573	8.51391
lincRNA	long_interg	1	4	0	0	1	0	0.037707	0.177743	0	0	0.042362	0
protein_co	zinc_finger_	113	65	88	140	107	150	1.468778	0.99563	1.507284	1.574232	1.562466	1.937665
sense_intrc	-	10	26	24	9	2	1	0.752003	2.304092	2.378294	0.585497	0.168966	0.074736
pseudogen	-	111	97	127	59	113	73	7.345563	7.564512	11.07492	3.377669	8.400973	4.801032
pseudogen	-	5	3	0	0	0	0	0.158887	0.112343	0	0	0	0
lincRNA	-	0	1	1	0	2	0	0	0.122569	0.137059	0	0.233697	0
protein_co	Uncharacte	0	0	0	2	0	0	0	0	0	0.044989	0	0
pseudogen	golgin_A5_	0	0	0	0	1	0	0	0	0	0	0.06069	0
lincRNA	-	0	4	2	0	0	0	0	0.136815	0.076495	0	0	0
lincRNA	-	0	0	0	0	0	3	0	0	0	0	0	0.075306
lincRNA	-	1	0	3	6	1	7	0.12032	0	0.475659	0.624531	0.135173	0.837042
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.068597
antisense	CNOT10_ar	1	0	0	0	1	0	0.113607	0	0	0	0.127631	0
lincRNA	-	0	0	0	0	2	6	0	0	0	0	0.032289	0.085691
pseudogen	-	10	9	10	9	11	6	0.588233	0.623877	0.775148	0.457989	0.726928	0.35076
processed_	-	11	1	3	0	0	0	0.798835	0.08558	0.287092	0	0	0
pseudogen	proteasom	0	0	0	0	0	1	0	0	0	0	0	0.076697
pseudogen	-	1	1	0	0	0	0	0.183187	0.215874	0	0	0	0
protein_co	zinc_finger_	54	56	41	73	69	50	0.810551	0.990562	0.810971	0.947922	1.163549	0.745875
processed_	-	2	4	1	1	2	0	0.039925	0.094099	0.026306	0.01727	0.044854	0
pseudogen	general_tra	1	0	4	0	9	3	0.078431	0	0.413412	0	0.793012	0.23384
antisense	-	18	38	16	0	0	0	2.089776	5.198977	2.447834	0	0	0
protein_co	ret_finger_	0	1	0	0	2	1	0	0.032836	0	0	0.062606	0.027692
lincRNA	-	1	8	1	0	1	3	0.096432	0.909111	0.127073	0	0.108335	0.287508
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.190628	0
processed_	-	18	29	10	10	20	20	0.896461	1.702017	0.656287	0.430846	1.11902	0.989916
antisense	-	0	0	0	2	3	3	0	0	0	0.233668	0.455173	0.402659
pseudogen	asparagine-	1	4	1	7	0	14	0.068934	0.324936	0.090838	0.417438	0	0.95911
antisense	-	0	0	1	0	4	1	0	0	0.13263	0	0.452288	0.100027
antisense	MAGI2_ant	1	3	0	0	0	0	0.112163	0.396532	0	0	0	0
antisense	-	4	2	0	4	0	1	0.266035	0.156753	0	0.230145	0	0.066098
lincRNA	-	0	0	0	3	0	0	0	0	0	0.323286	0	0
pseudogen	ALG1_chitc	13	10	5	9	12	23	0.710251	0.643836	0.359976	0.425377	0.736544	1.248837
pseudogen	-	0	5	1	0	6	3	0	0.251361	0.056215	0	0.287555	0.127189
lincRNA	-	0	0	0	7	0	2	0	0	0	0.501709	0	0.164676
lincRNA	-	0	1	5	0	0	0	0	0.069013	0.385859	0	0	0
pseudogen	-	0	0	0	1	2	0	0	0	0	0.099563	0.258591	0
pseudogen	NADH_deh	2	0	1	2	0	0	0.270798	0	0.178423	0.234266	0	0
antisense	-	0	1	0	4	4	5	0	0.081023	0	0.237916	0.308966	0.34165

lincRNA	-	0	0	0	2	0	0	0	0	0	0.222325	0	0
processed_	-	1	0	1	2	0	0	0.09112	0	0.120074	0.157655	0	0
antisense	-	0	0	0	4	0	1	0	0	0	0.30893	0	0.088725
protein_co	SH3_and_m	824	634	504	261	231	231	5.899835	5.349448	4.755301	1.616651	1.85812	1.643744
lincRNA	-	2	8	9	24	19	23	0.064484	0.30396	0.382381	0.669412	0.688211	0.736981
antisense	-	3	3	7	3	7	0	0.308994	0.364131	0.950084	0.267309	0.809983	0
processed_	-	0	0	0	1	6	5	0	0	0	0.08497	0.66207	0.488071
pseudogen	-	0	0	1	1	1	2	0	0	0.098258	0.064506	0.083769	0.148209
pseudogen	reticulon_3	1	1	3	0	0	4	0.07446	0.087746	0.29436	0	0	0.296
pseudogen	-	3	1	0	5	4	2	0.139686	0.05487	0	0.201402	0.209238	0.092549
pseudogen	heat_shock	5	6	16	0	12	11	0.155526	0.219933	0.655824	0	0.419337	0.340044
pseudogen	-	2	12	2	4	2	3	0.13592	0.961043	0.17911	0.235168	0.152698	0.202622
pseudogen	RAB5C_me	0	0	0	0	0	1	0	0	0	0	0	0.082597
lincRNA	WWC2_ant	19	17	12	11	15	14	0.460778	0.485841	0.38349	0.230778	0.408676	0.337424
lincRNA	-	4	0	6	2	0	0	0.338822	0	0.669728	0.146556	0	0
lincRNA	-	26	18	15	43	72	48	1.977681	1.613476	1.503519	2.82953	6.152681	3.628555
antisense	-	5	6	1	8	6	4	0.059712	0.084441	0.015737	0.082651	0.0805	0.047475
lincRNA	-	2	1	0	0	0	0	0.177654	0.104677	0	0	0	0
protein_co	zinc_finger_	160	136	118	173	124	120	1.96761	1.970902	1.912211	1.840467	1.713127	1.466594
lincRNA	-	2	4	6	1	4	2	0.063063	0.148631	0.249303	0.027277	0.141694	0.062673
lincRNA	long_interg	0	0	0	2	0	0	0	0	0	0.156044	0	0
pseudogen	-	1	0	2	6	1	0	0.51399	0	1.354627	2.667897	0.577436	0
antisense	-	0	0	0	1	0	1	0	0	0	0.052582	0	0.060406
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.215103	0
pseudogen	YTH_domai	0	1	2	1	0	0	0	0.037903	0.084767	0.027824	0	0
processed_	-	1	1	0	4	1	2	0.039865	0.046979	0	0.137949	0.044786	0.079238
processed_	-	15	7	11	9	6	19	0.324924	0.178688	0.313992	0.168654	0.146013	0.409029
pseudogen	aldehyde_d	0	1	0	0	0	0	0	0.040696	0	0	0	0
pseudogen	family_with	1	9	0	5	0	5	0.03806	0.403659	0	0.164626	0	0.189123
processed_	-	2	1	4	16	13	7	0.053154	0.031319	0.140087	0.367863	0.388146	0.184889
lincRNA	-	1	0	0	2	0	0	0.012847	0	0	0.022227	0	0
pseudogen	-	1	5	5	2	2	0	0.047695	0.281026	0.314249	0.082521	0.107164	0
antisense	-	24	34	9	12	8	17	2.406409	4.017392	1.189147	1.040884	0.90115	1.694013
lincRNA	-	2	0	0	3	1	0	0.415223	0	0	0.538811	0.233239	0
lincRNA	-	4	4	8	24	8	8	0.109722	0.129301	0.289174	0.56952	0.246532	0.218089
pseudogen	-	7	5	6	5	2	0	0.118969	0.100141	0.134376	0.073513	0.038187	0
processed_	-	26	15	11	37	14	13	0.684128	0.465117	0.38141	0.842226	0.413848	0.339952
pseudogen	NADH_deh	0	0	1	0	0	0	0	0	0.219381	0	0	0
antisense	-	0	0	0	1	0	0	0	0	0	0.084656	0	0
pseudogen	regulator_c	5	0	0	0	0	0	0.071833	0	0	0	0	0
processed_	-	26	43	25	5	3	5	0.629673	1.227206	0.797842	0.104755	0.081623	0.120343
antisense	-	0	0	0	0	1	0	0	0	0	0	0.325005	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.180311	0	0
antisense	-	0	0	0	31	9	18	0	0	0	2.134987	0.804937	1.42414

pseudogen	-	1	3	2	0	0	1	0.175884	0.621805	0.463543	0	0	0.174798
antisense	-	3	7	7	10	3	5	0.061919	0.170259	0.190387	0.178553	0.069562	0.102562
sense_intrc	-	0	0	2	1	0	0	0	0	0.250048	0.082077	0	0
antisense	-	3	1	1	4	0	7	0.586063	0.230213	0.257429	0.675999	0	1.359035
pseudogen	FK506_bin	0	0	2	0	1	1	0	0	0.103583	0	0.044154	0.03906
pseudogen	-	5	5	6	0	0	0	0.36612	0.43145	0.578948	0	0	0
pseudogen	-	2	5	0	100	57	73	0.07467	0.219985	0	3.229824	2.390781	2.708622
pseudogen	ribosomal_	307	248	207	158	196	216	5.771621	5.494374	5.128196	2.569683	4.139659	4.035737
pseudogen	-	0	0	2	0	0	0	0	0	0.283591	0	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.038077	0
pseudogen	-	2	2	3	5	7	8	0.173862	0.204886	0.343661	0.376017	0.683631	0.691153
pseudogen	-	6	0	0	6	2	5	0.403104	0	0	0.348723	0.150954	0.333845
protein_co	forkhead_b	10	13	7	6	0	1	0.23322	0.357287	0.215129	0.121054	0	0.023178
pseudogen	peptidylpr	0	6	0	2	0	2	0	0.759283	0	0.185797	0	0.213444
lincRNA	-	8	0	1	6	1	5	0.193303	0	0.031841	0.125419	0.027146	0.120069
lincRNA	-	1	0	0	0	0	0	0.053314	0	0	0	0	0
processed_	-	1	0	0	1	0	0	0.059284	0	0	0.051287	0	0
lincRNA	-	0	2	0	0	0	0	0	0.228526	0	0	0	0
pseudogen	-	2	6	5	0	2	0	0.197173	0.69707	0.649565	0	0.221512	0
pseudogen	inositol(my	1	2	0	0	0	0	0.062875	0.148189	0	0	0	0
antisense	-	9	11	14	0	5	1	0.974374	1.403405	1.997313	0	0.608138	0.107595
pseudogen	-	0	1	0	0	2	0	0	0.117935	0	0	0.224862	0
protein_co	Uncharacte	0	0	1	3	0	2	0	0	0.012652	0.024918	0	0.019084
lincRNA	-	0	0	0	4	0	1	0	0	0	0.11096	0	0.031868
pseudogen	sorting_ne	0	0	0	0	0	2	0	0	0	0	0	0.156823
processed_	-	3	4	4	2	5	1	0.271957	0.427313	0.477831	0.156846	0.509212	0.090093
pseudogen	MT-ND5_ps	4	2	2	2	0	5	0.146145	0.086111	0.096292	0.063215	0	0.181553
pseudogen	-	0	1	1	2	0	0	0	0.100788	0.112703	0.147977	0	0
pseudogen	-	7	3	4	12	17	7	1.203204	0.607673	0.906017	1.784373	3.282762	1.195774
antisense	-	2	5	8	0	9	7	0.241189	0.710566	1.271313	0	1.219324	0.838948
lincRNA	metastasis_	51619	54688	43035	5011	30617	32224	313.8219	391.8075	344.7707	26.35488	209.1151	194.6986
pseudogen	ALG3_alph	1	0	0	0	0	0	0.047523	0	0	0	0	0
lincRNA	-	0	0	0	4	1	4	0	0	0	0.235773	0.076546	0.270857
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.05208	0
processed_	-	0	0	0	0	4	0	0	0	0	0	0.288368	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.227441	0
antisense	-	0	12	4	3	0	1	0	1.774059	0.661263	0.325585	0	0.124678
processed_	-	7	9	4	20	24	20	0.729502	1.105294	0.549317	1.803107	2.809886	2.071419
lincRNA	-	0	0	0	3	0	0	0	0	0	0.173481	0	0
antisense	TET2_antis	2	1	2	1	4	0	0.197173	0.116178	0.259826	0.085287	0.443024	0
pseudogen	lactate_deh	0	0	0	1	1	2	0	0	0	0.046168	0.059956	0.106077
pseudogen	moesin_ps	1	2	1	0	0	0	0.030566	0.072041	0.040279	0	0	0
pseudogen	ATP-bindin	16	21	4	34	34	41	0.401448	0.620921	0.132253	0.737992	0.95838	1.022358
pseudogen	hydroxyacy	5	1	5	2	1	2	0.115895	0.027315	0.152722	0.040104	0.02604	0.046072

antisense	-	0	0	2	0	0	0	0	0	0.31075	0	0	0
antisense	-	38	32	18	67	38	37	0.882737	0.876001	0.551004	1.346436	0.9917	0.854199
antisense	-	5	1	1	23	14	20	0.87074	0.205223	0.229484	3.465049	2.739023	3.461451
lincRNA	-	1	0	0	0	1	0	0.067873	0	0	0	0.076251	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.288718	0
pseudogen	SET_pseudo	0	2	3	4	0	4	0	0.155001	0.259987	0.227572	0	0.261436
lincRNA	-	0	0	0	1	1	1	0	0	0	0.12793	0.166134	0.146967
pseudogen	heat_shock	3	1	0	0	0	0	0.104695	0.041126	0	0	0	0
lincRNA	-	32	27	19	24	12	32	0.740757	0.736541	0.579581	0.480618	0.312073	0.736183
lincRNA	-	0	0	0	6	0	0	0	0	0	0.4053	0	0
pseudogen	unc-93_ho	0	1	0	0	0	0	0	0.088493	0	0	0	0
lincRNA	-	0	0	0	4	2	5	0	0	0	0.321396	0.208687	0.461527
lincRNA	-	0	0	5	3	2	0	0	0	0.154071	0.060688	0.052541	0
pseudogen	-	25	10	9	24	12	22	0.464232	0.218828	0.220228	0.38554	0.250337	0.406001
sense_intro	EMCN_intr	0	0	0	5	2	3	0	0	0	0.47608	0.247301	0.328154
pseudogen	-	0	0	2	0	0	0	0	0	0.115886	0	0	0
pseudogen	-	0	0	0	8	4	2	0	0	0	0.299584	0.194525	0.086041
pseudogen	-	0	0	0	0	0	6	0	0	0	0	0	0.494029
antisense	-	0	3	1	0	1	0	0	0.399921	0.149067	0	0.127085	0
lincRNA	-	0	0	0	2	0	0	0	0	0	0.164154	0	0
protein_co	proline-rich	4	0	0	0	1	0	0.180532	0	0	0	0.050704	0
processed_	-	1	4	2	4	0	3	0.073022	0.344208	0.19245	0.252684	0	0.217713
processed_	-	19	38	28	0	0	0	0.873917	2.059717	1.697109	0	0	0
pseudogen	SMT3_supp	0	0	0	2	0	0	0	0	0	0.373869	0	0
protein_co	protocadhe	49	22	34	77	90	103	0.495721	0.262284	0.453268	0.673899	1.022899	1.035591
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.133369
sense_intro	ZNF346_in	11	10	6	18	4	9	0.781679	0.837419	0.561852	1.106551	0.319334	0.635606
pseudogen	-	5	0	0	0	0	4	0.278344	0	0	0	0	0.2213
pseudogen	family_with	27	9	20	52	23	31	0.502428	0.19736	0.490427	0.837098	0.480825	0.573299
antisense	-	9	7	18	22	55	34	0.717574	0.657702	1.891173	1.517434	4.926469	2.694093
lincRNA	-	1	1	0	0	0	0	0.077854	0.091747	0	0	0	0
antisense	-	0	1	0	0	0	2	0	0.098871	0	0	0	0.166764
pseudogen	-	5	4	3	2	5	8	0.447893	0.422252	0.354128	0.154988	0.50318	0.712204
antisense	-	3	5	2	3	9	4	0.200029	0.39287	0.175726	0.173044	0.67416	0.265058
pseudogen	-	8	10	10	31	26	36	1.366219	2.012507	2.250428	4.579891	4.988303	6.110019
protein_co	pentraxin_	2	0	1	0	0	0	0.069843	0	0.046018	0	0	0
antisense	-	51	38	41	49	43	43	1.146493	1.006681	1.214562	0.952928	1.085972	0.960681
lincRNA	-	2	0	0	0	0	1	0.134882	0	0	0	0	0.067024
antisense	-	3	4	3	2	0	2	0.390228	0.613147	0.514226	0.225056	0	0.258546
lincRNA	-	2	4	13	11	6	4	0.169411	0.399281	1.451076	0.806061	0.570969	0.33673
pseudogen	-	2	0	0	2	3	0	0.107823	0	0	0.093277	0.181698	0
antisense	-	0	0	0	1	1	3	0	0	0	0.068664	0.089169	0.236645
processed_	-	0	0	3	0	0	0	0	0	0.056687	0	0	0
pseudogen	trafficking_	1	0	0	0	0	0	0.12944	0	0	0	0	0

lincRNA	-	0	0	0	4	3	9	0	0	0	0.284908	0.277493	0.736433
antisense	-	2	3	1	1	2	5	0.189413	0.334818	0.1248	0.08193	0.212794	0.470609
pseudogen	-	0	0	0	4	0	0	0	0	0	0.175307	0	0
lincRNA	-	0	2	0	27	24	17	0	0.083073	0	0.823283	0.950348	0.595499
lincRNA	-	7	5	2	0	0	0	0.492147	0.414261	0.185294	0	0	0
lincRNA	-	0	0	0	0	0	3	0	0	0	0	0	0.214459
lincRNA	-	0	0	0	13	7	11	0	0	0	0.688307	0.481308	0.66908
lincRNA	-	5	8	2	0	0	0	0.512002	0.965381	0.269877	0	0	0
protein_co	protocadhe	14	16	16	13	25	17	0.156135	0.210281	0.235141	0.125424	0.313229	0.188422
lincRNA	-	104	59	56	5	5	0	5.037386	3.367682	3.574331	0.20951	0.272076	0
lincRNA	-	2	0	0	0	0	0	0.139502	0	0	0	0	0
pseudogen	-	0	2	1	0	1	3	0	0.760826	0.425386	0	0.362658	0.962452
antisense	KIAA0196_	2	0	2	0	0	0	0.180378	0	0.237694	0	0	0
antisense	-	0	0	1	0	0	0	0	0	0.094916	0	0	0
lincRNA	-	0	0	0	5	3	4	0	0	0	0.43618	0.339862	0.400869
antisense	-	1	0	3	1	0	0	0.081825	0	0.323477	0.070787	0	0
antisense	-	2	0	0	0	0	0	0.213472	0	0	0	0	0
pseudogen	-	4	0	0	0	0	0	0.547194	0	0	0	0	0
antisense	-	0	0	0	1	5	14	0	0	0	0.051809	0.336402	0.833254
pseudogen	-	0	1	0	6	0	2	0	0.166367	0	0.732782	0	0.280608
pseudogen	-	2	0	0	0	0	0	0.147674	0	0	0	0	0
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.121511
pseudogen	-	1	4	2	4	3	0	0.121424	0.572364	0.320015	0.420173	0.409238	0
antisense	-	0	0	0	0	0	3	0	0	0	0	0	0.128536
lincRNA	-	0	2	2	0	0	0	0	0.272435	0.304643	0	0	0
antisense	HOXA_clust	40	32	23	4	0	3	1.823979	1.719558	1.382046	0.157791	0	0.135954
lincRNA	-	0	2	0	0	2	0	0	0.130792	0	0	0.124687	0
pseudogen	Fc_fragmen	4	0	0	0	0	3	0.188738	0	0	0	0	0.140679
antisense	-	0	0	0	1	1	0	0	0	0	0.097238	0.126276	0
processed_	-	2	1	1	0	0	0	0.175884	0.103634	0.115886	0	0	0
antisense	-	21	15	13	19	7	19	0.404277	0.340297	0.32979	0.316429	0.151393	0.363515
pseudogen	glucuronid	28	18	14	61	36	39	1.111205	0.841813	0.732148	2.094253	1.605047	1.538192
pseudogen	-	0	0	1	0	0	0	0	0	0.252766	0	0	0
pseudogen	-	0	0	0	3	0	0	0	0	0	0.172826	0	0
antisense	-	5	7	2	1	13	9	0.524168	0.86478	0.27629	0.090691	1.531063	0.937676
pseudogen	-	0	4	0	1	0	1	0	0.223412	0	0.041002	0	0.047103
lincRNA	-	0	0	0	2	0	0	0	0	0	0.111705	0	0
pseudogen	Kruppel-lik	1	1	2	0	1	1	0.051801	0.061045	0.136523	0	0.058196	0.051481
lincRNA	-	0	0	0	0	0	5	0	0	0	0	0	0.537976
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.05794	0
pseudogen	phosphogly	2	0	0	0	0	0	0.130076	0	0	0	0	0
lincRNA	-	11	2	0	0	0	0	1.053076	0.225634	0	0	0	0
pseudogen	HIG1_hypo	0	0	0	1	1	0	0	0	0	0.164154	0.213175	0
processed_	long_interg	0	0	0	2	1	2	0	0	0	0.027474	0.017839	0.031562

pseudogen	MT-ND1_ps	0	2	0	0	5	2	0	0.133307	0	0	0.317713	0.112423
protein_co	uncharacte	88	77	97	81	75	65	5.211194	5.37344	7.569394	4.149565	4.98959	3.825406
protein_co	CDNA_FLJ2	13	7	18	59	37	39	0.389713	0.24729	0.711064	1.530088	1.246098	1.161918
antisense	-	0	0	4	0	0	0	0	0	0.437387	0	0	0
pseudogen	MT-ND4_ps	0	0	1	0	0	0	0	0	0.536641	0	0	0
sense_intrc	-	6	9	3	0	2	0	0.595959	1.053451	0.392664	0	0.223174	0
lincRNA	prostate_ca	0	0	0	4	0	0	0	0	0	0.318601	0	0
lincRNA	-	0	0	0	3	3	5	0	0	0	0.129132	0.167695	0.247246
lincRNA	-	0	0	0	2	0	2	0	0	0	0.196141	0	0.225328
pseudogen	-	1	0	0	0	0	0	0.065765	0	0	0	0	0
protein_co	coiled-coil_	226	197	209	167	122	149	2.827189	2.904155	3.445304	1.807282	1.71457	1.852432
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.022435	0
processed_	-	0	0	0	2	3	0	0	0	0	0.0542	0.105579	0
lincRNA	-	0	2	0	0	0	1	0	0.170691	0	0	0	0.071975
sense_intrc	-	4	8	6	18	16	16	0.039281	0.092581	0.077644	0.152918	0.176519	0.156154
lincRNA	-	0	0	0	3	0	0	0	0	0	0.032941	0	0
protein_co	homeobox_	315	308	319	11	3	1	6.562933	7.562149	8.758161	0.198264	0.07022	0.020706
sense_intrc	HTR4_intrc	0	0	0	1	0	2	0	0	0	0.026877	0	0.061754
lincRNA	-	0	1	0	0	0	0	0	0.031008	0	0	0	0
lincRNA	STAU2_anti	0	0	0	3	8	9	0	0	0	0.066183	0.229194	0.228096
protein_co	transmemb	181	180	145	192	215	229	3.753357	4.398665	3.96227	3.444336	5.008744	4.719396
protein_co	protocadhe	1907	1615	1703	250	461	294	21.95227	21.90828	25.8332	2.489612	5.961817	3.363455
antisense	-	0	0	0	0	4	1	0	0	0	0	0.599254	0.132529
protein_co	serpin_pep	16	22	26	42	27	29	0.369409	0.598574	0.791036	0.838881	0.700327	0.66542
protein_co	chromoson	2	0	0	80	72	82	0.071639	0	0	2.478966	2.897338	2.919047
lincRNA	-	0	0	0	3	2	0	0	0	0	0.239785	0.207595	0
lincRNA	-	0	2	0	0	0	0	0	0.15636	0	0	0	0
protein_co	HCG15011	13	9	6	8	3	7	0.910361	0.742711	0.553677	0.484645	0.236016	0.487167
pseudogen	-	0	0	0	0	1	5	0	0	0	0	0.047849	0.211641
antisense	RAD21_ant	1	0	0	11	4	3	0.026339	0	0	0.250641	0.11836	0.078528
pseudogen	-	1	0	2	0	0	0	0.179461	0	0.472971	0	0	0
pseudogen	-	18	27	17	5	9	12	0.860052	1.520279	1.070375	0.206674	0.483108	0.569827
lincRNA	-	2	0	0	0	0	0	0.157095	0	0	0	0	0
pseudogen	-	0	2	0	2	1	3	0	0.336322	0	0.246894	0.160312	0.425451
antisense	-	0	1	1	0	1	1	0	0.130518	0.145948	0	0.124427	0.110071
antisense	-	7	4	2	0	1	0	0.679976	0.457892	0.256012	0	0.10913	0
pseudogen	-	0	0	1	0	0	0	0	0	0.032463	0	0	0
pseudogen	-	1	1	4	1	1	2	0.052888	0.062325	0.278774	0.045753	0.059417	0.105123
antisense	-	0	1	0	0	0	0	0	0.074626	0	0	0	0
antisense	-	21	13	15	26	15	4	2.167175	1.580976	2.039862	2.321192	1.739062	0.410246
antisense	microRNA_	0	0	0	13	2	6	0	0	0	0.989013	0.197594	0.524393
protein_co	Uncharacte	1	0	0	0	1	0	0.073529	0	0	0	0.082605	0
antisense	taurine_up	1256	1100	1494	1636	1382	1057	11.72112	12.09704	18.37235	13.20765	14.48893	9.803111
lincRNA	-	6	6	2	0	0	0	0.671556	0.791388	0.294982	0	0	0

processed_	-	0	0	0	0	1	1	0	0	0	0	0.11943	0.105651
sense_intrc	-	0	1	0	38	16	38	0	0.13162	0	3.671642	2.007626	4.218004
antisense	-	0	0	0	0	2	1	0	0	0	0	0.298874	0.132196
lincRNA	-	0	0	0	0	1	7	0	0	0	0	0.156929	0.971763
pseudogen	-	3	5	5	2	4	4	0.248161	0.487404	0.545026	0.143122	0.371724	0.328838
protein_co	TMF1-regul	942	800	658	354	229	322	25.47008	25.49039	23.44445	8.280292	6.95607	8.652566
lincRNA	-	0	0	0	5	2	0	0	0	0	0.385513	0.200256	0
pseudogen	-	1	0	0	0	0	0	0.481282	0	0	0	0	0
sense_intrc	-	2	0	0	6	20	21	0.139686	0	0	0.362524	1.569285	1.457645
lincRNA	-	1	0	0	0	0	0	0.116868	0	0	0	0	0
lincRNA	-	0	0	2	0	1	0	0	0	0.17888	0	0.076251	0
protein_co	Uncharacte	3	3	1	0	7	3	0.088382	0.104153	0.038822	0	0.231681	0.087836
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.383716	0
pseudogen	-	0	0	0	0	3	2	0	0	0	0	0.159453	0.094038
lincRNA	-	1	2	3	6	8	14	0.068755	0.162046	0.271805	0.356875	0.617932	0.956619
lincRNA	-	0	1	0	0	0	0	0	0.369158	0	0	0	0
antisense	-	0	0	0	0	2	0	0	0	0	0	0.109331	0
lincRNA	-	7	7	4	14	5	11	0.588233	0.693197	0.442941	1.017753	0.472031	0.918658
antisense	-	3	0	2	1	1	0	0.204669	0	0.179802	0.059019	0.076644	0
lincRNA	long_interg	0	0	2	0	0	0	0	0	0.171831	0	0	0
lincRNA	-	0	0	0	1	0	3	0	0	0	0.106509	0	0.367075
sense_intrc	-	1	8	2	0	0	6	0.120048	1.13175	0.316387	0	0	0.715837
lincRNA	-	0	0	0	5	0	0	0	0	0	0.617236	0	0
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.179264
antisense	-	1	0	0	0	0	0	0.011679	0	0	0	0	0
antisense	-	4	1	0	0	1	0	0.259833	0.076549	0	0	0.072977	0
sense_intrc	-	1	8	2	2	4	5	0.103806	0.978631	0.273581	0.179604	0.466478	0.515824
antisense	-	0	1	0	0	0	0	0	0.096129	0	0	0	0
protein_co	Uncharacte	3	0	2	0	2	0	0.19228	0	0.168918	0	0.144009	0
lincRNA	-	0	0	0	4	0	0	0	0	0	0.441435	0	0
sense_intrc	-	0	4	0	0	0	0	0	0.491242	0	0	0	0
sense_intrc	-	0	0	0	0	0	2	0	0	0	0	0	0.98344
lincRNA	prostate_ca	0	0	0	23	28	11	0	0	0	0.528803	0.836007	0.290539
lincRNA	-	2	1	0	0	0	0	0.183187	0.107937	0	0	0	0
pseudogen	-	2	2	2	1	4	1	0.307796	0.362719	0.4056	0.133136	0.69158	0.152948
lincRNA	-	2	5	7	0	0	0	0.366374	1.079372	1.689768	0	0	0
antisense	-	7	8	1	0	0	0	0.68374	0.920852	0.128715	0	0	0
protein_co	small_integ	2	0	3	0	1	3	0.116997	0	0.231259	0	0.065719	0.174411
protein_co	Full-length_	2	2	0	3	6	11	0.062652	0.073832	0	0.0813	0.211157	0.342458
IG_V_pseu	immunoglo	0	0	0	2	0	0	0	0	0	0.254438	0	0
pseudogen	high_mobil	1	2	0	0	1	0	0.091752	0.216249	0	0	0.103078	0
pseudogen	-	0	0	2	0	0	0	0	0	0.237694	0	0	0
lincRNA	-	0	0	1	0	0	0	0	0	0.109691	0	0	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.142799	0

sense_intrc	-	0	2	0	2	1	2	0	0.440903	0	0.323667	0.210162	0.371831
lincRNA	-	6	8	7	6	7	7	0.601602	0.945269	0.924892	0.520442	0.788506	0.697535
antisense	-	18	12	2	32	42	48	1.319859	1.036915	0.19325	2.029868	3.459818	3.497887
lincRNA	-	0	0	0	7	1	8	0	0	0	0.282709	0.052448	0.371175
pseudogen	-	11	4	4	9	2	9	1.122063	0.48083	0.537675	0.794201	0.229194	0.912382
protein_co	protocadhe	4	4	4	0	3	7	0.046016	0.054227	0.060637	0	0.038772	0.08003
lincRNA	-	2	0	1	0	0	0	0.035531	0	0.02341	0	0	0
pseudogen	cadherin_1	0	1	1	0	0	0	0	0.211484	0.236486	0	0	0
lincRNA	-	2	0	3	0	0	0	0.194994	0	0.385432	0	0	0
antisense	-	3	0	0	1	0	0	0.152129	0	0	0.043869	0	0
lincRNA	-	0	0	1	0	0	0	0	0	0.128241	0	0	0
lincRNA	-	25	10	26	0	0	0	2.38044	1.122081	3.262312	0	0	0
sense_intrc	-	1	0	2	0	0	2	0.207612	0	0.547163	0	0	0.412659
antisense	-	2	0	0	0	0	0	0.256995	0	0	0	0	0
pseudogen	high_mobil	0	0	0	1	0	0	0	0	0	0.104088	0	0
antisense	-	2	0	1	1	0	1	0.057389	0	0.037812	0.024823	0	0.028517
pseudogen	-	0	0	0	0	7	2	0	0	0	0	1.435626	0.362856
lincRNA	hsa-mir-14	1	0	3	4	0	0	0.023008	0	0.090956	0.079616	0	0
lincRNA	-	1	0	1	0	0	0	0.060366	0	0.079548	0	0	0
pseudogen	-	2	0	0	0	0	0	0.072324	0	0	0	0	0
lincRNA	-	1	0	0	0	0	0	0.118969	0	0	0	0	0
pseudogen	-	1	0	0	0	0	0	0.188402	0	0	0	0	0
lincRNA	-	0	0	0	11	0	5	0	0	0	1.174331	0	0.613217
sense_intrc	-	0	0	0	0	1	1	0	0	0	0	0.09996	0.088427
antisense	-	0	0	1	0	0	1	0	0	0.094147	0	0	0.071004
pseudogen	-	0	1	0	2	1	5	0	0.112208	0	0.164744	0.106971	0.473148
protein_co	protocadhe	1	2	3	1	5	0	0.011496	0.027096	0.045448	0.009945	0.064578	0
antisense	-	0	0	1	0	0	0	0	0	0.107659	0	0	0
pseudogen	family_with	43	60	43	35	42	63	2.373788	3.903299	3.128072	1.671493	2.604785	3.456397
antisense	-	0	0	0	6	3	4	0	0	0	0.464964	0.301908	0.356102
pseudogen	-	0	3	0	2	0	0	0	0.421539	0	0.206301	0	0
antisense	HOXA_clust	44	51	35	18	16	21	0.948841	1.296038	0.994589	0.335796	0.387623	0.450059
processed_	-	1	4	6	0	1	0	0.036039	0.169878	0.284942	0	0.040487	0
pseudogen	-	1	0	0	1	0	0	0.037654	0	0	0.032574	0	0
lincRNA	-	5	1	1	0	0	0	0.36612	0.08629	0.096491	0	0	0
pseudogen	-	0	4	1	6	3	4	0	0.110421	0.030869	0.12159	0.07895	0.093122
antisense	OSGEPL1_a	3	8	5	16	17	7	0.280111	0.88025	0.615196	1.292385	1.783229	0.649556
antisense	-	0	0	1	0	0	1	0	0	0.141508	0	0	0.106722
antisense	-	1	3	0	0	2	0	0.119506	0.42249	0	0	0.268514	0
pseudogen	ring_finger_	6	1	1	1	2	6	0.588233	0.115533	0.129191	0.084813	0.220281	0.584601
lincRNA	-	0	0	0	0	4	1	0	0	0	0	0.814739	0.180185
antisense	-	1	0	0	0	0	0	0.129124	0	0	0	0	0
antisense	-	10	10	15	0	4	0	1.050417	1.237852	2.076288	0	0.472031	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.072074

lincRNA	-	0	4	4	0	0	0	0	0.373579	0.417744	0	0	0
sense_intrc	-	2	5	0	0	1	0	0.297421	0.876232	0	0	0.167067	0
antisense	-	4	5	4	0	0	0	0.134796	0.198561	0.177628	0	0	0
antisense	-	0	0	0	0	0	7	0	0	0	0	0	0.624234
protein_co	solute_carr	9	9	15	11	19	11	0.185541	0.218649	0.407496	0.196179	0.440048	0.225372
antisense	-	0	0	4	2	0	0	0	0	0.446485	0.146556	0	0
antisense	-	3	5	3	2	0	1	0.066957	0.131509	0.088233	0.038616	0	0.022181
antisense	-	0	1	2	3	0	0	0	0.1289	0.288278	0.283878	0	0
antisense	-	0	3	0	0	0	2	0	0.466741	0	0	0	0.262414
lincRNA	-	1	0	1	0	0	0	0.068223	0	0.089901	0	0	0
pseudogen	-	1	0	0	0	0	2	0.386431	0	0	0	0	0.768088
protein_co	eukaryotic_	15	10	9	80	19	63	0.207232	0.162807	0.163849	0.956136	0.294896	0.865001
lincRNA	-	0	0	0	1	0	0	0	0	0	0.107509	0	0
pseudogen	-	0	3	0	1	2	4	0	0.917467	0	0.224504	0.583097	1.031648
lincRNA	-	0	2	0	0	0	0	0	0.194354	0	0	0	0
protein_co	Uncharacte	1	7	1	0	5	0	0.071542	0.590154	0.094275	0	0.401864	0
lincRNA	-	0	0	1	0	0	0	0	0	0.118847	0	0	0
antisense	-	31	23	16	95	82	93	0.462432	0.404316	0.314515	1.22595	1.374197	1.378728
lincRNA	-	0	0	0	27	11	6	0	0	0	2.200303	1.164119	0.561716
antisense	-	0	0	1	0	0	0	0	0	0.057418	0	0	0
antisense	protease_se	1	0	0	11	16	12	0.047142	0	0	0.448609	0.847386	0.562216
pseudogen	superoxide_	0	0	0	0	1	0	0	0	0	0	0.131004	0
antisense	-	1	2	0	0	0	0	0.058113	0.136965	0	0	0	0
processed_	-	0	0	1	1	0	1	0	0	0.029473	0.019349	0	0.022228
antisense	-	0	4	1	132	70	83	0	0.376397	0.105224	9.118334	6.279509	6.586676
antisense	ZFHX4_anti	103	93	96	5	9	10	3.18698	3.391034	3.914246	0.133837	0.312848	0.307505
lincRNA	-	5	0	0	6	4	3	0.358193	0	0	0.371845	0.321926	0.213589
antisense	-	3	0	0	0	0	0	0.284629	0	0	0	0	0
pseudogen	-	10	10	10	16	37	27	0.213558	0.251665	0.281417	0.295596	0.8877	0.573045
lincRNA	-	16	12	13	9	4	13	0.305796	0.270272	0.327409	0.148805	0.085886	0.246925
processed_	-	0	0	0	5	0	0	0	0	0	0.307375	0	0
pseudogen	transgelin_	0	10	8	4	9	2	0	1.062823	0.950777	0.312088	0.911897	0.179264
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.121628	0
lincRNA	-	0	0	0	3	0	0	0	0	0	0.140344	0	0
pseudogen	-	0	1	0	0	0	0	0	0.369158	0	0	0	0
pseudogen	-	12	6	8	13	6	9	3.308812	1.949617	2.906803	3.100968	1.858622	2.466284
lincRNA	-	0	0	0	1	0	0	0	0	0	0.019398	0	0
lincRNA	-	9	4	2	0	2	0	0.62365	0.326637	0.182626	0	0.155696	0
antisense	-	0	0	2	0	0	0	0	0	0.157302	0	0	0
antisense	-	0	0	3	0	2	0	0	0	0.476742	0	0.270961	0
lincRNA	-	2	1	0	2	2	3	0.129917	0.076549	0	0.11239	0.145953	0.193671
pseudogen	-	5	5	3	0	0	2	1.838229	2.166241	1.453402	0	0	0.730751
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.079
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.105018

lincRNA	-	12	8	7	0	0	0	1.136479	0.892848	0.873601	0	0	0
processed_	-	9	7	4	2	4	5	0.266333	0.244111	0.155983	0.051201	0.132981	0.147049
processed_	-	2	1	1	4	1	0	0.03768	0.022202	0.024827	0.065194	0.021166	0
antisense	-	0	0	0	1	0	0	0	0	0	0.078557	0	0
protein_co	ALG11_alpl	123	79	113	88	107	96	1.423643	1.077532	1.723492	0.881133	1.391326	1.104274
lincRNA	-	5	0	0	0	0	1	0.540214	0	0	0	0	0.107376
antisense	-	49	46	30	63	28	53	3.765034	4.165219	3.037588	4.187708	2.417018	4.047235
processed_	-	0	0	0	0	3	1	0	0	0	0	0.498402	0.146967
protein_co	ataxin_7-lil	1788	1503	1472	1976	1709	2049	25.77144	25.5292	27.95849	24.63889	27.67338	29.35099
lincRNA	-	2	2	2	1	0	2	0.192863	0.227278	0.254147	0.083422	0	0.191672
sense_intrc	-	0	3	0	0	0	0	0	0.108689	0	0	0	0
protein_co	protein_kir	4068	3264	4321	7044	7092	5549	15.94344	15.07503	22.31619	23.8827	31.22618	21.61352
antisense	-	0	0	0	1	2	1	0	0	0	0.083727	0.217462	0.096187
protein_co	protocadhe	18	17	8	7	7	11	0.206935	0.230313	0.121196	0.069618	0.090409	0.12568
lincRNA	LZTS1_anti:	7	8	9	3	6	0	0.415456	0.559531	0.70389	0.154032	0.400062	0
antisense	-	3	2	4	0	0	0	0.451202	0.354476	0.792765	0	0	0
lincRNA	-	0	0	1	0	1	0	0	0	0.147491	0	0.125742	0
antisense	-	320	292	238	431	373	394	3.962835	4.261337	3.883897	4.617387	5.189361	4.849108
sense_intrc	-	7	3	0	4	1	4	3.46343	1.749189	0	1.712109	0.55585	1.96688
antisense	-	4	5	7	2	0	5	0.037256	0.05488	0.085915	0.016115	0	0.046283
antisense	-	0	0	1	0	0	0	0	0	0.145038	0	0	0
lincRNA	-	25	14	14	0	1	2	2.289835	1.511121	1.689768	0	0.1029	0.182056
antisense	-	3	2	1	3	1	2	0.355309	0.27914	0.15607	0.307375	0.133056	0.23541
lincRNA	-	3	2	3	1	0	4	0.28514	0.224013	0.375745	0.082224	0	0.377839
protein_co	protocadhe	10	10	16	12	19	10	0.114964	0.135478	0.242391	0.119346	0.245395	0.114254
lincRNA	-	4	3	6	0	0	0	0.465415	0.411348	0.919955	0	0	0
pseudogen	high_mobil	1	0	0	2	0	0	0.093206	0	0	0.161264	0	0
pseudogen	transmemb	1	7	2	21	13	6	0.068755	0.567161	0.181203	1.249061	1.004139	0.40998
pseudogen	-	0	0	0	5	5	3	0	0	0	0.326668	0.424222	0.225167
processed_	-	0	0	0	0	7	4	0	0	0	0	0.674767	0.341096
lincRNA	-	0	0	0	3	0	0	0	0	0	0.2373	0	0
antisense	-	0	0	0	0	1	3	0	0	0	0	0.057969	0.153842
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.209792	0
lincRNA	-	0	2	0	0	0	0	0	0.163962	0	0	0	0
pseudogen	zinc_finger_	1	0	0	0	0	0	0.051549	0	0	0	0	0
pseudogen	-	0	0	0	0	1	3	0	0	0	0	0.068838	0.182688
pseudogen	MT-ND1_ps	0	0	2	0	0	0	0	0	0.148433	0	0	0
protein_co	UTP14_U3_	497	365	453	467	438	413	4.758849	4.118561	5.71582	3.868347	4.711603	3.930114
processed_	-	0	1	5	0	0	0	0	0.084536	0.472651	0	0	0
lincRNA	-	39	32	23	0	0	0	2.343585	2.26607	1.821289	0	0	0
lincRNA	-	0	0	0	2	0	0	0	0	0	0.321396	0	0
antisense	-	4	13	1	0	0	0	0.376135	1.440569	0.123913	0	0	0
pseudogen	-	10	2	8	11	9	14	0.892765	0.210414	0.941157	0.849558	0.90267	1.242153
lincRNA	-	0	0	0	0	3	4	0	0	0	0	0.312483	0.368575

lincRNA	-	0	1	0	0	0	0	0	0.110031	0	0	0	0
lincRNA	-	0	2	0	0	0	0	0	0.263239	0	0	0	0
antisense	-	2	2	1	5	8	0	0.273597	0.322417	0.180267	0.591717	1.229476	0
processed_	-	15	4	6	1	3	3	0.776261	0.24394	0.409169	0.044769	0.174416	0.154293
lincRNA	-	1	0	0	0	0	0	0.087796	0	0	0	0	0
pseudogen	-	3	0	3	5	0	2	0.406197	0	0.535268	0.585664	0	0.269126
lincRNA	-	1	0	0	0	0	0	0.065038	0	0	0	0	0
processed_	-	59	40	40	5	12	19	0.71411	0.570533	0.637982	0.052354	0.163171	0.228548
lincRNA	-	5	1	2	1	0	0	0.393906	0.092839	0.207629	0.068153	0	0
protein_co	protocadhe	58	35	57	54	62	76	0.665059	0.472941	0.861275	0.53566	0.79868	0.866075
antisense	-	0	0	0	8	3	3	0	0	0	0.691304	0.336656	0.297815
antisense	-	44	23	38	18	24	21	2.480728	1.528134	2.823221	0.877934	1.520151	1.176672
protein_co	Uncharacte	0	0	0	4	5	1	0	0	0	0.369346	0.599556	0.106077
processed_	-	159	119	87	1	6	7	1.640541	1.446919	1.182889	0.008926	0.069549	0.071779
antisense	-	0	0	0	0	1	0	0	0	0	0	0.10115	0
antisense	FER1L6_ant	2	0	0	0	0	0	0.060643	0	0	0	0	0
pseudogen	phosphatid	0	2	0	0	0	0	0	0.19108	0	0	0	0
protein_co	protocadhe	11	20	16	98	141	107	0.147955	0.317011	0.283591	1.140318	2.130616	1.430311
antisense	-	0	2	1	0	7	0	0	0.213657	0.119458	0	0.712896	0
sense_intrc	-	19	10	14	9	15	20	1.418729	0.87994	1.377554	0.581368	1.258306	1.484176
pseudogen	-	31	25	22	1	3	7	0.552025	0.524619	0.516244	0.015405	0.060016	0.123881
pseudogen	-	0	0	0	2	0	0	0	0	0	0.078423	0	0
antisense	-	2	0	0	0	0	0	0.180995	0	0	0	0	0
lincRNA	-	3	0	0	0	0	0	0.323468	0	0	0	0	0
lincRNA	-	1	0	0	0	0	0	0.089126	0	0	0	0	0
antisense	family_with	2	4	2	1	2	0	0.133689	0.31509	0.17617	0.057827	0.150192	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.082017
lincRNA	-	0	2	0	0	0	0	0	0.216249	0	0	0	0
pseudogen	-	4	0	0	3	0	4	0.308245	0	0	0.199995	0	0.306341
protein_co	protocadhe	24	13	22	16	19	21	0.276094	0.176237	0.333505	0.159231	0.245555	0.24009
antisense	-	0	2	0	0	5	0	0	0.414536	0	0	0.987972	0
pseudogen	-	0	0	1	0	0	0	0	0	0.38122	0	0	0
pseudogen	MAPRE1_ps	0	0	0	1	1	0	0	0	0	0.057464	0.074625	0
pseudogen	-	0	0	0	2	5	3	0	0	0	0.101889	0.330789	0.175575
pseudogen	protein-kin	0	8	2	1	1	1	0	0.217948	0.060929	0.02	0.025972	0.022976
antisense	-	0	1	0	0	0	0	0	0.109452	0	0	0	0
pseudogen	-	3	0	0	3	0	0	0.162895	0	0	0.14092	0	0
antisense	-	1	2	4	0	0	4	0.024274	0.05721	0.127947	0	0	0.096495
lincRNA	-	0	0	0	0	3	0	0	0	0	0	0.231424	0
lincRNA	-	0	0	0	0	1	2	0	0	0	0	0.205089	0.362856
antisense	-	24	12	21	81	71	78	1.994637	1.175279	2.299888	5.823723	6.629184	6.442537
antisense	-	0	0	0	4	2	1	0	0	0	0.336757	0.218661	0.096717
antisense	-	0	0	4	0	0	0	0	0	0.080004	0	0	0
antisense	-	0	0	0	0	5	0	0	0	0	0	0.583097	0

antisense	-	0	0	2	0	0	0	0	0	0.28533	0	0	0
processed_	-	18	20	12	5	13	24	2.507731	3.283565	2.203051	0.602617	2.034702	3.322993
protein_co	protocadhe	536	420	431	155	185	153	6.198421	5.723645	6.567928	1.55064	2.403461	1.758399
pseudogen	high_mobil	3	1	0	2	3	0	0.140676	0.055259	0	0.081132	0.158041	0
antisense	-	12	2	4	7	0	0	0.357508	0.070217	0.157036	0.180412	0	0
protein_co	claudin_23	2	0	0	15	15	9	0.048816	0	0	0.316728	0.411313	0.218316
antisense	-	1	0	0	1	1	2	0.082334	0	0	0.071227	0.092498	0.163652
pseudogen	-	0	0	0	12	7	1	0	0	0	0.41106	0.311392	0.039352
lincRNA	-	0	0	0	1	0	0	0	0	0	0.019349	0	0
lincRNA	-	0	0	0	1	3	1	0	0	0	0.075952	0.2959	0.087254
antisense	-	2	0	1	0	0	0	0.110294	0	0.07267	0	0	0
protein_co	Uncharacte	0	0	0	1	9	3	0	0	0	0.056333	0.658405	0.194148
pseudogen	-	4	0	0	0	0	0	0.857344	0	0	0	0	0
antisense	-	2	8	2	8	6	14	0.210501	0.99225	0.277389	0.728412	0.709454	1.464407
pseudogen	asparagine-	10	8	5	27	18	18	0.692039	0.652421	0.455969	1.616432	1.399433	1.237978
antisense	-	316	235	160	93	129	184	17.10568	14.99092	11.41322	4.355111	7.844983	9.898758
lincRNA	-	6	2	0	7	1	17	0.44426	0.174511	0	0.448381	0.083183	1.250963
pseudogen	-	0	0	0	6	2	1	0	0	0	0.509821	0.22069	0.097614
lincRNA	-	0	0	1	0	0	0	0	0	0.210765	0	0	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.268514	0
antisense	-	3	1	0	0	1	3	0.275734	0.108312	0	0	0.103257	0.274032
protein_co	zinc_finger_	457	443	455	813	652	573	4.270038	4.877826	5.60224	6.571569	6.844034	5.320835
lincRNA	-	1	0	0	0	0	0	0.060504	0	0	0	0	0
pseudogen	asparagine-	5	5	1	23	4	16	0.624304	0.735704	0.164536	2.484375	0.561094	1.985436
IG_C_pseu	immunoglo	3	1	1	4	1	0	0.126451	0.049672	0.055544	0.145856	0.047353	0
lincRNA	-	0	1	0	0	0	0	0	0.127582	0	0	0	0
pseudogen	pyruvate_k	0	0	1	0	0	0	0	0	0.227985	0	0	0
antisense	-	0	0	0	6	0	12	0	0	0	0.559661	0	1.285883
antisense	-	0	2	6	1	4	1	0	0.201251	0.675129	0.073869	0.383716	0.084861
antisense	-	0	0	0	6	2	1	0	0	0	0.401158	0.173652	0.076809
antisense	-	0	0	0	3	5	0	0	0	0	0.250724	0.542663	0
antisense	-	0	0	1	7	2	5	0	0	0.103506	0.475656	0.176486	0.390312
pseudogen	-	0	0	0	1	0	0	0	0	0	0.092151	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.093077	0
sense_intrc	-	0	0	0	2	0	5	0	0	0	0.166239	0	0.477441
lincRNA	-	2	0	2	0	0	1	0.167006	0	0.220073	0	0	0.082987
lincRNA	-	1	1	0	1	2	0	0.100267	0.118159	0	0.08674	0.225288	0
pseudogen	-	0	2	1	5	1	1	0	0.288165	0.161116	0.528856	0.137358	0.121511
pseudogen	double_ho	0	0	0	0	0	1	0	0	0	0	0	0.089328
antisense	-	47	36	23	18	13	48	4.831508	4.361084	3.115642	1.600738	1.501334	4.903834
pseudogen	-	1	0	0	0	0	0	0.114343	0	0	0	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.116146
antisense	-	2	0	0	0	0	0	0.156399	0	0	0	0	0
lincRNA	-	0	0	0	4	1	5	0	0	0	0.362047	0.117541	0.519902

protein_co	v-yes-1_Yan	86	101	105	1519	1171	1192	1.507591	2.086477	2.425545	23.03594	23.06169	20.76687
pseudogen	-	1	0	1	1	0	1	0.03599	0	0.047426	0.031135	0	0.035768
lincRNA	-	3	0	0	0	0	0	0.608517	0	0	0	0	0
pseudogen	MT-ND2_ps	0	0	4	0	3	4	0	0	0.268837	0	0.171896	0.202752
protein_co	PIN2/TERF1	71	90	64	529	372	483	2.432887	3.634237	2.889871	15.68131	14.32042	16.44828
sense_intrc	-	2	0	0	0	1	5	0.200915	0	0	0	0.112858	0.499185
antisense	-	5	1	1	0	4	3	0.769491	0.18136	0.2028	0	0.69158	0.458843
lincRNA	-	0	0	0	1	2	7	0	0	0	0.085287	0.221512	0.685844
lincRNA	-	0	0	0	1	0	0	0	0	0	0.059172	0	0
processed_	-	1	0	1	0	0	0	0.019579	0	0.0258	0	0	0
pseudogen	VENT_hom	2	0	0	0	0	0	0.337204	0	0	0	0	0
protein_co	Uncharacte	0	0	1	0	0	0	0	0	0.134678	0	0	0
antisense	-	1	2	1	12	8	16	0.051349	0.121024	0.067666	0.533062	0.461501	0.816513
pseudogen	-	0	0	0	0	1	3	0	0	0	0	0.186445	0.494803
pseudogen	high_mobil	0	0	0	0	0	2	0	0	0	0	0	0.289088
antisense	-	0	0	3	0	0	0	0	0	0.260311	0	0	0
protein_co	protocadhe	1385	1105	1276	499	858	755	15.95372	14.99966	19.36857	4.97251	11.10321	8.643083
lincRNA	-	0	0	1	0	0	0	0	0	0.084767	0	0	0
antisense	-	1	1	0	0	0	0	0.110755	0.130518	0	0	0	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.080917	0	0
pseudogen	-	7	0	5	9	0	6	0.88235	0	0.830515	0.981405	0	0.751629
pseudogen	MT-ND6_ps	1	0	1	0	0	1	0.097677	0	0.128715	0	0	0.097074
lincRNA	-	1	0	0	0	0	0	0.076615	0	0	0	0	0
lincRNA	-	7	5	4	2	0	0	0.150584	0.126753	0.11339	0.03722	0	0
sense_intrc	-	0	0	0	0	4	0	0	0	0	0	0.332268	0
processed_	-	0	0	0	0	2	4	0	0	0	0	0.151146	0.267416
lincRNA	-	0	1	1	2	6	5	0	0.117491	0.131381	0.172501	0.672044	0.495424
lincRNA	-	0	0	0	5	4	19	0	0	0	0.449009	0.466478	1.960131
processed_	-	9	8	14	0	0	0	0.076701	0.080345	0.157226	0	0	0
lincRNA	-	19	19	10	21	14	12	0.267095	0.314755	0.185245	0.255384	0.2211	0.16765
antisense	-	2	0	0	0	0	0	0.230178	0	0	0	0	0
lincRNA	-	3	2	6	0	0	0	0.347534	0.273032	0.915929	0	0	0
antisense	-	28	21	16	45	30	27	2.093712	1.850483	1.576571	2.910947	2.520166	2.006468
lincRNA	-	0	0	1	0	0	3	0	0	0.190091	0	0	0.430088
sense_intrc	-	3	0	0	0	0	0	1.393184	0	0	0	0	0
lincRNA	-	0	1	0	3	4	0	0	0.144751	0	0.318786	0.551981	0
processed_	-	2	1	5	1	0	0	0.183187	0.107937	0.603489	0.079237	0	0
pseudogen	tRNA-yW_s	18	5	4	32	11	13	0.474571	0.155348	0.138971	0.729863	0.325814	0.340629
antisense	-	0	0	1	0	15	3	0	0	0.062067	0	0.793718	0.140429
antisense	-	0	0	0	3	0	1	0	0	0	0.169626	0	0.064956
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.410179	0
lincRNA	-	30	40	27	0	0	0	3.108082	4.88358	3.686123	0	0	0
pseudogen	-	42	59	63	50	103	61	5.517424	9.133687	10.90592	5.682246	15.20104	7.963913
lincRNA	-	0	0	0	47	60	77	0	0	0	3.363357	5.575867	6.330128

antisense	-	0	0	0	4	1	2	0	0	0	0.503285	0.163395	0.289088
protein_co	Protein_LO	47	48	20	47	23	39	0.681146	0.819768	0.381951	0.589255	0.374472	0.561716
sense_intrc	-	1	2	1	1	5	8	0.167535	0.394859	0.22077	0.144933	0.941075	1.332001
antisense	-	1	0	2	1	5	4	0.113122	0	0.298134	0.097861	0.635426	0.449693
protein_co	protocadhe	25	19	38	19	20	5	0.28835	0.25825	0.577561	0.189582	0.259154	0.057314
lincRNA	-	0	0	4	0	0	0	0	0	0.40857	0	0	0
antisense	-	0	1	0	0	0	0	0	0.163319	0	0	0	0
lincRNA	-	2	0	0	0	2	0	0.029485	0	0	0	0.033125	0
processed_	-	0	3	1	10	3	1	0	0.125951	0.046947	0.308203	0.120073	0.035406
lincRNA	-	3	0	1	1	2	5	0.198034	0	0.086987	0.057106	0.148319	0.328018
antisense	-	0	0	0	0	1	3	0	0	0	0	0.143662	0.381261
antisense	-	2	0	0	1	2	2	0.179461	0	0	0.077625	0.201613	0.178353
protein_co	protocadhe	6	5	7	0	0	1	0.068978	0.067739	0.106046	0	0	0.011425
antisense	-	0	0	1	0	0	0	0	0	0.213343	0	0	0
antisense	-	1	5	0	0	0	0	0.063555	0.374476	0	0	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.070623
antisense	-	0	0	0	0	3	0	0	0	0	0	0.06751	0
lincRNA	-	0	2	0	0	0	2	0	0.28166	0	0	0	0.237535
lincRNA	-	0	0	0	7	4	4	0	0	0	0.686493	0.50943	0.450656
lincRNA	-	0	6	1	7	4	0	0	0.186139	0.034691	0.159419	0.118301	0
lincRNA	-	2	0	2	0	0	0	0.243407	0	0.320751	0	0	0
pseudogen	-	0	0	2	0	3	0	0	0	0.337021	0	0.430985	0
pseudogen	teratocarci	2	2	6	3	5	5	0.233735	0.275443	0.924017	0.303304	0.656467	0.580729
processed_	-	0	1	0	0	0	0	0	0.030359	0	0	0	0
lincRNA	-	0	0	0	1	2	1	0	0	0	0.056682	0.147218	0.065116
pseudogen	keratin_8_p	2	0	1	32	25	51	0.073072	0	0.048146	1.011432	1.026155	1.85184
antisense	-	0	0	0	23	27	45	0	0	0	1.835148	2.797648	4.124795
lincRNA	-	0	0	0	0	3	4	0	0	0	0	0.075001	0.088464
lincRNA	-	0	0	0	10	2	15	0	0	0	0.264123	0.0686	0.455139
pseudogen	IMP_(inosi	1	0	0	1	0	3	0.034968	0	0	0.03025	0	0.104255
lincRNA	-	1	0	0	0	0	0	0.031835	0	0	0	0	0
pseudogen	mitochond	10	4	9	0	1	0	0.863638	0.407098	1.024257	0	0.097024	0
antisense	-	0	1	2	0	1	0	0	0.127063	0.284168	0	0.121132	0
antisense	-	0	1	0	0	3	2	0	0.068035	0	0	0.194578	0.114753
protein_co	chromoson	7	12	6	0	0	0	0.63025	1.273219	0.71187	0	0	0
lincRNA	-	0	0	0	0	0	3	0	0	0	0	0	0.271206
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.08092	0
sense_intrc	hsa-mir-15	3	3	1	0	2	0	1.7647	2.079591	0.775148	0	1.321687	0
sense_intrc	-	1	3	0	0	5	4	0.078664	0.278103	0	0	0.441872	0.312714
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.289088
sense_intrc	-	0	0	1	0	2	0	0	0	0.090719	0	0.154684	0
pseudogen	CDC28_prc	3	0	0	0	0	2	0.675842	0	0	0	0	0.447779
pseudogen	-	2	2	6	5	6	18	0.141553	0.166812	0.559599	0.306142	0.47708	1.266114
lincRNA	-	2	0	0	2	0	1	0.287723	0	0	0.248907	0	0.142973

lincRNA	-	0	0	0	6	2	4	0	0	0	0.533579	0.230974	0.408653
antisense	-	0	0	2	0	0	3	0	0	0.334596	0	0	0.378518
antisense	-	3	0	0	0	2	0	0.243968	0	0	0	0.182722	0
lincRNA	-	0	1	1	1	1	1	0	0.119517	0.133646	0.087737	0.113939	0.100793
pseudogen	MT-ND1_ps	0	0	0	0	0	1	0	0	0	0	0	0.055617
pseudogen	-	0	0	1	0	0	0	0	0	0.272513	0	0	0
lincRNA	-	2	0	0	0	0	0	0.149974	0	0	0	0	0
pseudogen	-	8	4	3	1	5	1	1.242017	0.731821	0.613753	0.134308	0.872081	0.154293
lincRNA	-	1	1	2	2	6	4	0.074881	0.088243	0.19735	0.129558	0.504746	0.297675
sense_intrc	-	1	0	1	0	0	0	0.093206	0	0.122823	0	0	0
lincRNA	-	0	0	0	1	0	1	0	0	0	0.078557	0	0.090247
lincRNA	-	0	0	1	0	0	0	0	0	0.101696	0	0	0
antisense	HOXA_clust	25	13	33	1	8	4	0.33196	0.203421	0.577424	0.011487	0.11934	0.052786
sense_intrc	-	1	1	2	6	2	7	0.103603	0.122089	0.273046	0.537756	0.232782	0.72074
antisense	-	0	0	0	0	1	0	0	0	0	0	0.187031	0
pseudogen	-	0	0	0	0	1	1	0	0	0	0	0.178606	0.158
processed_	-	0	0	0	0	1	0	0	0	0	0	0.020942	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.115487	0
pseudogen	deoxyuridi	0	1	0	1	1	4	0	0.134747	0	0.098918	0.128458	0.454549
antisense	RHPN1_ant	3	0	2	9	14	4	0.082807	0	0.072746	0.214906	0.434131	0.109727
lincRNA	-	0	0	2	1	0	0	0	0	0.247388	0.081204	0	0
antisense	-	0	1	1	0	5	7	0	0.104502	0.116856	0	0.498123	0.616915
pseudogen	-	0	2	0	1	0	0	0	0.228526	0	0.083881	0	0
processed_	-	0	0	2	0	0	0	0	0	0.076119	0	0	0
pseudogen	-	0	0	0	4	0	0	0	0	0	0.338624	0	0
processed_	-	0	2	3	0	2	4	0	0.167935	0.281682	0	0.160097	0.283252
antisense	-	1	3	1	0	0	1	0.062652	0.221495	0.08256	0	0	0.062265
processed_	-	0	0	0	14	10	11	0	0	0	0.890534	0.826054	0.803826
antisense	ANO1_antis	0	0	3	0	0	0	0	0	0.208456	0	0	0
antisense	-	1	0	0	2	12	4	0.220587	0	0	0.381658	2.973796	0.876901
sense_intrc	-	2	1	0	0	2	2	0.183504	0.108124	0	0	0.206156	0.182371
antisense	-	0	0	1	0	0	1	0	0	0.159641	0	0	0.120398
pseudogen	-	0	0	3	0	0	0	0	0	0.177214	0	0	0
lincRNA	-	3	1	1	10	7	19	0.182136	0.071546	0.080004	0.525217	0.477444	1.146407
antisense	-	29	29	15	45	57	82	2.935543	3.459358	2.000859	3.940632	6.482079	8.249239
antisense	-	73	60	34	329	252	368	7.637732	7.397754	4.687651	29.77834	29.62042	38.26476
antisense	-	9	0	0	0	0	1	0.659929	0	0	0	0	0.072873
antisense	-	0	0	0	2	0	0	0	0	0	0.304312	0	0
antisense	-	3	0	7	2	10	6	0.19228	0	0.591214	0.110893	0.720047	0.382184
protein_co	prostate_ar	0	0	1	0	0	0	0	0	0.027916	0	0	0
pseudogen	-	3	0	1	0	2	0	0.173577	0	0.076244	0	0.130002	0
processed_	-	0	0	0	0	0	3	0	0	0	0	0	0.193434
pseudogen	splicing_fa	0	2	0	0	0	0	0	0.082797	0	0	0	0
sense_intrc	ALG9_intrc	1	0	0	0	1	0	0.077399	0	0	0	0.086953	0

pseudogen	regulator_c	0	0	0	6	2	5	0	0	0	0.176489	0.076398	0.16896
lincRNA	-	0	1	0	0	0	0	0	0.1085	0	0	0	0
antisense	-	12	3	4	0	1	2	1.167816	0.34405	0.512965	0	0.109331	0.193434
processed_	-	2	4	0	0	0	3	0.180995	0.426583	0	0	0	0.269816
sense_intrc	-	0	0	0	0	0	3	0	0	0	0	0	0.408917
antisense	-	16	9	8	7	13	26	1.571532	1.041725	1.035448	0.594791	1.434484	2.537969
pseudogen	-	3	2	2	3	0	3	0.330881	0.259949	0.29068	0.286243	0	0.328838
pseudogen	protein-kin	0	0	1	0	0	0	0	0	0.030787	0	0	0
protein_co	Putative_sl	22	19	14	21	33	37	0.653959	0.665563	0.548392	0.540021	1.102024	1.093049
protein_co	adaptor-rel	124	119	112	209	197	232	1.364515	1.543159	1.624088	1.989601	2.43541	2.537198
antisense	-	18	15	19	26	12	11	0.937009	0.920173	1.303345	1.170867	0.701781	0.56908
processed_	hsa-mir-21	8	6	5	0	6	7	3.850254	3.402967	3.171058	0	3.244141	3.348167
antisense	-	5	0	1	5	13	7	0.301143	0	0.079367	0.260517	0.879621	0.418997
pseudogen	solute_carr	0	1	2	6	1	0	0	0.067301	0.150514	0.296433	0.06416	0
processed_	-	6	2	1	0	2	0	0.687545	0.270077	0.151003	0	0.257472	0
pseudogen	protein_tyr	0	0	1	3	0	0	0	0	0.138971	0.273699	0	0
sense_intrc	-	0	0	0	0	0	3	0	0	0	0	0	0.374034
processed_	-	1	4	3	21	9	9	0.063861	0.301026	0.252461	1.160165	0.645698	0.571202
lincRNA	-	0	0	0	1	0	2	0	0	0	0.013845	0	0.03181
antisense	-	3	0	3	2	3	2	0.403104	0	0.531193	0.232482	0.452862	0.267076
protein_co	charged_m	34	21	16	18	11	15	1.292171	0.940519	0.801301	0.591802	0.469659	0.566555
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.022191
pseudogen	-	4	1	4	4	10	2	0.489062	0.144083	0.644464	0.423085	1.373578	0.243021
processed_	-	10	12	5	35	34	25	0.558449	0.789718	0.36795	1.690888	2.133103	1.387501
pseudogen	-	1	2	3	0	2	4	0.065684	0.154808	0.259665	0	0.147583	0.261112
pseudogen	-	0	1	3	0	2	0	0	0.218139	0.731783	0	0.415916	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.106939
pseudogen	-	12	2	2	17	8	4	1.006802	0.197742	0.22112	1.233885	0.754053	0.333528
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.109727
lincRNA	-	0	0	2	0	0	0	0	0	0.311443	0	0	0
protein_co	Uncharacte	138	115	72	46	47	48	9.24792	9.081758	6.358173	2.666772	3.538441	3.196803
protein_co	poly(A)_bin	82	86	97	131	134	136	0.878067	1.085223	1.368738	1.213523	1.612009	1.447312
protein_co	Mitochond	0	0	0	0	1	0	0	0	0	0	0.037057	0
pseudogen	-	0	1	4	0	2	1	0	0.159969	0.715521	0	0.305005	0.134908
lincRNA	-	0	0	1	3	4	2	0	0	0.17617	0.346961	0.600767	0.265728
antisense	-	29	29	33	9	7	4	1.766731	2.081984	2.649239	0.474327	0.479093	0.242182
antisense	NAV2_antis	0	0	0	3	0	0	0	0	0	0.22976	0	0
antisense	-	6	0	2	4	0	1	0.591519	0	0.259826	0.341146	0	0.097978
protein_co	olfactory_r	3	2	2	2	0	1	0.322811	0.253609	0.283591	0.186174	0	0.106939
antisense	-	0	0	0	0	1	0	0	0	0	0	0.077645	0
protein_co	-	1	1	0	0	0	0	0.015359	0.018099	0	0	0	0
antisense	-	20	18	18	17	22	26	1.31858	1.39848	1.56381	0.969591	1.629477	1.703568
sense_intrc	-	12	19	8	3	10	11	0.371516	0.693197	0.326378	0.080349	0.347812	0.338453
antisense	-	0	1	0	0	0	0	0	0.113021	0	0	0	0

antisense	-	10	11	11	17	25	33	0.602287	0.780734	0.873033	0.885758	1.691579	1.975272
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.023509
antisense	-	0	2	2	2	1	0	0	0.389923	0.436021	0.286243	0.185862	0
pseudogen	MT-ND2_ps	2	2	2	1	3	3	0.102898	0.121259	0.135594	0.044508	0.173399	0.153394
processed_	-	20	4	4	5	5	7	5.785901	1.363666	1.52488	1.251336	1.625025	2.012559
pseudogen	proteasom	0	0	0	7	1	1	0	0	0	0.496273	0.092068	0.081446
protein_co	MAGE-like_	0	0	0	1	2	2	0	0	0	0.01843	0.047868	0.042345
lincRNA	-	0	0	0	0	5	0	0	0	0	0	0.180558	0
antisense	-	1	0	0	0	0	0	0.067613	0	0	0	0	0
pseudogen	-	1	1	2	7	7	9	0.059618	0.070256	0.157125	0.361027	0.468842	0.533251
pseudogen	-	21	42	34	26	16	26	1.620643	3.819657	3.457655	1.735819	1.387193	1.994119
protein_co	casein_kina	0	0	0	1	4	1	0	0	0	0.032344	0.168011	0.037157
processed_	-	48	35	27	33	41	53	0.910813	0.782642	0.675129	0.541707	0.874019	0.999478
antisense	-	5	4	8	3	1	5	0.491104	0.462989	1.035448	0.25491	0.110345	0.488071
lincRNA	-	0	1	1	0	0	0	0	0.083518	0.093391	0	0	0
protein_co	Uncharacte	10	3	7	1	0	0	1.297573	0.458733	1.196919	0.112252	0	0
pseudogen	-	0	0	0	4	1	1	0	0	0	0.180666	0.058655	0.051888
pseudogen	-	10	7	13	21	17	27	0.731229	0.603196	1.252656	1.328421	1.396534	1.962126
protein_co	Uncharacte	6	2	9	7	3	7	0.218464	0.085815	0.431822	0.22049	0.122715	0.2533
lincRNA	-	579	536	445	376	322	463	23.25708	25.37164	23.55437	13.06555	14.53054	18.48278
pseudogen	-	0	1	0	0	0	5	0	0.106464	0	0	0	0.448925
pseudogen	-	11	12	7	32	7	12	0.198755	0.255513	0.16667	0.500193	0.142093	0.215484
antisense	WAC_antis	294	292	211	499	340	421	5.968041	6.985129	5.644192	8.762904	7.753762	8.493296
protein_co	age-related	10	1	7	0	0	0	0.6472	0.076269	0.596996	0	0	0
lincRNA	-	6	0	1	7	7	7	0.486441	0	0.106835	0.490953	0.637567	0.56401
pseudogen	cytochrom	0	0	0	2	0	0	0	0	0	0.401745	0	0
pseudogen	-	0	0	2	0	1	0	0	0	0.371081	0	0.158181	0
lincRNA	-	1	0	0	2	3	5	0.04685	0	0	0.08106	0.157901	0.232806
antisense	-	0	0	3	8	0	16	0	0	0.573397	1.003812	0	2.306369
lincRNA	-	4	4	2	6	0	1	0.350023	0.412481	0.230622	0.454204	0	0.086965
antisense	-	3	0	3	3	2	1	0.510685	0	0.672958	0.44179	0.382482	0.169177
antisense	-	1	0	0	0	0	0	0.09337	0	0	0	0	0
protein_co	Uncharacte	1	1	1	1	6	0	0.047997	0.056562	0.063249	0.041522	0.323532	0
lincRNA	-	0	0	0	0	0	4	0	0	0	0	0	0.391911
antisense	STT3A_anti	7	0	1	11	6	3	0.863839	0	0.162618	1.174331	0.831831	0.36793
pseudogen	-	2	3	1	0	2	4	0.063516	0.112275	0.04185	0	0.071357	0.126248
antisense	-	0	0	0	1	0	0	0	0	0	0.165339	0	0
processed_	-	4	5	9	18	9	8	0.233993	0.344684	0.693778	0.910917	0.591473	0.465097
pseudogen	-	0	0	1	0	0	5	0	0	0.231772	0	0	0.873988
pseudogen	polycystic_	450	333	314	117	300	257	2.314979	2.018765	2.128624	0.520695	1.733823	1.313945
antisense	-	77	82	60	122	88	89	5.994789	7.523226	6.155584	8.216862	7.696883	6.886251
protein_co	fucose-1-ph	70	79	119	154	92	125	1.149463	1.528732	2.575009	2.187665	1.697204	2.039937
antisense	-	0	0	0	1	2	0	0	0	0	0.055447	0.144009	0
antisense	-	9	5	2	1	0	1	0.974374	0.637911	0.28533	0.093658	0	0.107595

lincRNA	-	4	0	0	2	0	0	0.454429	0	0	0.196562	0	0
antisense	-	15	10	4	20	14	23	1.788547	1.405129	0.628498	2.063014	1.875367	2.725503
antisense	-	9	1	4	5	5	5	0.864735	0.113226	0.506449	0.415598	0.539709	0.477441
antisense	-	12	6	7	4	9	3	1.75495	1.034051	1.349014	0.506065	1.478683	0.436028
processed_	-	0	0	1	0	0	0	0	0	0.161116	0	0	0
pseudogen	-	2	1	0	0	1	2	0.181305	0.106828	0	0	0.101842	0.180185
antisense	FLI1_antise	9	10	8	9	0	8	0.369356	0.483626	0.432641	0.319527	0	0.326289
antisense	-	0	0	0	4	1	0	0	0	0	0.236381	0.076743	0
antisense	-	0	1	4	0	2	9	0	0.115747	0.517724	0	0.22069	0.878528
pseudogen	-	0	1	1	0	0	5	0	0.070415	0.07874	0	0	0.296919
antisense	-	8	4	2	0	2	3	0.604177	0.355993	0.199039	0	0.169689	0.225167
pseudogen	glycine-N-a	12	7	2	4	9	8	0.704315	0.484162	0.154686	0.203099	0.59344	0.466643
antisense	-	2	0	1	11	1	8	0.037035	0	0.024401	0.176211	0.020803	0.147224
pseudogen	-	0	2	1	2	5	1	0	0.599882	0.3354	0.440374	1.42971	0.252952
pseudogen	family_witl	0	0	0	0	0	1	0	0	0	0	0	0.046072
protein_co	mex-3_hon	1905	1452	1635	1998	2225	2255	16.46842	14.79213	18.62557	14.94223	21.60907	19.37372
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.185862	0
lincRNA	-	0	0	1	0	4	0	0	0	0.161489	0	0.550703	0
protein_co	-	8	3	6	3	14	18	0.730221	0.322695	0.721689	0.236891	1.435626	1.63285
processed_	-	0	0	0	0	1	1	0	0	0	0	0.14471	0.128015
antisense	-	0	2	0	0	4	0	0	0.228109	0	0	0.434924	0
antisense	-	0	0	0	0	2	0	0	0	0	0	0.27599	0
pseudogen	olfactory_r	0	0	0	1	0	0	0	0	0	0.063171	0	0
antisense	-	0	0	0	2	0	0	0	0	0	0.160136	0	0
antisense	-	1	4	1	1	4	3	0.102599	0.483626	0.1352	0.088758	0.461054	0.305896
pseudogen	-	0	1	0	0	2	0	0	0.094527	0	0	0.18023	0
pseudogen	nucleosom	2	0	0	0	0	0	0.099607	0	0	0	0	0
antisense	-	0	0	0	5	3	0	0	0	0	0.841892	0.655984	0
pseudogen	tripartite_r	0	0	0	1	2	4	0	0	0	0.033825	0.087852	0.155433
antisense	-	0	0	0	1	0	0	0	0	0	0.072124	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.294435	0
antisense	-	0	0	0	0	0	3	0	0	0	0	0	0.362856
lincRNA	-	0	0	0	0	0	3	0	0	0	0	0	0.170456
pseudogen	GTPase_ver	0	4	0	0	0	0	0	0.113742	0	0	0	0
pseudogen	-	4	5	5	16	10	9	0.285396	0.420402	0.470103	0.987577	0.801562	0.638176
pseudogen	-	0	0	0	2	0	0	0	0	0	0.081638	0	0
antisense	-	0	0	1	0	0	0	0	0	0.198756	0	0	0
sense_intrc	FAR1_intro	11	6	7	2	12	8	1.582475	1.017191	1.327019	0.248907	1.939432	1.143784
pseudogen	farnesyl_di	0	4	2	1	0	1	0	0.237894	0.133009	0.04366	0	0.050156
protein_co	SYS1-DBND	0	3	0	2	0	0	0	0.142546	0	0.069762	0	0
lincRNA	-	7	3	6	0	0	0	0.569258	0.287501	0.64298	0	0	0
antisense	-	1	0	4	9	5	5	0.075522	0	0.398079	0.588003	0.424222	0.375279
antisense	-	5	0	0	0	0	1	0.119776	0	0	0	0	0.023807
protein_co	solute_carr	0	9	10	5	0	6	0	0.338451	0.420514	0.138032	0	0.190286

lincRNA	-	0	0	0	0	1	1	0	0	0	0	0.104527	0.092468
processed_	-	14	10	6	19	28	21	0.297302	0.250252	0.167902	0.349049	0.668001	0.443199
pseudogen	GTPase_ver	2	4	5	9	3	4	0.015004	0.035362	0.049428	0.058409	0.025284	0.029822
lincRNA	-	6	3	3	0	0	0	0.497099	0.2929	0.327527	0	0	0
processed_	-	0	1	0	1	0	1	0	0.028319	0	0.020789	0	0.023883
pseudogen	-	5	3	5	1	4	0	0.142929	0.10106	0.188346	0.024729	0.128458	0
antisense	-	2	0	2	0	0	0	0.226244	0	0.298134	0	0	0
lincRNA	-	1	4	3	2	3	7	0.102006	0.48083	0.403256	0.176489	0.343791	0.709631
pseudogen	-	28	28	17	89	52	86	1.803343	2.125129	1.442793	4.958762	3.762467	5.504633
antisense	-	3	12	0	21	33	35	0.303677	1.431458	0	1.838962	3.752783	3.521017
antisense	-	0	3	1	0	0	1	0	0.390737	0.145644	0	0	0.109841
pseudogen	NADH_deh	0	0	0	0	0	1	0	0	0	0	0	0.226785
protein_co	MPV17_mi	135	127	112	529	328	378	3.648307	4.044534	3.988508	12.36734	9.958193	10.15218
antisense	-	0	1	0	0	3	1	0	0.125277	0	0	0.358289	0.105651
antisense	TMEM9B_a	28	36	42	38	21	42	1.407738	2.132914	2.782581	1.652762	1.186129	2.098566
antisense	-	0	2	2	0	1	6	0	0.092426	0.103353	0	0.044056	0.23384
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.203143
antisense	-	0	2	0	2	2	0	0	0.226864	0	0.166541	0.216276	0
pseudogen	-	0	1	1	0	1	1	0	0.09554	0.106835	0	0.091081	0.080573
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.276632	0
processed_	-	0	3	0	0	0	0	0	0.059625	0	0	0	0
protein_co	Uncharacte	1	1	1	1	4	3	0.025526	0.030081	0.033637	0.022082	0.114708	0.076105
processed_	-	14	8	2	11	9	19	0.234475	0.157894	0.04414	0.159376	0.16934	0.31625
antisense	-	0	0	1	0	0	0	0	0	0.11905	0	0	0
pseudogen	-	5	0	2	3	0	2	0.651983	0	0.343661	0.338416	0	0.259183
lincRNA	-	1	5	0	0	0	0	0.141553	0.834061	0	0	0	0
antisense	-	5	2	0	0	0	0	0.348755	0.164395	0	0	0	0
pseudogen	-	2	0	0	0	0	0	0.231689	0	0	0	0	0
pseudogen	-	24	14	17	26	17	25	0.655616	0.450685	0.611959	0.614433	0.521719	0.678716
pseudogen	-	1	0	3	0	1	0	0.090343	0	0.35715	0	0.101495	0
antisense	-	0	0	1	0	0	0	0	0	0.160745	0	0	0
antisense	-	7	2	3	3	3	2	0.690106	0.232357	0.389739	0.25586	0.332268	0.195955
protein_co	MEF2B_nei	67	94	37	133	134	144	0.95918	1.585843	0.69801	1.647175	2.155158	2.048789
antisense	-	0	0	0	1	0	2	0	0	0	0.093087	0	0.213878
antisense	-	2	0	4	1	4	2	0.134539	0	0.354578	0.058194	0.302292	0.133708
pseudogen	-	6	7	7	14	11	31	1.527144	2.099587	2.347803	3.082619	3.145361	7.841517
antisense	-	16	14	19	1	4	2	2.160857	2.228133	3.381384	0.116834	0.606897	0.268439
antisense	small_Cajal	136	134	187	34	109	117	20.39653	23.68259	36.95675	4.411226	18.36508	17.43865
pseudogen	-	6	1	2	4	1	0	0.259091	0.050887	0.113806	0.149425	0.048512	0
antisense	-	1	0	1	0	0	0	0.130397	0	0.171831	0	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.227242	0	0	0
pseudogen	-	0	0	0	2	1	8	0	0	0	0.062781	0.040765	0.288494
protein_co	Protein_LO	0	0	0	14	13	9	0	0	0	0.709275	0.855295	0.523812
pseudogen	-	0	0	3	0	1	0	0	0	0.654031	0	0.185862	0

pseudogen	-	0	5	1	0	1	2	0	0.462817	0.103506	0	0.088243	0.156125
antisense	-	7	1	2	0	0	0	0.604546	0.101774	0.227613	0	0	0
lincRNA	long_interg	0	0	1	185	148	125	0	0	0.087423	10.61754	11.03062	8.241549
sense_intrc	-	10	13	10	18	19	13	0.303561	0.465046	0.400019	0.472695	0.64796	0.392192
pseudogen	-	9	1	4	6	8	1	1.063547	0.139258	0.622886	0.613378	1.06207	0.117442
pseudogen	ATP_syntha	9	10	1	3	1	1	0.626933	0.820891	0.091794	0.180785	0.078258	0.069229
pseudogen	guanine_nu	1	0	0	0	0	3	0.255754	0	0	0	0	0.762522
processed_	-	1	3	3	153	141	141	0.021151	0.074776	0.083616	2.799534	3.350421	2.963876
antisense	-	7	1	3	0	0	0	4.028119	0.678127	2.27489	0	0	0
antisense	-	0	0	0	0	2	1	0	0	0	0	0.1361	0.060199
processed_	-	0	0	0	0	2	1	0	0	0	0	0.141947	0.062785
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.139125	0
lincRNA	-	0	0	0	25	8	17	0	0	0	0.632931	0.263022	0.494438
pseudogen	olfactory_r	0	0	0	3	0	0	0	0	0	0.149507	0	0
pseudogen	asparagine-	24	1	12	12	21	7	2.31436	0.113639	1.52488	1.001069	2.275035	0.670853
antisense	-	0	2	1	1	2	0	0	0.108031	0.060401	0.039653	0.102989	0
antisense	-	1	4	0	0	0	3	0.140427	0.661939	0	0	0	0.418679
pseudogen	high_mobil	0	0	0	3	4	4	0	0	0	0.200579	0.347305	0.307235
pseudogen	ferritin_ligh	1	1	0	0	10	3	0.125453	0.147838	0	0	1.409382	0.374034
sense_intrc	RSF1_intro	2	2	0	3	3	5	0.187071	0.220451	0	0.24275	0.315243	0.464788
protein_co	dipeptidyl-	824	659	679	1401	1217	1424	14.17264	13.35722	15.38963	20.84609	23.51598	24.34126
lincRNA	-	1	3	2	1	2	9	0.094201	0.333031	0.248268	0.081493	0.211658	0.842574
antisense	-	0	0	3	2	0	1	0	0	0.368468	0.161264	0	0.09263
lincRNA	-	1	0	2	3	1	1	0.067613	0	0.178195	0.175475	0.075959	0.067195
lincRNA	-	0	1	0	2	4	0	0	0.069397	0	0.101889	0.264631	0
protein_co	STX16-NPEI	13	10	1	2	2	6	0.200476	0.181729	0.020321	0.026682	0.03465	0.091956
protein_co	ANKHD1-EI	20	19	14	12	23	9	0.128404	0.143751	0.118444	0.066649	0.165892	0.057425
protein_co	keratin_ass	3	0	0	2	0	0	0.133689	0	0	0.077103	0	0
protein_co	BRICK1_SC/	4458	3749	3077	3541	2811	3984	191.412	189.6931	174.097	131.5279	135.5935	170.0035
pseudogen	-	2	1	1	1	0	0	0.102798	0.060571	0.067731	0.044465	0	0
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.234884
lincRNA	-	1	0	0	1	2	0	0.068844	0	0	0.059556	0.154684	0
antisense	-	0	5	0	14	9	17	0	0.283839	0	0.583426	0.487064	0.813866
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.194049	0
pseudogen	-	0	0	1	0	0	0	0	0	0.231772	0	0	0
antisense	-	11	8	8	8	7	2	0.717181	0.614657	0.687323	0.451221	0.512723	0.129591
processed_	-	5	0	0	0	0	0	0.329645	0	0	0	0	0
processed_	-	9	16	15	14	11	12	0.602363	1.261952	1.322945	0.8106	0.827099	0.79819
processed_	-	2	0	1	0	0	0	0.016383	0	0.010794	0	0	0
protein_co	Uncharacte	4	0	0	0	0	0	0.421841	0	0	0	0	0
pseudogen	-	0	0	1	1	5	0	0	0	0.073435	0.048209	0.313031	0
antisense	-	0	0	0	0	2	0	0	0	0	0	0.267307	0
protein_co	Uncharacte	5	4	5	2	2	1	0.326393	0.307708	0.430107	0.112944	0.146673	0.064876
antisense	-	1	1	3	1	11	11	0.045133	0.053186	0.178423	0.039044	0.557745	0.493397

protein_co	Uncharacte	23	12	10	30	38	40	2.392226	1.470831	1.370595	2.699346	4.440245	4.134699
sense_intrc	-	0	0	0	1	1	0	0	0	0	0.109305	0.141947	0
pseudogen	-	0	0	0	0	0	4	0	0	0	0	0	0.411047
antisense	GRM5_anti	2	0	0	1	0	0	0.021963	0	0	0.0095	0	0
antisense	-	2	0	5	12	2	1	0.147674	0	0.486494	0.766509	0.165902	0.073381
pseudogen	-	0	1	0	2	0	0	0	0.090026	0	0.132176	0	0
processed_	-	19	10	15	6	1	0	1.048883	0.65055	1.091188	0.286542	0.062019	0
antisense	-	1	2	0	0	0	0	0.212614	0.501106	0	0	0	0
antisense	-	0	1	0	0	0	0	0	0.110031	0	0	0	0
lincRNA	-	3	0	1	0	2	0	0.197051	0	0.086555	0	0.147583	0
sense_intrc	-	0	2	1	0	0	6	0	0.222416	0.124355	0	0	0.562717
protein_co	Protein_LO	0	0	0	1	0	0	0	0	0	0.107762	0	0
antisense	-	2	4	1	2	5	7	0.315125	0.742711	0.207629	0.272613	0.885058	1.096126
protein_co	KIAA0754	223	201	341	29	294	116	1.966329	2.088597	3.962238	0.221214	2.912378	1.016527
pseudogen	-	0	0	1	0	0	0	0	0	0.054631	0	0	0
antisense	-	0	0	2	1	0	0	0	0	0.260311	0.085446	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.10893	0
protein_co	charged_m	552	386	377	714	435	479	9.568903	7.885286	8.611905	10.70741	8.471521	8.252171
pseudogen	-	0	2	0	0	6	0	0	0.436278	0	0	1.247747	0
antisense	-	0	0	0	0	0	4	0	0	0	0	0	0.426025
lincRNA	-	2	3	5	68	52	81	0.077912	0.137721	0.256671	2.29163	2.275753	3.135937
pseudogen	-	2	4	0	8	6	12	0.569258	1.341672	0	1.969845	1.918578	3.394455
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.106077
lincRNA	-	0	4	0	1	0	0	0	0.81023	0	0.148698	0	0
pseudogen	olfactory_r	0	0	0	1	1	5	0	0	0	0.049406	0.06416	0.283787
processed_	-	77	51	46	189	126	184	1.563058	1.220005	1.230487	3.319016	2.873453	3.712034
lincRNA	-	1	0	0	0	0	0	0.098403	0	0	0	0	0
processed_	-	0	0	0	1	2	0	0	0	0	0.352299	0.915014	0
antisense	-	9	0	2	8	14	7	0.792794	0	0.232157	0.609636	1.385462	0.612809
pseudogen	-	0	0	0	1	0	0	0	0	0	0.054008	0	0
antisense	-	15	24	11	17	11	33	2.796179	5.272202	2.702099	2.741484	2.303645	6.113604
antisense	-	0	0	0	3	9	14	0	0	0	0.252567	0.983977	1.354038
lincRNA	-	0	0	0	2	0	3	0	0	0	0.048464	0	0.083514
antisense	-	5	5	3	3	0	2	0.461963	0.544396	0.365253	0.239785	0	0.183644
protein_co	EP300_inte	14	13	5	24	30	25	0.506266	0.553989	0.238263	0.750802	1.218769	0.898464
antisense	-	14	11	8	11	4	10	0.789323	0.730847	0.594362	0.536515	0.253359	0.56032
protein_co	Hydroxyacy	4	0	2	9	9	5	0.064879	0	0.042747	0.126284	0.163996	0.080598
sense_intrc	KLHL22_int	1	3	1	1	0	7	0.485697	1.717093	0.64003	0.420173	0	3.378884
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.250953	0
antisense	-	8	19	14	8	0	4	0.464395	1.299744	1.070928	0.401745	0	0.230763
antisense	-	12	2	9	0	10	4	0.747402	0.146795	0.73867	0	0.699717	0.247596
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.091784	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.031499	0	0
antisense	-	0	0	4	2	5	0	0	0	0.635656	0.208651	0.677402	0

sense_intrc	-	0	0	1	0	3	1	0	0	0.150352	0	0.384543	0.113392
processed_	-	0	0	3	0	0	0	0	0	0.37174	0	0	0
antisense	-	46	60	30	9	8	12	1.754529	2.696876	1.507852	0.296967	0.342801	0.454877
protein_co	coiled-coil_	0	0	0	0	0	3	0	0	0	0	0	0.119577
processed_	-	3	5	0	0	0	0	0.060504	0.118834	0	0	0	0
pseudogen	-	5	7	1	1	0	0	0.201297	0.332102	0.053052	0.034828	0	0
sense_intrc	-	1	1	1	2	1	0	0.350603	0.413164	0.462008	0.606608	0.39388	0
pseudogen	glycine-N-a	0	0	0	0	0	1	0	0	0	0	0	0.032741
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.121792
pseudogen	Nanog_hon	0	0	0	2	1	0	0	0	0	0.099998	0.06493	0
pseudogen	SSU72_RNA	0	0	0	2	0	0	0	0	0	0.156577	0	0
antisense	-	2	0	2	1	2	0	0.124421	0	0.163956	0.053818	0.139779	0
lincRNA	small_nucl	34	38	24	73	52	63	3.821643	5.033405	3.554817	7.098344	6.566343	7.037548
pseudogen	-	0	13	3	9	2	5	0	0.344537	0.088908	0.175102	0.050532	0.111755
antisense	-	5	11	4	12	3	14	0.495702	1.28514	0.522571	1.029189	0.334134	1.379395
antisense	-	0	0	2	0	2	0	0	0	0.215319	0	0.183568	0
pseudogen	olfactory_r	3	0	1	1	5	2	0.178654	0	0.078474	0.051517	0.33451	0.118367
antisense	-	0	0	1	0	0	0	0	0	0.090133	0	0	0
lincRNA	-	0	0	0	3	6	2	0	0	0	0.244478	0.634974	0.187239
pseudogen	DEAD_(Asp	1	0	0	1	0	0	0.040537	0	0	0.035068	0	0
protein_co	caspase_rec	0	0	0	0	0	2	0	0	0	0	0	0.225811
pseudogen	SET_pseudo	3	0	2	0	0	2	0.194398	0	0.170779	0	0	0.128798
antisense	-	16	7	12	39	7	25	0.670139	0.345502	0.66231	1.413099	0.329376	1.040626
lincRNA	-	2	0	0	0	0	0	0.188067	0	0	0	0	0
processed_	-	1	0	0	0	0	0	0.089883	0	0	0	0	0
lincRNA	-	3	0	0	0	0	0	0.397057	0	0	0	0	0
processed_	-	2	0	1	5	3	5	0.040061	0	0.026395	0.086642	0.06751	0.099535
antisense	-	1	0	0	1	6	0	0.096082	0	0	0.08312	0.647651	0
antisense	-	6	3	8	7	0	5	0.478382	0.281872	0.840521	0.48282	0	0.39619
pseudogen	ret_finger_	0	0	0	0	1	0	0	0	0	0	0.069972	0
pseudogen	-	0	0	0	2	0	0	0	0	0	0.196985	0	0
processed_	-	0	0	0	6	2	2	0	0	0	0.097791	0.042332	0.037448
antisense	-	0	2	0	0	0	0	0	0.495141	0	0	0	0
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.148837
lincRNA	-	0	0	0	5	0	0	0	0	0	0.40965	0	0
sense_over	-	1064	1102	892	139	64	82	16.7149	20.40097	18.46553	1.889035	1.129513	1.280223
lincRNA	-	2	0	0	0	0	1	0.210501	0	0	0	0	0.1046
pseudogen	-	0	0	0	1	0	0	0	0	0	0.261708	0	0
sense_intrc	-	0	1	1	0	1	0	0	0.126291	0.141221	0	0.120397	0
processed_	TMPRSS4_a	0	0	0	1	0	0	0	0	0	0.150654	0	0
antisense	RRM1_anti	0	0	0	1	0	0	0	0	0	0.132367	0	0
pseudogen	ATP-bindin	7	2	0	1	7	0	0.516858	0.174024	0	0.063876	0.580657	0
lincRNA	-	2	0	0	0	0	0	0.198653	0	0	0	0	0
pseudogen	Wilms_tum	0	2	4	7	10	1	0	0.047228	0.105622	0.121345	0.225117	0.019914

protein_co	Protein_LO	109	77	57	97	55	135	7.543227	6.279549	5.198048	5.807181	4.276046	9.284832
pseudogen	-	0	1	4	1	1	2	0	0.176736	0.790519	0.129742	0.168487	0.298097
lincRNA	-	0	0	0	0	2	1	0	0	0	0	0.224862	0.099459
pseudogen	-	0	0	2	1	2	0	0	0	0.249155	0.081784	0.212414	0
lincRNA	-	0	0	1	0	0	0	0	0	0.119253	0	0	0
protein_co	EP300_inte	1844	1825	1532	2144	1126	1465	42.48181	49.54639	46.50885	42.7297	29.14268	33.54203
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.053578
antisense	-	3	11	1	8	3	4	0.214916	0.92864	0.094402	0.495793	0.241445	0.284785
protein_co	olfactory_r	0	0	0	0	2	0	0	0	0	0	0.110243	0
antisense	-	0	0	0	1	1	0	0	0	0	0.088758	0.115263	0
pseudogen	-	0	0	1	0	0	0	0	0	0.209499	0	0	0
sense_intrc	-	134	137	114	230	163	173	3.658635	4.408004	4.101606	5.432567	4.999781	4.694291
antisense	-	0	0	0	0	4	0	0	0	0	0	0.262008	0
pseudogen	-	0	3	0	0	0	0	0	0.362719	0	0	0	0
lincRNA	-	49	39	18	16	7	12	3.121671	2.927944	1.511118	0.881808	0.501001	0.75977
pseudogen	-	0	3	0	0	0	0	0	0.139155	0	0	0	0
antisense	-	33	29	15	23	28	15	4.400637	4.55729	2.635892	2.653337	4.194775	1.987936
antisense	-	1	2	2	5	1	2	0.076837	0.181096	0.202506	0.332358	0.086322	0.152726
lincRNA	-	1	0	3	3	0	3	0.077061	0	0.304643	0.199995	0	0.229756
lincRNA	-	0	0	11	0	0	0	0	0	1.216159	0	0	0
antisense	-	6	3	0	2	1	1	0.487935	0.287501	0	0.140703	0.091361	0.08082
lincRNA	-	1	0	0	0	0	2	0.064016	0	0	0	0	0.127241
pseudogen	H2A_histor	2	1	3	3	2	4	0.280854	0.165485	0.555145	0.364448	0.315522	0.558239
sense_intrc	-	2	1	0	0	0	0	0.328826	0.193751	0	0	0	0
antisense	-	2	2	2	12	1	3	0.153009	0.180311	0.201628	0.794201	0.085948	0.228096
antisense	-	0	0	1	0	0	0	0	0	0.157125	0	0	0
pseudogen	olfactory_r	0	0	0	0	0	2	0	0	0	0	0	0.160654
pseudogen	-	2	0	0	0	1	0	0.23322	0	0	0	0.131004	0
processed_	-	1	0	0	0	0	0	0.167535	0	0	0	0	0
lincRNA	-	0	0	0	2	0	1	0	0	0	0.201314	0	0.115635
lincRNA	-	5	7	6	4	5	5	0.139539	0.230213	0.220654	0.096571	0.156763	0.138677
protein_co	NADPH_oxi	0	0	1	1	8	8	0	0	0.00812	0.00533	0.055378	0.048989
antisense	-	0	0	1	0	0	0	0	0	0.208872	0	0	0
pseudogen	-	3	14	7	2	5	7	0.104078	0.572364	0.320015	0.060025	0.194875	0.241349
antisense	-	0	0	0	0	2	0	0	0	0	0	0.200256	0
antisense	-	1	5	0	1	4	2	0.077512	0.456718	0	0.067055	0.348322	0.154067
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.103165
lincRNA	-	0	2	3	0	1	3	0	0.321586	0.539407	0	0.153288	0.40681
lincRNA	-	8	7	4	0	0	0	0.765873	0.789718	0.504617	0	0	0
lincRNA	-	2	0	0	0	0	0	0.042506	0	0	0	0	0
processed_	-	2	5	0	3	0	4	0.107713	0.317333	0	0.139773	0	0.214096
pseudogen	cytochrom	1	0	0	0	0	0	0.167535	0	0	0	0	0
antisense	-	1	0	0	0	1	0	0.102599	0	0	0	0.115263	0
lincRNA	-	0	0	0	2	0	0	0	0	0	0.141792	0	0

protein_co	Protein_LO	0	3	0	0	0	0	0	0.117935	0	0	0	0
pseudogen	cytochrom	0	1	0	0	0	0	0	0.196188	0	0	0	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.214751
processed_	-	0	1	2	0	0	0	0	0.139883	0.31284	0	0	0
protein_co	-	0	1	1	0	1	1	0	0.029908	0.033444	0	0.028512	0.025222
lincRNA	-	0	1	0	0	0	0	0	0.072628	0	0	0	0
antisense	-	28	32	17	21	16	22	0.612287	0.824621	0.48987	0.397264	0.393067	0.478112
protein_co	chromoson	5	3	2	0	0	0	0.187203	0.132364	0.098675	0	0	0
pseudogen	-	0	0	0	1	2	3	0	0	0	0.021135	0.054892	0.072839
protein_co	hydroxycar	0	0	0	4	0	1	0	0	0	0.085726	0	0.024621
antisense	TBX5_antis	7	0	0	0	0	1	0.102372	0	0	0	0	0.014534
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.216276	0
protein_co	protocadhe	56	47	46	33	14	9	0.56363	0.557457	0.610097	0.287332	0.158301	0.090024
sense_intro	RSF1_intro	0	1	0	8	0	3	0	0.098715	0	0.579733	0	0.24975
antisense	-	1	3	2	0	0	0	0.108708	0.384319	0.286502	0	0	0
processed_	-	0	0	0	2	0	0	0	0	0	0.037069	0	0
pseudogen	-	0	1	4	0	2	9	0	0.095103	0.425386	0	0.181329	0.721839
lincRNA	-	3	0	0	3	1	0	0.231858	0	0	0.200579	0.086826	0
antisense	-	3	0	0	1	0	0	0.557274	0	0	0.160698	0	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.139943	0
protein_co	endogenou	31	11	19	20	25	22	0.977469	0.408734	0.789459	0.54555	0.885585	0.689404
pseudogen	olfactory_r	0	0	0	0	2	2	0	0	0	0	0.13043	0.115382
sense_intro	-	6	1	1	0	4	0	0.581769	0.114263	0.127772	0	0.435721	0
antisense	-	0	0	1	0	1	3	0	0	0.120489	0	0.102722	0.272612
antisense	-	22	16	11	0	6	9	0.477924	0.409603	0.314894	0	0.146432	0.194307
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.144346
antisense	-	5	11	4	0	1	0	0.450945	1.169106	0.475389	0	0.101322	0
pseudogen	-	2	4	10	4	1	1	0.15663	0.369158	1.032001	0.270999	0.087982	0.077831
antisense	-	4	0	0	5	3	3	0.415223	0	0	0.449009	0.349858	0.309494
lincRNA	-	2	0	0	0	2	1	0.225761	0	0	0	0.253629	0.112183
processed_	-	2	5	1	3	1	3	0.148711	0.438116	0.097982	0.192973	0.083534	0.221688
lincRNA	-	76	56	92	63	65	53	1.00739	0.87474	1.606966	0.722416	0.967936	0.698183
antisense	-	5	1	0	0	1	1	0.665088	0.156753	0	0	0.149437	0.132196
lincRNA	-	9	7	3	9	6	9	0.449075	0.411606	0.197257	0.388492	0.336339	0.446302
pseudogen	zinc_finger_	0	2	0	0	0	0	0	0.371356	0	0	0	0
antisense	-	2	3	0	0	0	0	0.109836	0.194153	0	0	0	0
protein_co	Uncharacte	54	62	22	26	27	34	3.751724	5.076167	2.014163	1.562692	2.107414	2.347609
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.148209
antisense	-	1	4	3	7	5	3	0.045797	0.215874	0.181047	0.277329	0.257249	0.136542
lincRNA	-	4	0	1	7	7	8	0.169547	0	0.055855	0.256679	0.333332	0.337
antisense	-	1	1	3	0	0	0	0.090343	0.106464	0.35715	0	0	0
antisense	-	2	0	0	0	0	0	0.187734	0	0	0	0	0
lincRNA	-	0	7	0	0	0	0	0	0.525528	0	0	0	0
antisense	-	2	3	0	0	0	3	0.413602	0.731106	0	0	0	0.616571

pseudogen	-	0	0	5	0	2	0	0	0	0.942747	0	0.321491	0
antisense	-	10	15	7	9	7	2	0.388986	0.687594	0.358812	0.302858	0.305901	0.077317
processed_	-	8	0	3	0	2	0	1.183039	0	0.584609	0	0.332268	0
lincRNA	-	10	3	2	8	6	7	1.214243	0.429273	0.320015	0.840347	0.818476	0.844721
antisense	-	0	0	0	0	4	0	0	0	0	0	0.408068	0
antisense	-	3	0	0	1	0	3	0.232537	0	0	0.067055	0	0.231101
protein_co	microRNA_	37	17	33	29	14	14	0.386812	0.209437	0.454619	0.262277	0.164428	0.145457
antisense	-	0	0	0	2	0	1	0	0	0	0.062652	0	0.035988
antisense	-	26	17	36	3	6	16	1.458121	1.123508	2.660464	0.145547	0.378025	0.891764
antisense	-	0	1	2	0	1	0	0	0.187915	0.420261	0	0.179144	0
antisense	-	0	0	1	0	0	0	0	0	0.063306	0	0	0
antisense	-	0	0	1	0	0	0	0	0	0.108497	0	0	0
protein_co	Protein_LO	1	0	0	0	1	2	0.025724	0	0	0	0.0289	0.051131
protein_co	polymerase	740	687	697	644	469	547	9.32992	10.20728	11.58014	7.024171	6.643059	6.853986
pseudogen	-	3	3	0	0	0	0	0.54956	0.647623	0	0	0	0
pseudogen	olfactory_r	0	0	0	6	3	6	0	0	0	0.359677	0.233544	0.413199
antisense	-	1	0	0	4	2	1	0.144253	0	0	0.499171	0.324119	0.143363
pseudogen	-	0	0	0	0	1	1	0	0	0	0	0.252017	0.222941
antisense	-	0	0	1	0	0	0	0	0	0.134678	0	0	0
lincRNA	-	0	0	0	0	3	0	0	0	0	0	0.311937	0
antisense	-	0	0	2	0	0	0	0	0	0.255076	0	0	0
pseudogen	-	1	1	0	2	5	2	0.056987	0.067156	0	0.098598	0.320107	0.11327
lincRNA	-	0	1	0	0	0	0	0	0.079172	0	0	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.037477	0
lincRNA	-	2	0	0	3	1	5	0.228194	0	0	0.296114	0.128181	0.566962
antisense	ZNF252P_a	4	2	2	12	1	4	0.06544	0.038559	0.043117	0.169835	0.018379	0.065036
protein_co	ferredoxin-	7	14	12	38	32	30	0.132874	0.313169	0.300165	0.624008	0.682406	0.565945
lincRNA	-	16	4	4	0	1	4	1.821626	0.536669	0.600114	0	0.127905	0.452594
pseudogen	-	8	16	6	14	11	1	0.840333	1.980563	0.830515	1.272192	1.298085	0.104393
sense_intrc	BRWD1_int	3	0	2	1	1	4	0.158823	0	0.139527	0.045799	0.059476	0.210456
lincRNA	-	0	0	0	1	0	2	0	0	0	0.01685	0	0.038715
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.072709	0
pseudogen	-	5	3	2	0	3	10	0.258754	0.182955	0.13639	0	0.174416	0.514311
protein_co	RAB44_mer	4	2	1	13	2	2	0.094622	0.055753	0.031172	0.266035	0.053151	0.047019
lincRNA	-	0	0	0	1	0	0	0	0	0	0.078828	0	0
sense_intrc	-	0	0	0	0	2	3	0	0	0	0	0.212414	0.281861
processed_	-	6	0	1	0	3	0	0.132187	0	0.029032	0	0.074252	0
protein_co	Protocadhe	10	16	8	2	10	0	0.17284	0.325891	0.182209	0.029905	0.194175	0
pseudogen	-	0	0	0	2	2	4	0	0	0	0.059868	0.077746	0.137553
antisense	-	0	1	0	0	1	0	0	0.135038	0	0	0.128736	0
pseudogen	-	2	0	0	0	0	0	1.41176	0	0	0	0	0
antisense	-	0	0	0	1	0	0	0	0	0	0.100436	0	0
pseudogen	-	1	0	3	2	0	2	0.079971	0	0.316148	0.138365	0	0.158955
antisense	FAM222A_	2	3	3	0	0	2	0.121564	0.214883	0.240287	0	0	0.120813

processed_	-	5	3	5	2	1	4	1.155917	0.817306	1.523216	0.39999	0.25972	0.919023
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.087254
lincRNA	RERG_antis	2	0	1	0	0	2	0.31419	0	0.207013	0	0	0.31225
protein_co	Uncharacte	2	2	0	3	8	0	0.044582	0.052537	0	0.057851	0.20034	0
protein_co	-	1	0	0	0	0	0	0.072621	0	0	0	0	0
lincRNA	-	0	0	0	1	5	0	0	0	0	0.071116	0.46177	0
lincRNA	-	6	13	1	0	0	2	0.577538	1.474619	0.126842	0	0	0.191324
lincRNA	-	1	3	3	0	1	0	0.128498	0.45428	0.507985	0	0.144359	0
antisense	-	1	0	1	0	0	1	0.096256	0	0.126842	0	0	0.095662
pseudogen	-	1	5	1	0	3	0	0.320855	1.890537	0.422808	0	1.08138	0
pseudogen	-	2	0	1	6	32	20	0.020967	0	0.013815	0.054415	0.376877	0.208372
protein_co	Uncharacte	3	0	0	2	2	7	0.352157	0	0	0.203099	0.263751	0.816626
pseudogen	-	0	1	2	0	0	0	0	0.162046	0.362407	0	0	0
pseudogen	-	10	11	6	10	8	18	0.51399	0.666277	0.406388	0.44465	0.461949	0.919469
processed_	small_nucl	875	979	606	3024	1995	2596	16.73532	22.0656	15.27332	50.03464	42.86649	49.34468
processed_	-	2	0	0	0	0	0	0.303387	0	0	0	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.04281
lincRNA	-	10	11	10	0	0	1	0.875058	1.134322	1.153112	0	0	0.086965
processed_	IFNG_antis	3	0	0	0	0	0	0.088678	0	0	0	0	0
pseudogen	-	3	5	3	44	56	43	0.095275	0.187126	0.125549	1.208849	1.997991	1.357171
protein_co	HCG20144	4	0	0	0	0	0	0.141176	0	0	0	0	0
antisense	-	9	2	6	0	5	8	0.83738	0.219289	0.735641	0	0.522635	0.739741
lincRNA	-	0	0	0	2	0	2	0	0	0	0.136713	0	0.157057
protein_co	Uncharacte	10	4	11	31	6	12	1.004573	0.473531	1.45616	2.694053	0.677145	1.198043
antisense	-	2	0	0	0	3	2	0.149551	0	0	0	0.252017	0.148627
pseudogen	-	0	0	1	0	9	14	0	0	0.11905	0	0.913453	1.256991
pseudogen	-	0	0	0	1	0	4	0	0	0	0.03395	0	0.156009
lincRNA	-	1	0	2	0	0	0	0.10401	0	0.274119	0	0	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.063084	0	0
lincRNA	-	3	0	0	0	0	0	0.24322	0	0	0	0	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.050831	0	0
pseudogen	-	0	0	2	0	0	0	0	0	0.549317	0	0	0
pseudogen	-	0	3	2	0	1	0	0	0.575887	0.429313	0	0.183003	0
processed_	rhabdomyc	0	0	0	6	1	0	0	0	0	0.105771	0.022893	0
protein_co	Uncharacte	1	4	0	1	0	3	0.073427	0.346118	0	0.063521	0	0.218921
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.187907
antisense	-	0	1	1	0	2	0	0	0.159969	0.17888	0	0.305005	0
protein_co	MT-RNR2-li	2	0	0	1	1	0	0.082079	0	0	0.035503	0.046105	0
pseudogen	-	7	2	16	1	2	7	0.306017	0.103035	0.921728	0.037819	0.098226	0.304127
protein_co	taste_recep	12	8	15	16	4	11	0.460023	0.361406	0.757747	0.530617	0.172269	0.419084
antisense	-	1	1	1	0	2	4	0.091593	0.107937	0.120698	0	0.205799	0.364111
antisense	-	0	0	1	0	0	0	0	0	0.196516	0	0	0
antisense	-	0	0	0	3	0	0	0	0	0	0.097306	0	0
pseudogen	-	2	0	3	0	0	0	0.70588	0	1.395266	0	0	0

pseudogen	-	1	0	0	0	0	0	0.066011	0	0	0	0	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.030052	0	0
antisense	PXN_antise	14	24	8	47	34	70	0.633482	1.279748	0.477014	1.839785	1.72836	3.147849
lincRNA	-	1	0	0	0	1	0	0.111455	0	0	0	0.125212	0
lincRNA	-	4	3	6	2	12	7	0.254524	0.224956	0.503101	0.110094	0.857826	0.442666
lincRNA	-	6	1	2	0	0	0	0.717034	0.14083	0.314958	0	0	0
antisense	DENND5B_	5	2	4	7	7	3	0.239335	0.112817	0.252308	0.289866	0.37643	0.142714
lincRNA	-	0	0	1	0	0	0	0	0	0.032031	0	0	0
protein_co	-	1	0	4	3	1	0	0.020433	0	0.107701	0.053028	0.022955	0
protein_co	long_interg	4	2	13	3	7	5	0.36199	0.213291	1.550295	0.234866	0.711678	0.449693
pseudogen	-	2	1	1	6	1	0	0.119641	0.070495	0.078829	0.310501	0.067204	0
antisense	-	2	2	4	8	1	3	0.182241	0.21476	0.480298	0.630622	0.102368	0.271673
processed_	-	6	2	5	5	3	8	0.292492	0.114895	0.321194	0.210861	0.164298	0.38758
processed_	-	0	0	0	3	2	0	0	0	0	0.246673	0.213558	0
processed_	-	0	0	0	0	0	2	0	0	0	0	0	0.146557
antisense	-	3	5	1	0	6	13	0.320855	0.630179	0.140936	0	0.72092	1.381783
antisense	-	0	2	2	0	0	0	0	0.171395	0.191657	0	0	0
antisense	-	0	2	0	0	0	3	0	0.594169	0	0	0	0.751629
lincRNA	-	10	7	5	2	8	7	0.79491	0.655727	0.523748	0.137534	0.714425	0.553001
antisense	-	6	0	0	0	4	2	0.544847	0	0	0	0.408068	0.180494
antisense	-	2	0	0	0	0	5	0.211341	0	0	0	0	0.52509
pseudogen	-	0	0	0	0	0	6	0	0	0	0	0	0.660427
pseudogen	-	0	1	0	0	0	0	0	0.479906	0	0	0	0
antisense	-	8	8	4	10	5	6	0.887899	1.046335	0.585017	0.960145	0.623437	0.661812
pseudogen	-	1	0	0	3	3	3	0.023169	0	0	0.06013	0.078087	0.069078
antisense	-	9	6	5	4	6	2	0.614799	0.483002	0.450086	0.236381	0.460459	0.135778
lincRNA	-	0	2	1	0	0	0	0	0.039801	0.022253	0	0	0
pseudogen	-	0	0	0	0	1	1	0	0	0	0	2.12414	1.879073
protein_co	cytochrom	12	3	22	1	2	2	0.360143	0.106102	0.870064	0.025963	0.067433	0.059653
pseudogen	neurexophi	1	0	0	0	0	0	0.072921	0	0	0	0	0
lincRNA	-	2	4	2	5	21	7	0.14913	0.35148	0.196516	0.322528	1.759147	0.51873
lincRNA	-	3	1	2	0	2	9	0.372824	0.14645	0.327527	0	0.27923	1.111564
pseudogen	proteasom	0	0	0	0	3	0	0	0	0	0	0.133654	0
protein_co	coiled-coil_	1	0	0	0	0	0	0.096256	0	0	0	0	0
lincRNA	-	0	0	0	1	0	4	0	0	0	0.090691	0	0.416745
sense_intrc	-	1	17	1	4	3	2	0.196078	3.928116	0.258383	0.678502	0.660844	0.389734
protein_co	histone_clu	1	0	1	8	33	24	0.113364	0	0.149386	0.784564	4.202795	2.703934
pseudogen	-	1	0	1	3	0	0	0.113364	0	0.149386	0.294211	0	0
antisense	CACNA1C_a	0	6	0	0	6	3	0	0.509288	0	0	0.485518	0.214751
pseudogen	chromobo	2	4	3	5	4	1	0.250312	0.589955	0.494775	0.541358	0.56242	0.124383
pseudogen	mitochond	0	3	4	4	4	2	0	0.309873	0.462008	0.303304	0.39388	0.174219
protein_co	cathepsin_	271	226	265	110	78	77	4.856808	4.773063	6.258385	1.705443	1.570454	1.371456
lincRNA	-	3	5	14	0	1	5	0.121517	0.238668	0.747273	0	0.045506	0.201278
protein_co	apoptogeni	204	184	125	375	216	246	4.280604	4.549878	3.456366	6.807209	5.091874	5.130026

pseudogen	-	16	39	21	6	16	13	0.912776	2.621898	1.578695	0.296114	1.025447	0.73705
protein_co	trafficking_	42	21	14	59	41	45	1.275687	0.751659	0.560348	1.550278	1.399032	1.358366
protein_co	dyslexia_su	10	3	5	4	7	15	0.265635	0.09391	0.175021	0.09192	0.208897	0.395991
pseudogen	alpha-2-ma	0	0	0	2	0	2	0	0	0	0.022179	0	0.025479
protein_co	chromoson	7	4	2	6	10	3	0.454151	0.305822	0.170988	0.336757	0.728872	0.193434
antisense	-	20	28	11	2	12	4	2.332202	3.847701	1.6903	0.201757	1.572051	0.46356
protein_co	zinc_finger_	298	281	254	374	269	280	3.495771	3.884545	3.926407	3.795433	3.545097	3.264333
pseudogen	-	0	5	0	0	0	0	0	0.459409	0	0	0	0
lincRNA	-	30	38	29	29	35	36	0.827203	1.234757	1.053716	0.691754	1.084196	0.986513
protein_co	long_interg	1	0	0	0	0	1	0.107604	0	0	0	0	0.106939
pseudogen	-	0	1	0	0	1	0	0	0.299941	0	0	0.285942	0
lincRNA	-	0	0	1	0	3	0	0	0	0.115694	0	0.2959	0
pseudogen	-	2	1	0	0	3	0	0.184463	0.108689	0	0	0.31085	0
antisense	-	0	2	2	0	0	2	0	0.135185	0.151166	0	0	0.114007
lincRNA	-	1	0	0	0	1	0	0.092393	0	0	0	0.103797	0
lincRNA	-	2	1	0	4	7	5	0.1657	0.097633	0	0.286691	0.651536	0.411691
pseudogen	-	0	1	1	0	0	3	0	0.08665	0.096893	0	0	0.219225
processed_	-	0	6	3	7	9	4	0	0.694483	0.388293	0.594791	0.993104	0.390457
pseudogen	-	4	0	0	3	2	2	0.145843	0	0	0.094626	0.081923	0.072471
pseudogen	-	0	1	1	0	0	1	0	0.382747	0.427996	0	0	0.322786
pseudogen	-	3	1	0	0	2	0	0.329508	0.129435	0	0	0.246788	0
protein_co	small_leuci	3	0	0	0	0	0	0.063226	0	0	0	0	0
antisense	-	4	2	3	7	2	4	0.381557	0.224821	0.377099	0.577644	0.214328	0.3792
pseudogen	activating_	1	0	0	1	5	0	0.027431	0	0	0.02373	0.154083	0
pseudogen	glycine_cle	1	0	0	0	0	0	0.120595	0	0	0	0	0
pseudogen	-	1	3	1	7	7	10	0.167535	0.592289	0.22077	1.014533	1.317504	1.665002
lincRNA	-	62	50	51	52	28	41	19.08338	18.13597	20.68562	13.84618	9.682126	12.54172
protein_co	taste_recep	7	0	7	2	3	1	0.219672	0	0.289474	0.054296	0.105766	0.031188
pseudogen	-	0	4	0	2	0	0	0	0.277896	0	0.102002	0	0
lincRNA	long_interg	0	0	0	0	5	0	0	0	0	0	0.153685	0
antisense	-	3	9	8	0	0	0	0.041392	0.146336	0.145454	0	0	0
antisense	-	0	0	1	6	3	4	0	0	0.080745	0.318048	0.206514	0.243584
sense_intrc	TSPAN9_int	0	0	0	0	0	2	0	0	0	0	0	0.187239
lincRNA	-	0	0	1	0	0	0	0	0	0.097982	0	0	0
pseudogen	-	0	0	6	0	2	1	0	0	0.892494	0	0.253629	0.112183
lincRNA	-	0	0	0	13	8	3	0	0	0	0.344751	0.275511	0.091397
protein_co	MT-RNR2-li	1	0	2	3	3	1	0.03828	0	0.100887	0.099347	0.129015	0.038043
protein_co	zinc_finger_	93	130	117	158	75	107	1.10865	1.826256	1.837943	1.629414	1.004435	1.267666
protein_co	zinc_finger_	170	181	123	771	491	497	2.345574	2.942971	2.236352	9.202751	7.610809	6.815007
lincRNA	-	0	0	0	21	10	27	0	0	0	1.108038	0.685206	1.636612
antisense	-	2	1	3	0	2	1	0.151476	0.089253	0.299413	0	0.170174	0.07527
protein_co	small_integ	0	2	2	0	0	0	0	0.053506	0.059831	0	0	0
pseudogen	-	3	0	0	0	0	0	0.050694	0	0	0	0	0
pseudogen	ribosomal_	1	0	1	0	0	0	0.112163	0	0.147804	0	0	0

lincRNA	-	0	3	0	0	5	1	0	0.974808	0	0	1.548852	0.274032
lincRNA	-	1	0	0	2	0	0	0.030584	0	0	0.052916	0	0
lincRNA	-	0	0	1	0	4	0	0	0	0.118847	0	0.405287	0
pseudogen	-	3	1	1	0	0	0	0.140925	0.055357	0.061902	0	0	0
pseudogen	DEAD/H_(A	0	1	0	0	4	0	0	0.170458	0	0	0.65001	0
lincRNA	-	24	26	19	1	0	5	2.076117	2.650459	2.165854	0.074835	0	0.429853
protein_co	hydroxyme	472	322	326	1115	800	1055	11.83151	9.511766	10.76839	24.17887	22.52876	26.28211
antisense	CACNA1C_a	0	1	3	0	0	2	0	0.102443	0.343661	0	0	0.172788
antisense	-	5	6	7	5	3	3	0.260025	0.367708	0.479708	0.224946	0.175273	0.155051
pseudogen	-	0	0	4	1	1	0	0	0	1.007412	0.165339	0.214715	0
pseudogen	-	17	21	6	2	8	12	0.954398	1.389334	0.443881	0.097134	0.504568	0.669532
pseudogen	-	0	0	0	3	1	0	0	0	0	0.80349	0.347812	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.106262	0	0
lincRNA	-	0	0	0	1	0	5	0	0	0	0.070568	0	0.405347
protein_co	zinc_finger_	73	77	104	49	43	62	1.522732	1.892772	2.8587	0.884218	1.007669	1.285292
pseudogen	-	0	0	0	2	1	0	0	0	0	0.418255	0.27158	0
lincRNA	-	3	0	0	0	1	0	0.501019	0	0	0	0.187621	0
pseudogen	-	1	3	2	12	27	12	0.023901	0.084498	0.062992	0.24812	0.724989	0.285042
processed_	-	0	1	0	0	0	0	0	0.163319	0	0	0	0
pseudogen	-	1	0	1	0	0	0	0.139686	0	0.184072	0	0	0
lincRNA	-	0	1	0	0	0	1	0	0.159559	0	0	0	0.134563
antisense	-	0	2	0	3	1	0	0	0.25887	0	0.285055	0.123394	0
protein_co	histone_clu	3	0	5	1	6	2	0.340822	0	0.748533	0.098281	0.765784	0.225811
lincRNA	-	1	0	0	0	0	0	0.032499	0	0	0	0	0
pseudogen	-	6	6	4	5	7	6	1.604273	1.890537	1.409359	1.156538	2.102684	1.594365
antisense	-	12	7	9	4	7	14	1.698642	1.167685	1.678796	0.489828	1.113186	1.96951
sense_intrc	-	1	2	1	3	0	0	0.213472	0.503127	0.281304	0.554019	0	0
pseudogen	ribosomal_	5	3	4	7	2	5	0.867885	0.61365	0.914928	1.051122	0.390006	0.862525
pseudogen	ATP-bindin	2	2	1	4	3	7	0.035978	0.042397	0.023705	0.062248	0.060628	0.125144
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.047505	0
pseudogen	-	0	0	0	6	6	11	0	0	0	0.359677	0.467088	0.757532
pseudogen	-	0	4	1	0	0	0	0	0.727554	0.203391	0	0	0
pseudogen	heat_shock	0	0	0	0	0	1	0	0	0	0	0	0.02543
lincRNA	-	7	6	5	18	7	21	0.96759	0.977353	0.910748	2.152429	1.087027	2.884843
pseudogen	-	1	2	0	1	2	6	0.122266	0.288165	0	0.105771	0.274716	0.729063
lincRNA	-	1	0	1	0	0	0	0.104626	0	0.137872	0	0	0
antisense	-	4	13	4	17	2	10	0.190778	0.730667	0.251399	0.701425	0.107164	0.474
lincRNA	-	1	1	4	0	2	0	0.092554	0.109069	0.487855	0	0.207958	0
pseudogen	-	18	4	5	40	21	22	0.640846	0.167822	0.234577	1.231981	0.839942	0.778419
processed_	-	20	6	3	5	8	11	0.651181	0.230213	0.128715	0.140833	0.292624	0.355938
pseudogen	-	54	30	16	24	17	31	36.65146	23.99528	14.31042	14.09197	12.9627	20.91071
protein_co	acid-sensin	0	0	0	2	1	0	0	0	0	0.054136	0.035151	0
pseudogen	-	3	5	0	0	0	0	0.130183	0.255687	0	0	0	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.120886	0

protein_co	NADH-cyto	0	0	0	1	0	0	0	0	0	0.019227	0	0
lincRNA	-	0	0	1	3	4	1	0	0	0.070326	0.138505	0.239822	0.053038
lincRNA	-	2	4	0	2	0	0	0.146246	0.344684	0	0.126516	0	0
protein_co	taste_recep	10	3	4	2	1	8	0.518521	0.183314	0.273314	0.089714	0.058253	0.412255
antisense	-	0	2	0	0	0	0	0	0.23454	0	0	0	0
lincRNA	-	0	3	0	7	18	12	0	0.102219	0	0.175091	0.58469	0.344822
antisense	-	0	7	0	0	0	0	0	1.307527	0	0	0	0
pseudogen	-	1	0	0	0	0	1	0.05711	0	0	0	0	0.056757
antisense	-	4	12	3	5	7	5	1.340278	4.738309	1.324619	1.449332	2.635009	1.665002
antisense	-	0	0	4	1	1	0	0	0	0.65352	0.107257	0.139288	0
protein_co	sal-like_3_(	1	0	1	201	186	146	0.013245	0	0.017454	2.303122	2.767706	1.921854
pseudogen	-	3	2	4	7	0	3	0.222753	0.175001	0.391379	0.449639	0	0.221377
antisense	-	2	0	0	0	0	0	0.178553	0	0	0	0	0
antisense	-	2	3	1	2	1	9	0.144648	0.255687	0.095305	0.125134	0.081251	0.646894
antisense	-	0	0	0	1	1	0	0	0	0	0.10155	0.131876	0
antisense	-	10	17	8	0	3	5	0.355309	0.711806	0.374568	0	0.11975	0.176557
lincRNA	-	0	0	0	1	2	0	0	0	0	0.105771	0.274716	0
protein_co	polymerase	227	187	168	350	256	301	6.94258	6.739749	6.770786	9.260322	8.795976	9.148948
protein_co	-	0	0	0	1	1	0	0	0	0	0.036406	0.047278	0
pseudogen	-	3	1	1	1	0	0	0.149833	0.058856	0.065814	0.043207	0	0
lincRNA	-	1	0	2	12	5	3	0.066676	0	0.175726	0.692175	0.374533	0.198794
processed_	-	25	3	11	33	31	22	1.482111	0.209589	0.859346	1.692457	2.064673	1.296203
pseudogen	-	4	0	0	4	2	1	0.341555	0	0	0.295477	0.191858	0.084861
pseudogen	-	1	0	2	0	1	0	0.168602	0	0.444352	0	0.189414	0
pseudogen	NANOGNB_	1	0	1	0	0	0	0.125751	0	0.165709	0	0	0
antisense	-	4	2	0	4	0	3	0.351184	0.206924	0	0.303807	0	0.261761
sense_intrc	-	0	0	0	2	5	0	0	0	0	0.17786	0.577436	0
protein_co	olfactory_r	0	0	0	2	0	0	0	0	0	0.04408	0	0
lincRNA	-	6	5	3	3	2	5	0.215062	0.211197	0.141699	0.093024	0.080536	0.178111
lincRNA	-	2	0	0	0	1	0	0.189075	0	0	0	0.106207	0
sense_intrc	-	3	0	0	0	1	3	0.2521	0	0	0	0.094406	0.250543
pseudogen	-	2	0	0	0	0	1	0.104523	0	0	0	0	0.051939
protein_co	Uncharacte	13	7	6	13	4	21	0.779426	0.49458	0.474043	0.674276	0.269427	1.251297
pseudogen	-	41	49	54	38	37	45	0.831003	1.170367	1.442273	0.666293	0.8425	0.906444
lincRNA	-	1	1	0	0	2	1	0.023467	0.027654	0	0	0.052727	0.023322
antisense	-	0	1	1	0	2	1	0	0.106464	0.11905	0	0.202989	0.089785
pseudogen	-	4	1	3	1	0	0	0.231183	0.068109	0.228482	0.049999	0	0
pseudogen	cytochrom	6	1	2	0	0	1	0.107458	0.021105	0.047201	0	0	0.017799
pseudogen	-	17	8	29	4	5	4	0.267458	0.148321	0.601229	0.054441	0.088374	0.062543
protein_co	MT-RNR2-li	0	0	0	1	0	0	0	0	0	0.029453	0	0
pseudogen	-	0	0	0	0	3	1	0	0	0	0	0.181513	0.053524
protein_co	-	2	2	1	7	3	3	0.091435	0.107751	0.060245	0.27685	0.154083	0.136306
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.161619	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.079238

pseudogen	-	0	0	1	1	0	1	0	0	0.151659	0.099563	0	0.114378
protein_co	Proteasom	0	0	0	0	2	1	0	0	0	0	0.048951	0.021652
sense_intrc	RERG_intrc	2	7	12	0	0	0	0.351767	1.450877	2.78126	0	0	0
pseudogen	-	1	2	1	0	1	0	0.056141	0.132318	0.07398	0	0.063071	0
lincRNA	-	1	4	0	0	0	0	0.073224	0.34516	0	0	0	0
protein_co	transmemb	8	10	17	9	12	11	0.2889	0.425564	0.808988	0.281167	0.486842	0.394785
pseudogen	-	0	0	3	4	0	0	0	0	0.226995	0.198694	0	0
antisense	-	1	0	0	0	0	0	0.35294	0	0	0	0	0
antisense	A2ML1_ant	0	0	0	0	4	1	0	0	0	0	0.526336	0.116403
pseudogen	-	108	89	100	292	330	295	4.018009	3.901973	4.90255	9.397948	13.79273	10.90734
pseudogen	killer_cell_l	83	80	57	120	64	103	2.074647	2.356477	1.877482	2.594839	1.797195	2.558662
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.414284
pseudogen	-	1	0	0	17	17	18	0.132352	0	0	1.946453	2.527726	2.367632
pseudogen	-	2	0	1	1	0	0	0.073529	0	0.048447	0.031805	0	0
pseudogen	-	0	1	0	0	0	0	0	0.133023	0	0	0	0
pseudogen	coiled-coil_	0	0	0	0	2	0	0	0	0	0	0.275351	0
pseudogen	-	0	0	0	2	3	1	0	0	0	0.097444	0.189817	0.055972
protein_co	zinc_finger_	94	96	88	103	80	108	2.128509	2.561686	2.625821	2.017659	2.035104	2.430418
antisense	-	6	1	0	4	0	3	0.562205	0.110421	0	0.32424	0	0.279367
antisense	-	0	0	0	1	1	4	0	0	0	0.076459	0.099292	0.351346
sense_intrc	-	5	9	6	2	2	1	0.687545	1.458414	1.08722	0.237916	0.308966	0.13666
protein_co	pepsinogen	0	3	2	0	0	0	0	0.123215	0.091854	0	0	0
sense_intrc	CACNA1C_i	1	1	0	0	4	2	0.085114	0.100302	0	0	0.382482	0.169177
pseudogen	-	5	0	0	0	3	0	0.224326	0	0	0	0.15121	0
antisense	-	0	0	0	0	3	0	0	0	0	0	0.318621	0
lincRNA	-	3	4	2	6	20	16	0.291954	0.458733	0.256483	0.505135	2.186615	1.547472
pseudogen	-	2	0	3	7	10	7	0.192863	0	0.38122	0.583957	1.08335	0.670853
antisense	-	0	4	4	0	5	7	0	0.507217	0.567181	0	0.60443	0.748574
antisense	-	0	0	1	0	2	0	0	0	0.102744	0	0.175187	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.110345	0
antisense	-	1	0	0	2	0	2	0.101032	0	0	0.174805	0	0.200817
protein_co	saitohin	0	0	0	4	0	1	0	0	0	0.411676	0	0.118234
antisense	CACNA1C_a	0	0	0	0	2	0	0	0	0	0	0.26791	0
protein_co	zinc_finger_	100	116	104	293	241	219	1.504433	2.056544	2.061774	3.813322	4.07323	3.274361
antisense	-	2	0	0	2	0	2	0.250312	0	0	0.216543	0	0.248766
lincRNA	-	4	0	2	0	0	0	0.350603	0	0.231004	0	0	0
protein_co	killer_cell_l	3	0	0	1	0	0	0.217268	0	0	0.062652	0	0
pseudogen	-	3	0	0	0	0	0	0.2517	0	0	0	0	0
antisense	-	175	135	129	31	24	25	3.661926	3.32899	3.5571	0.561172	0.564198	0.519902
protein_co	calpain_sm	1	0	0	1	1	4	0.052107	0	0	0.045078	0.058539	0.207142
processed_	-	1	0	0	0	0	0	0.107823	0	0	0	0	0
pseudogen	-	1	0	0	0	2	0	0.315125	0	0	0	0.708047	0
processed_	-	1	0	3	2	0	0	0.081448	0	0.321984	0.14092	0	0
pseudogen	-	0	4	1	0	0	4	0	0.934648	0.261286	0	0	0.788225

pseudogen	-	2	3	3	0	3	6	0.298259	0.52722	0.589549	0	0.502613	0.889252
sense_intrc	CACNA1C_i	0	2	0	0	0	0	0	0.181624	0	0	0	0
pseudogen	-	0	2	2	1	2	0	0	0.065293	0.073012	0.023966	0.062246	0
pseudogen	-	2	0	1	0	0	0	0.070682	0	0.046571	0	0	0
processed_	-	0	0	1	0	0	0	0	0	0.141221	0	0	0
antisense	-	0	1	2	0	1	0	0	0.092017	0.205791	0	0.087723	0
protein_co	solute_carr	0	0	0	0	0	1	0	0	0	0	0	0.012593
protein_co	nucleolar_	52	41	31	82	30	84	0.965264	0.896878	0.758297	1.316799	0.625623	1.549642
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.200434
pseudogen	-	9	8	6	6	18	12	0.728546	0.763153	0.64003	0.420173	1.636952	0.965395
antisense	-	8	22	25	1	2	0	0.748283	2.424965	3.081417	0.080917	0.210162	0
antisense	-	28	22	17	30	22	31	2.430078	2.250049	1.944223	2.252405	2.145033	2.673829
pseudogen	-	2	3	3	0	3	0	0.199026	0.351811	0.393402	0	0.335391	0
pseudogen	-	2	2	0	0	0	0	0.197541	0.23279	0	0	0	0
pseudogen	-	4	1	4	0	3	2	1.534522	0.452085	2.022124	0	1.292955	0.762522
pseudogen	-	0	0	0	0	2	4	0	0	0	0	0.047695	0.084385
processed_	-	0	2	1	1	0	0	0	0.217379	0.121539	0.079789	0	0
lincRNA	-	2	9	4	2	0	0	0.193569	1.026489	0.510152	0.167455	0	0
antisense	-	0	0	0	6	0	3	0	0	0	0.369843	0	0.212439
pseudogen	-	0	0	0	0	0	4	0	0	0	0	0	0.243866
antisense	-	0	0	0	0	1	0	0	0	0	0	0.137995	0
antisense	-	11	4	4	0	0	0	1.481809	0.63499	0.710059	0	0	0
protein_co	Homo_sapi	0	0	0	0	0	2	0	0	0	0	0	0.077317
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.126173
lincRNA	-	0	0	1	0	0	3	0	0	0.246513	0	0	0.557746
antisense	-	17	4	8	10	16	30	1.201598	0.333179	0.745135	0.611467	1.270514	2.107372
pseudogen	small_nucl	0	1	0	1	0	0	0	0.223612	0	0.164154	0	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.219468	0
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.318873
lincRNA	-	17	12	19	2	0	0	1.219508	1.014435	1.796074	0.124116	0	0
pseudogen	taste_recep	4	4	3	0	9	6	0.232708	0.274232	0.229989	0	0.588223	0.346906
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.052457
lincRNA	-	0	1	0	0	0	0	0	0.032494	0	0	0	0
protein_co	haptoglobi	0	1	4	3	2	2	0	0.020631	0.092279	0.045435	0.039336	0.034798
antisense	-	0	2	0	1	0	0	0	0.144751	0	0.053131	0	0
sense_intrc	-	37	26	36	47	78	57	0.781027	0.646763	1.001387	0.858273	1.849729	1.195774
pseudogen	-	6	0	1	0	0	2	0.22401	0	0.049198	0	0	0.074209
antisense	-	7	8	5	13	9	21	0.218635	0.294455	0.205791	0.35126	0.315801	0.651855
protein_co	-	0	0	0	5	0	0	0	0	0	0.107207	0	0
antisense	-	3	0	0	0	1	0	0.200534	0	0	0	0.075096	0
antisense	-	0	0	1	0	3	0	0	0	0.083951	0	0.214715	0
antisense	-	0	1	0	0	1	1	0	0.077022	0	0	0.073427	0.064956
pseudogen	-	0	1	0	0	0	0	0	0.623877	0	0	0	0
antisense	-	13	11	6	6	14	11	1.760187	1.755154	1.070536	0.702797	2.129572	1.480191

pseudogen	-	1	0	3	0	0	0	0.158033	0	0.624746	0	0	0
pseudogen	ribosomal_	1	0	0	1	0	2	0.113852	0	0	0.098492	0	0.226297
pseudogen	-	1	0	0	0	0	0	0.108932	0	0	0	0	0
lincRNA	-	0	0	0	0	4	1	0	0	0	0	0.306972	0.067889
antisense	-	0	0	0	1	5	3	0	0	0	0.130854	0.849656	0.450978
processed_	-	4	7	3	5	3	6	0.248258	0.511974	0.245357	0.268458	0.209177	0.370087
protein_co	paraneopla	1	0	0	0	0	0	0.035795	0	0	0	0	0
protein_co	KIAA1147	149	132	132	220	233	170	1.081169	1.128725	1.262165	1.380998	1.899382	1.22593
lincRNA	-	0	0	1	0	4	0	0	0	0.039979	0	0.136334	0
pseudogen	leucine_ric	0	0	0	2	0	0	0	0	0	0.319156	0	0
protein_co	LSM14A_SC	1950	1711	1664	3666	3367	3573	28.2758	29.23731	31.7957	45.98707	54.84947	51.49
antisense	-	0	0	0	0	4	0	0	0	0	0	0.479644	0
protein_co	NHL_repeat	1	2	0	7	8	2	0.025246	0.059502	0	0.152881	0.226899	0.05018
antisense	-	0	0	0	4	0	0	0	0	0	0.332478	0	0
pseudogen	-	2	4	6	0	2	3	0.205596	0.484565	0.812776	0	0.230974	0.30649
pseudogen	RNA_polym	26	21	35	127	105	136	0.421066	0.400778	0.74693	1.779278	1.910361	2.188899
protein_co	chronic_lyr	0	0	0	0	0	1	0	0	0	0	0	0.013501
pseudogen	-	2	0	0	0	0	0	0.227703	0	0	0	0	0
processed_	-	10	4	2	0	0	1	0.304784	0.143668	0.080326	0	0	0.03029
processed_	-	1	1	0	0	0	0	0.091593	0.107937	0	0	0	0
pseudogen	phosphogly	5	5	9	3	2	4	0.123233	0.145223	0.292304	0.063965	0.055378	0.097978
lincRNA	-	205	221	224	659	509	556	2.350131	2.985641	3.383927	6.535617	6.555488	6.33465
lincRNA	-	0	0	0	1	0	0	0	0	0	0.076459	0	0
pseudogen	-	4	0	0	0	0	0	0.33454	0	0	0	0	0
processed_	TMPO_anti	20	14	20	69	63	76	0.315407	0.260181	0.415629	0.941354	1.11617	1.191143
pseudogen	-	3	3	3	0	2	1	0.421281	0.496454	0.555145	0	0.315522	0.13956
antisense	-	6	0	8	6	4	11	0.133465	0	0.234498	0.115459	0.09996	0.243174
sense_intrc	hsa-mir-10	1	0	1	0	6	2	0.02013	0	0.026526	0	0.135687	0.040011
pseudogen	high_mobil	0	0	0	0	2	3	0	0	0	0	0.435721	0.578176
processed_	-	1	0	2	0	0	0	0.100077	0	0.263755	0	0	0
protein_co	Uncharacte	22	14	26	0	0	0	1.522486	1.141736	2.37104	0	0	0
antisense	-	3	2	0	1	5	1	0.22182	0.174267	0	0.063965	0.415335	0.073483
lincRNA	-	1	0	0	0	0	0	0.057172	0	0	0	0	0
pseudogen	-	0	1	0	0	1	5	0	0.067228	0	0	0.06409	0.283481
processed_	-	0	1	0	0	0	0	0	0.143751	0	0	0	0
pseudogen	family_with	0	0	1	0	1	2	0	0	0.017402	0	0.014836	0.026248
antisense	-	0	0	0	3	1	0	0	0	0	0.243611	0.105454	0
protein_co	LIM_and_se	1	2	1	0	0	0	0.016534	0.038968	0.021787	0	0	0
protein_co	glutamyl-tR	333	267	260	534	366	481	8.471577	8.004577	8.71622	11.75234	10.46044	12.16115
processed_	-	88	86	64	0	0	0	4.301761	4.95415	4.122669	0	0	0
pseudogen	-	2	0	0	0	0	3	0.158506	0	0	0	0	0.236291
antisense	-	47	39	36	0	9	16	4.147045	4.055202	4.185797	0	0.892139	1.403041
antisense	-	0	2	6	9	12	9	0	0.333624	1.119197	1.102113	1.908318	1.266114
antisense	-	4	5	0	0	1	4	0.075874	0.111766	0	0	0.02131	0.075405

pseudogen	-	0	0	1	0	0	0	0	0	0.262268	0	0	0
processed_	-	1	0	0	4	0	0	0.121984	0	0	0.42211	0	0
protein_co	uncharacte	7	4	0	4	10	3	0.168372	0.113381	0	0.083233	0.270222	0.071714
pseudogen	-	7	7	3	2	0	11	0.685004	0.807235	0.386857	0.169312	0	1.069787
pseudogen	-	4	3	4	3	2	1	0.280854	0.248227	0.370097	0.182224	0.157761	0.06978
antisense	-	5	9	1	7	4	12	0.32519	0.689791	0.085704	0.393848	0.292265	0.775637
antisense	-	0	0	4	0	1	1	0	0	0.858625	0	0.183003	0.161889
lincRNA	-	2	0	0	1	1	0	0.178553	0	0	0.077233	0.100297	0
lincRNA	-	0	0	3	0	0	0	0	0	0.10597	0	0	0
processed_	-	17	13	8	33	13	21	1.085642	0.978336	0.673228	1.823117	0.932674	1.332805
lincRNA	microRNA_	0	0	0	0	3	2	0	0	0	0	0.263946	0.155663
pseudogen	zinc_finger_	477	471	409	851	701	684	4.928348	5.734703	5.568537	7.606337	8.136733	7.023421
antisense	-	24	19	17	66	48	63	2.855245	2.663746	2.665114	6.792647	6.41538	7.448731
lincRNA	-	2	1	1	0	3	0	0.176176	0.103807	0.116079	0	0.296885	0
antisense	-	17	10	11	5	8	5	0.214489	0.148684	0.182888	0.054574	0.113395	0.062695
antisense	-	1	6	2	0	1	0	0.098039	0.693197	0.258383	0	0.110141	0
antisense	-	2	2	0	5	13	10	0.179157	0.211126	0	0.38747	1.308269	0.890255
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.138639	0
sense_intrc	-	24	15	21	4	14	9	0.269591	0.198561	0.310848	0.03887	0.176674	0.100472
pseudogen	fumarylace	0	0	0	6	0	0	0	0	0	0.292645	0	0
antisense	-	20	10	8	20	16	18	2.422929	1.427637	1.277131	2.09606	2.177608	2.167169
pseudogen	-	2	0	0	0	0	1	0.14934	0	0	0	0	0.074209
protein_co	zinc_finger_	70	38	117	0	22	8	0.871969	0.55782	1.920542	0	0.307875	0.099038
antisense	-	0	1	0	0	4	0	0	0.086529	0	0	0.329963	0
protein_co	Uncharacte	0	0	0	0	1	0	0	0	0	0	0.088243	0
processed_	-	0	1	0	2	0	0	0	0.174267	0	0.25586	0	0
protein_co	maltase-glu	0	0	0	1	3	0	0	0	0	0.004993	0.019454	0
antisense	-	29	36	44	35	23	17	0.536252	0.784477	1.072157	0.559889	0.477802	0.312413
protein_co	-	0	0	0	0	1	2	0	0	0	0	0.06069	0.107376
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.066232	0
antisense	-	0	1	0	0	0	0	0	0.087012	0	0	0	0
antisense	-	42	25	42	30	13	12	4.006345	2.810258	5.279384	2.475617	1.39313	1.137601
pseudogen	-	0	0	1	0	0	0	0	0	0.055324	0	0	0
protein_co	farnesyltrar	6	10	8	2	13	2	0.112084	0.22014	0.196932	0.032321	0.272825	0.037131
pseudogen	-	0	1	0	0	0	0	0	0.092701	0	0	0	0
lincRNA	-	0	1	0	0	0	0	0	0.113021	0	0	0	0
pseudogen	-	8	10	5	0	0	1	0.546488	0.805003	0.450086	0	0	0.067889
lincRNA	microRNA_	0	0	0	1	0	0	0	0	0	0.06765	0	0
protein_co	Uncharacte	0	1	1	0	7	1	0	0.034526	0.038607	0	0.230399	0.029117
lincRNA	microRNA_	1	0	0	0	3	0	0.024996	0	0	0	0.084244	0
pseudogen	-	3	1	4	0	1	1	0.622835	0.244658	1.094326	0	0.233239	0.20633
pseudogen	-	0	0	0	1	1	0	0	0	0	0.056333	0.073156	0
processed_	-	16	16	15	18	6	13	0.591933	0.697557	0.731271	0.576087	0.249375	0.477975
lincRNA	-	3	0	1	3	2	0	0.050564	0	0.022211	0.043743	0.037871	0

lincRNA	-	16	5	16	21	5	15	0.256761	0.094556	0.338349	0.291536	0.090142	0.239227
antisense	-	11	1	5	11	7	11	0.773374	0.082852	0.463236	0.669041	0.552897	0.768598
antisense	-	2	0	0	0	0	0	0.190778	0	0	0	0	0
protein_co	zinc_finger	5	4	1	21	7	15	0.152392	0.143668	0.040163	0.5537	0.239684	0.454353
processed_	-	14	3	1	0	0	2	1.30259	0.328934	0.122607	0	0	0.184935
antisense	-	3	2	3	0	0	0	0.45508	0.357523	0.599684	0	0	0
pseudogen	-	1	2	0	3	0	0	0.231183	0.544871	0	0.599986	0	0
lincRNA	-	2	0	0	0	1	0	0.098039	0	0	0	0.05507	0
lincRNA	-	0	2	7	9	47	24	0	0.152911	0.59846	0.505135	3.425696	1.547472
sense_intrc	-	7	17	10	9	9	4	0.691394	1.978715	1.301554	0.769011	0.998663	0.392642
pseudogen	-	0	0	0	4	9	3	0	0	0	0.197409	0.576814	0.170089
antisense	-	0	0	0	0	1	0	0	0	0	0	0.079196	0
processed_	-	3	3	0	1	2	0	0.282603	0.333031	0	0.081493	0.211658	0
antisense	-	32	33	21	8	11	7	2.086345	2.535462	1.804223	0.451221	0.805708	0.453569
3prime_ov	-	1	11	0	0	0	0	0.029494	0.38232	0	0	0	0
processed_	-	0	0	1	0	0	0	0	0	0.164925	0	0	0
sense_intrc	-	8	6	5	28	17	21	0.80062	0.707611	0.659388	2.424139	1.911324	2.088648
pseudogen	-	17	20	5	2	22	15	0.895519	1.241547	0.347081	0.091142	1.30196	0.785284
pseudogen	-	2	1	0	6	2	8	0.093453	0.055064	0	0.242536	0.104988	0.371503
processed_	-	1	0	0	0	0	2	0.091752	0	0	0	0	0.182371
lincRNA	-	0	0	0	4	0	0	0	0	0	0.421139	0	0
processed_	-	0	0	6	0	3	0	0	0	1.674319	0	0.713711	0
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.258546
pseudogen	-	3	11	0	6	8	9	0.448652	1.938602	0	0.776253	1.344089	1.337645
lincRNA	-	6	7	4	1	9	2	0.421281	0.579196	0.370097	0.060741	0.709925	0.13956
pseudogen	heat_shock	1	0	0	0	0	0	0.02933	0	0	0	0	0
pseudogen	olfactory_r	0	0	1	8	2	2	0	0	0.04906	0.257659	0.083651	0.074
lincRNA	-	7	1	6	9	6	3	0.977802	0.164611	1.104432	1.087573	0.941571	0.41647
protein_co	Uncharacte	0	0	0	0	2	3	0	0	0	0	0.208687	0.276916
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.022906
lincRNA	-	17	10	4	12	6	8	0.932639	0.646505	0.289174	0.56952	0.369798	0.436179
antisense	-	3	9	6	2	6	3	0.133465	0.47184	0.351748	0.076973	0.299879	0.13264
pseudogen	-	0	0	0	1	0	0	0	0	0	0.077757	0	0
antisense	-	1	9	7	0	2	2	0.06243	0.662134	0.575876	0	0.140273	0.12409
pseudogen	glutathione	0	0	0	1	0	2	0	0	0	0.14357	0	0.329869
pseudogen	-	11	6	8	0	2	0	0.557274	0.358207	0.534073	0	0.11383	0
pseudogen	-	0	4	0	5	2	1	0	0.146622	0	0.134544	0.069889	0.030913
processed_	-	1	1	1	0	0	0	0.10442	0.123053	0.1376	0	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.097662	0
protein_co	zinc_finger	0	5	8	3	4	2	0	0.185899	0.332602	0.081881	0.141778	0.06271
protein_co	UDP-N-acet	6	7	14	0	5	5	0.058834	0.080888	0.180901	0	0.05508	0.048726
lincRNA	-	0	2	0	0	0	0	0	0.397374	0	0	0	0
antisense	-	4	3	3	18	17	32	0.288114	0.254644	0.284748	1.121606	1.375633	2.29068
protein_co	Uncharacte	0	0	2	2	0	0	0	0	0.144887	0.095117	0	0

pseudogen	-	0	0	1	1	20	10	0	0	0.287092	0.188473	4.895137	2.165187
processed_	-	15	20	18	9	7	5	1.246648	1.958798	1.971333	0.64708	0.653582	0.412983
processed_	-	1	0	3	0	3	2	0.084167	0	0.332734	0	0.283669	0.167294
processed_	-	619	506	435	658	472	563	13.2406	12.75482	12.26143	12.17603	11.34248	11.96837
antisense	-	4	0	1	0	1	0	0.347724	0	0.114554	0	0.097662	0
antisense	-	1	0	0	2	1	1	0.096432	0	0	0.166845	0.108335	0.095836
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.172394	0
lincRNA	-	24	23	37	29	59	29	2.975606	3.360463	6.045062	3.110464	8.217984	3.57332
lincRNA	-	1	0	0	0	0	0	0.144648	0	0	0	0	0
processed_	-	0	0	1	0	0	0	0	0	0.096225	0	0	0
pseudogen	-	2	0	0	0	4	0	0.120595	0	0	0	0.270961	0
lincRNA	-	0	0	1	0	5	3	0	0	0.147491	0	0.628709	0.333704
processed_	-	0	0	0	0	2	0	0	0	0	0	0.183851	0
pseudogen	chromobo	1	5	0	0	0	3	0.101614	0.598731	0	0	0	0.30296
processed_	-	0	0	0	28	26	42	0	0	0	0.757454	0.913393	1.305251
antisense	-	6	8	4	23	16	7	0.430415	0.67629	0.378121	1.427337	1.289451	0.499049
antisense	-	0	3	2	1	0	0	0	0.447759	0.333796	0.109567	0	0
processed_	-	78	50	50	43	26	26	5.440576	4.109864	4.595737	2.594668	2.037383	1.802326
antisense	LBX2_antis	2	7	3	30	30	42	0.050831	0.209656	0.100475	0.65961	0.85659	1.060869
protein_co	proline_ric	569	376	259	350	225	254	35.94681	27.99259	21.56168	19.12842	15.96907	15.94746
processed_	-	0	0	1	0	0	0	0	0	0.106346	0	0	0
antisense	-	5	4	1	1	5	8	0.503241	0.474431	0.13263	0.08707	0.56536	0.800214
protein_co	canopy_2_l	64	71	66	105	95	138	2.802501	3.663796	3.808417	3.977572	4.673459	6.005574
antisense	-	0	4	0	0	2	0	0	0.355993	0	0	0.169689	0
antisense	-	0	0	0	3	0	0	0	0	0	0.244478	0	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.062311	0	0
antisense	-	27	28	14	140	47	89	3.270954	3.997383	2.234979	14.67242	6.396723	10.71545
lincRNA	-	1	0	0	0	0	0	0.042017	0	0	0	0	0
lincRNA	-	103	82	94	230	170	174	1.088842	1.021524	1.309455	2.103384	2.018951	1.828044
pseudogen	-	1	4	0	0	0	0	0.075307	0.35498	0	0	0	0
antisense	-	3	2	1	1	0	0	0.384559	0.30212	0.168918	0.110893	0	0
lincRNA	-	0	1	0	0	0	0	0	0.110421	0	0	0	0
processed_	-	0	0	1	0	0	0	0	0	0.132378	0	0	0
pseudogen	-	0	0	0	0	1	4	0	0	0	0	0.072267	0.255718
antisense	-	0	0	1	0	0	0	0	0	0.131629	0	0	0
processed_	-	0	0	1	0	0	0	0	0	0.198756	0	0	0
pseudogen	formin_bin	12	19	6	10	11	4	0.318602	0.594467	0.20992	0.229684	0.328102	0.105545
pseudogen	MRS2_mag	1	3	2	0	2	0	0.044081	0.155839	0.116175	0	0.099044	0
pseudogen	-	0	0	1	0	3	4	0	0	0.04798	0	0.122715	0.144743
antisense	-	0	0	2	0	0	1	0	0	0.258383	0	0	0.097433
processed_	-	12	18	11	28	9	25	0.71947	1.271777	0.869078	1.452287	0.60621	1.489639
lincRNA	-	0	3	1	13	6	6	0	0.140724	0.052454	0.447658	0.268312	0.237357
pseudogen	-	0	0	2	4	2	1	0	0	0.128124	0.168224	0.10923	0.048314
antisense	-	2	0	1	4	4	0	0.108597	0	0.071552	0.187893	0.244004	0

pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.022351	0
lincRNA	-	0	2	0	0	0	0	0	0.487404	0	0	0	0
pseudogen	-	0	0	3	1	7	4	0	0	0.18391	0.040245	0.365845	0.184935
pseudogen	MT-ND1_ps	0	0	0	0	2	0	0	0	0	0	0.138155	0
lincRNA	-	2	0	7	3	0	4	0.042302	0	0.195103	0.054893	0	0.084082
pseudogen	-	0	2	0	1	1	1	0	0.217758	0	0.079928	0.103797	0.091822
pseudogen	-	1	3	0	0	0	0	0.107385	0.379641	0	0	0	0
3prime_ov	-	6	3	0	6	4	6	0.558253	0.328934	0	0.482941	0.418108	0.554805
processed_	-	0	0	1	0	0	1	0	0	0.080932	0	0	0.061037
sense_intrc	-	0	0	0	0	2	4	0	0	0	0	0.249375	0.441208
lincRNA	-	1	3	0	0	0	0	0.060435	0.213657	0	0	0	0
antisense	-	3	0	0	0	0	0	0.54956	0	0	0	0	0
lincRNA	-	0	0	1	0	0	1	0	0	0.110385	0	0	0.08325
lincRNA	-	7	5	3	2	8	27	0.320855	0.270077	0.181203	0.079305	0.411954	1.229939
pseudogen	-	5	8	5	7	5	5	0.45482	0.857563	0.599341	0.550846	0.510961	0.452011
lincRNA	-	0	0	6	0	0	1	0	0	0.763832	0	0	0.096011
processed_	-	0	0	0	1	0	0	0	0	0	0.055784	0	0
pseudogen	-	1	2	0	0	1	0	0.227215	0.535517	0	0	0.255261	0
processed_	-	1	2	1	2	1	0	0.092716	0.218521	0.122177	0.160416	0.104161	0
antisense	-	5	6	5	5	3	0	0.125215	0.17707	0.165003	0.108323	0.084403	0
processed_	-	0	0	0	8	0	2	0	0	0	0.452894	0	0.130072
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.091344
protein_co	cut-like_ho	1002	884	801	1541	1595	1361	3.854591	4.007466	4.060485	5.128333	6.893191	5.203293
lincRNA	-	0	0	2	0	0	0	0	0	0.248268	0	0	0
lincRNA	-	0	0	1	0	0	0	0	0	0.125927	0	0	0
pseudogen	-	0	1	3	1	0	0	0	0.107937	0.362093	0.079237	0	0
protein_co	-	20	10	10	31	23	48	0.179309	0.105652	0.118143	0.240435	0.231659	0.427684
pseudogen	-	0	0	1	8	3	2	0	0	0.073512	0.386081	0.188017	0.110883
antisense	-	8	19	8	3	5	2	0.694308	1.943224	0.914928	0.225241	0.487508	0.172505
pseudogen	-	2	2	1	5	1	1	0.163651	0.192852	0.107826	0.353933	0.091926	0.08132
pseudogen	-	0	1	0	7	16	5	0	0.162046	0	0.832707	2.471726	0.683299
pseudogen	glutaminyl	2	0	0	0	0	0	0.080457	0	0	0	0	0
antisense	-	2	10	4	4	3	10	0.185758	1.094522	0.489567	0.321396	0.313031	0.923054
pseudogen	-	1	2	0	0	2	0	0.247388	0.583063	0	0	0.55585	0
protein_co	Uncharacte	0	0	0	2	1	1	0	0	0	0.144249	0.093663	0.082857
antisense	-	1	0	0	5	0	0	0.082591	0	0	0.357246	0	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.083575	0	0
antisense	-	0	0	0	0	2	2	0	0	0	0	0.213558	0.188919
antisense	-	0	2	0	0	0	0	0	0.065984	0	0	0	0
pseudogen	high_mobil	1	0	0	0	0	0	0.163398	0	0	0	0	0
pseudogen	-	0	6	4	0	0	2	0	0.313244	0.233517	0	0	0.088057
antisense	-	0	4	1	0	3	4	0	0.278206	0.077774	0	0.198916	0.234622
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.123944
antisense	-	0	0	0	0	1	0	0	0	0	0	0.067433	0

pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.094707	0
antisense	-	2	3	1	1	1	0	0.211341	0.373579	0.139248	0.091415	0.118714	0
pseudogen	-	0	0	0	1	1	2	0	0	0	0.188473	0.244757	0.433037
antisense	-	2	7	6	1	7	4	0.158744	0.654744	0.627556	0.068664	0.624185	0.315527
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.168011	0
protein_co	Uncharacte	0	0	0	0	3	0	0	0	0	0	0.315801	0
antisense	-	39	38	35	63	45	68	1.620643	1.860858	1.916574	2.264781	2.100798	2.808285
antisense	BCDIN3D_a	10	16	3	6	3	14	0.171998	0.324303	0.067995	0.089277	0.057969	0.23931
processed_	-	0	0	0	0	1	0	0	0	0	0	0.158181	0
pseudogen	-	0	0	0	8	0	1	0	0	0	0.539604	0	0.077488
processed_	-	47	39	30	4	0	7	3.326506	3.252836	2.797993	0.244914	0	0.492377
lincRNA	-	2	0	0	0	0	0	0.125156	0	0	0	0	0
processed_	-	10	10	6	0	4	1	0.969615	1.142632	0.766629	0	0.435721	0.096363
processed_	-	7	8	5	1	0	5	0.499443	0.672644	0.470103	0.061724	0	0.354542
processed_	-	11	2	2	0	2	3	0.928789	0.199004	0.22253	0	0.189716	0.251742
antisense	-	5	1	5	7	4	10	0.545783	0.128634	0.719209	0.661015	0.490523	1.084826
lincRNA	-	1	0	0	1	0	0	0.059218	0	0	0.051229	0	0
antisense	-	6	3	9	13	10	13	0.471285	0.27769	0.931557	0.883362	0.882432	1.014811
processed_	-	1	0	0	0	0	0	0.072324	0	0	0	0	0
pseudogen	-	0	0	1	0	0	6	0	0	0.16974	0	0	0.768088
processed_	-	0	0	0	1	0	0	0	0	0	0.055921	0	0
lincRNA	-	2	0	0	0	0	0	0.156168	0	0	0	0	0
processed_	-	0	0	0	1	0	0	0	0	0	0.105527	0	0
protein_co	Uncharacte	11	10	13	3	0	3	0.343976	0.368504	0.53569	0.081156	0	0.093232
processed_	-	0	0	0	1	0	0	0	0	0	0.079928	0	0
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.211869
processed_	-	16	26	9	6	13	7	0.5042	0.965524	0.373732	0.163568	0.46023	0.219225
processed_	-	3	2	0	0	0	0	0.281601	0.221233	0	0	0	0
pseudogen	-	0	0	0	0	1	1	0	0	0	0	0.11731	0.103775
pseudogen	-	0	3	0	2	1	0	0	0.607673	0	0.297395	0.193104	0
antisense	-	0	0	0	2	0	7	0	0	0	0.047167	0	0.189649
lincRNA	-	0	0	0	0	3	0	0	0	0	0	0.140605	0
antisense	-	1	0	1	0	0	0	0.107385	0	0.141508	0	0	0
processed_	-	0	1	6	0	0	5	0	0.118834	0.797295	0	0	0.501086
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.103617	0
lincRNA	-	1	0	1	0	0	3	0.090343	0	0.11905	0	0	0.269355
sense_over	-	4	2	1	0	0	1	0.525469	0.309617	0.17311	0	0	0.130556
lincRNA	-	0	0	0	0	1	2	0	0	0	0	0.108138	0.191324
pseudogen	-	0	0	1	0	0	0	0	0	0.14534	0	0	0
processed_	-	2	0	0	0	4	1	0.111926	0	0	0	0.251484	0.055617
pseudogen	-	0	0	0	0	1	1	0	0	0	0	0.039026	0.034524
processed_	-	0	7	3	0	0	0	0	0.919398	0.44061	0	0	0
protein_co	C-type_lect	0	0	0	0	1	0	0	0	0	0	0.01694	0
pseudogen	-	5	1	2	6	3	4	0.46603	0.109838	0.245645	0.483791	0.314133	0.370521

protein_co	Protein_LO	4	2	0	0	0	0	0.146347	0.08623	0	0	0	0
lincRNA	-	0	0	0	9	2	9	0	0	0	0.698627	0.201613	0.802587
pseudogen	-	13	15	9	5	1	4	2.271396	3.088501	2.072177	0.755758	0.19629	0.694575
protein_co	Uncharacte	0	2	0	0	0	0	0	0.620773	0	0	0	0
protein_co	Uncharacte	0	0	0	0	1	0	0	0	0	0	0.075286	0
antisense	-	0	1	6	0	0	3	0	0.115107	0.772287	0	0	0.291222
lincRNA	-	3	0	0	0	0	0	0.419058	0	0	0	0	0
pseudogen	-	0	2	3	0	0	1	0	0.848813	1.42374	0	0	0.357919
antisense	-	2	0	1	2	1	3	0.066718	0	0.043959	0.057718	0.037477	0.099459
pseudogen	-	0	0	0	3	0	0	0	0	0	0.238123	0	0
pseudogen	polymerase	6	0	4	4	1	4	1.89075	0	1.661031	1.09045	0.354023	1.252715
lincRNA	-	1	0	2	3	4	1	0.050276	0	0.132504	0.130481	0.225929	0.049966
protein_co	churchill_d	766	769	668	775	695	598	11.99432	14.18993	13.78346	10.49812	12.2259	9.305886
antisense	-	142	143	133	176	82	176	3.214032	3.814213	3.966873	3.446177	2.08509	3.958988
pseudogen	-	0	1	0	0	0	0	0	0.162468	0	0	0	0
lincRNA	-	21	14	9	38	21	20	0.662946	0.520828	0.3744	1.037781	0.744779	0.627478
3prime_ov	-	4	2	4	2	2	5	0.247967	0.146107	0.32676	0.107257	0.139288	0.308045
processed_	-	4	3	2	0	0	2	0.271841	0.240261	0.17911	0	0	0.135081
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.050884
protein_co	Uncharacte	7	3	11	7	3	10	0.109576	0.055341	0.226906	0.094794	0.052758	0.155571
lincRNA	-	0	0	0	0	0	6	0	0	0	0	0	0.60592
protein_co	chromoson	1	5	1	5	4	2	0.022595	0.133136	0.029775	0.097736	0.101538	0.044912
pseudogen	-	2	3	1	0	0	0	0.094034	0.16622	0.061957	0	0	0
antisense	-	9	9	1	9	9	10	0.540214	0.636609	0.079097	0.467336	0.606897	0.596531
processed_	-	4	6	0	6	7	0	0.355309	0.628064	0	0.461063	0.698543	0
antisense	-	1	4	0	1	1	2	0.120595	0.568453	0	0.104326	0.13548	0.2397
lincRNA	-	0	2	0	0	0	0	0	0.149253	0	0	0	0
antisense	-	0	0	3	2	1	0	0	0	0.050238	0.021987	0.014277	0
sense_intro	-	3	4	4	6	0	3	0.322156	0.506188	0.566031	0.55739	0	0.320167
sense_over	-	2	0	0	0	0	0	0.221975	0	0	0	0	0
processed_	-	1	0	0	0	3	0	0.113364	0	0	0	0.382072	0
sense_over	-	2	0	8	17	8	13	0.186741	0	0.984314	1.373159	0.839166	1.206319
processed_	-	0	0	0	1	0	0	0	0	0	0.076332	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.130233
lincRNA	microRNA_	1	1	0	2	0	0	0.036286	0.042761	0	0.062781	0	0
processed_	-	4	4	0	1	3	2	0.678731	0.799843	0	0.146791	0.571884	0.33727
pseudogen	-	0	2	0	2	0	0	0	0.159969	0	0.117433	0	0
pseudogen	PEST_conta	2	2	1	3	5	3	0.207205	0.244179	0.136523	0.268878	0.581956	0.308889
protein_co	Uncharacte	8	3	7	6	4	7	0.53207	0.23513	0.613496	0.345218	0.298874	0.462686
protein_co	regulator_c	11	17	9	3	8	5	0.115776	0.210853	0.124825	0.027315	0.094594	0.0523
pseudogen	solute_carr	2	0	0	0	0	2	0.12032	0	0	0	0	0.119577
antisense	-	12	21	8	4	1	2	0.377476	0.778457	0.331614	0.108851	0.035339	0.062524
antisense	-	0	1	0	5	4	4	0	0.143091	0	0.525217	0.545651	0.482698
processed_	-	1	0	0	4	0	0	0.155252	0	0	0.537231	0	0

processed_	-	0	0	0	2	4	5	0	0	0	0.204004	0.529852	0.585903
antisense	-	6	7	3	4	0	2	0.170961	0.235045	0.112643	0.098598	0	0.056635
protein_co	Epidermal_	4	3	1	4	10	8	0.050649	0.044765	0.016686	0.043816	0.142253	0.100673
lincRNA	-	0	0	1	0	0	0	0	0	0.052296	0	0	0
lincRNA	-	0	0	0	0	3	0	0	0	0	0	0.334134	0
antisense	-	0	0	5	0	1	0	0	0	0.599341	0	0.102192	0
antisense	-	2	0	2	0	0	4	0.186412	0	0.245645	0	0	0.370521
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.125871
lincRNA	-	0	3	0	0	0	0	0	0.359929	0	0	0	0
protein_co	zinc_finger_	1	0	0	2	4	6	0.010074	0	0	0.017431	0.045272	0.060073
sense_intrc	-	3	7	0	0	2	0	0.345267	0.949378	0	0	0.258591	0
lincRNA	-	1	0	1	3	0	1	0.095561	0	0.125927	0.248009	0	0.094971
processed_	-	0	0	1	0	1	1	0	0	0.09453	0	0.080591	0.071293
pseudogen	-	0	0	2	0	0	0	0	0	0.259343	0	0	0
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.235937
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.131293	0
processed_	-	0	0	0	0	2	0	0	0	0	0	0.206514	0
processed_	-	11	3	2	8	8	13	1.94117	0.623877	0.465089	1.221304	1.586024	2.279942
pseudogen	-	2	0	0	5	1	4	0.20168	0	0	0.43618	0.113287	0.400869
antisense	-	2	1	1	6	0	2	0.251501	0.148189	0.165709	0.652716	0	0.249948
protein_co	peptide_de	77	66	32	181	135	225	3.520256	3.555777	1.927828	7.158551	6.933721	10.22294
lincRNA	-	3	0	0	0	0	0	0.22213	0	0	0	0	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.095315
pseudogen	-	1	2	1	0	0	6	0.097677	0.230213	0.128715	0	0	0.582443
processed_	long_interg	447	367	396	620	643	512	4.362143	4.220516	5.092398	5.234161	7.049404	4.965603
processed_	-	2	0	0	1	2	5	0.113001	0	0	0.048878	0.12695	0.280758
pseudogen	-	1	0	1	0	1	3	0.085665	0	0.112886	0	0.096239	0.255408
pseudogen	-	0	0	2	2	0	0	0	0	0.460484	0.302303	0	0
pseudogen	-	0	0	0	0	3	2	0	0	0	0	0.349174	0.205926
sense_intrc	-	6	4	8	1	7	3	0.792135	0.622321	1.391786	0.114212	1.038233	0.393621
lincRNA	-	0	0	0	1	0	0	0	0	0	0.050053	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.192725
processed_	-	0	6	1	1	0	4	0	0.719858	0.13416	0.088075	0	0.404723
antisense	-	2	0	0	0	1	0	0.291686	0	0	0	0.163846	0
antisense	-	14	5	9	8	8	11	0.725929	0.305523	0.614955	0.358855	0.466021	0.566851
processed_	-	0	6	0	5	4	8	0	0.565448	0	0.345913	0.359371	0.635819
processed_	-	0	1	0	0	0	6	0	0.016075	0	0	0	0.081341
protein_co	DDB1-_and	0	2	0	0	1	0	0	0.047353	0	0	0.022572	0
protein_co	-	4	0	0	2	1	2	0.316066	0	0	0.136713	0.08877	0.157057
pseudogen	charged_m	3	3	4	7	5	3	0.270107	0.318305	0.47458	0.545225	0.505748	0.268439
antisense	-	2	0	0	2	0	1	0.075738	0	0	0.065521	0	0.037635
protein_co	Uncharacte	29	20	20	228	169	158	0.425996	0.346214	0.387144	2.897378	2.788965	2.306609
lincRNA	long_interg	2	0	0	0	0	1	0.149551	0	0	0	0	0.074314
lincRNA	-	0	0	0	8	1	4	0	0	0	0.534098	0.0867	0.306787

protein_co	sperm_equ	3	2	4	0	0	2	0.110987	0.087195	0.195006	0	0	0.073535
pseudogen	-	1	6	1	4	1	6	0.057796	0.408653	0.076161	0.199995	0.06493	0.344634
antisense	RNA_7SL_c	37023	27541	124421	4392	21727	30032	6533.448	5727.402	28933.39	670.496	4307.444	5267.017
pseudogen	-	1	2	1	0	0	2	0.072029	0.169763	0.094916	0	0	0.143167
antisense	-	0	0	0	0	2	2	0	0	0	0	0.231424	0.204724
lincRNA	DIO3_oppc	12	12	7	26	8	34	0.204405	0.240879	0.157125	0.383131	0.153091	0.575572
pseudogen	-	1	0	1	0	0	0	0.163904	0	0.215985	0	0	0
lincRNA	-	0	0	0	1	1	0	0	0	0	0.075327	0.097822	0
pseudogen	-	0	1	0	0	2	1	0	0.126291	0	0	0.240793	0.106506
protein_co	Uncharacte	0	0	0	0	2	2	0	0	0	0	0.186153	0.164676
pseudogen	-	0	0	0	1	0	4	0	0	0	0.194889	0	0.895558
antisense	-	3	6	16	4	8	6	0.332266	0.78311	2.335173	0.383254	0.995413	0.660427
lincRNA	-	0	1	0	0	0	1	0	0.107937	0	0	0	0.091028
antisense	-	10	2	4	13	6	6	0.959076	0.226042	0.505531	1.078597	0.646477	0.571892
pseudogen	5'3'-nucleo	10	5	3	0	0	0	1.040098	0.612846	0.411178	0	0	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.029872	0
lincRNA	-	4	1	0	2	4	5	0.247099	0.072798	0	0.106882	0.277601	0.306966
pseudogen	ankyrin_rep	2	3	2	4	13	5	0.133521	0.236019	0.175948	0.231016	0.975015	0.331741
pseudogen	barrier_to_	8	1	6	1	6	2	1.610372	0.237216	1.591558	0.17414	1.356865	0.400107
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.102192	0
sense_over	-	0	0	2	0	0	2	0	0	0.023324	0	0	0.017591
pseudogen	-	0	0	0	4	9	10	0	0	0	0.563679	1.647025	1.618894
lincRNA	FRMD6_ant	0	0	0	0	1	0	0	0	0	0	0.102368	0
protein_co	-	1	0	0	2	0	0	0.015471	0	0	0.026767	0	0
processed_	-	2	0	0	1	2	2	0.050372	0	0	0.021788	0.05659	0.050061
antisense	-	0	0	0	2	2	0	0	0	0	0.182466	0.236956	0
protein_co	Uncharacte	1	0	1	0	1	0	0.008533	0	0.011245	0	0.009587	0
antisense	-	0	0	0	0	2	1	0	0	0	0	0.276632	0.122358
processed_	-	12	10	8	11	9	14	0.464734	0.456384	0.408271	0.368535	0.391575	0.538842
antisense	-	0	1	0	0	0	0	0	0.113846	0	0	0	0
lincRNA	-	2	0	0	2	1	4	0.087796	0	0	0.075952	0.049317	0.174508
pseudogen	-	0	3	0	0	0	0	0	0.355824	0	0	0	0
pseudogen	-	9	15	9	12	20	5	0.421654	0.828156	0.555637	0.48636	1.052671	0.232806
pseudogen	ras_homolo	8	0	4	2	2	4	0.731482	0	0.481957	0.1582	0.205444	0.363482
lincRNA	-	0	0	1	0	0	3	0	0	0.129191	0	0	0.2923
pseudogen	pituitary_t	0	2	1	0	1	0	0	0.354476	0.198191	0	0.168966	0
protein_co	Uncharacte	4	6	5	0	2	0	0.213257	0.376965	0.351275	0	0.11979	0
pseudogen	-	1	0	1	0	0	0	0.113852	0	0.150029	0	0	0
pseudogen	-	0	3	0	0	2	1	0	0.638782	0	0	0.405979	0.17957
pseudogen	neurobeach	5	8	6	10	9	13	0.087189	0.164395	0.137872	0.150853	0.176312	0.225291
pseudogen	-	0	4	0	0	2	1	0	0.681833	0	0	0.325005	0.143754
lincRNA	-	0	0	0	18	5	8	0	0	0	0.742016	0.267668	0.378859
lincRNA	-	0	0	0	3	12	9	0	0	0	0.13148	0.682977	0.453135
pseudogen	-	0	0	0	1	8	1	0	0	0	0.079237	0.823196	0.091028

lincRNA	-	2	2	0	49	33	46	0.182241	0.21476	0	3.862558	3.37815	4.165656
antisense	-	0	0	0	0	0	5	0	0	0	0	0	0.423624
pseudogen	-	0	0	0	3	1	0	0	0	0	0.508877	0.220281	0
pseudogen	DnaJ_(Hsp4	0	0	0	6	0	0	0	0	0	0.782887	0	0
pseudogen	-	4	3	4	0	1	2	0.207408	0.183314	0.273314	0	0.058253	0.103064
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.217864
pseudogen	-	0	0	0	2	0	0	0	0	0	0.506065	0	0
sense_intrc	-	1	3	0	0	1	0	0.120048	0.424406	0	0	0.134866	0
antisense	-	1	2	1	0	0	3	0.114839	0.270663	0.15133	0	0	0.342391
pseudogen	cytochrom	1	1	0	7	9	0	0.168067	0.198056	0	1.017753	1.699312	0
pseudogen	-	1	0	0	0	0	0	0.519029	0	0	0	0	0
antisense	-	1	0	0	0	0	0	0.076394	0	0	0	0	0
antisense	-	120	125	106	149	159	140	1.506859	1.849731	1.75401	1.618605	2.243043	1.747146
lincRNA	-	16	15	18	44	47	66	1.598219	1.76569	2.369319	3.802173	5.274279	6.551938
antisense	-	0	0	1	0	1	4	0	0	0.177064	0	0.150954	0.534153
pseudogen	ribosomal_	0	1	0	6	0	1	0	0.132177	0	0.582189	0	0.11147
protein_co	BCL2L2-PA	7	13	7	6	3	8	0.271294	0.593734	0.357499	0.201166	0.130621	0.308135
pseudogen	-	0	0	0	4	0	0	0	0	0	0.598679	0	0
antisense	-	3	3	2	12	0	1	0.324791	0.382747	0.28533	1.1239	0	0.107595
pseudogen	ubiquitin-c	7	4	13	0	2	3	0.66893	0.450453	1.637045	0	0.214715	0.284914
pseudogen	-	0	1	0	0	3	0	0	0.37583	0	0	1.074866	0
protein_co	Uncharacte	0	0	1	0	0	0	0	0	0.01888	0	0	0
lincRNA	-	79	94	52	18	18	6	4.616268	6.472899	4.004074	0.909912	1.181641	0.348437
antisense	ARHGAP5_	6	5	14	48	26	31	0.231015	0.226864	0.710317	1.598798	1.124636	1.186208
antisense	-	0	0	0	0	1	0	0	0	0	0	0.093516	0
antisense	-	5	0	4	5	0	0	0.663421	0	0.699381	0.573921	0	0
protein_co	tripartite_r	0	2	1	4	2	2	0	0.05005	0.027984	0.073484	0.047714	0.042209
antisense	-	55	41	30	51	40	55	4.201666	3.691049	3.020055	3.370482	3.432953	4.175718
antisense	-	0	0	0	0	1	0	0	0	0	0	0.022762	0
lincRNA	HIF1A_anti	40	20	41	7	6	5	3.973058	2.341003	5.366406	0.601487	0.669523	0.493565
antisense	-	0	3	3	0	0	0	0	0.215626	0.241117	0	0	0
lincRNA	-	3	0	1	0	4	0	0.322156	0	0.141508	0	0.482563	0
lincRNA	-	0	0	0	1	5	4	0	0	0	0.071898	0.466844	0.330387
processed_	-	3	0	0	0	0	0	0.080214	0	0	0	0	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.026694
processed_	-	26	39	29	43	25	34	2.389698	4.224169	3.512387	3.419016	2.58142	3.10569
pseudogen	-	8	0	1	2	0	1	0.369248	0	0.060822	0.079859	0	0.045871
processed_	-	14	8	20	2	1	6	0.152192	0.102485	0.286502	0.018809	0.012213	0.064822
processed_	-	1	0	0	2	1	0	0.087942	0	0	0.152156	0.098797	0
antisense	-	0	0	1	0	0	0	0	0	0.13263	0	0	0
pseudogen	sal-like_4_(	0	4	0	0	0	0	0	0.079984	0	0	0	0
lincRNA	-	0	1	0	0	0	0	0	0.161626	0	0	0	0
lincRNA	-	1	0	0	0	0	0	0.151693	0	0	0	0	0
lincRNA	long_interg	0	0	0	6	2	3	0	0	0	0.317313	0.137358	0.182266

lincRNA	long_interg	17	16	9	23	12	19	0.357425	0.396427	0.249352	0.418338	0.283444	0.397008
lincRNA	-	0	1	2	0	1	0	0	0.02059	0.046048	0	0.019629	0
processed_	-	36	9	24	27	13	15	3.160656	0.93116	2.776648	2.050697	1.282234	1.308807
protein_co	HCG18042	1	0	4	9	6	12	0.027516	0	0.145038	0.214236	0.185476	0.328154
processed_	cancer/test	0	0	0	1	0	0	0	0	0	0.013466	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.012617	0
protein_co	chromosor	0	0	1	0	0	0	0	0	0.095566	0	0	0
lincRNA	-	21	12	13	0	0	0	1.539835	1.036915	1.256126	0	0	0
antisense	-	6	2	4	9	13	6	0.208292	0.08182	0.182986	0.270289	0.507008	0.207006
antisense	-	3	3	1	5	2	8	0.048974	0.057713	0.021512	0.070612	0.03668	0.129791
antisense	ITPK1_anti	2	3	0	0	4	2	0.022523	0.039813	0	0	0.050607	0.022384
antisense	-	2	0	0	0	0	1	0.098403	0	0	0	0	0.048898
pseudogen	-	55	48	48	14	23	8	7.703055	7.922251	8.858829	1.696256	3.618905	1.113525
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.08081	0
lincRNA	-	0	0	0	0	1	1	0	0	0	0	0.118242	0.1046
pseudogen	SUB1_hom	0	0	0	0	2	1	0	0	0	0	0.447187	0.197797
antisense	-	13	23	11	20	10	20	0.325098	0.677807	0.362492	0.432677	0.280944	0.497062
pseudogen	enolase_1_	5	4	0	0	2	5	0.271771	0.256212	0	0	0.122127	0.270093
pseudogen	-	2	0	0	1	0	0	0.283866	0	0	0.122785	0	0
lincRNA	-	0	0	1	11	4	9	0	0	0.08842	0.638515	0.301526	0.60016
protein_co	Uncharacte	1	0	0	3	1	1	0.075847	0	0	0.196843	0.085209	0.075378
antisense	-	0	3	1	0	0	3	0	0.349838	0.130399	0	0	0.295032
antisense	-	0	0	0	0	0	3	0	0	0	0	0	0.34165
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.122127	0
processed_	-	0	1	1	0	0	2	0	0.103807	0.116079	0	0	0.175088
lincRNA	-	1	0	0	0	0	0	0.137509	0	0	0	0	0
lincRNA	-	5	8	1	0	0	0	0.076065	0.14342	0.020047	0	0	0
processed_	-	0	0	0	0	0	9	0	0	0	0	0	0.824959
lincRNA	-	32	24	41	23	41	28	0.442442	0.391043	0.747008	0.275104	0.636854	0.384746
pseudogen	RAP1A_me	0	5	1	1	1	0	0	0.69166	0.154686	0.10155	0.131876	0
lincRNA	-	1	0	0	0	0	0	0.095389	0	0	0	0	0
lincRNA	-	5	6	12	0	1	4	0.461963	0.653275	1.461011	0	0.103797	0.367288
lincRNA	HIF1A_anti	19	7	23	21	17	26	1.542759	0.669807	2.460975	1.475118	1.550752	2.098106
pseudogen	-	19	9	5	5	2	1	0.881577	0.492103	0.305711	0.200696	0.104252	0.046112
processed_	-	0	0	0	0	0	1	0	0	0	0	0	0.114628
pseudogen	-	1	1	1	0	0	0	0.220587	0.259949	0.29068	0	0	0
processed_	-	7	6	1	8	13	9	0.516138	0.521346	0.097163	0.510294	1.076862	0.659508
protein_co	KIAA0391	3	1	0	7	8	6	0.041178	0.016175	0	0.08312	0.123362	0.081847
processed_	long_interg	3	2	1	0	3	2	0.179867	0.141309	0.079007	0	0.20207	0.119171
processed_	-	0	0	0	1	3	0	0	0	0	0.151152	0.58887	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.333
polymorph	olfactory_r	0	0	0	1	0	0	0	0	0	0.048722	0	0
lincRNA	-	0	3	0	0	0	0	0	0.22659	0	0	0	0
processed_	-	1	0	2	0	0	0	0.092554	0	0.243928	0	0	0

lincRNA	-	1	0	2	7	2	2	0.092554	0	0.243928	0.560476	0.207958	0.183965
antisense	-	0	0	0	0	3	4	0	0	0	0	0.606897	0.715837
lincRNA	-	6	0	1	1	10	5	0.097617	0	0.021439	0.014075	0.182778	0.080845
lincRNA	-	0	1	3	0	0	0	0	0.126291	0.423664	0	0	0
lincRNA	-	0	1	0	11	4	13	0	0.120208	0	0.97069	0.458389	1.317886
antisense	-	0	0	0	3	0	0	0	0	0	0.195166	0	0
antisense	-	3	1	2	4	6	0	0.385493	0.151427	0.338657	0.44465	0.866154	0
pseudogen	-	0	0	0	2	0	2	0	0	0	0.119423	0	0.137194
antisense	-	1	1	3	8	3	4	0.096256	0.113432	0.380527	0.666166	0.324414	0.382648
sense_intrc	-	0	0	0	0	1	0	0	0	0	0	0.071831	0
pseudogen	-	1	0	0	0	0	0	0.08973	0	0	0	0	0
antisense	-	3	6	1	0	0	0	0.29576	0.69707	0.129913	0	0	0
protein_co	melanocort	28	45	19	15	15	42	0.407574	0.771913	0.364449	0.188887	0.245295	0.607586
lincRNA	-	0	0	0	1	0	0	0	0	0	0.142233	0	0
antisense	-	0	0	0	8	0	0	0	0	0	0.934672	0	0
antisense	-	0	0	1	3	3	1	0	0	0.126154	0.248457	0.322654	0.095143
lincRNA	-	0	0	0	4	3	0	0	0	0	0.36566	0.356143	0
antisense	-	6	2	2	0	3	2	0.44364	0.174267	0.19487	0	0.249201	0.146967
lincRNA	-	0	0	3	0	0	0	0	0	0.384724	0	0	0
processed_	-	2	3	1	0	0	0	0.169683	0.299941	0.1118	0	0	0
pseudogen	eukaryotic_	10	10	3	9	7	11	1.552522	1.829552	0.613753	1.208769	1.220913	1.697227
lincRNA	-	1	0	0	0	0	0	0.08095	0	0	0	0	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.117425	0
lincRNA	-	6	14	7	0	0	0	0.547665	1.505911	0.841971	0	0	0
lincRNA	-	5	0	2	0	0	0	0.473533	0	0.2496	0	0	0
lincRNA	-	0	0	0	0	1	1	0	0	0	0	0.089572	0.079238
pseudogen	-	0	0	2	0	1	0	0	0	0.365253	0	0.155696	0
lincRNA	-	0	0	1	6	0	2	0	0	0.181675	0.715608	0	0.274032
protein_co	centrosom	388	362	322	713	523	590	5.641611	6.20279	6.169672	8.968585	8.543231	8.525759
antisense	-	11	12	7	2	6	6	0.164135	0.211007	0.137639	0.025817	0.100579	0.088975
pseudogen	-	0	0	0	0	1	1	0	0	0	0	0.114377	0.101181
pseudogen	-	2	0	0	0	2	0	0.303387	0	0	0	0.340836	0
pseudogen	heterogene	6	6	8	32	43	54	0.414681	0.488677	0.728598	1.91327	3.338726	3.709084
lincRNA	-	0	0	0	0	3	1	0	0	0	0	0.319763	0.09429
lincRNA	-	1	0	1	0	0	0	0.071833	0	0.094658	0	0	0
sense_intrc	-	21	1	9	11	4	3	2.085855	0.11705	1.177992	0.945193	0.446348	0.296139
lincRNA	-	3	0	1	9	11	14	0.228522	0	0.100379	0.593079	0.941345	1.059851
lincRNA	-	1	0	1	0	0	0	0.061992	0	0.08169	0	0	0
lincRNA	-	0	0	0	0	0	3	0	0	0	0	0	1.242852
pseudogen	-	3	0	1	0	0	0	0.096198	0	0.042255	0	0	0
pseudogen	zinc_finger_	12	0	1	4	2	0	0.807232	0	0.088645	0.232777	0.151146	0
antisense	FOXN3_ant	22	10	7	61	33	52	1.081432	0.579273	0.453429	2.593996	1.822382	2.540326
processed_	-	5	3	2	3	5	6	0.570485	0.403369	0.300704	0.296114	0.640904	0.680354
protein_co	Uncharacte	1	0	4	0	0	0	0.100077	0	0.527511	0	0	0

lincRNA	-	1	1	4	3	3	2	0.023008	0.027113	0.121275	0.059712	0.077544	0.045731
pseudogen	-	0	3	0	0	0	0	0	0.656713	0	0	0	0
pseudogen	-	0	0	0	3	5	3	0	0	0	0.203853	0.441216	0.234187
lincRNA	-	1	0	0	0	0	0	0.071833	0	0	0	0	0
lincRNA	-	4	0	2	0	1	0	0.378826	0	0.2496	0	0.106397	0
antisense	-	8	5	6	9	5	12	0.147725	0.108803	0.145999	0.143771	0.103725	0.220219
antisense	-	0	1	4	4	0	0	0	0.045907	0.205337	0.134802	0	0
lincRNA	-	18	7	7	0	0	2	1.082884	0.496266	0.554935	0	0	0.119577
antisense	-	7	5	13	0	4	1	0.476946	0.401465	1.167211	0	0.306182	0.067714
protein_co	Tubulin_be	140	97	93	172	144	184	1.995085	1.628966	1.746429	2.120434	2.305392	2.605918
antisense	-	2	2	3	0	0	3	0.294117	0.346598	0.581361	0	0	0.43845
pseudogen	-	2	0	1	2	3	0	0.08686	0	0.05723	0.075142	0.146372	0
antisense	-	35	32	39	0	0	0	3.239396	3.490223	4.756587	0	0	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.015384	0	0
lincRNA	long_interg	10	7	10	1	0	0	0.776261	0.640343	1.022922	0.067154	0	0
lincRNA	-	0	0	2	1	3	6	0	0	0.076411	0.025082	0.097715	0.172883
antisense	-	8	6	8	8	10	6	0.748283	0.661354	0.986053	0.647334	1.050811	0.557746
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.242461
pseudogen	-	1	3	3	0	0	0	0.199026	0.703621	0.786804	0	0	0
pseudogen	-	5	9	3	6	0	3	0.754145	1.599685	0.596267	0.782887	0	0.449693
lincRNA	-	0	2	0	0	0	0	0	0.485508	0	0	0	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.197409	0	0
lincRNA	-	1	2	2	1	0	0	0.079372	0.18707	0.209185	0.068664	0	0
pseudogen	eukaryotic_	2	0	2	3	4	0	0.256373	0	0.337837	0.33268	0.576038	0
antisense	-	1	0	1	3	2	0	0.159943	0	0.210765	0.415096	0.359371	0
processed_	-	3	4	6	6	7	0	0.322811	0.507217	0.850772	0.558523	0.846202	0
protein_co	Ubiquitin-c	0	0	2	3	1	0	0	0	0.048079	0.047346	0.020495	0
antisense	-	26	10	10	36	7	31	3.760836	1.704583	1.906101	4.50481	1.137518	4.456381
protein_co	transmemb	0	0	0	3	1	2	0	0	0	0.05474	0.023696	0.041924
pseudogen	-	0	0	0	1	0	0	0	0	0	0.036176	0	0
pseudogen	neurofibro	0	0	0	1	2	0	0	0	0	0.018283	0.047486	0
lincRNA	-	2	3	2	0	0	0	0.036461	0.06445	0.048046	0	0	0
antisense	-	2	3	5	0	4	1	0.176176	0.31142	0.580393	0	0.395846	0.087544
antisense	-	78	155	290	12	154	90	6.47241	15.15689	31.71058	0.861421	14.35626	7.422045
processed_	-	0	0	0	0	0	1	0	0	0	0	0	0.09654
lincRNA	-	2	1	0	4	3	6	0.179766	0.105921	0	0.311028	0.302933	0.535967
processed_	-	1	2	0	0	0	0	0.053747	0.126676	0	0	0	0
pseudogen	-	0	0	0	1	1	1	0	0	0	0.192432	0.249899	0.221067
pseudogen	-	1	0	2	4	4	13	0.183187	0	0.482791	0.633895	0.823196	2.366722
protein_co	FPGT-TNNI3	7	11	5	0	1	0	0.048981	0.090704	0.046103	0	0.007861	0
lincRNA	-	10	2	2	0	0	3	0.957342	0.225634	0.252308	0	0	0.285429
pseudogen	endosulfine	1	2	1	2	2	3	0.150401	0.354476	0.198191	0.260221	0.337931	0.448415
lincRNA	-	0	0	0	2	0	0	0	0	0	0.204459	0	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.094122

antisense	-	0	2	5	0	3	3	0	0.447224	1.250238	0	0.639526	0.565742
antisense	-	1	0	4	0	0	0	0.074775	0	0.394143	0	0	0
antisense	-	0	0	0	1	0	0	0	0	0	0.058343	0	0
pseudogen	cysteine_ar	2	0	0	0	0	0	0.097139	0	0	0	0	0
pseudogen	-	0	1	0	1	0	0	0	0.187351	0	0.137534	0	0
antisense	-	0	0	0	1	0	0	0	0	0	0.040494	0	0
pseudogen	double_ho	0	0	0	0	0	1	0	0	0	0	0	0.113637
lincRNA	-	1	2	0	0	0	0	0.070028	0.165047	0	0	0	0
antisense	ACTN1_ant	1	0	0	6	3	15	0.088382	0	0	0.458754	0.297876	1.317547
antisense	-	7	4	5	8	2	4	0.646749	0.435516	0.608755	0.639426	0.207595	0.367288
protein_co	Uncharacte	3	1	0	0	0	3	0.278637	0.109452	0	0	0	0.276916
lincRNA	-	2	0	0	0	0	1	0.181305	0	0	0	0	0.090093
lincRNA	long_interg	0	0	0	0	1	0	0	0	0	0	0.013235	0
lincRNA	-	19	12	13	19	17	17	2.255334	1.678594	2.033459	1.951074	2.267019	2.005468
processed_	FOXN3_ant	0	3	2	0	0	0	0	0.148307	0.11056	0	0	0
protein_co	POC1B-GAL	0	0	1	1	0	0	0	0	0.012834	0.008425	0	0
pseudogen	polypyrimi	0	0	1	0	0	0	0	0	0.043575	0	0	0
pseudogen	-	0	1	0	0	0	0	0	0.157148	0	0	0	0
antisense	-	3	1	3	2	2	0	0.212047	0.083295	0.279426	0.122293	0.158814	0
lincRNA	-	4	1	1	1	1	7	0.399555	0.117713	0.131629	0.086413	0.112219	0.694903
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.35076
processed_	-	0	1	0	0	0	0	0	0.164611	0	0	0	0
antisense	-	5	4	4	9	3	8	0.590859	0.557033	0.622886	0.920067	0.398276	0.939537
pseudogen	-	3	0	0	0	0	0	0.132795	0	0	0	0	0
pseudogen	-	47	53	43	6	3	9	3.499616	4.650562	4.219158	0.386489	0.250953	0.666001
pseudogen	-	1	0	1	0	0	0	0.03116	0	0.041061	0	0	0
antisense	-	0	8	1	4	3	3	0	1.114067	0.155722	0.408919	0.398276	0.352326
antisense	-	0	0	0	0	9	0	0	0	0	0	0.971476	0
lincRNA	-	0	0	1	0	2	1	0	0	0.138971	0	0.236956	0.104809
antisense	-	24	14	12	10	16	5	2.277032	1.565284	1.500286	0.820769	1.705403	0.471452
antisense	-	7	11	8	1	4	7	0.465562	0.862142	0.701139	0.057536	0.298874	0.462686
protein_co	small_integ	6	2	0	5	8	15	0.331918	0.130382	0	0.239284	0.497186	0.824672
pseudogen	-	1	1	3	0	3	0	0.263388	0.310387	1.041243	0	0.8877	0
pseudogen	trans-golgi_	0	0	0	0	1	0	0	0	0	0	0.096395	0
antisense	-	11	26	14	3	1	1	0.90287	2.514854	1.514242	0.213018	0.092211	0.081572
lincRNA	-	0	0	2	0	0	0	0	0	0.530519	0	0	0
lincRNA	long_interg	16	5	6	37	47	38	0.293607	0.108124	0.145088	0.587369	0.968932	0.69301
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.191672
antisense	-	1	4	1	6	4	2	0.144253	0.679975	0.190091	0.748756	0.648239	0.286725
processed_	-	1	2	2	3	4	0	0.089126	0.21006	0.234893	0.231308	0.400511	0
pseudogen	-	0	0	0	2	0	0	0	0	0	0.043535	0	0
antisense	-	0	5	1	7	11	1	0	0.608068	0.135991	0.624936	1.275312	0.102562
pseudogen	CAP_adeny	0	1	1	1	1	3	0	0.044883	0.050189	0.032949	0.042788	0.113556
sense_intrc	-	5	0	0	0	1	0	0.832406	0	0	0	0.187031	0

lincRNA	-	8	5	2	100	137	90	0.673335	0.495928	0.221823	7.281225	12.95421	7.528242
pseudogen	-	1	0	1	2	4	4	0.10084	0	0.132882	0.174472	0.45315	0.400869
lincRNA	ADAM_met	3	3	6	0	0	1	0.052348	0.061689	0.137963	0	0	0.017341
pseudogen	-	0	0	1	0	1	0	0	0	0.095697	0	0.081586	0
pseudogen	-	0	2	0	5	0	8	0	0.140197	0	0.257297	0	0.472935
processed_	-	1	0	2	2	0	0	0.042798	0	0.112794	0.074048	0	0
pseudogen	DEAD_(Asp	4	4	11	0	5	3	0.106307	0.125277	0.385239	0	0.149287	0.079238
antisense	-	0	0	0	0	2	2	0	0	0	0	0.108138	0.095662
antisense	-	1	3	0	10	9	5	0.020441	0.072264	0	0.17683	0.206673	0.101572
pseudogen	-	1	0	0	3	0	0	0.075094	0	0	0.194889	0	0
antisense	-	0	4	2	0	0	0	0	0.099028	0.055368	0	0	0
processed_	-	0	0	0	0	2	1	0	0	0	0	0.051339	0.022708
antisense	-	0	0	0	2	1	2	0	0	0	0.199995	0.12986	0.229756
lincRNA	-	1	0	0	0	0	0	0.114591	0	0	0	0	0
pseudogen	ubiquitin-c	1	0	0	0	0	0	0.098955	0	0	0	0	0
antisense	-	0	0	0	4	0	0	0	0	0	0.503285	0	0
lincRNA	-	50	40	49	8	4	1	4.103953	3.869006	5.299846	0.568048	0.368843	0.081572
antisense	-	0	0	0	0	1	0	0	0	0	0	0.046321	0
pseudogen	-	0	3	0	1	1	1	0	0.285745	0	0.069922	0.090803	0.080327
pseudogen	-	0	1	1	0	1	4	0	0.079882	0.089326	0	0.076154	0.26947
pseudogen	-	1	8	1	0	0	0	0.304259	2.868401	0.400938	0	0	0
sense_intrc	HMBOX1_i	0	0	1	0	0	0	0	0	0.201047	0	0	0
lincRNA	-	4	7	5	7	7	1	0.245951	0.507217	0.405129	0.372349	0.483544	0.061108
antisense	-	5	4	4	2	4	1	0.519029	0.489316	0.547163	0.179604	0.466478	0.103165
protein_co	Uncharacte	3	6	1	0	0	0	0.336489	0.793064	0.147804	0	0	0
pseudogen	protein_kir	1	1	6	4	9	10	0.047184	0.055604	0.373066	0.163276	0.47708	0.468931
protein_co	integrin_be	89	68	85	10	14	8	1.179411	1.061919	1.484325	0.114641	0.208426	0.10536
antisense	-	0	1	7	0	6	10	0	0.125277	0.980608	0	0.716577	1.056507
antisense	-	1	3	1	1	3	1	0.072621	0.25674	0.095697	0.062824	0.244757	0.072173
antisense	-	1	8	4	2	6	1	0.11169	1.052957	0.58872	0.193244	0.75286	0.111
antisense	-	0	0	0	0	0	3	0	0	0	0	0	0.212725
pseudogen	-	0	2	0	3	2	0	0	0.254644	0	0.280401	0.242759	0
antisense	-	0	0	2	2	5	4	0	0	0.058306	0.038277	0.124271	0.087947
protein_co	solute_carr	17	15	8	2	8	9	0.753135	0.78311	0.467035	0.076651	0.398165	0.396256
lincRNA	-	0	4	1	0	0	0	0	0.217568	0.060822	0	0	0
pseudogen	-	3	0	2	0	0	0	0.40413	0	0.355029	0	0	0
pseudogen	-	0	1	2	3	0	1	0	0.065533	0.146562	0.144324	0	0.055267
lincRNA	-	0	0	0	2	0	0	0	0	0	0.057141	0	0
pseudogen	-	1	2	2	0	0	0	0.178253	0.420119	0.469786	0	0	0
pseudogen	-	9	11	8	11	8	4	0.264999	0.381682	0.310404	0.280194	0.264631	0.11705
antisense	-	1	0	1	0	0	0	0.131694	0	0.173541	0	0	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.027289
processed_	-	1	0	3	0	1	0	0.107604	0	0.425386	0	0.120886	0
lincRNA	-	0	2	0	0	0	0	0	0.19743	0	0	0	0

antisense	-	4	11	12	8	0	5	0.117191	0.379781	0.463287	0.202762	0	0.145584
antisense	-	72	51	51	104	59	93	7.032752	5.870432	6.564442	8.787982	6.474316	9.027872
antisense	-	0	0	6	0	0	0	0	0	0.217897	0	0	0
sense_intrc	-	1	0	0	0	1	0	0.102599	0	0	0	0.115263	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.113364	0	0
pseudogen	-	0	2	2	4	0	0	0	0.467324	0.522571	0.686126	0	0
pseudogen	NADH_deh	0	0	0	0	0	3	0	0	0	0	0	0.631369
antisense	-	0	0	0	10	13	15	0	0	0	0.340766	0.575288	0.58721
antisense	-	1	0	0	0	4	0	0.121984	0	0	0	0.548165	0
lincRNA	-	4	0	3	0	3	0	0.376135	0	0.37174	0	0.316923	0
antisense	-	2	0	0	3	3	3	0.186412	0	0	0.241896	0.314133	0.277891
antisense	-	0	0	1	0	0	0	0	0	0.092894	0	0	0
processed_	-	1	0	0	0	0	0	0.092232	0	0	0	0	0
lincRNA	-	0	0	2	0	0	1	0	0	0.186035	0	0	0.070152
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.158715
antisense	-	0	0	0	0	2	0	0	0	0	0	0.1559	0
pseudogen	-	2	2	4	0	0	0	0.115089	0.135625	0.303319	0	0	0
antisense	-	9	11	12	17	18	4	1.065926	1.535269	1.87284	1.741793	2.395003	0.470819
protein_co	Uncharacte	0	0	3	6	2	4	0	0	0.075638	0.099311	0.042989	0.076059
sense_intrc	-	1	2	1	0	0	5	0.148711	0.350493	0.195964	0	0	0.738961
antisense	-	25	7	8	20	16	9	1.133155	0.373899	0.477831	0.784228	0.814739	0.405416
antisense	-	2	0	0	3	1	0	0.170228	0	0	0.220895	0.09562	0
pseudogen	-	46	31	17	0	8	3	0.312617	0.24827	0.152243	0	0.061079	0.020262
antisense	-	0	0	0	0	0	4	0	0	0	0	0	0.543814
antisense	-	3	5	6	7	3	0	0.238115	0.467674	0.627556	0.480648	0.267508	0
pseudogen	-	0	0	1	0	0	0	0	0	0.04762	0	0	0
pseudogen	tubulin_be	3	0	1	0	1	0	0.128915	0	0.056626	0	0.048276	0
protein_co	ZHX1-C8OR	4	1	0	0	2	0	0.168736	0.049711	0	0	0.094782	0
lincRNA	-	0	0	0	0	3	0	0	0	0	0	0.229933	0
pseudogen	-	0	0	0	0	4	1	0	0	0	0	0.58887	0.130233
antisense	-	5	0	0	0	0	0	0.328011	0	0	0	0	0
pseudogen	-	14	6	3	26	10	12	0.445953	0.225226	0.125927	0.716469	0.357858	0.379885
processed_	-	6	8	3	29	28	27	0.188738	0.296555	0.124355	0.789167	0.989498	0.844076
pseudogen	-	1	0	2	0	0	0	0.143861	0	0.379148	0	0	0
pseudogen	-	3	7	10	1	4	16	0.540214	1.485422	2.372901	0.155779	0.809196	2.86335
antisense	-	3	1	10	16	4	3	0.039129	0.01537	0.171873	0.180533	0.058611	0.038887
lincRNA	-	7	2	3	6	3	21	0.4961	0.167035	0.280174	0.367863	0.238859	1.47911
antisense	-	1	8	1	0	0	0	0.117909	1.111585	0.155375	0	0	0
pseudogen	-	0	0	0	1	2	1	0	0	0	0.050663	0.131584	0.058201
antisense	-	6	7	5	2	3	7	0.1492	0.205126	0.16384	0.043024	0.083808	0.172991
lincRNA	-	4	10	1	1	0	0	0.242293	0.713818	0.079821	0.052401	0	0
pseudogen	-	22	14	14	14	8	21	1.004053	0.752955	0.841971	0.552745	0.410179	0.952496
antisense	-	291	243	221	723	493	647	25.93574	25.52225	25.9557	55.74513	49.36301	57.30857
pseudogen	-	0	0	0	2	0	0	0	0	0	0.051809	0	0

processed_	-	0	0	1	0	1	0	0	0	0.051985	0	0.044319	0
lincRNA	-	0	1	0	1	0	0	0	0.157944	0	0.115947	0	0
antisense	-	0	0	0	0	2	2	0	0	0	0	0.163171	0.144346
antisense	-	2	0	4	4	0	1	0.137688	0	0.362878	0.238226	0	0.068419
pseudogen	-	0	0	0	2	2	6	0	0	0	0.150654	0.195644	0.519218
processed_	-	19	17	23	4	0	1	0.729956	0.76966	1.164409	0.132943	0	0.038181
lincRNA	-	1	0	0	0	0	0	0.071445	0	0	0	0	0
lincRNA	-	4	6	7	0	0	0	0.377476	0.667248	0.870487	0	0	0
antisense	-	20	5	10	5	15	9	1.900933	0.560033	1.252483	0.411121	1.601685	0.850137
pseudogen	-	0	0	0	3	0	1	0	0	0	0.292333	0	0.111945
antisense	-	0	1	0	18	5	12	0	0.026006	0	0.343635	0.12396	0.26318
antisense	-	0	0	0	0	0	5	0	0	0	0	0	0.147709
lincRNA	-	3	6	3	1	1	0	0.248549	0.5858	0.327527	0.071673	0.093077	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.013795
protein_co	Uncharacte	20	20	17	3	3	6	1.59221	1.876323	1.783422	0.206612	0.268312	0.474713
antisense	-	8	4	2	0	3	5	0.725219	0.427313	0.238915	0	0.305527	0.450463
lincRNA	-	6	7	2	0	0	0	0.571306	0.785457	0.250947	0	0	0
3prime_ov	-	13	24	22	7	30	8	1.246799	2.71251	2.780421	0.580783	3.232387	0.762522
antisense	-	4	1	5	0	2	2	0.320855	0.094527	0.52851	0	0.18023	0.159437
antisense	-	2	1	0	5	9	12	0.035555	0.02095	0	0.076895	0.179746	0.212011
lincRNA	-	1	0	0	0	0	0	0.080457	0	0	0	0	0
antisense	-	1	3	2	0	0	0	0.107823	0.381188	0.284168	0	0	0
pseudogen	DDB1_and_	1	6	0	4	0	2	0.039686	0.280604	0	0.137328	0	0.078882
pseudogen	-	0	1	0	0	0	0	0	0.034621	0	0	0	0
lincRNA	-	3	0	0	0	2	0	0.064275	0	0	0	0.048139	0
pseudogen	-	1	4	3	0	0	0	0.043323	0.204215	0.171268	0	0	0
protein_co	growth_ho	0	0	1	0	0	1	0	0	0.084052	0	0	0.06339
pseudogen	H3_histone	2	0	0	0	0	1	0.317012	0	0	0	0	0.157527
pseudogen	-	0	0	1	0	0	0	0	0	0.2028	0	0	0
pseudogen	-	0	0	0	0	3	0	0	0	0	0	0.187424	0
sense_intrc	-	0	0	0	1	4	3	0	0	0	0.096216	0.499798	0.331601
pseudogen	-	5	0	2	3	9	6	0.361619	0	0.19061	0.1877	0.731261	0.431263
sense_intrc	-	6	1	6	4	2	2	0.833716	0.163747	1.098634	0.480828	0.31221	0.276189
sense_intrc	-	3	2	6	3	3	13	0.301945	0.237216	0.795779	0.26121	0.339216	1.300347
pseudogen	elongation_	0	0	1	2	0	2	0	0	0.0388	0.050944	0	0.058525
pseudogen	iron-sulfur_	4	0	0	1	0	3	1.580328	0	0	0.341783	0	1.177926
antisense	-	7	6	2	6	1	8	0.384426	0.388305	0.144737	0.285055	0.061697	0.436631
antisense	-	13	0	7	8	14	13	1.267464	0	0.899342	0.674754	1.533449	1.259637
processed_	-	0	2	0	0	0	0	0	0.360623	0	0	0	0
pseudogen	-	2	0	0	0	2	1	0.098221	0	0	0	0.110345	0.048807
pseudogen	hect_doma	3	2	3	0	0	1	0.218764	0.171867	0.288278	0	0	0.072471
antisense	-	2	0	0	4	8	6	0.123839	0	0	0.214264	0.5565	0.369221
antisense	-	1	2	3	9	13	10	0.007684	0.01811	0.030376	0.059824	0.112219	0.076363
antisense	-	5	0	0	0	2	0	0.488386	0	0	0	0.219468	0

antisense	-	0	1	0	1	7	0	0	0.026503	0	0.019456	0.176861	0
processed_	-	0	0	0	3	0	0	0	0	0	0.197409	0	0
antisense	-	1	0	0	0	2	0	0.158506	0	0	0	0.356143	0
pseudogen	-	0	0	0	0	3	1	0	0	0	0	0.045286	0.013354
processed_	-	7	9	1	35	32	30	0.208429	0.315798	0.039237	0.901553	1.070433	0.887751
pseudogen	ubiquitin-c	4	0	1	0	1	1	0.26176	0	0.086234	0	0.073518	0.065036
protein_co	thiamine_t	76	59	56	15	24	46	1.406824	1.28702	1.365994	0.240204	0.499099	0.84624
sense_intrc	-	2	0	1	0	0	1	0.186741	0	0.123039	0	0	0.092794
antisense	-	2	0	1	0	0	1	0.05416	0	0.035685	0	0	0.026913
lincRNA	-	0	7	0	0	0	1	0	0.504872	0	0	0	0.060825
pseudogen	nucleopho	2	0	0	0	1	0	0.13471	0	0	0	0.075669	0
antisense	-	7	11	8	10	3	15	0.339676	0.629024	0.511555	0.419788	0.163545	0.723383
lincRNA	-	1	7	5	5	3	1	0.100648	0.830255	0.663149	0.435351	0.339216	0.100027
antisense	-	0	0	0	1	8	2	0	0	0	0.095614	0.993335	0.219683
processed_	-	0	0	0	0	4	0	0	0	0	0	0.508341	0
lincRNA	-	0	0	0	6	2	2	0	0	0	0.140129	0.060659	0.05366
lincRNA	-	8	6	4	0	0	0	0.901123	0.796439	0.59373	0	0	0
sense_intrc	-	5	4	2	0	4	3	0.354832	0.334519	0.187033	0	0.318906	0.211585
antisense	-	4	11	6	22	6	14	0.370217	1.199764	0.731783	1.761496	0.623873	1.287756
protein_co	Uncharacte	0	0	2	0	6	3	0	0	0.057537	0	0.147157	0.06509
lincRNA	-	11	8	3	0	0	0	0.713665	0.611644	0.256483	0	0	0
pseudogen	acidic_(leu	1	0	0	0	0	0	0.074987	0	0	0	0	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.024609
antisense	-	1	2	0	0	0	3	0.127877	0.30139	0	0	0	0.381261
pseudogen	adenosylhc	0	0	0	2	0	0	0	0	0	0.070029	0	0
pseudogen	NADH_deh	1	0	1	0	0	0	0.102006	0	0.134419	0	0	0
lincRNA	-	0	0	0	5	0	3	0	0	0	0.424064	0	0.2923
pseudogen	keratin_8_p	1	0	0	0	0	0	0.036536	0	0	0	0	0
protein_co	HCG20035	0	2	0	0	0	0	0	0.14979	0	0	0	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.078005
antisense	-	0	1	1	0	3	0	0	0.191962	0.214656	0	0.549008	0
antisense	-	9	0	5	0	4	1	0.810321	0	0.593225	0	0.404598	0.08948
pseudogen	-	22	8	21	10	6	24	1.02798	0.440514	1.293053	0.404227	0.314965	1.114508
pseudogen	-	1	0	0	0	0	0	0.049757	0	0	0	0	0
antisense	-	1	1	1	0	1	1	0.111221	0.131067	0.146562	0	0.124949	0.110534
antisense	-	3	0	0	0	0	0	0.269649	0	0	0	0	0
processed_	-	3	0	0	0	0	0	0.307201	0	0	0	0	0
processed_	-	21	12	16	15	13	10	0.368499	0.248145	0.369974	0.227704	0.256277	0.174392
lincRNA	-	0	0	0	24	27	27	0	0	0	1.94544	2.842212	2.5143
antisense	-	4	0	1	9	4	2	0.281601	0	0.09277	0.548125	0.316361	0.139931
protein_co	mitochond	39	30	44	65	68	60	0.371282	0.336564	0.551984	0.535323	0.727273	0.567675
antisense	-	33	27	20	886	768	878	0.520886	0.502227	0.416	12.09834	13.61881	13.77315
lincRNA	-	3	11	4	3	2	0	0.242478	1.047733	0.426035	0.209766	0.181606	0
pseudogen	-	0	0	1	4	2	4	0	0	0.112703	0.295954	0.192168	0.339994

lincRNA	-	0	0	0	1	0	0	0	0	0	0.081638	0	0
pseudogen	-	4	1	0	2	3	7	0.17603	0.05186	0	0.076141	0.148319	0.30615
processed_	-	0	0	0	2	0	0	0	0	0	0.161548	0	0
protein_co	uncharacte	16	6	14	0	1	1	1.697507	0.750153	1.957286	0	0.11919	0.105439
pseudogen	heterogene	4	5	2	0	0	0	0.219217	0.322918	0.144437	0	0	0
pseudogen	-	3	0	0	0	0	0	0.493239	0	0	0	0	0
antisense	-	2	6	5	1	0	3	0.139686	0.493834	0.46018	0.060421	0	0.208235
antisense	-	1	2	3	9	9	26	0.063938	0.150695	0.252766	0.497814	0.646477	1.652132
pseudogen	acidic_(leu	0	6	2	2	0	3	0	0.348535	0.129913	0.085287	0	0.146967
antisense	-	5	4	3	7	5	9	0.420167	0.396113	0.332206	0.508877	0.472031	0.751629
antisense	-	0	3	2	1	5	9	0	0.421539	0.314249	0.103151	0.669774	1.066501
antisense	-	9	12	6	19	6	15	0.328373	0.515956	0.288477	0.59971	0.245938	0.543908
processed_	-	20	5	10	4	16	22	1.497624	0.441214	0.986751	0.259117	1.34599	1.637212
lincRNA	long_interg	0	0	0	7	1	8	0	0	0	0.179503	0.033301	0.235673
antisense	-	0	0	1	0	0	1	0	0	0.131381	0	0	0.099085
protein_co	E3_ubiquit	7	2	4	17	27	8	0.077238	0.026006	0.05816	0.162272	0.334691	0.087727
pseudogen	-	0	2	3	11	9	2	0	0.079882	0.133988	0.322528	0.342691	0.067368
lincRNA	-	4	6	1	1	0	4	0.448652	0.793064	0.147804	0.097032	0	0.445882
antisense	-	5	2	0	0	0	0	0.118066	0.055654	0	0	0	0
pseudogen	-	6	1	0	0	0	0	1.549493	0.30433	0	0	0	0
antisense	-	3	0	0	5	0	1	0.251302	0	0	0.362333	0	0.08325
antisense	-	0	0	0	0	1	0	0	0	0	0	0.027949	0
lincRNA	-	0	2	4	2	0	0	0	0.22202	0.496536	0.162985	0	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.210908	0
antisense	-	1	1	1	0	0	3	0.093042	0.109645	0.122607	0	0	0.277403
pseudogen	-	0	1	1	0	6	2	0	0.104327	0.116661	0	0.596748	0.175967
pseudogen	cytochrom	0	0	0	5	4	1	0	0	0	0.760779	0.790378	0.174798
lincRNA	-	0	4	0	0	0	0	0	0.457053	0	0	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.083534	0
pseudogen	-	16	20	17	14	21	16	0.813694	1.198612	1.139266	0.615931	1.199802	0.808669
pseudogen	-	3	7	16	28	13	14	0.228522	0.628366	1.606061	1.845136	1.112499	1.059851
antisense	-	0	10	3	0	3	0	0	1.252766	0.420261	0	0.358289	0
antisense	-	0	1	1	0	1	0	0	0.15636	0.174845	0	0.149062	0
pseudogen	-	6	7	16	0	0	4	0.816571	1.122658	2.869441	0	0	0.541019
protein_co	BH3-like_m	0	0	11	0	0	0	0	0	0.890251	0	0	0
antisense	-	0	0	1	0	0	0	0	0	0.145038	0	0	0
lincRNA	-	0	1	1	0	3	4	0	0.031637	0.035377	0	0.090481	0.106722
pseudogen	TYRO3P_pr	5	12	9	0	14	4	0.097858	0.276766	0.232114	0	0.307824	0.077803
antisense	-	6	10	4	12	5	15	0.098863	0.194173	0.086851	0.171051	0.092555	0.24563
processed_	-	0	0	0	6	0	0	0	0	0	0.318048	0	0
pseudogen	-	0	0	1	0	1	1	0	0	0.058526	0	0.049896	0.044139
antisense	-	0	0	0	0	5	0	0	0	0	0	0.630041	0
lincRNA	-	0	0	0	0	0	5	0	0	0	0	0	0.814459
antisense	-	0	0	4	0	0	0	0	0	0.34622	0	0	0

pseudogen	PRELI_dom	0	2	1	4	2	6	0	0.243702	0.136256	0.357804	0.232328	0.616571
pseudogen	-	1	0	0	0	0	0	0.215207	0	0	0	0	0
lincRNA	-	0	0	0	0	3	1	0	0	0	0	0.260859	0.076921
antisense	-	1	0	5	0	2	0	0.084706	0	0.558106	0	0.190323	0
3prime_ov	-	4	8	11	0	5	2	0.689785	1.625739	2.499662	0	0.968663	0.342763
antisense	-	0	0	0	2	0	0	0	0	0	0.137534	0	0
processed_	-	31	47	16	31	34	70	1.155754	2.064946	0.786065	0.999835	1.424071	2.59365
antisense	YLP_motif_	22	1	9	0	2	1	1.673422	0.089638	0.902111	0	0.170908	0.075595
lincRNA	-	0	0	0	19	2	1	0	0	0	1.828108	0.249899	0.110534
pseudogen	eukaryotic_	2	4	0	0	1	0	0.076726	0.180834	0	0	0.043098	0
pseudogen	-	2	0	0	0	0	0	0.125601	0	0	0	0	0
processed_	-	2	0	0	0	0	0	0.235293	0	0	0	0	0
antisense	-	3	0	3	0	4	2	0.317646	0	0.41858	0	0.475807	0.210456
lincRNA	-	0	2	0	0	0	1	0	0.420119	0	0	0	0.177152
pseudogen	-	0	0	0	0	2	1	0	0	0	0	0.051967	0.022986
antisense	-	0	0	0	1	1	3	0	0	0	0.17414	0.226144	0.60016
sense_over	-	155	160	92	243	261	222	2.800633	3.406838	2.190519	3.798339	5.298025	3.986457
processed_	-	0	0	2	0	0	0	0	0	0.226137	0	0	0
pseudogen	-	1	6	0	0	3	1	0.130397	0.921986	0	0	0.439477	0.129591
pseudogen	-	1	2	2	3	1	1	0.029412	0.06932	0.077515	0.076332	0.033042	0.02923
pseudogen	-	0	0	1	2	0	0	0	0	0.683954	0.898018	0	0
antisense	-	7	13	6	6	12	15	0.230321	0.504065	0.260149	0.170785	0.443574	0.490498
lincRNA	-	1	0	0	0	0	0	0.075522	0	0	0	0	0
sense_over	-	0	0	2	0	2	2	0	0	0.29374	0	0.250425	0.221533
processed_	-	0	0	1	0	0	0	0	0	0.032892	0	0	0
protein_co	chromoson	8	1	7	1	9	10	0.203424	0.029965	0.234555	0.021998	0.257101	0.252709
sense_intrc	-	10	12	9	7	6	11	0.393321	0.556206	0.466471	0.238182	0.265123	0.429981
sense_intrc	-	0	1	0	9	7	4	0	0.089896	0	0.593934	0.599901	0.303251
pseudogen	-	0	1	1	1	1	0	0	0.036742	0.041086	0.026972	0.035027	0
protein_co	Uncharacte	10	16	8	2	0	0	0.829796	1.564583	0.874775	0.14357	0	0
lincRNA	-	0	0	0	0	0	3	0	0	0	0	0	0.597887
antisense	-	0	0	1	0	3	2	0	0	0.143251	0	0.366381	0.216074
lincRNA	-	0	2	9	1	1	1	0	0.167935	0.845046	0.061641	0.080048	0.070813
pseudogen	phosphatid	8	9	1	5	13	1	0.749607	0.993787	0.123475	0.4053	1.368472	0.093122
protein_co	Uncharacte	42	44	34	7	11	26	3.557635	4.392096	3.795123	0.512948	1.046776	2.188744
sense_intrc	-	19	14	12	7	15	8	1.540396	1.337562	1.28202	0.490953	1.366216	0.644583
pseudogen	DNM1_pse	12	13	7	7	6	7	0.042232	0.053915	0.032463	0.021312	0.023722	0.024483
antisense	-	9	16	5	44	28	35	0.070463	0.14762	0.051585	0.298011	0.246277	0.272329
lincRNA	-	0	0	0	2	4	1	0	0	0	0.0675	0.175316	0.038772
pseudogen	-	0	0	0	0	5	0	0	0	0	0	0.803729	0
antisense	-	0	0	0	0	3	1	0	0	0	0	0.103737	0.03059
antisense	-	4	10	14	0	1	8	0.201105	0.592476	0.927527	0	0.056482	0.399727
antisense	-	0	0	1	0	0	0	0	0	0.171831	0	0	0
lincRNA	IQCH_antis	10	9	14	31	19	23	0.092023	0.097599	0.16977	0.246787	0.196427	0.210346

processed_	-	1	0	1	0	0	0	0.134028	0	0.176616	0	0	0
lincRNA	-	0	0	0	0	2	1	0	0	0	0	0.208322	0.092144
pseudogen	-	2	2	2	7	2	5	0.141933	0.167259	0.187033	0.429748	0.159453	0.352641
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.093954
sense_intrc	-	0	7	2	0	2	3	0	1.116916	0.356845	0	0.304225	0.403688
pseudogen	-	34	56	24	0	1	2	1.855664	3.601766	1.726102	0	0.061315	0.108483
antisense	-	25	4	10	45	24	41	2.184034	0.4118	1.151209	3.400909	2.355482	3.559696
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.149472
lincRNA	-	8	1	2	2	4	4	0.592347	0.087256	0.195142	0.128109	0.332732	0.294344
sense_intrc	-	0	0	0	2	7	0	0	0	0	0.027302	0.124093	0
pseudogen	FK506_bin	0	0	1	0	0	0	0	0	0.246513	0	0	0
lincRNA	-	2	0	0	13	24	16	0.186084	0	0	1.046372	2.50865	1.479481
lincRNA	-	0	2	0	0	0	0	0	0.228526	0	0	0	0
lincRNA	-	0	7	2	0	2	0	0	0.764823	0.244355	0	0.208322	0
processed_	long_interg	0	0	0	0	0	3	0	0	0	0	0	0.106434
lincRNA	-	6	11	7	6	8	7	0.163482	0.353199	0.251335	0.141427	0.244883	0.189551
pseudogen	heat_shock	3	1	0	0	1	8	0.06662	0.026169	0	0	0.024948	0.176557
antisense	-	7	1	4	3	7	4	0.414064	0.069707	0.311791	0.153516	0.465175	0.235147
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.13666
lincRNA	-	0	3	0	5	0	0	0	0.521346	0	0.637868	0	0
antisense	-	6	6	5	2	0	1	0.50023	0.58949	0.549317	0.144249	0	0.082857
sense_over	-	0	2	0	0	4	0	0	0.249053	0	0	0.474858	0
lincRNA	long_interg	0	0	3	0	0	0	0	0	0.52192	0	0	0
lincRNA	-	52	44	23	54	51	72	4.498254	4.485392	2.621823	4.04108	4.956326	6.189888
lincRNA	long_interg	0	2	0	0	0	2	0	0.25674	0	0	0	0.216519
processed_	-	1	0	0	0	0	0	0.092393	0	0	0	0	0
lincRNA	-	13	26	27	0	3	1	0.395991	0.933303	1.083779	0	0.102663	0.030273
pseudogen	-	3	0	2	0	0	0	0.648257	0	0.569496	0	0	0
antisense	-	0	0	0	2	0	0	0	0	0	0.169	0	0
lincRNA	-	2	0	0	0	0	0	0.03337	0	0	0	0	0
antisense	-	0	0	1	0	0	0	0	0	0.125248	0	0	0
pseudogen	-	105	91	78	21	27	22	1.132139	1.15627	1.108256	0.195881	0.327057	0.235745
lincRNA	-	1	1	0	151	106	101	0.043217	0.050929	0	5.645416	5.146488	4.337975
pseudogen	-	6	2	4	0	0	0	0.12189	0.04788	0.107081	0	0	0
processed_	-	1	1	2	0	2	9	0.089277	0.105207	0.235289	0	0.200593	0.798527
sense_over	-	42	27	29	7	14	5	3.512673	2.661088	3.196106	0.506465	1.315423	0.415593
sense_intrc	-	3	3	5	2	0	3	0.319563	0.376586	0.701844	0.184301	0	0.31759
antisense	-	5	1	3	2	0	4	0.402899	0.094958	0.318554	0.139418	0	0.320329
lincRNA	-	0	0	1	0	0	0	0	0	0.022933	0	0	0
pseudogen	-	0	1	0	0	1	2	0	0.077985	0	0	0.074345	0.131535
sense_intrc	-	6	8	11	8	4	9	0.420723	0.661062	1.016419	0.485286	0.315104	0.627187
pseudogen	-	0	1	2	4	0	0	0	0.201902	0.451542	0.592866	0	0
pseudogen	-	1	0	0	0	0	0	0.067527	0	0	0	0	0
pseudogen	-	0	0	2	2	1	1	0	0	0.110823	0.072754	0.047241	0.04179

protein_co	-	0	0	0	0	4	0	0	0	0	0	0.378827	0
antisense	-	3	1	2	0	0	2	0.220587	0.08665	0.193787	0	0	0.14615
antisense	-	2	0	0	0	3	0	0.183504	0	0	0	0.309234	0
lincRNA	-	546	571	640	1297	1313	1027	3.092851	3.811619	4.777284	6.355786	8.355647	5.781578
antisense	-	0	1	3	0	0	0	0	0.31509	1.057019	0	0	0
lincRNA	-	0	0	0	0	4	4	0	0	0	0	0.467394	0.41347
antisense	-	1	5	4	3	7	3	0.107168	0.631455	0.564885	0.278131	0.842776	0.319519
lincRNA	-	10	17	12	0	2	0	1.184362	2.372688	1.87284	0	0.266111	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.082338
sense_intrc	-	6	2	5	1	0	3	0.699661	0.274836	0.768318	0.100879	0	0.34767
processed_	-	7	1	5	7	13	16	0.802136	0.135038	0.755014	0.693923	1.673565	1.822132
sense_intrc	-	3	3	5	0	0	1	0.354516	0.417775	0.778608	0	0	0.117442
antisense	-	1	0	0	0	1	0	0.174148	0	0	0	0.195644	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.037788	0	0
antisense	-	16	10	4	13	7	5	1.220542	0.898959	0.402094	0.857905	0.599901	0.379064
lincRNA	-	1	0	0	0	0	0	0.017583	0	0	0	0	0
pseudogen	-	182	166	120	731	522	695	14.91526	16.03152	12.95912	51.82508	48.05949	56.6049
sense_intrc	-	5	5	2	1	0	1	0.32559	0.383688	0.171619	0.056333	0	0.064716
sense_overl	-	171	108	116	9	15	5	2.679168	1.994044	2.394951	0.121986	0.264024	0.077854
antisense	-	1	0	3	0	0	1	0.109609	0	0.433312	0	0	0.108932
antisense	-	3	0	0	4	1	8	0.069507	0	0	0.080173	0.026029	0.184207
sense_overl	-	1	1	6	75	47	42	0.031588	0.037224	0.249749	2.049474	1.667881	1.318491
sense_intrc	-	4	3	0	8	7	6	0.494776	0.437297	0	0.856054	0.972737	0.73758
antisense	-	0	0	0	3	6	3	0	0	0	0.284465	0.738831	0.326795
antisense	-	2	6	0	0	0	0	0.184785	0.653275	0	0	0	0
antisense	-	12	13	12	13	16	19	0.705096	0.900156	0.929145	0.660806	1.056176	1.109508
protein_co	solute_carr	6	7	3	2	2	2	0.18998	0.261193	0.125173	0.054783	0.071143	0.062935
antisense	-	8	3	2	7	1	2	0.47111	0.20819	0.155202	0.35661	0.066158	0.11705
antisense	-	2	0	0	0	0	0	0.140427	0	0	0	0	0
lincRNA	-	123	79	88	120	101	107	17.50468	13.24901	16.50314	14.77384	16.14803	15.13361
lincRNA	-	3	4	1	0	1	0	0.075666	0.11889	0.033236	0	0.028335	0
3prime_ov	-	5	0	0	1	0	2	0.10853	0	0	0.018778	0	0.043144
processed_	-	4	0	4	0	0	0	0.280111	0	0.369118	0	0	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.075486
lincRNA	-	4	11	1	0	0	0	0.137777	0.446496	0.045389	0	0	0
antisense	-	3	1	1	2	0	0	0.044228	0.017373	0.019427	0.025508	0	0
lincRNA	-	12	28	19	105	65	60	0.101598	0.279363	0.211979	0.769052	0.618253	0.504853
antisense	-	7	6	16	19	7	24	0.165885	0.167559	0.499647	0.389516	0.186361	0.565236
lincRNA	-	10	11	7	4	0	0	0.132485	0.171738	0.122208	0.045845	0	0
lincRNA	-	0	0	0	11	7	5	0	0	0	0.144725	0.119601	0.075573
pseudogen	transcriptic	0	0	0	1	0	2	0	0	0	0.137949	0	0.316952
lincRNA	-	10	5	10	0	0	1	1.187018	0.699414	1.564199	0	0	0.117969
antisense	-	0	0	0	0	1	0	0	0	0	0	0.11943	0
pseudogen	hect_doma	0	0	0	5	1	3	0	0	0	0.095693	0.024854	0.06596

lincRNA	-	11	4	8	0	0	0	1.062684	0.455385	1.018442	0	0	0
lincRNA	-	3	11	3	0	0	0	0.211764	0.91502	0.279053	0	0	0
pseudogen	RAB43_pse	0	2	2	2	1	1	0	0.211843	0.236887	0.155514	0.100978	0.089328
lincRNA	-	2	2	0	0	0	0	0.232197	0.27363	0	0	0	0
lincRNA	SH3RF3_an	57	61	48	3	11	20	1.88132	2.372601	2.087679	0.085659	0.407877	0.656036
lincRNA	-	88	70	51	355	186	267	3.739011	3.504929	2.855479	13.04864	8.878427	11.27444
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.050661	0
antisense	-	0	1	3	4	5	0	0	0.042268	0.141795	0.124116	0.201477	0
lincRNA	-	0	0	0	2	0	0	0	0	0	0.094626	0	0
pseudogen	-	0	0	0	2	0	0	0	0	0	0.384865	0	0
antisense	-	0	2	0	0	1	0	0	0.221626	0	0	0.105641	0
antisense	-	36	37	24	102	54	47	0.786252	0.952288	0.690726	1.927182	1.324959	1.020157
antisense	-	0	9	2	0	1	7	0	0.728261	0.180968	0	0.077141	0.477689
lincRNA	-	4	0	1	0	1	2	0.495934	0	0.16338	0	0.139288	0.246436
antisense	-	33	15	28	46	45	60	0.783081	0.41946	0.875559	0.944307	1.199649	1.41499
pseudogen	-	3	1	0	0	0	0	0.167006	0.065602	0	0	0	0
lincRNA	-	2	0	0	7	0	6	0.265368	0	0	0.80349	0	0.791189
antisense	-	18	2	4	2	4	11	0.291954	0.038228	0.085494	0.028063	0.072887	0.177315
antisense	-	2	0	1	0	3	0	0.151693	0	0.099947	0	0.255627	0
antisense	-	71	32	40	91	87	87	1.578669	0.838474	1.172	1.750399	2.173207	1.922479
pseudogen	-	1	2	1	2	5	1	0.049803	0.11738	0.065629	0.086169	0.279755	0.049496
antisense	-	2	2	0	0	0	0	0.222441	0.262133	0	0	0	0
antisense	-	0	0	0	0	3	0	0	0	0	0	0.254171	0
lincRNA	-	9	3	1	0	1	0	0.21638	0.084997	0.031682	0	0.02701	0
pseudogen	-	3	2	5	8	8	8	0.101161	0.079475	0.222176	0.23337	0.303062	0.268097
lincRNA	-	10	2	6	0	1	3	0.182429	0.042996	0.144238	0	0.020495	0.054391
sense_intrc	-	6	0	2	4	0	1	0.081239	0	0.035685	0.046853	0	0.013456
pseudogen	-	4	1	1	0	0	2	0.219672	0.064718	0.072369	0	0	0.109158
lincRNA	-	0	0	0	0	0	8	0	0	0	0	0	0.217301
sense_intrc	-	0	2	0	0	8	2	0	0.176736	0	0	0.673948	0.149048
pseudogen	-	0	0	2	0	0	0	0	0	0.514858	0	0	0
sense_intrc	-	0	2	0	0	1	0	0	0.200282	0	0	0.095467	0
sense_overl	-	3	2	6	2	2	4	0.264705	0.207959	0.697633	0.152663	0.198253	0.35076
sense_intrc	-	0	0	4	2	0	1	0	0	0.516765	0.169626	0	0.097433
lincRNA	-	0	0	0	25	12	25	0	0	0	1.120325	0.698347	1.287036
antisense	-	5	8	5	4	1	5	0.157188	0.296379	0.207136	0.108786	0.035318	0.156217
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.103436	0
antisense	-	40	52	33	74	48	77	1.374198	2.105232	1.493957	2.199299	1.852592	2.628995
lincRNA	-	5	11	6	6	5	0	0.146246	0.379152	0.231259	0.15182	0.164298	0
pseudogen	-	0	0	4	0	4	0	0	0	0.631342	0	0.538244	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.108731	0
sense_overl	-	17	20	25	136	86	67	0.200534	0.27802	0.38861	1.387846	1.13969	0.785459
antisense	IL21R_anti	0	1	0	3	2	0	0	0.023858	0	0.052542	0.045488	0
lincRNA	-	67	65	69	123	83	94	0.840931	0.961404	1.14122	1.33553	1.170342	1.172527

processed_	-	2	0	0	0	1	2	0.128654	0	0	0	0.072267	0.127859
lincRNA	-	4	3	3	0	4	1	0.38087	0.336624	0.376421	0	0.427884	0.09463
sense_overl	-	93	101	53	3	7	3	5.018871	6.423201	3.769066	0.140058	0.424395	0.160899
antisense	-	19	29	15	16	10	10	1.481412	2.664572	1.541162	1.079208	0.875934	0.774876
lincRNA	long_interg	0	1	0	0	0	0	0	0.012701	0	0	0	0
lincRNA	-	64	42	34	8	10	18	2.018001	1.560622	1.412717	0.21822	0.354234	0.564058
lincRNA	-	5	4	7	4	4	5	0.372824	0.35148	0.687807	0.258022	0.335076	0.370521
pseudogen	mitochond	1	1	0	0	0	0	0.225281	0.26548	0	0	0	0
pseudogen	cell_divisio	0	0	2	0	2	0	0	0	0.145492	0	0.124037	0
pseudogen	-	0	0	2	4	0	0	0	0	0.303979	0.399119	0	0
antisense	-	2	1	1	123	55	49	0.090575	0.053368	0.059678	4.818875	2.798268	2.205379
antisense	-	4	0	0	7	2	4	0.506612	0	0	0.766967	0.284574	0.503484
pseudogen	-	0	1	1	0	0	0	0	0.024485	0.02738	0	0	0
sense_overl	-	41	35	25	56	48	53	0.669726	0.673734	0.538131	0.791342	0.880853	0.860396
processed_	-	0	1	2	0	0	0	0	0.146107	0.32676	0	0	0
antisense	-	11	10	7	11	15	16	0.383883	0.411257	0.321914	0.332095	0.588094	0.554927
protein_co	transformi	18	11	19	6	13	13	0.7563	0.544655	1.051986	0.21809	0.61364	0.542843
antisense	-	16	9	4	19	10	12	0.187984	0.124609	0.061929	0.193116	0.131993	0.140117
lincRNA	-	73	39	48	114	72	71	1.449622	0.912649	1.256053	1.958393	1.606251	1.401199
sense_overl	-	0	0	3	0	5	3	0	0	0.106944	0	0.151957	0.080655
lincRNA	-	2	0	1	3	1	0	0.294117	0	0.193787	0.381658	0.165211	0
pseudogen	-	2	3	0	0	0	0	0.139318	0.246267	0	0	0	0
pseudogen	LSM3_hom	0	0	0	0	0	2	0	0	0	0	0	0.343883
sense_intrc	-	0	0	0	0	2	0	0	0	0	0	0.290836	0
antisense	-	0	0	0	3	2	0	0	0	0	0.3806	0.329506	0
antisense	-	14	12	4	14	22	21	1.422599	1.436953	0.535611	1.230681	2.511459	2.12072
antisense	-	6	11	4	5	2	8	0.599332	1.29484	0.526515	0.432065	0.224437	0.794174
lincRNA	-	38	31	26	59	29	34	5.041999	4.847167	4.545978	6.772269	4.322811	4.483403
pseudogen	mitochond	0	0	10	0	2	5	0	0	2.93123	0	0.499798	1.105337
lincRNA	-	23	28	14	76	57	85	3.326893	4.772832	2.668541	9.510155	9.262643	12.21911
protein_co	homeobox	33	21	24	279	163	190	0.444656	0.333454	0.426144	3.2522	2.467441	2.544329
antisense	-	21	25	21	1	6	4	0.970123	1.360989	1.278385	0.039964	0.311392	0.183644
lincRNA	long_interg	12379	10761	11549	5526	7533	6510	122.7489	125.7453	150.9077	47.40303	83.91685	64.15386
pseudogen	-	0	0	0	2	0	0	0	0	0	0.195305	0	0
antisense	-	15	15	11	221	222	190	0.140154	0.165163	0.135439	1.786367	2.330331	1.764326
pseudogen	-	0	0	1	0	0	0	0	0	0.096491	0	0	0
lincRNA	-	2	2	1	1	8	1	0.168067	0.198056	0.110735	0.072697	0.75525	0.083514
sense_intrc	-	0	2	7	2	3	1	0	0.348535	1.364087	0.25586	0.498402	0.146967
lincRNA	-	0	0	1	0	0	0	0	0	0.042931	0	0	0
antisense	-	1	10	2	3	8	2	0.092879	1.094522	0.244783	0.241047	0.83475	0.184611
lincRNA	-	0	1	0	0	0	1	0	0.115747	0	0	0	0.097614
pseudogen	ATP-bindin	0	0	0	1	0	0	0	0	0	0.02097	0	0
lincRNA	-	446	446	261	432	406	495	15.04887	17.73418	11.60498	12.61002	15.3902	16.59908
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.064796

lincRNA	-	1	0	0	0	0	2	0.019154	0	0	0	0	0.038071
antisense	-	10	2	14	4	5	13	0.635546	0.14979	1.172492	0.219923	0.356998	0.821108
antisense	-	4	13	9	8	13	3	0.105882	0.40552	0.313935	0.183196	0.386593	0.078921
sense_intrc	-	0	0	4	0	0	0	0	0	0.336614	0	0	0
lincRNA	-	92	94	71	69	52	69	1.594817	1.920251	1.621871	1.034749	1.012688	1.188726
pseudogen	-	2	0	0	0	0	0	0.437529	0	0	0	0	0
antisense	-	1	2	0	0	0	1	0.075094	0.176986	0	0	0	0.07463
pseudogen	N-ethylmal	0	0	0	0	2	0	0	0	0	0	0.080865	0
lincRNA	-	17	5	8	17	18	19	0.572517	0.198434	0.355029	0.495281	0.681022	0.63592
antisense	-	8	9	9	5	2	8	0.560964	0.743695	0.831615	0.303304	0.157552	0.5575
pseudogen	-	1	1	1	0	0	0	0.088235	0.10398	0.116272	0	0	0
antisense	microRNA_	9	8	3	8	10	21	0.333428	0.349267	0.146459	0.256397	0.416207	0.773195
antisense	-	0	0	0	0	2	0	0	0	0	0	0.217462	0
lincRNA	-	2	1	0	4	2	4	0.123984	0.073054	0	0.214515	0.139288	0.246436
lincRNA	-	0	4	2	8	0	1	0	0.339064	0.189574	0.497814	0	0.071486
pseudogen	ADAM_met	3	0	4	0	1	0	0.189075	0	0.332206	0	0.070805	0
lincRNA	-	10	10	9	13	11	27	0.58758	0.692428	0.696859	0.660806	0.726121	1.57667
antisense	-	0	1	0	4	1	0	0	0.016548	0	0.048593	0.015776	0
antisense	-	3	0	2	9	6	7	0.400058	0	0.351452	1.038262	0.89888	0.927704
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.054579
lincRNA	-	1	0	4	0	0	2	0.027761	0	0.146331	0	0	0.05518
pseudogen	-	9	3	6	27	11	18	0.140759	0.055292	0.123657	0.365309	0.193275	0.279779
pseudogen	-	1	0	0	0	0	2	0.023128	0	0	0	0	0.045971
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.049896	0
pseudogen	-	0	1	1	0	0	0	0	0.307329	0.343661	0	0	0
sense_intrc	-	93	68	62	63	35	54	2.168948	1.868884	1.905429	1.271071	0.91703	1.251612
antisense	-	0	0	0	3	0	1	0	0	0	0.192432	0	0.073689
lincRNA	-	0	0	0	10	3	21	0	0	0	0.319825	0.1246	0.771575
antisense	-	6	9	8	25	31	35	0.172166	0.30433	0.302497	0.620581	0.999324	0.998099
lincRNA	-	0	0	1	0	0	0	0	0	0.077861	0	0	0
lincRNA	-	11	12	11	0	0	0	0.149974	0.192803	0.19763	0	0	0
pseudogen	unc-51-like	0	0	0	2	0	1	0	0	0	0.114784	0	0.065932
antisense	-	1	0	1	0	3	0	0.139686	0	0.184072	0	0.470786	0
lincRNA	-	10	11	10	10	19	17	0.725219	0.940089	0.955661	0.627382	1.548003	1.225259
lincRNA	-	1	4	0	6	0	0	0.051499	0.242754	0	0.267309	0	0
pseudogen	-	4	12	1	4	3	4	0.177357	0.627012	0.058428	0.15343	0.149437	0.176261
antisense	-	2	4	0	0	0	0	0.157562	0.371356	0	0	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.168011	0
antisense	-	0	0	2	0	3	0	0	0	0.295607	0	0.378025	0
antisense	-	1	1	1	0	2	1	0.096082	0.113226	0.126612	0	0.215884	0.095488
sense_over	-	62	43	24	48	22	33	4.862728	3.974329	2.480472	3.256811	1.938474	2.572242
lincRNA	-	2	0	0	6	0	1	0.023655	0	0	0.061393	0	0.011755
pseudogen	-	0	0	0	4	5	0	0	0	0	1.040884	1.689657	0
processed_	-	0	0	0	0	1	0	0	0	0	0	0.27923	0

antisense	-	1	0	0	5	7	19	0.109836	0	0	0.475092	0.863758	2.073998
lincRNA	-	29	30	23	39	31	29	2.684071	3.272084	2.805167	3.122653	3.223345	2.667496
lincRNA	-	4	4	1	10	9	16	0.13592	0.160174	0.044777	0.29396	0.343571	0.540324
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.129591
pseudogen	-	3	1	3	0	0	0	0.322156	0.126547	0.424523	0	0	0
sense_over	-	3	6	1	4	2	10	0.193687	0.456496	0.085077	0.223409	0.145063	0.641635
lincRNA	-	3	5	0	15	17	21	0.124665	0.24485	0	0.539234	0.793635	0.867265
antisense	-	2	2	2	0	4	1	0.143277	0.168844	0.188805	0	0.321926	0.071196
antisense	-	79	47	66	87	53	82	1.45069	1.017074	1.597078	1.382069	1.093383	1.49648
lincRNA	-	20	27	7	19	25	20	0.397157	0.631834	0.183174	0.326399	0.557726	0.394704
sense_intrc	-	0	1	0	1	1	1	0	0.035108	0	0.025773	0.03347	0.029608
antisense	-	4	0	2	0	0	0	0.370217	0	0.243928	0	0	0
lincRNA	-	0	0	1	3	2	7	0	0	0.064596	0.127219	0.110141	0.341017
pseudogen	-	6	4	4	3	6	0	0.125601	0.098676	0.110341	0.054328	0.141105	0
antisense	-	1	1	2	16	6	6	0.067099	0.079072	0.17684	0.928748	0.452288	0.400107
sense_over	-	467	420	400	176	125	135	5.405213	5.72865	6.100855	1.762267	1.62538	1.552885
processed_	-	11	4	7	21	35	28	1.403255	0.601328	1.17673	2.317535	5.016041	3.549864
antisense	-	3	0	2	1	0	10	0.275256	0	0.241814	0.079374	0	0.911855
pseudogen	-	1	4	0	5	5	4	0.106521	0.502115	0	0.460754	0.598349	0.423453
sense_over	-	11	29	9	0	4	12	0.103144	0.320447	0.111206	0	0.042137	0.111826
antisense	-	18	24	11	26	35	32	0.400394	0.62912	0.322435	0.500324	0.874646	0.707416
processed_	-	28	24	13	17	15	25	0.76331	0.771012	0.467004	0.400917	0.459392	0.677318
antisense	-	31	29	26	15	44	55	0.858802	0.946753	0.94916	0.359489	1.369409	1.514271
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.023158
sense_over	-	0	0	4	297	278	320	0	0	0.106712	5.201635	6.32287	6.438431
antisense	-	0	0	0	0	1	0	0	0	0	0	0.121132	0
pseudogen	SUB1_hom	0	1	0	0	4	4	0	0.184035	0	0	0.701781	0.620815
lincRNA	-	5	15	2	4	4	10	0.229978	0.813046	0.121222	0.159162	0.206693	0.457116
antisense	-	8	11	11	4	4	0	0.081229	0.13162	0.14718	0.035135	0.045628	0
antisense	-	0	5	0	4	4	10	0	0.845362	0	0.496465	0.644725	1.425855
sense_over	-	1	0	0	3	1	0	0.070494	0	0	0.182952	0.079196	0
pseudogen	-	0	0	0	0	8	3	0	0	0	0	0.434924	0.14428
lincRNA	-	86	56	29	506	203	346	2.66253	2.043107	1.18312	13.55219	7.060591	10.64588
pseudogen	-	3	1	2	0	0	1	0.183187	0.071958	0.16093	0	0	0.060685
protein_co	Uncharacte	15	11	3	7	5	22	1.101408	0.951824	0.290277	0.44465	0.412454	1.605422
lincRNA	-	351	404	273	337	324	523	54.33418	73.69779	55.68823	45.12933	56.34561	80.4595
lincRNA	-	9	6	5	31	42	57	0.135824	0.106706	0.099435	0.404722	0.712083	0.854903
sense_over	-	3	7	5	14	17	6	0.101679	0.279586	0.223314	0.41049	0.647305	0.202103
lincRNA	-	0	0	0	1	9	3	0	0	0	0.058343	0.681889	0.201073
pseudogen	-	0	0	0	1	0	0	0	0	0	0.013725	0	0
antisense	-	56	64	35	64	41	47	0.979741	1.319503	0.806912	0.968648	0.805853	0.817204
processed_	-	11	7	2	4	5	12	0.738087	0.553503	0.17684	0.232187	0.376907	0.800214
antisense	-	6	6	0	10	6	2	0.364273	0.429273	0	0.525217	0.409238	0.120674
lincRNA	-	2	0	2	19	5	8	0.074043	0	0.097571	0.608517	0.207958	0.294344

antisense	-	28	33	14	38	29	66	0.647879	0.899823	0.426873	0.760646	0.753847	1.517713
antisense	-	1	2	2	1	1	1	0.102798	0.242282	0.270925	0.08893	0.115487	0.102163
antisense	-	1	4	2	0	0	4	0.022819	0.107565	0.060141	0	0	0.090714
antisense	-	39	22	34	12	24	40	5.136067	3.414254	5.900377	1.367132	3.550801	5.235229
antisense	-	5	6	4	2	2	2	0.53584	0.757746	0.564885	0.185421	0.240793	0.213012
pseudogen	tryptase_ps	1	0	0	0	0	0	0.086789	0	0	0	0	0
antisense	-	24	20	25	17	24	28	0.312721	0.307102	0.42926	0.191627	0.351322	0.362588
protein_co	Uncharacte	0	0	0	0	2	0	0	0	0	0	0.146132	0
processed_	-	0	0	0	2	0	0	0	0	0	0.057356	0	0
pseudogen	-	2	6	0	6	4	1	0.075522	0.266995	0	0.196001	0.169689	0.037528
sense_intrc	-	9	8	12	5	0	5	0.945375	0.990281	1.661031	0.454354	0	0.521965
sense_overl	-	8	18	7	28	20	27	0.366057	0.970596	0.422077	1.108357	1.028106	1.227813
pseudogen	-	1	0	1	0	3	0	0.048929	0	0.064476	0	0.164906	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.046721	0
lincRNA	-	0	0	1	0	0	0	0	0	0.016774	0	0	0
lincRNA	-	24	18	21	17	10	15	0.763113	0.674462	0.879897	0.467616	0.357213	0.474
sense_intrc	-	0	0	0	3	3	0	0	0	0	0.315855	0.410179	0
sense_intrc	-	5	7	2	0	9	3	0.083372	0.137548	0.043945	0	0.168593	0.049714
lincRNA	-	18	14	20	37	38	36	0.527943	0.483894	0.773	0.938814	1.252125	1.049366
pseudogen	cytochrom	6	2	15	6	10	7	1.477423	0.580351	4.867206	1.278109	2.766322	1.713016
pseudogen	-	1	5	0	0	0	0	0.064327	0.379026	0	0	0	0
antisense	-	21	19	15	7	3	8	0.756815	0.806921	0.712355	0.218238	0.121462	0.28653
lincRNA	-	5	0	0	2	0	0	0.323205	0	0	0.111841	0	0
pseudogen	-	0	0	1	1	1	0	0	0	0.458969	0.301309	0.391289	0
sense_overl	-	514	540	427	353	334	336	6.939982	8.592036	7.597277	4.123186	5.066298	4.508626
processed_	-	0	2	0	0	3	0	0	0.032749	0	0	0.046831	0
antisense	HEXA_antis	0	1	0	7	12	1	0	0.023314	0	0.119803	0.266708	0.019661
antisense	-	21	28	25	15	34	16	1.520877	2.38968	2.385885	0.939786	2.766322	1.151607
antisense	-	0	0	0	0	0	3	0	0	0	0	0	0.367075
antisense	-	0	0	1	1	2	0	0	0	0.139806	0.091781	0.23838	0
antisense	-	7	0	1	9	1	2	0.800404	0	0.150677	0.890259	0.128458	0.227275
antisense	-	10	18	14	34	8	10	0.228984	0.485718	0.422442	0.673513	0.205799	0.227569
lincRNA	-	18	4	6	8	2	3	0.30329	0.079424	0.133221	0.116611	0.037859	0.050236
lincRNA	-	3	0	2	3	1	7	0.126351	0	0.111	0.109305	0.047316	0.292998
lincRNA	-	2	6	1	22	18	29	0.060992	0.215626	0.040186	0.580401	0.616686	0.878921
sense_overl	-	1	2	3	0	3	0	0.193215	0.455385	0.763832	0	0.651196	0
antisense	-	6	8	2	11	14	11	0.680184	1.068741	0.298772	1.078775	1.783004	1.239303
sense_overl	-	4	10	2	8	6	5	0.185433	0.546302	0.122177	0.320833	0.312483	0.230359
lincRNA	-	14	8	0	10	2	5	0.744898	0.50161	0	0.460291	0.11955	0.264392
antisense	AQP4_antis	0	0	1	5	0	2	0	0	0.029165	0.095733	0	0.043992
lincRNA	-	0	0	0	0	0	3	0	0	0	0	0	0.133765
antisense	-	1	3	1	0	7	0	0.067355	0.238121	0.088757	0	0.529684	0
antisense	-	0	0	3	0	4	3	0	0	0.314249	0	0.357213	0.237
lincRNA	long_interg	1	0	8	10	8	6	0.021451	0	0.226137	0.185571	0.192791	0.127911

pseudogen	WW_doma	0	0	0	2	0	0	0	0	0	0.03082	0	0
sense_over	-	26	24	18	31	28	32	0.542343	0.589955	0.494775	0.559403	0.656157	0.663377
antisense	-	2	1	1	0	0	0	0.086789	0.051137	0.057183	0	0	0
lincRNA	-	1	0	3	4	0	1	0.036841	0	0.145644	0.127485	0	0.036614
sense_over	-	2	10	0	1	8	0	0.028205	0.16619	0	0.0122	0.126747	0
sense_over	-	69	78	33	224	190	189	1.59169	2.120367	1.003132	4.470133	4.923932	4.332922
sense_over	-	0	0	0	79	69	125	0	0	0	1.076499	1.221017	1.956786
processed_	-	172	148	135	181	184	207	2.071866	2.100884	2.142899	1.886144	2.490004	2.478068
lincRNA	-	5	5	8	4	1	7	0.165234	0.194718	0.348381	0.114354	0.037126	0.229899
pseudogen	-	3	0	0	1	1	0	0.156476	0	0	0.045122	0.058597	0
sense_over	-	15	7	7	12	18	5	0.115407	0.063467	0.07097	0.07987	0.155583	0.038231
lincRNA	-	193	150	105	23	16	37	3.572592	3.272084	2.561239	0.368313	0.332732	0.680671
lincRNA	-	11	4	2	1	10	10	0.168553	0.072229	0.040384	0.013256	0.172144	0.152284
lincRNA	-	0	0	0	15	5	13	0	0	0	1.836854	0.795133	1.828831
lincRNA	-	0	0	1	4	1	14	0	0	0.015899	0.041749	0.013554	0.167866
antisense	-	12	16	11	17	15	31	1.460441	2.294721	1.764129	1.789842	2.050894	3.749507
sense_over	-	1	0	0	0	0	0	0.028448	0	0	0	0	0
lincRNA	-	1	0	3	0	0	0	0.06295	0	0.248858	0	0	0
lincRNA	-	0	0	0	21	21	17	0	0	0	0.207997	0.270111	0.193434
lincRNA	-	0	0	1	0	0	0	0	0	0.067274	0	0	0
antisense	-	0	1	0	0	2	0	0	0.217379	0	0	0.414466	0
antisense	-	20	29	9	0	2	0	0.752003	1.284975	0.44593	0	0.084483	0
antisense	-	2	2	3	1	2	1	0.231689	0.273032	0.457965	0.100216	0.260288	0.115129
antisense	-	3	6	5	6	15	8	0.284629	0.670836	0.625119	0.492461	1.598815	0.754323
pseudogen	-	0	0	0	1	0	1	0	0	0	0.315855	0	0.362856
antisense	-	6	5	1	0	1	1	0.506612	0.49751	0.111265	0	0.094858	0.083914
lincRNA	-	14	6	16	22	32	24	0.96759	0.488677	1.457196	1.315373	2.484634	1.648482
pseudogen	TP53RK_bi	0	2	2	0	0	0	0	0.262685	0.29374	0	0	0
lincRNA	-	2	2	0	0	0	0	0.075901	0.089445	0	0	0	0
lincRNA	-	0	0	3	5	1	2	0	0	0.107881	0.118038	0.030658	0.054241
protein_co	chromoson	8	9	6	9	10	10	0.256684	0.340297	0.253685	0.249812	0.36046	0.318873
pseudogen	ferritin_ligh	0	0	0	22	34	16	0	0	0	2.081768	4.17806	1.739307
lincRNA	-	0	1	0	0	0	0	0	0.034129	0	0	0	0
sense_over	-	40	26	23	49	26	20	0.886784	0.679263	0.671924	0.93976	0.64756	0.440654
lincRNA	-	6	3	7	8	13	5	0.179867	0.105981	0.276525	0.20747	0.437818	0.148964
processed_	-	3	0	0	4	2	5	0.304259	0	0	0.350949	0.227877	0.503966
lincRNA	-	0	0	0	14	1	0	0	0	0	1.27726	0.118478	0
lincRNA	-	0	0	1	0	0	0	0	0	0.134419	0	0	0
lincRNA	-	5	7	4	10	8	11	0.122719	0.202464	0.129371	0.212327	0.220588	0.268315
lincRNA	-	0	2	4	1	1	2	0	0.121495	0.271717	0.044595	0.057912	0.102462
antisense	-	5	4	0	0	2	4	0.306371	0.288832	0	0	0.137676	0.243584
lincRNA	-	198	154	223	157	203	128	4.255914	3.900816	6.316367	2.919378	4.901994	2.734307
lincRNA	-	0	0	0	0	0	10	0	0	0	0	0	0.242238
antisense	-	1	0	3	0	1	0	0.088088	0	0.348236	0	0.098962	0

pseudogen	-	3	0	1	13	5	5	0.31326	0	0.1376	1.174331	0.586548	0.518876
antisense	-	0	1	0	0	1	4	0	0.049357	0	0	0.047054	0.1665
pseudogen	-	0	0	0	3	1	2	0	0	0	0.190037	0.082263	0.145544
antisense	-	4	5	3	29	14	16	0.078635	0.115833	0.077716	0.493193	0.309195	0.312597
processed_	-	0	1	0	7	0	4	0	0.1085	0	0.557552	0	0.366011
antisense	-	1	2	0	0	0	1	0.104626	0.246592	0	0	0	0.10398
lincRNA	-	0	0	2	0	4	1	0	0	0.106104	0	0.180915	0.040011
processed_	-	0	0	0	0	2	0	0	0	0	0	0.338894	0
sense_over	-	300	240	316	59	66	57	2.980352	2.809731	4.136836	0.507062	0.736613	0.56277
lincRNA	-	3	0	9	0	0	0	0.063327	0	0.250347	0	0	0
lincRNA	-	0	2	2	0	0	0	0	0.21513	0.240563	0	0	0
pseudogen	-	7	5	7	5	3	0	0.31459	0.264804	0.414553	0.194393	0.151467	0
antisense	-	0	1	0	0	0	0	0	0.144083	0	0	0	0
antisense	-	0	2	0	0	0	0	0	0.283581	0	0	0	0
lincRNA	-	6	11	3	4	0	2	0.106593	0.23029	0.070231	0.061475	0	0.035311
antisense	-	3	7	6	15	13	9	0.078007	0.214496	0.205589	0.337418	0.379758	0.232577
processed_	family_with	32	42	28	33	37	55	0.775692	1.199764	0.894401	0.692016	1.007605	1.324988
lincRNA	-	1	0	0	0	0	0	0.02986	0	0	0	0	0
sense_over	-	80	62	60	45	28	45	1.965327	1.794914	1.942365	0.956358	0.772773	1.098669
antisense	-	5	2	2	9	14	9	0.576699	0.271842	0.303979	0.898018	1.81408	1.031648
lincRNA	-	893	746	547	720	555	640	19.17125	18.87317	15.47466	13.37194	13.3857	13.6549
sense_over	-	13	3	9	14	3	3	3.128331	0.850742	2.853952	2.914476	0.811035	0.717464
antisense	-	1	0	0	0	1	2	0.127569	0	0	0	0.143315	0.253562
pseudogen	metallothi	22	8	6	11	6	2	2.833824	1.21436	1.018442	1.225761	0.868262	0.256029
antisense	-	24	8	8	48	25	13	2.086345	0.819543	0.916431	3.609766	2.44154	1.123124
lincRNA	-	0	0	0	2	4	0	0	0	0	0.030091	0.078155	0
processed_	-	37	24	25	113	77	79	4.441761	3.395251	3.954835	11.73532	10.38468	9.425193
lincRNA	-	5	1	3	1	1	3	0.493853	0.116395	0.390466	0.085446	0.110963	0.294482
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.715837
lincRNA	-	36	44	29	56	24	42	1.594875	2.297121	1.693	2.146225	1.194495	1.849197
processed_	endogenou	212	175	231	123	147	155	2.012099	1.957306	2.889085	1.009908	1.5674	1.462025
pseudogen	-	0	2	1	0	1	1	0	0.250553	0.140087	0	0.11943	0.105651
antisense	-	0	0	0	3	4	7	0	0	0	0.080115	0.138719	0.214751
pseudogen	-	1	0	0	0	3	1	0.115089	0	0	0	0.387886	0.114378
antisense	-	0	0	0	0	6	11	0	0	0	0	0.648828	1.052281
lincRNA	-	58	33	35	8	3	8	0.966807	0.648235	0.768802	0.115362	0.05618	0.132529
antisense	-	16	16	12	20	11	15	2.13903	2.520716	2.114039	2.313076	1.652109	1.992956
antisense	-	0	1	0	5	0	0	0	0.039813	0	0.146136	0	0
pseudogen	tyrosylprot	0	0	0	0	3	4	0	0	0	0	0.161913	0.190977
antisense	long_interg	3	0	0	2	2	5	0.28514	0	0	0.164448	0.213558	0.472298
sense_intro	-	1	0	0	0	0	0	0.075847	0	0	0	0	0
lincRNA	-	15	9	7	25	12	27	0.448652	0.317226	0.2759	0.646877	0.403227	0.802587
antisense	-	4	5	10	34	23	25	0.081605	0.120208	0.268837	0.600063	0.527147	0.506879
lincRNA	-	1	1	3	2	0	5	0.154347	0.181888	0.610174	0.267049	0	0.766969

antisense	-	0	0	0	0	4	0	0	0	0	0	0.375835	0
antisense	-	0	3	2	3	1	2	0	0.402501	0.300057	0.295477	0.127905	0.226297
antisense	-	0	0	2	1	0	0	0	0	0.308687	0.101325	0	0
lincRNA	-	130	96	158	3	7	1	2.568033	2.234784	4.11291	0.051267	0.155348	0.019632
pseudogen	high_mobil	0	0	0	1	0	0	0	0	0	0.117133	0	0
lincRNA	-	13	10	12	1	0	1	0.097346	0.088243	0.11841	0.006478	0	0.007442
antisense	-	0	1	0	1	7	0	0	0.148189	0	0.108786	0.988911	0
antisense	-	0	0	0	6	10	0	0	0	0	0.420173	0.909418	0
antisense	-	2	0	0	0	0	1	0.134539	0	0	0	0	0.066854
antisense	-	15	11	10	4	7	0	1.250575	1.080732	1.098634	0.288497	0.65564	0
lincRNA	-	2	3	0	0	0	0	0.043129	0.076238	0	0	0	0
antisense	-	0	0	2	5	0	3	0	0	0.254147	0.417112	0	0.287508
antisense	-	6	0	1	2	0	9	0.490952	0	0.107826	0.141573	0	0.73188
lincRNA	-	0	0	4	0	0	0	0	0	0.498309	0	0	0
pseudogen	-	18	12	25	10	6	7	0.570621	0.448295	1.044361	0.274245	0.213686	0.220538
antisense	SNAI3_anti	226	174	159	66	83	86	5.708332	5.179134	5.292157	1.442141	2.355201	2.158783
lincRNA	-	0	3	2	5	3	5	0	0.096178	0.071699	0.117674	0.091689	0.135185
antisense	-	6	5	4	0	0	5	0.750936	0.737444	0.6597	0	0	0.621915
lincRNA	-	0	0	0	0	0	3	0	0	0	0	0	0.2844
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.227275
antisense	-	40	31	28	3	18	9	0.375003	0.342486	0.345913	0.024331	0.189581	0.083855
processed_	-	3	0	2	4	4	3	0.205463	0	0.1805	0.236993	0.307767	0.204194
lincRNA	-	55	43	26	28	17	20	1.371528	1.263623	0.854378	0.604036	0.476256	0.495658
lincRNA	-	0	0	2	0	3	5	0	0	0.204584	0	0.261624	0.385734
antisense	-	5	4	1	7	4	11	0.353411	0.333179	0.093142	0.428027	0.317628	0.772703
sense_intrc	-	0	0	0	1	0	1	0	0	0	0.011376	0	0.013069
antisense	-	0	0	1	0	4	2	0	0	0.145644	0	0.496667	0.219683
lincRNA	-	5	9	2	11	0	1	0.245552	0.520862	0.129431	0.467336	0	0.048807
lincRNA	-	0	2	0	0	2	0	0	0.31509	0	0	0.300383	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.073075
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.040348
processed_	-	7	4	1	0	1	1	0.1758	0.118383	0.033095	0	0.028214	0.024959
sense_intrc	-	0	0	0	0	6	4	0	0	0	0	1.031374	0.608255
lincRNA	-	1	7	5	1	0	2	0.021688	0.178908	0.142899	0.018762	0	0.043109
lincRNA	-	0	6	1	1	4	1	0	0.134892	0.02514	0.016504	0.085731	0.01896
pseudogen	-	5	3	0	1	0	1	0.3887	0.274836	0	0.067252	0	0.07726
sense_over	-	4	2	21	28	4	18	0.097229	0.057289	0.672649	0.588783	0.10923	0.434827
pseudogen	-	8	9	2	3	8	3	0.453456	0.601167	0.149386	0.147106	0.50943	0.168996
lincRNA	-	8	2	2	0	0	1	0.604177	0.177996	0.199039	0	0	0.075056
lincRNA	-	10	4	1	2	1	1	0.178373	0.08408	0.023505	0.030862	0.020039	0.017727
antisense	-	0	0	0	2	7	4	0	0	0	0.1582	0.719053	0.363482
lincRNA	long_interg	0	6	0	13	9	10	0	0.202887	0	0.322702	0.290126	0.285171
antisense	-	34	39	17	71	57	96	2.686558	3.631525	1.770113	4.853317	5.059891	7.53873
sense_intrc	-	0	1	0	16	13	9	0	0.020522	0	0.241047	0.254338	0.155765

pseudogen	-	0	1	1	0	0	0	0	0.01557	0.01741	0	0	0
antisense	-	0	0	0	1	1	0	0	0	0	0.027656	0.035915	0
pseudogen	vomeronas	0	0	0	3	0	0	0	0	0	0.150489	0	0
sense_intrc	-	1	0	3	0	0	1	0.121703	0	0.481126	0	0	0.120952
lincRNA	-	0	0	0	22	21	16	0	0	0	0.641768	0.795538	0.536194
pseudogen	solute_carr	3	3	4	13	15	33	0.29576	0.348535	0.519652	1.108726	1.661338	3.233266
processed_	-	0	0	0	0	4	0	0	0	0	0	0.05439	0
antisense	-	2	0	1	1	0	0	0.147263	0	0.097028	0.063698	0	0
antisense	-	4	9	1	5	0	2	0.08151	0.216124	0.026853	0.088143	0	0.040504
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.078646
lincRNA	-	0	0	0	1	3	0	0	0	0	0.084035	0.32739	0
antisense	-	0	0	0	22	12	17	0	0	0	0.264248	0.187178	0.234576
sense_over	-	5	8	12	16	6	14	0.169033	0.318711	0.534585	0.467933	0.227877	0.470368
antisense	-	0	3	4	5	1	1	0	0.244978	0.365253	0.299731	0.077848	0.068867
pseudogen	-	0	5	1	5	0	0	0	0.705744	0.157835	0.518087	0	0
lincRNA	-	10	12	3	3	3	9	0.953892	1.348924	0.377099	0.247562	0.321491	0.853201
sense_intrc	-	18	16	8	33	25	17	0.930603	0.974808	0.545026	1.475941	1.452049	0.873475
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.021581
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.047887	0
sense_over	-	68	48	52	69	25	26	1.954391	1.625739	1.96943	1.715594	0.807219	0.742652
antisense	-	2	5	0	16	0	4	0.211764	0.623877	0	1.465565	0	0.420912
processed_	-	16	12	5	14	9	26	0.294015	0.259859	0.121075	0.222556	0.185798	0.474823
lincRNA	-	3	1	2	1	2	1	0.058049	0.022803	0.050997	0.016739	0.043477	0.01923
lincRNA	hsa-mir-94	28	25	11	21	20	30	2.729922	2.872363	1.413252	1.771228	2.190642	2.906854
pseudogen	Rho_GTPas	9	5	7	1	3	2	0.245983	0.161042	0.252113	0.023644	0.092116	0.054325
pseudogen	-	0	0	2	4	1	0	0	0	0.075995	0.09978	0.032394	0
pseudogen	-	0	2	0	2	0	1	0	0.107937	0	0.079237	0	0.045514
lincRNA	-	6	0	4	3	4	1	0.234252	0	0.205791	0.101325	0.175445	0.038801
antisense	-	0	0	1	4	0	0	0	0	0.077001	0.202203	0	0
antisense	-	0	0	0	1	1	1	0	0	0	0.032367	0.042032	0.037183
lincRNA	-	2	4	2	0	0	3	0.027747	0.065396	0.036564	0	0	0.041363
antisense	-	28	11	9	8	13	5	0.825361	0.382107	0.349593	0.204004	0.430505	0.146476
antisense	-	4	2	1	5	6	9	0.392156	0.231066	0.129191	0.424064	0.660844	0.876901
antisense	-	0	0	0	2	1	1	0	0	0	0.162985	0.105829	0.093619
pseudogen	-	2	0	0	0	2	1	0.073631	0	0	0	0.08272	0.036588
antisense	-	0	1	0	0	3	0	0	0.044722	0	0	0.127905	0
lincRNA	-	4	2	1	0	0	1	0.046086	0.027155	0.015182	0	0	0.01145
processed_	-	0	0	0	0	0	2	0	0	0	0	0	0.136129
lincRNA	-	373	294	239	728	456	520	6.272869	5.826554	5.296513	10.59136	8.615317	8.691012
lincRNA	-	4	6	13	39	19	34	0.111513	0.197118	0.477579	0.940578	0.595072	0.94201
antisense	-	6	4	7	51	36	30	0.210083	0.165047	0.322978	1.544804	1.416093	1.04393
lincRNA	-	36	24	14	65	66	79	0.511507	0.401853	0.262127	0.798961	1.053519	1.115542
lincRNA	-	4	4	2	2	11	7	0.376135	0.443252	0.247827	0.162696	1.162052	0.654171
lincRNA	-	0	0	0	0	1	2	0	0	0	0	0.084363	0.14926

processed_	-	12	5	6	29	22	11	1.902072	0.933948	1.253233	3.976552	3.917575	1.732798
sense_intrc	-	0	0	0	4	0	1	0	0	0	0.073869	0	0.021215
sense_overl	-	112	108	98	85	66	85	1.197615	1.360912	1.380893	0.786287	0.792852	0.903291
pseudogen	high_mobil	0	0	0	3	0	0	0	0	0	0.244914	0	0
antisense	-	3	1	0	6	7	3	0.252501	0.099186	0	0.436874	0.661894	0.250941
sense_intrc	-	1	4	8	1	9	3	0.011807	0.055654	0.124466	0.010214	0.119376	0.035201
antisense	-	0	0	0	0	1	0	0	0	0	0	0.039837	0
processed_	-	65	69	62	61	37	67	4.901944	6.132127	6.161429	3.979677	3.134771	5.021569
lincRNA	-	0	1	0	1	7	1	0	0.046662	0	0.034255	0.311392	0.039352
lincRNA	-	33	22	33	15	12	8	1.124954	0.883793	1.482414	0.442359	0.459569	0.271032
lincRNA	-	0	0	1	0	1	4	0	0	0.021166	0	0.018045	0.063852
sense_overl	-	56	44	55	25	11	22	0.96007	0.888944	1.242546	0.370781	0.211864	0.374841
pseudogen	-	3	0	2	0	0	0	0.223066	0	0.195964	0	0	0
antisense	FBXL19_an	154	137	124	398	309	440	2.063506	2.16328	2.189483	4.613507	4.651495	5.859322
antisense	-	18	21	31	103	49	69	1.663068	2.286461	3.774279	8.232613	5.086073	6.335723
antisense	-	39	37	22	2	1	5	0.594671	0.664846	0.442048	0.026382	0.01713	0.075769
sense_intrc	-	2	0	0	0	0	0	0.407238	0	0	0	0	0
pseudogen	-	0	0	0	3	6	6	0	0	0	0.15386	0.399614	0.35351
sense_intrc	-	2	0	3	1	3	4	0.026228	0	0.051843	0.011345	0.044198	0.052132
pseudogen	-	0	0	0	2	3	0	0	0	0	0.256577	0.499798	0
antisense	-	2	0	0	0	0	0	0.320855	0	0	0	0	0
lincRNA	-	12	5	9	10	6	15	0.337204	0.165573	0.333264	0.243094	0.189414	0.418902
sense_overl	-	0	0	0	0	6	0	0	0	0	0	0.398276	0
antisense	-	25	10	25	16	18	22	0.555403	0.261803	0.731885	0.307504	0.449252	0.485736
lincRNA	-	5	3	2	1	5	4	0.335494	0.237216	0.17684	0.058047	0.376907	0.266738
lincRNA	-	0	0	2	0	0	0	0	0	0.093391	0	0	0
lincRNA	-	0	0	0	7	0	7	0	0	0	0.86413	0	0.992718
antisense	-	0	0	1	3	0	1	0	0	0.044549	0.087737	0	0.033598
lincRNA	-	2	0	0	0	4	0	0.09813	0	0	0	0.220485	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.27158	0
processed_	-	29	19	12	9	10	15	2.992766	2.310657	1.63189	0.80349	1.159375	1.538423
antisense	-	0	1	0	3	3	6	0	0.135625	0	0.298689	0.387886	0.68627
lincRNA	-	13	10	18	0	5	1	1.106484	1.003018	2.018873	0	0.478102	0.084589
lincRNA	-	1	0	3	5	0	0	0.023869	0	0.09436	0.103244	0	0
pseudogen	DNM1_pse	0	0	0	0	2	0	0	0	0	0	0.263168	0
processed_	ADPGK_ant	7	13	13	1	1	0	0.135746	0.297084	0.332206	0.016776	0.021786	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.015529	0
sense_overl	-	0	1	0	8	1	3	0	0.014372	0	0.084402	0.013701	0.036361
lincRNA	-	1	0	2	2	2	2	0.141176	0	0.372071	0.244261	0.317205	0.280608
lincRNA	-	3	0	0	7	2	6	0.189075	0	0	0.381658	0.141609	0.375815
pseudogen	-	2	0	0	0	0	0	0.266035	0	0	0	0	0
lincRNA	long_interg	57	65	45	2	6	4	1.294567	1.739684	1.346782	0.039296	0.153091	0.090286
lincRNA	-	5	8	3	0	0	2	0.574197	1.08265	0.453991	0	0	0.228261
sense_overl	-	13	28	22	186	125	180	0.350246	0.888985	0.781065	4.335164	3.783455	4.819608

protein_co	cell_cycle_	50	35	45	54	32	59	0.388017	0.320078	0.46018	0.362524	0.278984	0.455032
sense_over	-	194	139	132	125	116	104	2.424015	2.046706	2.173414	1.35116	1.628323	1.291447
sense_over	-	56	56	62	2	4	0	0.423528	0.499102	0.617903	0.013085	0.033986	0
sense_over	-	88	62	42	74	51	45	1.904664	1.581373	1.197898	1.385576	1.240095	0.967961
antisense	-	0	0	0	0	7	0	0	0	0	0	0.638545	0
processed_	-	4	4	2	0	7	1	0.102998	0.121377	0.067863	0	0.202496	0.02559
antisense	-	26	20	15	37	44	78	0.957209	0.867701	0.727712	1.178414	1.819847	2.853891
antisense	-	7	5	11	6	11	9	0.642265	0.540622	1.329976	0.476245	1.133856	0.82067
antisense	-	2	0	0	2	0	0	0.165441	0	0	0.143122	0	0
lincRNA	-	1	0	0	0	0	0	0.022918	0	0	0	0	0
lincRNA	-	5	1	3	0	5	4	0.128622	0.030315	0.101696	0	0.144499	0.102262
antisense	-	0	1	1	8	0	4	0	0.160793	0.179802	0.944307	0	0.542413
sense_intrc	FTO_intron	3	5	3	8	3	0	0.129863	0.25506	0.171128	0.299584	0.145894	0
sense_over	-	4	1	1	13	10	9	0.35294	0.10398	0.116272	0.99231	0.991265	0.789211
pseudogen	-	0	0	1	0	0	0	0	0	0.07821	0	0	0
sense_over	-	0	0	2	0	0	3	0	0	0.235687	0	0	0.266625
sense_over	long_interg	19	12	10	18	16	20	0.640687	0.476849	0.444352	0.525083	0.606124	0.670243
antisense	-	53	26	40	127	55	98	0.701468	0.40552	0.697633	1.454115	0.817794	1.289044
antisense	-	0	4	1	0	0	0	0	0.782291	0.218694	0	0	0
lincRNA	-	0	0	3	0	0	1	0	0	0.059323	0	0	0.014913
sense_over	-	25	34	27	19	14	18	0.654239	1.048533	0.931097	0.430143	0.411598	0.468143
sense_over	-	7	4	7	8	4	15	0.406791	0.273931	0.536052	0.402186	0.261146	0.866313
processed_	-	0	0	0	0	1	0	0	0	0	0	0.106018	0
sense_intrc	-	4	0	0	1	0	0	0.524168	0	0	0.113364	0	0
lincRNA	-	0	3	10	3	3	5	0	0.425371	1.585529	0.312265	0.405518	0.597887
lincRNA	long_interg	2	0	0	0	0	0	0.082785	0	0	0	0	0
sense_over	-	47	34	45	32	19	21	0.486647	0.414861	0.613993	0.286635	0.221014	0.216095
antisense	-	0	0	1	0	3	0	0	0	0.157479	0	0.402771	0
lincRNA	-	3	1	6	4	4	0	0.117473	0.046145	0.3096	0.1355	0.175964	0
lincRNA	-	27	30	22	1	4	9	0.580352	0.759899	0.623139	0.018595	0.096591	0.192256
lincRNA	-	2	0	1	0	0	3	0.247967	0	0.16338	0	0	0.369654
antisense	-	0	2	3	2	2	0	0	0.257269	0.431525	0.188861	0.245262	0
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.124236
antisense	DOCK9_ant	1	0	1	8	6	3	0.065602	0	0.086448	0.454016	0.4422	0.195591
sense_over	-	1	0	1	0	0	0	0.027703	0	0.036506	0	0	0
antisense	-	1	1	1	0	1	1	0.10401	0.122569	0.137059	0	0.116849	0.103367
antisense	-	0	6	2	1	3	5	0	0.454832	0.169534	0.055649	0.216802	0.319648
sense_over	-	1	0	0	0	0	1	0.010206	0	0	0	0	0.010143
lincRNA	-	7	18	25	13	13	21	0.161405	0.489102	0.759618	0.259314	0.336754	0.481226
processed_	-	4	3	2	6	9	13	0.09652	0.085307	0.063595	0.125248	0.243976	0.311751
sense_over	-	20	28	10	18	9	14	0.401829	0.662944	0.264756	0.312858	0.203144	0.279543
lincRNA	-	3	3	4	3	6	4	0.116099	0.136815	0.203986	0.100436	0.260859	0.153842
lincRNA	-	6	0	1	0	5	5	0.50023	0	0.109863	0	0.468314	0.414284
lincRNA	-	0	0	0	2	0	5	0	0	0	0.037494	0	0.107683

sense_over	-	1	1	1	2	0	0	0.010595	0.012485	0.013961	0.018331	0	0
antisense	-	0	0	0	1	0	1	0	0	0	0.038682	0	0.044438
lincRNA	-	0	1	2	0	0	0	0	0.120673	0.269877	0	0	0
lincRNA	-	2	8	1	0	0	0	0.195354	0.920852	0.128715	0	0	0
processed_	-	60	48	54	2	3	1	5.041999	4.753351	5.97971	0.145393	0.283219	0.083514
antisense	-	2	0	0	0	0	0	0.153009	0	0	0	0	0
pseudogen	-	0	0	0	1	0	1	0	0	0	0.114212	0	0.131207
antisense	-	1	4	0	2	2	2	0.188402	0.888082	0	0.325971	0.423316	0.374477
sense_over	-	150	167	93	124	70	91	2.670191	3.503279	2.181569	1.909571	1.399904	1.609912
sense_over	-	10	13	16	5	6	7	0.252702	0.387131	0.532798	0.109305	0.170337	0.175799
protein_co	sulfotransf	1	2	0	2	1	0	0.022347	0.05267	0	0.038665	0.025106	0
antisense	-	3	0	0	2	0	1	0.061992	0	0	0.035752	0	0.020536
pseudogen	-	4	11	12	6	10	3	0.134967	0.43739	0.533562	0.175139	0.379069	0.1006
processed_	-	0	0	1	4	0	0	0	0	0.136791	0.359207	0	0
sense_intrc	-	62	34	38	415	241	328	4.584276	2.962546	3.702521	26.54545	20.01913	24.10253
sense_over	-	5	9	1	6	6	0	0.104958	0.222637	0.027662	0.108959	0.141497	0
lincRNA	-	6	5	2	0	0	0	0.584983	0.574473	0.256955	0	0	0
processed_	-	16	1	6	3	9	9	0.159943	0.01178	0.079037	0.025943	0.101073	0.089412
lincRNA	-	6	9	3	31	19	24	0.157095	0.27769	0.103506	0.702159	0.558874	0.624499
lincRNA	-	39	35	41	33	60	39	1.670468	1.766643	2.314154	1.222786	2.88718	1.660152
lincRNA	-	0	2	1	0	0	0	0	0.126036	0.070468	0	0	0
antisense	-	22	13	12	44	29	36	1.114547	0.776115	0.801109	1.928375	1.650528	1.812541
pseudogen	-	0	1	3	0	0	2	0	0.068558	0.229989	0	0	0.115635
lincRNA	-	0	1	0	0	0	0	0	0.044028	0	0	0	0
lincRNA	-	7	0	1	3	11	4	0.156696	0	0.029498	0.058096	0.276632	0.088988
lincRNA	-	3	2	0	0	0	0	0.104972	0.082469	0	0	0	0
pseudogen	-	5	0	2	0	0	0	0.272892	0	0.143842	0	0	0
lincRNA	-	1	8	2	0	0	4	0.029893	0.281819	0.078784	0	0	0.118835
lincRNA	-	28	21	14	24	26	19	0.524725	0.463767	0.34573	0.389088	0.547389	0.353864
lincRNA	-	115	103	89	291	167	163	3.199272	3.37674	3.262707	7.003406	5.219379	4.506616
pseudogen	-	0	0	1	0	1	0	0	0	0.067797	0	0.0578	0
sense_over	-	58	36	30	69	62	91	1.540681	1.126923	1.050125	1.585612	1.850229	2.402347
sense_over	-	3	1	1	10	0	4	0.063352	0.024885	0.027827	0.182684	0	0.083947
lincRNA	long_interg	2	2	0	0	0	0	0.07563	0.089125	0	0	0	0
lincRNA	-	21	15	11	59	38	26	0.268541	0.226042	0.185361	0.65269	0.545914	0.330426
sense_over	-	8	1	24	3	10	6	0.650581	0.095834	2.571918	0.211055	0.913609	0.484922
pseudogen	ATP_syntha	0	0	0	4	2	0	0	0	0	0.688705	0.447187	0
antisense	-	6	6	2	0	4	10	0.561212	0.661354	0.246513	0	0.420325	0.929577
lincRNA	-	0	0	0	1	7	7	0	0	0	0.013993	0.127202	0.112526
processed_	-	2	8	3	2	5	0	0.192863	0.909111	0.38122	0.166845	0.541675	0
antisense	-	32	31	19	26	19	37	2.532305	2.890911	1.981319	1.779928	1.689152	2.909895
sense_intrc	-	10	3	1	0	5	2	0.757382	0.267758	0.099804	0	0.425436	0.150541
protein_co	transmemb	1	0	1	235	331	257	0.005014	0	0.006608	1.019392	1.864608	1.280717
sense_over	-	7	11	8	231	168	167	0.191716	0.355026	0.288725	5.473123	5.169143	4.545549

lincRNA	-	0	9	2	0	1	0	0	0.690639	0.171619	0	0.073156	0
processed_	-	19	19	6	26	24	15	1.154855	1.360926	0.480574	1.367132	1.638831	0.906097
lincRNA	-	2	0	2	1	0	0	0.048238	0	0.063566	0.020865	0	0
sense_intrc	-	3	13	2	3	0	10	0.266482	1.360806	0.234105	0.230531	0	0.882786
antisense	-	3	2	4	0	0	7	0.315125	0.24757	0.553677	0	0	0.730751
processed_	-	13	22	27	15	4	22	0.132684	0.26461	0.36314	0.132443	0.045865	0.223156
lincRNA	-	27	22	25	87	38	42	0.309798	0.297471	0.377998	0.863568	0.489832	0.478932
sense_intrc	-	3	1	3	10	3	0	0.494776	0.194354	0.651993	1.426757	0.55585	0
lincRNA	-	0	0	2	4	0	3	0	0	0.1257	0.165041	0	0.1422
antisense	-	11	3	16	12	10	10	0.191123	0.061425	0.366332	0.18037	0.195195	0.172675
processed_	-	2	0	1	1	3	15	0.031438	0	0.020714	0.013598	0.052977	0.234326
antisense	-	21	16	19	33	35	26	2.422137	2.174736	2.887805	3.292732	4.535201	2.980317
antisense	-	8	8	2	7	5	4	0.714212	0.841656	0.235289	0.540628	0.501483	0.354901
pseudogen	-	8	1	3	0	1	0	0.113974	0.016789	0.056321	0	0.016005	0
pseudogen	-	0	4	0	0	0	0	0	2.354254	0	0	0	0
lincRNA	-	0	0	0	16	4	7	0	0	0	0.155712	0.050553	0.078261
protein_co	Uncharacte	0	0	1	2	0	2	0	0	0.018177	0.023866	0	0.027417
antisense	-	0	0	0	2	2	0	0	0	0	0.098811	0.128319	0
lincRNA	-	29	5	5	8	3	10	1.893081	0.384635	0.430107	0.451777	0.22001	0.648755
lincRNA	-	2	0	0	0	0	0	0.208429	0	0	0	0	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.082377	0
sense_over	-	32	23	37	29	48	34	0.487795	0.413164	0.743231	0.382427	0.822011	0.515081
sense_over	-	19	15	9	0	0	0	0.654869	0.609255	0.408769	0	0	0
processed_	-	0	1	1	0	0	0	0	0.108689	0.121539	0	0	0
processed_	-	55	65	23	54	25	45	4.943556	6.884894	2.724203	4.198881	2.524445	4.019749
antisense	-	0	1	0	1	1	0	0	0.120906	0	0.088758	0.115263	0
pseudogen	-	0	0	0	0	0	3	0	0	0	0	0	0.299511
processed_	-	0	0	0	1	1	0	0	0	0	0.083271	0.108138	0
sense_over	-	11	14	4	182	244	171	0.10231	0.153448	0.049025	1.464406	2.549565	1.58064
antisense	-	0	0	0	32	20	41	0	0	0	2.279261	1.849951	3.354862
lincRNA	-	1	0	0	0	0	0	0.035483	0	0	0	0	0
antisense	-	0	0	1	2	7	8	0	0	0.063191	0.082969	0.377112	0.381261
lincRNA	-	7	5	5	4	6	10	0.326508	0.274836	0.307327	0.161406	0.31441	0.46356
antisense	-	35	24	28	45	25	43	0.911877	0.736863	0.961305	1.014247	0.731741	1.113388
antisense	-	10	1	0	123	99	158	0.596182	0.070256	0	6.343767	6.630761	9.361509
antisense	-	0	0	0	3	1	0	0	0	0	0.24318	0.105267	0
processed_	-	0	1	3	0	1	3	0	0.111606	0.3744	0	0.106397	0.282365
antisense	-	1	0	2	3	0	1	0.077173	0	0.203391	0.200287	0	0.076697
lincRNA	-	0	0	1	0	0	0	0	0	0.017568	0	0	0
lincRNA	-	0	0	0	1	3	1	0	0	0	0.031305	0.12196	0.035963
lincRNA	-	8	3	3	17	10	24	0.978125	0.432248	0.483348	1.798109	1.373578	2.916252
lincRNA	long_interg	0	0	0	0	0	1	0	0	0	0	0	0.019216
antisense	-	28	14	15	8	10	11	2.623624	1.545891	1.852123	0.64848	1.052671	1.024344
lincRNA	-	1	3	3	23	9	17	0.015922	0.05629	0.062944	0.316804	0.160987	0.269004

sense_over	-	0	2	3	0	1	0	0	0.352473	0.591214	0	0.168011	0
lincRNA	-	1	0	0	4	10	3	0.037547	0	0	0.129926	0.421815	0.111945
processed_	-	3	0	0	0	0	3	0.048659	0	0	0	0	0.048359
antisense	-	6	7	0	4	5	17	0.827203	1.137276	0	0.477072	0.774426	2.329268
lincRNA	-	0	0	0	0	1	2	0	0	0	0	0.093811	0.165975
lincRNA	-	21	11	5	16	14	20	1.63735	1.0107	0.513721	1.079208	1.226308	1.549751
protein_co	zinc_finger_	828	631	478	1174	838	1009	10.9451	9.829378	8.326304	13.4252	12.44465	13.25532
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.017027	0
lincRNA	-	0	0	0	5	0	4	0	0	0	0.302104	0	0.277647
antisense	-	2	0	0	6	1	6	0.127723	0	0	0.331476	0.071744	0.380801
antisense	-	0	2	6	21	6	5	0	0.256212	0.859507	1.974901	0.732763	0.540185
pseudogen	ankyrin_rep	0	0	0	7	0	0	0	0	0	0.067621	0	0
antisense	-	4	1	1	0	0	0	0.464395	0.136815	0.15299	0	0	0
antisense	-	3	6	0	19	5	7	0.144911	0.341539	0	0.793959	0.271332	0.336039
antisense	-	1	0	1	0	2	0	0.088827	0	0.117052	0	0.199584	0
protein_co	golgin_A8_	3	0	0	0	0	0	0.083767	0	0	0	0	0
processed_	-	1	0	0	2	3	0	0.111455	0	0	0.192837	0.375637	0
antisense	-	0	0	0	3	0	0	0	0	0	0.041711	0	0
antisense	-	0	2	3	8	4	8	0	0.085287	0.143055	0.250438	0.162614	0.287705
lincRNA	-	0	1	0	4	1	2	0	0.238121	0	0.69922	0.227007	0.401634
antisense	-	20	14	14	4	9	6	0.878689	0.724837	0.810528	0.15203	0.444218	0.261979
sense_over	-	23	24	12	19	38	23	0.240308	0.295501	0.165218	0.171735	0.44604	0.238824
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.055122
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.14869	0
antisense	-	3	9	5	4	9	18	0.335778	1.187082	0.737455	0.387306	1.131677	2.002226
antisense	-	2	0	3	2	2	3	0.24174	0	0.477831	0.209127	0.27158	0.36037
sense_over	-	0	0	0	0	0	2	0	0	0	0	0	0.042345
sense_intrc	-	4	3	3	0	2	3	0.352353	0.31142	0.348236	0	0.197923	0.262633
protein_co	mucin_22	3	7	2	0	0	0	0.026387	0.072556	0.023181	0	0	0
antisense	-	0	2	0	0	0	0	0	0.340917	0	0	0	0
pseudogen	unc-51-like	0	2	1	0	0	0	0	0.142601	0.079729	0	0	0
lincRNA	-	5	2	0	14	8	14	0.133018	0.062701	0	0.322203	0.239099	0.370149
antisense	-	6	7	4	4	8	8	0.105953	0.145668	0.09308	0.061106	0.158708	0.140398
sense_intrc	-	9	1	2	1	1	0	0.934253	0.122329	0.273581	0.089802	0.116619	0
sense_over	-	0	0	0	0	1	3	0	0	0	0	0.029619	0.078607
antisense	-	2	0	0	0	1	0	0.21092	0	0	0	0.118478	0
antisense	-	106	65	106	1	3	2	8.606971	6.219636	11.34188	0.070244	0.273662	0.161393
antisense	-	1	2	0	1	5	0	0.052005	0.122569	0	0.044989	0.292121	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.031982	0	0
sense_over	-	0	0	0	1	0	0	0	0	0	0.054718	0	0
pseudogen	-	28	14	4	87	111	121	0.757459	0.44631	0.142592	2.036027	3.373442	3.253092
lincRNA	-	69	61	67	38	36	50	1.184862	1.234399	1.516101	0.564502	0.694497	0.853293
antisense	-	0	0	0	0	1	0	0	0	0	0	0.04313	0
sense_over	-	0	0	0	0	0	1	0	0	0	0	0	0.074

pseudogen	La_ribonuc	0	0	1	1	0	5	0	0	0.032046	0.021038	0	0.120841
sense_over	-	96	75	89	84	48	66	0.936318	0.862026	1.143871	0.708752	0.525948	0.639743
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.044887	0
lincRNA	-	87	113	72	128	101	79	0.846045	1.294969	0.922659	1.07683	1.103429	0.763503
antisense	-	13	12	8	0	0	0	0.524168	0.570185	0.425062	0	0	0
antisense	-	8	0	0	1	1	3	0.623753	0	0	0.067451	0.087593	0.232463
lincRNA	-	1	0	4	0	1	2	0.027374	0	0.144288	0	0.030753	0.05441
antisense	-	5	2	4	9	10	3	0.154167	0.072671	0.162524	0.240064	0.346394	0.091929
pseudogen	eukaryotic_	0	0	0	0	0	1	0	0	0	0	0	0.029311
antisense	-	8	7	5	5	12	14	0.555811	0.573116	0.457764	0.300518	0.936629	0.966662
sense_over	-	53	51	27	91	56	65	1.371394	1.555119	0.92063	2.036999	1.627884	1.671512
lincRNA	-	5	0	1	8	3	20	0.534758	0	0.140936	0.740184	0.36046	2.12582
sense_intrc	-	17	23	6	28	17	30	0.567821	0.905311	0.264088	0.809066	0.637912	0.99585
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.198544
pseudogen	-	12	1	3	0	2	2	1.384078	0.135921	0.455969	0	0.259154	0.229255
antisense	-	0	1	0	6	3	6	0	0.057874	0	0.25491	0.165517	0.292843
lincRNA	-	19	15	13	12	11	11	2.941166	2.736304	2.651821	1.606979	1.912968	1.692265
sense_over	-	21	35	15	27	22	31	0.302438	0.594007	0.284671	0.33639	0.355949	0.443698
lincRNA	-	0	0	0	1	0	0	0	0	0	0.065055	0	0
antisense	-	3	13	4	18	15	6	0.056783	0.289968	0.099769	0.294737	0.318963	0.112865
antisense	MANEA_ant	2	1	9	3	12	0	0.046685	0.027508	0.276838	0.060581	0.314687	0
antisense	-	0	1	1	4	2	3	0	0.112817	0.126154	0.331276	0.215103	0.285429
antisense	-	0	0	3	0	1	0	0	0	0.240563	0	0.068363	0
sense_over	-	15	10	2	10	17	20	1.18348	0.929772	0.207938	0.682547	1.506841	1.568228
antisense	-	35	26	22	267	156	133	1.057008	0.925317	0.875523	6.975646	5.29278	3.991825
sense_over	-	0	0	2	0	0	0	0	0	0.087532	0	0	0
pseudogen	-	0	3	0	0	0	1	0	0.148307	0	0	0	0.041691
pseudogen	-	0	1	3	8	3	6	0	0.058361	0.195781	0.342742	0.166911	0.295308
lincRNA	-	12	5	7	2	1	1	0.619193	0.304034	0.475968	0.089277	0.057969	0.051281
lincRNA	-	9	7	1	6	11	4	0.597079	0.547261	0.087423	0.344353	0.819843	0.26373
lincRNA	-	0	1	0	0	0	1	0	0.080813	0	0	0	0.068153
antisense	-	0	3	2	0	0	4	0	0.347242	0.258862	0	0	0.390457
pseudogen	-	0	0	0	0	5	3	0	0	0	0	1.093307	0.580302
antisense	-	1	0	1	0	0	3	0.099889	0	0.131629	0	0	0.297815
antisense	-	4	1	2	0	3	1	0.452487	0.133307	0.298134	0	0.381256	0.112423
pseudogen	-	2	1	0	1	1	1	0.14788	0.087134	0	0.063965	0.083067	0.073483
lincRNA	-	0	0	0	1	0	0	0	0	0	0.011914	0	0
processed_	-	1	0	0	3	1	1	0.054804	0	0	0.142233	0.061569	0.054466
processed_	TEN1-CDK3	4	2	0	4	3	7	0.05434	0.032018	0	0.047009	0.045786	0.094508
sense_over	-	3	2	6	9	6	14	0.03179	0.024975	0.083783	0.082504	0.071428	0.147437
antisense	-	0	0	0	0	1	0	0	0	0	0	0.105641	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.114377	0
pseudogen	-	0	1	1	0	0	0	0	0.084766	0.094787	0	0	0
pseudogen	-	7	5	6	2	8	3	1.026557	0.864096	1.159501	0.253734	1.318026	0.437236

antisense	-	1	0	0	3	10	7	0.03236	0	0	0.083983	0.363545	0.225121
lincRNA	-	5	5	12	17	18	15	0.113852	0.134167	0.360069	0.334874	0.460459	0.339445
lincRNA	-	54	52	31	0	0	0	1.290078	1.463972	0.97593	0	0	0
sense_intrc	-	1	0	0	2	2	0	0.012947	0	0	0.022401	0.029091	0
protein_co	-	0	0	0	0	0	1	0	0	0	0	0	0.065036
antisense	-	13	14	12	48	22	29	0.244488	0.310276	0.297392	0.78094	0.464821	0.542028
pseudogen	developme	0	0	0	0	0	1	0	0	0	0	0	0.059925
sense_intrc	-	0	0	0	2	2	3	0	0	0	0.298364	0.387465	0.514144
antisense	-	0	0	0	2	0	0	0	0	0	0.489828	0	0
lincRNA	-	0	1	0	2	1	0	0	0.115319	0	0.169312	0.109937	0
sense_overl	-	3	0	0	0	0	0	0.281601	0	0	0	0	0
antisense	-	0	0	0	29	27	35	0	0	0	0.608414	0.735616	0.84356
sense_overl	-	37	29	35	29	9	31	1.600341	1.478141	1.994865	1.085105	0.437323	1.332545
antisense	-	2	0	1	6	0	0	0.095475	0	0.062906	0.247785	0	0
antisense	-	4	6	0	5	7	3	0.137242	0.242596	0	0.148409	0.269819	0.102296
lincRNA	-	15	1	0	0	0	3	0.822917	0.06465	0	0	0	0.163567
antisense	-	1	0	3	0	0	0	0.082591	0	0.326505	0	0	0
sense_overl	-	0	3	2	6	2	3	0	0.040328	0.030064	0.05921	0.025631	0.03401
lincRNA	-	14	10	8	82	65	106	0.381262	0.320925	0.287092	1.931847	1.988649	2.868873
lincRNA	-	40	28	27	101	51	80	1.200476	0.990281	1.067805	2.622273	1.719542	2.386125
antisense	-	1	3	6	4	2	11	0.016817	0.059455	0.132967	0.058194	0.037786	0.183848
pseudogen	ubiquitin-c	0	1	0	1	0	12	0	0.113432	0	0.083271	0	1.147943
sense_overl	-	5	4	8	7	2	2	0.138155	0.130246	0.291287	0.167324	0.062083	0.054921
sense_intrc	-	4	0	0	3	1	4	0.397306	0	0	0.25778	0.111587	0.394852
antisense	-	7	2	7	0	5	16	0.152254	0.051264	0.200634	0	0.122177	0.345861
lincRNA	-	28	32	32	21	8	22	3.301443	4.446342	4.971993	2.142042	1.059705	2.577971
sense_intrc	-	9	11	4	12	10	17	0.559236	0.805475	0.327527	0.645055	0.698074	1.049811
lincRNA	-	2	0	0	0	0	0	0.190093	0	0	0	0	0
antisense	-	1	0	0	1	2	0	0.106307	0	0	0.091966	0.238859	0
antisense	PAN3_antis	32	33	33	27	28	33	1.253969	1.523905	1.704062	0.9153	1.232661	1.285169
antisense	-	9	6	1	45	38	23	0.245983	0.193251	0.036016	1.063991	1.166797	0.624741
lincRNA	-	0	0	0	0	2	5	0	0	0	0	0.466478	1.031648
sense_overl	-	44	50	55	105	81	118	0.663648	0.888714	1.093157	1.370053	1.372521	1.768791
sense_overl	-	1	0	0	0	1	0	0.033528	0	0	0	0.037667	0
lincRNA	-	12	3	6	0	5	3	0.461695	0.13602	0.3042	0	0.216119	0.114711
antisense	-	91	98	61	111	116	103	1.550573	1.967814	1.369669	1.636202	2.220536	1.744206
lincRNA	-	55	56	29	100	87	98	1.830141	2.195923	1.271612	2.878624	3.252297	3.24084
antisense	-	0	6	3	3	1	10	0	0.481759	0.269356	0.17683	0.076546	0.677144
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.055093
antisense	DLGAP1_ar	3	0	1	8	12	7	0.061227	0	0.026894	0.141246	0.275139	0.141981
lincRNA	-	3	1	2	44	22	30	0.286684	0.112613	0.251853	3.637458	2.36186	2.849136
lincRNA	-	4	8	3	7	10	11	0.164413	0.387501	0.162492	0.248907	0.46177	0.449344
pseudogen	-	3	0	1	4	3	6	0.219976	0	0.096625	0.253734	0.24713	0.437236
pseudogen	-	7	4	1	0	4	0	0.51045	0.343734	0.096093	0	0.327691	0

sense_intrc	-	10	2	5	2	5	1	0.330262	0.077839	0.217602	0.057141	0.185514	0.032822
sense_overl	-	3	6	1	3	7	6	0.073393	0.172979	0.032238	0.063492	0.19239	0.14588
sense_overl	-	109	73	99	26	26	27	1.527009	1.205161	1.827617	0.315102	0.409202	0.375914
sense_intrc	-	0	0	0	4	0	0	0	0	0	0.231016	0	0
3prime_ov	-	0	0	0	3	0	0	0	0	0	0.322528	0	0
lincRNA	-	18	20	15	27	18	31	0.463942	0.607475	0.509469	0.60203	0.521211	0.794078
antisense	-	0	1	0	0	0	0	0	0.112613	0	0	0	0
sense_intrc	-	0	0	6	0	0	0	0	0	0.97799	0	0	0
antisense	-	6	0	2	0	7	0	0.150901	0	0.066283	0	0.197782	0
pseudogen	-	0	0	0	23	31	34	0	0	0	1.448934	2.536112	2.46063
antisense	-	12	9	12	4	14	21	1.369164	1.210107	1.804223	0.394818	1.794532	2.381239
processed_	-	2	3	12	2	15	9	0.02565	0.04534	0.2028	0.022189	0.216119	0.114711
pseudogen	-	0	0	0	2	3	3	0	0	0	0.153174	0.298374	0.26395
pseudogen	-	78	60	53	136	83	108	1.569516	1.422753	1.405342	2.367408	1.876283	2.159756
pseudogen	-	2	0	1	0	0	0	0.071494	0	0.047106	0	0	0
sense_intrc	-	16	12	5	19	18	21	0.566593	0.500771	0.233322	0.58206	0.716098	0.73906
protein_co	Uncharacte	8	7	1	0	8	3	1.465495	1.511121	0.241395	0	1.646392	0.546167
lincRNA	-	4	0	2	2	0	1	0.131123	0	0.086394	0.056717	0	0.032578
antisense	-	0	0	0	1	0	0	0	0	0	0.096622	0	0
sense_intrc	-	8	3	4	10	0	4	0.22397	0.098976	0.147569	0.242194	0	0.111294
antisense	-	0	0	2	0	0	0	0	0	0.3354	0	0	0
sense_intrc	-	3	6	5	0	2	0	0.37815	0.891253	0.830515	0	0.283219	0
pseudogen	-	0	1	1	8	2	7	0	0.127063	0.142084	0.746214	0.242264	0.750098
sense_overl	-	77	62	70	24	28	20	0.972437	0.922719	1.16494	0.262207	0.397263	0.251021
pseudogen	-	0	0	1	1	0	0	0	0	0.096225	0.063171	0	0
antisense	-	20	13	16	4	0	9	2.00155	1.533158	2.110043	0.346306	0	0.895135
lincRNA	-	17	20	12	44	27	35	0.52204	0.723756	0.485591	1.168882	0.931467	1.068151
processed_	-	13	11	3	176	204	221	0.328669	0.327729	0.099947	3.849383	5.794215	5.552868
pseudogen	-	0	0	0	0	0	4	0	0	0	0	0	0.812572
lincRNA	-	161	132	103	65	59	52	1.772037	1.712096	1.493891	0.618904	0.729538	0.568801
processed_	-	0	7	1	2	1	0	0	0.851295	0.135991	0.178553	0.115937	0
protein_co	trophoblas	143	109	83	15	9	16	2.710549	2.434752	2.073166	0.245966	0.191652	0.301405
sense_intrc	-	0	4	6	15	0	2	0	0.377535	0.633252	1.03931	0	0.159195
sense_overl	-	43	46	61	44	35	21	0.556049	0.700986	1.039463	0.492221	0.508465	0.269882
antisense	-	9	10	12	9	0	0	0.224221	0.293589	0.393957	0.193972	0	0
lincRNA	microRNA_	172	154	132	588	475	514	1.195621	1.261517	1.209133	3.535945	3.709435	3.550896
lincRNA	-	0	1	1	1	0	0	0	0.03501	0.039149	0.025701	0	0
antisense	-	2	3	1	0	4	1	0.052915	0.093535	0.034864	0	0.118892	0.026294
pseudogen	Y_box_binc	0	0	0	1	0	1	0	0	0	0.042017	0	0.04827
antisense	-	9	7	8	7	13	17	0.177986	0.163136	0.208482	0.119758	0.288826	0.33412
lincRNA	-	0	0	1	2	0	0	0	0	0.023301	0.030594	0	0
pseudogen	high_mobil	0	1	0	2	0	3	0	0.151427	0	0.222325	0	0.383112
lincRNA	-	1	0	0	0	0	0	0.014414	0	0	0	0	0
sense_overl	-	122	117	92	1	2	6	5.030219	5.684863	4.998615	0.035669	0.092642	0.24586

lincRNA	-	0	2	0	0	0	0	0	0.245621	0	0	0	0
antisense	-	8	0	3	2	7	11	0.774274	0	0.382614	0.167455	0.761118	1.058052
antisense	-	0	2	1	5	12	12	0	0.159764	0.089326	0.293207	0.913843	0.808411
antisense	-	0	0	0	0	6	4	0	0	0	0	0.641826	0.378518
processed_	-	0	0	0	1	0	0	0	0	0	0.018933	0	0
pseudogen	-	1	0	1	1	0	0	0.073022	0	0.096225	0.063171	0	0
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.235548	0
sense_over	-	31	29	15	77	40	65	1.906122	2.101329	1.215388	4.095837	2.763109	3.972025
antisense	-	4	1	1	0	0	0	0.184143	0.05425	0.060664	0	0	0
processed_	DISC1_fusi	0	4	0	0	2	0	0	0.143916	0	0	0.0686	0
lincRNA	-	7	6	6	0	0	0	0.167762	0.169455	0.189488	0	0	0
pseudogen	golgin_A6_	2	0	0	0	2	0	0.053368	0	0	0	0.059956	0
protein_co	uncharacte	3	4	2	1	6	5	0.217864	0.34232	0.191394	0.062824	0.489514	0.360865
sense_over	-	7	5	4	5	4	6	0.061919	0.05212	0.046625	0.038261	0.03975	0.052746
sense_over	-	3	14	3	0	0	0	0.080908	0.444946	0.106617	0	0	0
processed_	-	0	0	3	0	1	1	0	0	0.392664	0	0.111587	0.098713
sense_over	-	9	8	10	10	5	3	0.145888	0.152817	0.213605	0.140229	0.091053	0.048329
processed_	-	42	48	34	25	32	36	0.651486	0.877413	0.694976	0.335474	0.557641	0.554968
sense_over	-	53	34	34	19	14	12	2.06466	1.560841	1.745365	0.640308	0.612703	0.464583
antisense	-	11	14	5	50	34	38	0.739024	1.108411	0.44266	2.906022	2.56622	2.537226
antisense	-	17	5	3	44	36	36	0.234191	0.081171	0.05446	0.524369	0.557151	0.492872
antisense	-	7	9	2	1	4	9	0.640047	0.969757	0.240979	0.0791	0.410887	0.817835
lincRNA	-	3	2	0	0	0	1	0.034549	0.027143	0	0	0	0.011445
lincRNA	-	2	1	3	1	3	2	0.119641	0.070495	0.236486	0.05175	0.201613	0.118902
lincRNA	-	2	0	0	0	0	0	0.270798	0	0	0	0	0
pseudogen	-	0	0	2	0	0	0	0	0	0.32448	0	0	0
lincRNA	-	654	477	477	121	147	113	10.06202	8.648343	9.67076	1.610482	2.540819	1.727808
antisense	-	23	37	27	43	36	35	1.255302	2.379738	1.941865	2.030261	2.207354	1.898445
sense_intrc	-	0	4	0	1	2	1	0	0.601328	0	0.110359	0.286631	0.126781
antisense	-	0	0	4	5	3	1	0	0	0.082633	0.06781	0.052836	0.01558
antisense	-	0	0	0	2	0	0	0	0	0	0.1582	0	0
lincRNA	-	0	0	0	23	19	7	0	0	0	0.721984	0.774532	0.252432
processed_	-	0	0	0	0	0	1	0	0	0	0	0	0.030625
protein_co	haptoglobi	5	9	3	1	5	0	0.212785	0.451358	0.168239	0.036816	0.239051	0
lincRNA	-	84	61	46	90	108	96	5.836015	4.994293	4.211432	5.40932	8.429658	6.628542
antisense	-	0	0	0	1	1	0	0	0	0	0.057249	0.074345	0
lincRNA	-	8	13	14	6	0	7	0.80062	1.533158	1.846287	0.519458	0	0.696216
pseudogen	-	0	2	1	1	2	1	0	0.267758	0.149707	0.098281	0.255261	0.112906
lincRNA	-	0	0	0	0	0	3	0	0	0	0	0	0.128746
sense_over	-	174	179	163	135	109	114	2.034843	2.466844	2.51191	1.365773	1.432047	1.32494
processed_	-	2	5	4	6	7	3	0.168871	0.49751	0.445061	0.438267	0.664005	0.251742
lincRNA	-	0	0	0	5	0	2	0	0	0	0.254156	0	0.11679
antisense	-	0	0	0	16	5	3	0	0	0	0.573831	0.232874	0.123604
antisense	-	6	6	6	4	6	19	0.720286	0.848813	0.94916	0.41541	0.809196	2.266818

protein_co	-	10	15	8	6	15	18	0.099401	0.175707	0.104789	0.051595	0.167506	0.177817
sense_intrc	-	1	0	1	0	0	2	0.089427	0	0.117843	0	0	0.17775
antisense	-	8	4	7	8	10	25	0.440716	0.259678	0.508161	0.38126	0.618896	1.368732
protein_co	BolA-like_p	2	1	3	2	10	13	0.034122	0.020106	0.067448	0.029519	0.191672	0.220426
lincRNA	-	12	7	7	0	2	4	0.360961	0.248133	0.277468	0	0.067586	0.119577
antisense	-	15	24	18	5	16	9	1.083376	2.042709	1.71315	0.312407	1.298246	0.646012
sense_overl	-	0	0	0	5	0	0	0	0	0	0.457989	0	0
lincRNA	-	0	0	0	14	10	1	0	0	0	0.232566	0.215727	0.019084
lincRNA	-	3	0	0	0	0	0	0.096843	0	0	0	0	0
antisense	-	3	3	6	3	5	13	0.050404	0.059398	0.13284	0.043604	0.094376	0.217068
lincRNA	-	0	0	3	4	1	1	0	0	0.244212	0.213764	0.0694	0.061393
antisense	-	2	1	2	18	10	16	0.049156	0.028964	0.064776	0.382721	0.276118	0.390819
pseudogen	keratin_18_	0	0	1	0	3	0	0	0	0.054545	0	0.139506	0
sense_intrc	-	3	5	0	0	0	0	0.372824	0.73225	0	0	0	0
antisense	-	9	10	8	5	8	5	0.875862	1.146833	1.025931	0.420946	0.874646	0.483585
lincRNA	-	12	13	18	34	30	30	0.173293	0.221233	0.342537	0.424758	0.48671	0.430557
sense_overl	-	1	2	0	0	0	0	0.066845	0.157545	0	0	0	0
lincRNA	-	2	0	4	4	11	4	0.293302	0	0.773	0.507467	1.812286	0.582981
processed_	-	3	1	6	24	18	25	0.107969	0.042412	0.284555	0.747229	0.727781	0.894188
processed_	-	9	0	3	2	7	3	0.408986	0	0.179648	0.078625	0.357366	0.135487
processed_	-	6	5	1	12	4	8	0.849321	0.834061	0.186533	1.469484	0.636106	1.125434
lincRNA	-	79	82	85	168	107	118	0.825407	1.00963	1.170294	1.518495	1.255955	1.225273
protein_co	transcriptic	0	0	2	4	2	0	0	0	0.05695	0.074774	0.048552	0
lincRNA	-	0	0	2	2	2	0	0	0	0.212369	0.139418	0.181053	0
antisense	-	2	2	0	0	0	0	0.063708	0.075075	0	0	0	0
protein_co	golgin_A8_	14	7	5	0	4	10	0.390297	0.229971	0.183684	0	0.125278	0.277062
lincRNA	-	1	0	0	0	0	0	0.016503	0	0	0	0	0
sense_overl	-	113	113	106	132	111	107	1.887171	2.223916	2.332779	1.907084	2.082595	1.775932
antisense	LOXL1_anti	456	366	373	37	15	19	10.23795	9.683592	11.0355	0.718643	0.378346	0.423947
lincRNA	-	0	0	0	7	5	5	0	0	0	0.44465	0.412454	0.364869
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.107816
polymorph	tubulin_be	0	0	0	1	4	8	0	0	0	0.021654	0.112484	0.199013
pseudogen	-	7	4	4	0	6	9	0.194841	0.131204	0.146716	0	0.187621	0.248962
antisense	-	0	0	0	1	0	0	0	0	0	0.058343	0	0
lincRNA	-	2	0	2	0	0	1	0.1262	0	0.166301	0	0	0.06271
lincRNA	long_interg	233	183	216	326	205	226	4.973892	4.603611	6.076157	6.02034	4.916356	4.794667
sense_overl	-	0	0	0	0	1	5	0	0	0	0	0.099458	0.439917
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.117705
sense_intrc	-	2	0	1	0	0	1	0.149762	0	0.098675	0	0	0.074419
antisense	-	0	0	1	6	5	8	0	0	0.170988	0.673513	0.728872	1.031648
lincRNA	-	0	0	3	0	0	0	0	0	0.073954	0	0	0
antisense	-	14	8	17	26	20	38	0.649014	0.437042	1.038508	1.042707	1.04161	1.75073
lincRNA	-	3	0	0	0	1	0	0.071671	0	0	0	0.026839	0
protein_co	melanoma_	0	0	0	9	1	9	0	0	0	0.6522	0.094107	0.749251

lincRNA	-	0	0	0	9	4	6	0	0	0	0.323794	0.186884	0.247985
processed_	-	2	0	0	0	7	1	0.192863	0	0	0	0.758345	0.095836
pseudogen	-	0	5	6	3	5	4	0	0.235071	0.315433	0.103539	0.224099	0.158595
antisense	-	1	1	1	3	0	0	0.078664	0.092701	0.10366	0.204156	0	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.080917	0	0
antisense	-	13	12	7	8	11	9	0.401302	0.436532	0.284748	0.213639	0.381478	0.276109
protein_co	-	18	10	11	12	25	18	0.167623	0.109741	0.134986	0.096673	0.261548	0.166588
processed_	-	0	0	0	0	0	1	0	0	0	0	0	0.1332
lincRNA	-	95	64	69	12	12	34	1.893597	1.503319	1.812374	0.206923	0.268716	0.673523
lincRNA	-	1	0	2	4	4	5	0.070777	0	0.186533	0.244914	0.318053	0.351698
processed_	-	103	97	70	21	42	89	1.938472	2.151301	1.736022	0.341904	0.888016	1.664646
sense_intrc	-	5	10	8	4	1	8	0.517002	1.21851	1.090051	0.357804	0.116164	0.822095
antisense	-	11	10	4	6	13	15	0.185876	0.199131	0.089069	0.087709	0.246788	0.251903
protein_co	protocadhe	11	16	11	3	11	4	0.126461	0.216765	0.166644	0.029836	0.142071	0.045702
pseudogen	-	0	3	0	0	0	1	0	1.497306	0	0	0	0.420912
protein_co	Homo_sapi	0	0	0	0	0	3	0	0	0	0	0	0.084138
pseudogen	-	0	0	0	0	3	2	0	0	0	0	0.225288	0.132864
pseudogen	-	8	10	6	3	4	9	1.154027	1.699938	1.140544	0.374378	0.648239	1.290263
antisense	-	48	40	26	67	33	35	1.174835	1.153726	0.838579	1.418644	0.9074	0.85136
antisense	-	0	4	3	0	2	0	0	0.601328	0.504313	0	0.286631	0
antisense	-	2	0	1	0	0	1	0.120457	0	0.079367	0	0	0.059857
lincRNA	-	1	1	1	18	7	12	0.01383	0.016298	0.018224	0.215355	0.10876	0.164934
antisense	DLGAP1_ar	38	25	30	89	71	109	0.889765	0.689825	0.925652	1.802788	1.867665	2.536458
protein_co	Uncharacte	17	7	24	5	6	6	1.097557	0.532578	2.041852	0.279262	0.43519	0.384981
lincRNA	-	1	0	0	0	4	0	0.107604	0	0	0	0.483544	0
pseudogen	-	0	0	1	0	0	0	0	0	0.361468	0	0	0
antisense	-	0	0	0	3	0	7	0	0	0	0.225241	0	0.603768
sense_intrc	-	0	0	0	0	0	3	0	0	0	0	0	0.320167
protein_co	Uncharacte	2	7	0	0	0	3	0.277178	1.143231	0	0	0	0.413199
antisense	-	14	17	18	56	27	78	0.374898	0.536465	0.635174	1.297288	0.812266	2.07582
lincRNA	-	12	1	0	7	8	8	0.923389	0.09068	0	0.465977	0.69158	0.611791
sense_over	-	2	5	13	1	7	0	0.020954	0.061733	0.179482	0.009064	0.082393	0
lincRNA	-	37	21	13	8	15	15	5.710836	3.819657	2.644089	1.068196	2.600988	2.300906
lincRNA	-	0	0	0	4	0	0	0	0	0	0.076046	0	0
pseudogen	protocadhe	4	3	2	2	2	0	0.090228	0.079746	0.059449	0.039028	0.050683	0
processed_	-	0	0	1	0	0	0	0	0	0.091794	0	0	0
processed_	-	5	0	0	0	3	0	0.719307	0	0	0	0.484858	0
lincRNA	-	0	2	0	0	0	0	0	0.313506	0	0	0	0
antisense	-	0	0	1	1	1	1	0	0	0.086662	0.056893	0.073883	0.065359
lincRNA	breast_can	0	2	0	0	0	0	0	0.098017	0	0	0	0
pseudogen	-	0	0	0	2	0	0	0	0	0	0.059946	0	0
antisense	-	2	7	5	3	3	3	0.180995	0.74652	0.596267	0.234866	0.305005	0.269816
antisense	-	2	0	0	1	6	3	0.178855	0	0	0.077363	0.602796	0.266625
pseudogen	-	5	1	5	3	0	2	0.30046	0.070815	0.395932	0.155955	0	0.119442

pseudogen	-	0	8	0	2	4	5	0	3.178993	0	0.583426	1.51531	1.675607
antisense	-	8	7	9	19	8	17	1.331849	1.373315	1.974433	2.736413	1.496249	2.812701
lincRNA	long_interg	2	1	0	6	3	20	0.03128	0.018431	0	0.08118	0.052711	0.310866
lincRNA	-	3	8	3	1	5	3	0.084706	0.266188	0.111621	0.024426	0.158602	0.084182
processed_	-	17	8	8	6	7	9	1.601418	0.888082	0.993072	0.488956	0.740803	0.842574
antisense	-	7	12	5	9	7	5	0.691394	1.39674	0.650777	0.769011	0.776738	0.490803
sense_intrc	-	3	6	1	1	4	2	0.358517	0.844981	0.157479	0.103384	0.537029	0.237535
lincRNA	-	0	0	0	0	0	4	0	0	0	0	0	0.257596
protein_co	oculomedi	17	22	13	13	16	12	1.018096	1.552636	1.025931	0.673513	1.076487	0.714218
sense_overl	-	25	8	21	2	1	2	0.949444	0.358036	1.050953	0.065709	0.042666	0.075486
lincRNA	-	1	2	1	0	0	0	0.034377	0.081023	0.045301	0	0	0
lincRNA	-	18	10	10	39	7	26	1.839648	1.204396	1.346782	3.44818	0.803729	2.64086
lincRNA	-	0	0	0	10	6	7	0	0	0	0.782887	0.610009	0.62957
lincRNA	-	1	5	4	15	1	5	0.08311	0.4897	0.438074	1.078467	0.093369	0.412983
protein_co	protocadhe	0	3	2	0	3	0	0	0.039594	0.029517	0	0.037747	0
antisense	-	21	6	16	9	15	13	0.517821	0.174349	0.519894	0.191984	0.415528	0.318576
lincRNA	-	0	0	1	5	1	5	0	0	0.099378	0.326203	0.084724	0.374744
antisense	-	3	4	2	1	0	7	0.288245	0.452905	0.253224	0.08312	0	0.668418
protein_co	coronin_7	39	25	35	133	78	114	0.577054	0.435912	0.682425	1.702419	1.296568	1.676356
pseudogen	-	6	8	1	5	8	10	0.923389	1.450877	0.2028	0.665682	1.383161	1.529478
sense_intrc	-	2	6	0	24	26	12	0.095218	0.336624	0	0.988466	1.390624	0.567778
sense_intrc	-	4	10	4	1	2	2	0.52809	1.555804	0.695893	0.114212	0.296638	0.262414
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.035406
antisense	-	0	0	0	1	2	0	0	0	0	0.234866	0.610009	0
antisense	-	0	1	2	3	2	1	0	0.113639	0.254147	0.250267	0.21667	0.095836
protein_co	transient_r	0	0	1	1	1	0	0	0	0.014678	0.009636	0.012513	0
sense_overl	-	1	2	0	2	2	0	0.110294	0.259949	0	0.190829	0.247816	0
antisense	-	3	0	0	1	0	4	0.321504	0	0	0.09271	0	0.426025
pseudogen	-	1	0	0	1	0	0	0.072127	0	0	0.062396	0	0
antisense	-	1	1	0	1	3	0	0.019806	0.02334	0	0.017134	0.066752	0
pseudogen	heterogene	5	2	12	19	17	24	0.277178	0.130655	0.876607	0.911182	1.058734	1.322238
antisense	-	0	1	1	0	7	0	0	0.15558	0.173973	0	1.038233	0
lincRNA	-	0	0	0	0	0	4	0	0	0	0	0	0.228757
antisense	-	3	4	0	8	1	6	0.399053	0.627012	0	0.920581	0.149437	0.793177
protein_co	double_C2	0	0	0	1	0	0	0	0	0	0.035752	0	0
sense_overl	-	0	1	0	22	7	15	0	0.102611	0	1.657197	0.684756	1.298044
antisense	-	4	0	2	0	5	3	0.696592	0	0.458969	0	0.978222	0.519218
sense_intrc	-	6	0	0	3	2	5	0.631503	0	0	0.273155	0.236485	0.523002
pseudogen	-	2	1	6	0	3	0	0.222909	0.131343	0.88122	0	0.375637	0
pseudogen	-	3	0	0	0	0	0	0.877475	0	0	0	0	0
sense_intrc	-	4	11	1	2	1	2	0.32985	1.068949	0.108666	0.142676	0.092642	0.163907
lincRNA	-	1	0	0	0	0	0	0.052835	0	0	0	0	0
antisense	-	4	5	2	2	0	3	0.081542	0.120115	0.053726	0.035271	0	0.060779
antisense	-	24	19	22	16	7	6	2.61437	2.439026	3.158009	1.507783	0.856649	0.649556

lincRNA	-	0	2	1	0	2	0	0	0.169302	0.094658	0	0.1614	0
lincRNA	-	22	33	3	12	11	26	1.789097	3.162512	0.32149	0.844219	1.004969	2.101329
lincRNA	-	11	12	11	24	13	26	0.278237	0.357694	0.366649	0.525167	0.369416	0.653591
pseudogen	trans-golgi_	0	0	0	0	2	0	0	0	0	0	0.190934	0
pseudogen	sterile_alpl	1	0	0	0	0	0	0.080092	0	0	0	0	0
antisense	-	2	8	3	1	1	4	0.207612	0.978631	0.410372	0.089802	0.116619	0.412659
protein_co	uncharacte	5	5	0	0	0	2	0.25043	0.295117	0	0	0	0.099554
pseudogen	-	2	2	0	0	1	0	0.246237	0.290175	0	0	0.138316	0
pseudogen	-	0	0	1	2	1	1	0	0	0.097845	0.128468	0.083416	0.073792
pseudogen	-	1	0	1	6	6	2	0.073529	0	0.096893	0.381658	0.495633	0.14615
sense_intrc	-	4	1	6	1	4	5	0.178403	0.052559	0.352637	0.038584	0.200424	0.221626
pseudogen	-	1	1	2	0	0	3	0.109609	0.129167	0.288875	0	0	0.326795
antisense	-	1	0	0	6	0	0	0.127569	0	0	0.662153	0	0
3prime_ov	-	0	1	3	11	13	10	0	0.0213	0.071454	0.172	0.263976	0.179631
protein_co	protocadhe	26	14	13	0	10	2	0.299102	0.189793	0.197071	0	0.129239	0.022866
processed_	-	6	25	12	40	37	36	0.072209	0.354556	0.190307	0.416448	0.500252	0.430576
pseudogen	-	0	0	0	3	7	7	0	0	0	0.215693	0.653582	0.578176
lincRNA	-	4	0	5	0	2	0	0.040175	0	0.066177	0	0.022567	0
pseudogen	-	2	5	9	1	3	2	0.184463	0.543447	1.093849	0.079789	0.31085	0.183324
processed_	-	47	37	26	25	39	27	3.202351	2.970844	2.334421	1.473581	2.985278	1.828287
lincRNA	long_interg	0	0	0	5	11	14	0	0	0	0.194558	0.55585	0.625826
pseudogen	-	0	0	0	0	0	4	0	0	0	0	0	0.513308
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.404723
sense_intrc	-	4	0	10	0	13	0	0.356505	0	1.174466	0	1.301661	0
3prime_ov	-	1	2	2	2	0	1	0.010592	0.024965	0.027916	0.018327	0	0.010527
antisense	-	1	0	1	3	0	0	0.096432	0	0.127073	0.250267	0	0
lincRNA	-	1	4	0	1	2	13	0.105042	0.495141	0	0.090871	0.236016	1.357108
antisense	-	0	0	0	1	0	0	0	0	0	0.072812	0	0
antisense	-	1	13	4	2	9	10	0.097677	1.496385	0.514858	0.169	0.987607	0.970739
lincRNA	-	2	6	2	1	0	3	0.311418	1.10096	0.410372	0.134703	0	0.464242
processed_	-	29	38	19	1	1	5	0.573511	0.885593	0.495145	0.017108	0.022217	0.098271
antisense	-	14	13	13	24	21	32	2.546989	2.787081	3.116573	3.777229	4.292077	5.785737
pseudogen	-	0	5	4	3	1	3	0	0.166901	0.149306	0.073513	0.031822	0.084453
antisense	-	0	4	0	5	13	3	0	0.2279	0	0.209127	0.706107	0.144148
pseudogen	-	0	0	1	2	0	3	0	0	0.117447	0.154205	0	0.265728
sense_intrc	-	9	7	3	32	25	28	0.244468	0.224071	0.107383	0.751957	0.762903	0.755871
lincRNA	-	0	0	1	14	24	17	0	0	0.032569	0.299339	0.666397	0.417572
lincRNA	-	9	9	2	1	0	4	0.493239	0.581252	0.144437	0.047411	0	0.217864
antisense	-	1	1	0	1	0	0	0.01073	0.012644	0	0.009282	0	0
processed_	-	0	0	0	4	1	5	0	0	0	0.296433	0.096239	0.42568
lincRNA	-	194	157	102	361	212	251	4.874491	4.64873	3.377245	7.846894	5.984288	6.267739
pseudogen	mitochond	4	1	0	1	0	6	0.823984	0.242754	0	0.178206	0	1.228344
sense_intrc	-	28	16	11	9	12	22	2.729922	1.838312	1.413252	0.759098	1.314385	2.131693
antisense	-	0	0	1	0	0	0	0	0	0.115311	0	0	0

lincRNA	-	2	3	0	0	0	1	0.059218	0.104677	0	0	0	0.029426
antisense	-	6	11	9	4	3	3	0.557274	1.203974	1.101526	0.321396	0.313031	0.276916
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.031552	0
lincRNA	-	1	0	0	8	0	4	0.069294	0	0	0.47957	0	0.275466
pseudogen	-	0	0	0	2	1	4	0	0	0	0.117283	0.076154	0.26947
antisense	-	0	0	0	0	1	1	0	0	0	0	0.112644	0.099648
protein_co	mitochond	22	15	33	97	64	81	1.132978	0.910327	2.239483	4.321492	3.702781	4.14566
antisense	-	1	4	2	0	3	1	0.103199	0.486454	0.271982	0	0.347812	0.102562
3prime_ov	-	12	10	20	1	5	7	0.125329	0.123077	0.275255	0.009035	0.058666	0.072657
antisense	-	0	0	0	1	3	7	0	0	0	0.053629	0.208932	0.431263
antisense	-	11	6	3	0	11	2	0.181757	0.116831	0.065321	0	0.204193	0.032843
processed_	-	12	2	4	11	9	16	1.527144	0.299941	0.670801	1.211029	1.286739	2.023617
antisense	-	0	0	0	1	0	0	0	0	0	0.080774	0	0
pseudogen	cytochrom	2	2	2	0	1	0	0.360143	0.424406	0.47458	0	0.202299	0
lincRNA	-	1	2	1	0	0	0	0.060922	0.143585	0.08028	0	0	0
processed_	-	12	10	16	40	25	57	0.406978	0.399665	0.715062	1.173579	0.952529	1.921205
processed_	-	179	152	160	81	98	88	8.766363	8.772373	10.32574	3.43174	5.391896	4.283105
processed_	-	0	0	1	0	0	0	0	0	0.035323	0	0	0
antisense	-	0	0	0	1	1	0	0	0	0	0.017989	0.023361	0
sense_over	-	8	9	5	0	0	0	0.547194	0.725439	0.450667	0	0	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.073278	0	0
antisense	-	36	41	15	60	39	47	2.180636	2.926655	1.19731	3.14409	2.65396	2.82936
pseudogen	-	0	1	3	23	1	3	0	0.051946	0.174263	0.877081	0.049522	0.131426
antisense	-	2	0	1	1	0	0	0.178855	0	0.117843	0.077363	0	0
pseudogen	arachidona	7	1	2	44	61	51	0.085665	0.014422	0.032253	0.465823	0.838657	0.620277
sense_intrc	-	299	268	289	306	242	261	8.270302	8.735586	10.53375	7.322082	7.519944	7.174643
lincRNA	-	1	6	0	3	0	2	0.085665	0.605706	0	0.222325	0	0.170272
pseudogen	-	3	1	0	0	0	0	0.293573	0.115319	0	0	0	0
antisense	-	6	5	2	0	0	1	0.056012	0.055006	0.024604	0	0	0.009278
sense_intrc	-	1	0	0	5	1	1	0.081073	0	0	0.350681	0.091081	0.080573
antisense	-	0	0	0	3	0	0	0	0	0	0.060288	0	0
protein_co	zinc_finger	274	251	224	196	211	223	4.47021	4.825676	4.815709	2.766282	3.867309	3.615696
lincRNA	-	12	17	12	7	12	16	0.891013	1.487505	1.174137	0.449639	1.000997	1.18068
pseudogen	Rho-associa	0	3	6	12	5	2	0	0.33422	0.747464	0.981405	0.531035	0.187907
sense_over	-	3	2	3	3	7	3	0.525904	0.413164	0.693013	0.454956	1.378581	0.522656
sense_intrc	-	18	9	24	19	22	25	0.822207	0.48446	1.444624	0.750802	1.128965	1.134902
pseudogen	-	0	1	0	0	3	4	0	0.187351	0	0	0.535819	0.632001
processed_	-	0	0	2	1	0	3	0	0	0.231772	0.076078	0	0.262196
pseudogen	-	0	0	0	0	4	0	0	0	0	0	1.272212	0
lincRNA	-	18	12	4	8	5	13	2.151101	1.689961	0.629917	0.827068	0.671286	1.543979
antisense	-	0	0	1	0	0	3	0	0	0.296865	0	0	0.671669
protein_co	Uncharacte	34	15	11	61	55	55	0.952378	0.495141	0.40603	1.478166	1.730781	1.531097
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.132463	0
antisense	-	20	19	11	7	13	8	0.290008	0.324669	0.210188	0.087809	0.211774	0.115287

antisense	-	161	134	111	286	162	237	5.353957	5.251228	4.864148	8.227693	6.052198	7.832619
antisense	-	0	0	2	2	1	8	0	0	0.195415	0.128288	0.0833	0.589513
lincRNA	-	0	0	0	0	1	1	0	0	0	0	0.026457	0.023405
antisense	-	0	5	1	0	8	7	0	0.072866	0.016296	0	0.111144	0.086031
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.25479
lincRNA	-	2	1	0	0	0	3	0.332962	0.196188	0	0	0	0.496359
sense_intrc	-	3	0	0	0	1	0	0.067412	0	0	0	0.025244	0
3prime_ov	-	0	0	0	0	1	2	0	0	0	0	0.015223	0.026933
pseudogen	-	193	170	212	85	125	71	2.177203	2.259943	3.151463	0.829514	1.584166	0.795994
lincRNA	-	2	0	0	31	31	33	0.084301	0	0	1.130387	1.467957	1.382376
processed_	-	0	0	0	0	0	2	0	0	0	0	0	0.158238
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.431263
lincRNA	-	1	0	2	0	4	0	0.106307	0	0.280174	0	0.477718	0
processed_	-	0	0	0	0	0	1	0	0	0	0	0	0.091028
pseudogen	-	0	0	0	1	0	0	0	0	0	0.050888	0	0
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.0888
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.08583
antisense	ZNF205_an	7	6	6	3	2	6	0.304009	0.307077	0.34338	0.112713	0.097581	0.25897
pseudogen	receptor-lil	1	2	6	2	3	7	0.030461	0.071793	0.24084	0.052703	0.102663	0.211909
antisense	-	3	1	3	1	2	6	0.310201	0.121851	0.408769	0.089451	0.232328	0.616571
pseudogen	ATP_synth	0	6	0	0	0	0	0	0.248392	0	0	0	0
sense_over	-	0	4	3	12	10	3	0	0.233662	0.195964	0.514594	0.556891	0.147792
sense_intrc	-	1228	1037	978	956	819	888	10.94286	10.88976	11.48434	7.369762	8.199087	7.864211
processed_	-	0	0	0	1	1	1	0	0	0	0.078964	0.102545	0.090714
protein_co	Protein_LO	7	4	3	2	6	6	0.237861	0.160174	0.134332	0.058792	0.229047	0.202622
antisense	-	58	86	55	207	137	143	1.584405	2.768496	1.979866	4.891834	4.204438	3.882254
sense_over	-	2	0	1	2	8	1	0.035037	0	0.023085	0.03031	0.157448	0.01741
antisense	-	0	0	0	3	1	1	0	0	0	0.284465	0.123139	0.108932
lincRNA	-	1	0	1	3	1	3	0.079372	0	0.104593	0.205992	0.089169	0.236645
antisense	-	4	4	0	0	1	3	0.395821	0.46645	0	0	0.11117	0.295032
antisense	-	0	3	3	0	3	0	0	0.391555	0.437845	0	0.37328	0
antisense	-	6	1	5	6	9	3	0.565206	0.11101	0.62067	0.488956	0.952461	0.280858
pseudogen	-	0	0	1	0	0	0	0	0	0.17311	0	0	0
antisense	-	0	1	3	0	0	0	0	0.115747	0.388293	0	0	0
antisense	-	12	7	9	1	4	9	0.534308	0.367295	0.528065	0.038519	0.200087	0.398256
lincRNA	-	1	0	0	10	3	2	0.158982	0	0	1.375343	0.535819	0.316
pseudogen	-	4	1	3	2	3	2	0.31326	0.09229	0.3096	0.1355	0.263946	0.155663
antisense	TAPT1_anti	10	27	15	18	11	38	0.244531	0.778046	0.483348	0.380776	0.302187	0.92348
antisense	-	2	3	7	8	10	5	0.126653	0.223879	0.584142	0.438267	0.711434	0.314677
sense_intrc	-	0	0	0	2	0	5	0	0	0	0.163568	0	0.469768
antisense	-	25	15	26	33	8	20	1.56445	1.106165	2.144025	1.786482	0.56242	1.243831
lincRNA	-	10	4	7	18	18	41	0.710617	0.334968	0.655494	1.106551	1.437002	2.895538
pseudogen	-	1	1	0	1	0	2	0.063175	0.074448	0	0.054653	0	0.125571
antisense	-	0	2	2	0	2	4	0	0.462131	0.516765	0	0.440562	0.779467

antisense	-	2	2	0	0	0	0	0.619193	0.729681	0	0	0	0
antisense	-	1	3	4	7	4	3	0.095734	0.338451	0.504617	0.579733	0.430206	0.285429
antisense	-	4	14	6	0	5	3	0.24174	0.997064	0.477831	0	0.339474	0.180185
processed_	-	17	15	14	40	20	18	0.309277	0.321586	0.335631	0.629538	0.408769	0.325448
lincRNA	-	0	0	0	0	1	3	0	0	0	0	0.118714	0.315054
antisense	-	13	16	3	12	9	17	1.574904	2.284219	0.478924	1.257636	1.224904	2.046771
lincRNA	-	2	0	2	11	10	23	0.159461	0	0.21013	0.758717	0.895722	1.822475
antisense	-	7	3	2	2	1	6	0.414991	0.209589	0.156245	0.102573	0.066602	0.35351
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.305005	0
antisense	-	1	1	3	2	2	7	0.037494	0.044184	0.148222	0.064871	0.084244	0.260835
lincRNA	-	3	0	0	4	1	0	0.324791	0	0	0.374633	0.121628	0
antisense	-	5	4	5	0	0	1	0.471005	0.444041	0.62067	0	0	0.093619
antisense	-	0	1	4	2	7	7	0	0.075075	0.335804	0.110226	0.501001	0.443199
pseudogen	adenylate_	2	4	2	6	2	4	0.158744	0.374139	0.209185	0.411984	0.178339	0.315527
lincRNA	-	0	0	0	1	3	1	0	0	0	0.059019	0.229933	0.067802
protein_co	ubiquitin_E	2	0	0	3	2	1	0.072572	0	0	0.094172	0.08153	0.036062
lincRNA	-	22	20	20	5	10	18	1.476175	1.581438	1.768398	0.290234	0.753814	1.200321
pseudogen	-	4	0	0	1	1	3	0.167535	0	0	0.036233	0.047054	0.124875
antisense	-	1	1	8	0	5	4	0.043006	0.050681	0.453376	0	0.241576	0.170964
lincRNA	-	3	0	4	2	3	0	0.419058	0	0.736288	0.241683	0.470786	0
antisense	-	0	0	1	4	0	0	0	0	0.118043	0.309976	0	0
pseudogen	-	0	0	3	0	0	3	0	0	0.617374	0	0	0.465611
lincRNA	-	0	2	4	0	0	0	0	0.253094	0.566031	0	0	0
antisense	-	0	2	5	5	7	9	0	0.216624	0.605584	0.39756	0.722798	0.822095
sense_intrc	-	0	0	0	2	0	0	0	0	0	0.678502	0	0
processed_	-	0	0	1	0	1	1	0	0	0.109691	0	0.093516	0.082726
lincRNA	-	0	2	2	0	0	0	0	0.292214	0.32676	0	0	0
antisense	-	2	0	0	0	0	0	0.101908	0	0	0	0	0
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.404723
antisense	-	0	0	0	4	2	2	0	0	0	0.567169	0.368272	0.325784
protein_co	Protein_LO	2	0	0	0	0	0	0.029346	0	0	0	0	0
sense_intrc	-	0	0	0	0	3	3	0	0	0	0	0.424828	0.375815
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.140491
sense_intrc	-	0	0	0	0	1	0	0	0	0	0	0.075096	0
antisense	DLGAP1_ar	0	0	0	0	4	4	0	0	0	0	0.189113	0.167294
sense_intrc	-	6	0	3	1	4	8	1.185246	0	0.780932	0.170891	0.8877	1.570569
lincRNA	-	42	24	18	119	109	91	0.829054	0.558279	0.46821	2.032092	2.417179	1.78519
lincRNA	-	6	0	0	6	0	0	0.407761	0	0	0.352752	0	0
lincRNA	long_interg	215	220	175	287	215	268	2.860597	3.449435	3.068252	3.303414	3.213702	3.543746
antisense	-	0	0	1	0	2	0	0	0	0.108328	0	0.184708	0
antisense	-	3	6	0	4	3	3	0.216675	0.510677	0	0.249926	0.243421	0.215337
sense_intrc	-	22	28	26	58	70	93	1.62441	2.436341	2.52977	3.704793	5.806575	6.824417
antisense	-	0	2	0	2	0	0	0	0.229367	0	0.168378	0	0
protein_co	KRAB-A_do	4	2	5	3	2	4	0.068599	0.04042	0.112995	0.044508	0.038533	0.068175

protein_co	Uncharacte	7	7	4	0	0	0	0.165293	0.194788	0.124466	0	0	0
pseudogen	-	2	3	5	0	0	1	0.045936	0.081199	0.15133	0	0	0.022826
antisense	-	3	1	1	13	20	12	0.100394	0.039436	0.044098	0.37635	0.751908	0.399095
antisense	-	9	13	9	5	15	10	0.198529	0.337934	0.261612	0.095414	0.371724	0.219225
antisense	-	8	3	2	30	19	27	0.167601	0.074065	0.055214	0.543715	0.447187	0.56216
pseudogen	cytokine_ir	0	0	0	0	1	0	0	0	0	0	0.063884	0
antisense	-	12	7	6	9	17	18	1.167816	0.802783	0.769448	0.757702	1.858622	1.740906
lincRNA	long_interg	33	28	17	17	15	21	0.738712	0.738629	0.50147	0.32921	0.377226	0.467186
antisense	DLGAP1_ar	0	0	0	0	9	3	0	0	0	0	0.707111	0.20851
pseudogen	-	0	2	0	0	1	0	0	0.243227	0	0	0.115937	0
lincRNA	-	10	2	0	16	9	5	0.248433	0.058553	0	0.343868	0.251189	0.123449
sense_intrc	-	2	1	0	0	0	0	0.318922	0.187915	0	0	0	0
lincRNA	-	81	63	63	111	77	73	1.591767	1.458956	1.631435	1.887037	1.699943	1.425696
sense_intrc	-	12	10	6	17	10	9	1.315304	1.291671	0.866625	1.61197	1.231385	0.980386
processed_	-	0	0	1	1	0	1	0	0	0.11216	0.073632	0	0.084589
antisense	-	6	1	7	3	0	5	0.912776	0.179275	1.403284	0.394818	0	0.755949
lincRNA	-	4	5	7	0	8	2	0.425229	0.626383	0.980608	0	0.955436	0.211301
lincRNA	-	1	2	8	5	1	14	0.075738	0.178506	0.798435	0.327603	0.085087	1.053786
antisense	-	0	0	2	0	2	0	0	0	0.275744	0	0.235083	0
lincRNA	-	0	2	5	22	22	45	0	0.273032	0.763274	2.204761	2.863173	5.180815
antisense	-	2	1	2	0	0	5	0.188067	0.110813	0.247827	0	0	0.467265
antisense	-	11	4	7	0	0	2	1.463193	0.627012	1.226992	0	0	0.264392
lincRNA	-	11	8	10	6	6	14	1.193342	1.02275	1.429575	0.563101	0.731261	1.509419
antisense	-	0	0	0	0	1	4	0	0	0	0	0.13043	0.461527
sense_intrc	-	0	2	0	1	2	0	0	0.195573	0	0.071785	0.186445	0
antisense	-	0	0	0	3	1	0	0	0	0	0.382721	0.165671	0
lincRNA	-	0	0	0	15	3	10	0	0	0	1.222391	0.317487	0.936193
lincRNA	-	5	0	0	2	0	0	0.396859	0	0	0.137328	0	0
lincRNA	-	24	17	13	45	29	34	0.570536	0.476242	0.40724	0.925438	0.774496	0.803268
processed_	-	0	0	0	0	1	0	0	0	0	0	0.045194	0
pseudogen	-	1	3	2	1	5	2	0.088382	0.312459	0.232932	0.076459	0.49646	0.175673
protein_co	-	25	9	13	24	25	15	0.528987	0.224416	0.362479	0.439318	0.594284	0.315432
lincRNA	microRNA_	0	0	1	0	0	0	0	0	0.077948	0	0	0
pseudogen	dead_end_l	0	4	3	20	2	3	0	0.235648	0.19763	0.864946	0.112325	0.149048
antisense	-	0	0	0	2	0	0	0	0	0	0.190829	0	0
lincRNA	-	0	0	1	0	0	0	0	0	0.123913	0	0	0
antisense	-	25	26	11	28	25	26	0.682229	0.836124	0.395565	0.661015	0.766442	0.705137
antisense	-	13	3	0	11	20	13	1.398847	0.380413	0	1.023959	2.41772	1.390209
lincRNA	-	598	537	431	457	487	482	6.704514	7.09492	6.367635	4.432465	6.134005	5.3706
protein_co	HCG19963	0	6	2	0	0	0	0	0.69837	0.260311	0	0	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.252346
pseudogen	-	2	2	0	1	4	3	0.637843	0.751659	0	0.275897	1.433155	0.950856
lincRNA	-	0	1	0	0	1	0	0	0.149611	0	0	0.142628	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.277277	0

lincRNA	-	0	0	0	1	0	0	0	0	0	0.033875	0	0
pseudogen	-	0	1	0	0	0	0	0	0.144751	0	0	0	0
pseudogen	mago-nashi	8	9	5	5	1	0	0.971394	1.28782	0.800038	0.525217	0.136413	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.010618
pseudogen	-	0	0	0	2	0	0	0	0	0	0.214515	0	0
protein_co	Uncharacte	0	1	2	0	0	1	0	0.03685	0.082414	0	0	0.031077
sense_intrc	-	0	0	2	4	0	4	0	0	0.415258	0.545225	0	0.626358
antisense	-	0	1	0	0	7	1	0	0.043115	0	0	0.28772	0.036361
antisense	-	0	0	3	4	6	0	0	0	0.3354	0.293583	0.571884	0
lincRNA	-	0	0	0	0	4	0	0	0	0	0	0.420325	0
antisense	-	0	0	1	0	0	5	0	0	0.549317	0	0	2.071419
antisense	-	4	0	0	9	5	1	0.204603	0	0	0.398251	0.287323	0.050835
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.285942	0
lincRNA	-	163	131	120	229	168	213	2.49188	2.360033	2.41744	3.028573	2.885346	3.236152
lincRNA	-	0	1	0	0	0	0	0	0.124775	0	0	0	0
antisense	-	1	2	2	0	0	0	0.080335	0.189341	0.211725	0	0	0
antisense	-	11	11	4	3	11	1	1.028889	1.212482	0.493027	0.24275	1.155892	0.092958
antisense	-	0	1	0	0	0	2	0	0.121614	0	0	0	0.205123
antisense	-	1	1	0	0	1	2	0.114343	0.134747	0	0	0.128458	0.227275
protein_co	Uncharacte	25	39	12	65	62	75	1.022027	1.878858	0.646455	2.298787	2.847496	3.047146
pseudogen	-	38	19	19	28	15	19	5.041999	2.970844	3.322061	3.213958	2.235937	2.505431
sense_intrc	-	1	4	2	0	3	6	0.113852	0.536669	0.300057	0	0.383716	0.678891
pseudogen	-	2	3	0	0	0	0	0.237937	0.420591	0	0	0	0
lincRNA	-	0	0	0	4	0	0	0	0	0	0.239785	0	0
antisense	-	4	3	8	0	10	12	0.376804	0.333031	0.993072	0	1.05829	1.123432
protein_co	Uncharacte	0	0	3	3	2	0	0	0	0.04137	0.027159	0.023513	0
lincRNA	-	9	19	8	0	0	0	0.978376	2.434018	1.146009	0	0	0
pseudogen	small_nucl	0	2	0	5	4	5	0	0.552104	0	1.01325	1.052671	1.164028
lincRNA	-	246	245	269	414	458	412	3.264849	3.831786	4.704518	4.753258	6.828772	5.434191
antisense	-	1	3	2	9	6	15	0.09337	0.330094	0.246079	0.726967	0.629375	1.391906
antisense	-	0	0	1	3	2	6	0	0	0.183588	0.36157	0.313031	0.830748
lincRNA	-	207	194	176	43	21	57	22.27395	24.60004	24.95597	4.00275	2.538606	6.09553
antisense	-	0	1	1	3	2	0	0	0.134456	0.150352	0.296114	0.256362	0
lincRNA	-	10	22	14	231	170	140	0.366374	0.949848	0.675907	7.321486	6.997167	5.097555
antisense	-	3	2	6	5	1	0	0.256166	0.201251	0.675129	0.369346	0.095929	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.075056
sense_intrc	-	9	23	12	26	25	31	0.286857	0.863888	0.504009	0.7169	0.895182	0.98196
antisense	-	0	0	2	0	1	0	0	0	0.374066	0	0.159453	0
lincRNA	-	43	31	28	83	42	30	1.772946	1.506246	1.521318	2.960521	1.945474	1.2293
protein_co	Uncharacte	3	0	4	0	0	0	0.28412	0	0.499201	0	0	0
antisense	-	3	0	1	7	0	10	0.345267	0	0.151659	0.69694	0	1.143784
antisense	-	9	3	4	2	6	0	0.996797	0.391555	0.583793	0.191627	0.74656	0
lincRNA	-	414	401	291	103	62	70	39.99557	45.65233	37.04583	8.608188	6.729027	6.720773
processed_	-	0	0	0	0	2	1	0	0	0	0	0.04607	0.020377

lincRNA	-	12	4	6	7	6	5	1.726337	0.678127	1.137445	0.871175	0.969716	0.714865
antisense	-	0	0	0	0	1	1	0	0	0	0	0.023088	0.020425
pseudogen	-	2	3	7	3	2	4	0.162396	0.28706	0.748992	0.210731	0.182441	0.322786
pseudogen	-	231	215	170	392	258	375	7.839339	8.598309	7.602409	11.50844	9.836402	12.64761
sense_intrc	-	2	5	9	4	5	5	0.062028	0.182741	0.36782	0.10732	0.174212	0.154113
antisense	-	7	4	9	20	11	3	0.156498	0.105385	0.265148	0.386815	0.276282	0.066656
antisense	-	1	7	1	0	0	0	0.07467	0.615958	0.098397	0	0	0
lincRNA	long_interg	23	15	6	22	10	16	0.64941	0.499102	0.223243	0.537374	0.317205	0.448973
antisense	-	68	46	63	141	120	203	4.004436	3.192253	4.888862	7.183143	7.938943	11.88059
sense_intrc	-	4	1	1	0	0	0	0.131286	0.038678	0.043251	0	0	0
sense_intrc	-	7	1	4	49	23	32	0.809142	0.136218	0.609286	4.899883	2.986782	3.676091
antisense	-	0	2	1	0	7	2	0	0.059051	0.033016	0	0.197033	0.0498
sense_intrc	-	4	2	2	1	4	5	0.13194	0.077742	0.086932	0.028535	0.148227	0.163907
antisense	-	0	0	0	2	1	3	0	0	0	0.329489	0.213942	0.567778
pseudogen	-	1	0	3	5	3	2	0.108708	0	0.429753	0.470215	0.366381	0.216074
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.031505
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.089979	0
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.229255
lincRNA	-	1	0	2	0	0	0	0.025526	0	0.067274	0	0	0
pseudogen	-	1	2	0	1	2	0	0.027747	0.065396	0	0.024004	0.062344	0
lincRNA	-	0	0	0	13	7	3	0	0	0	0.22838	0.159698	0.060546
pseudogen	divergent-p	0	0	6	2	3	0	0	0	0.736936	0.161264	0.314133	0
antisense	-	3	4	1	0	0	8	0.194398	0.305448	0.08539	0	0	0.515193
antisense	-	0	0	0	0	6	0	0	0	0	0	2.062749	0
antisense	-	13	6	9	1	16	9	1.222439	0.664878	1.115221	0.081348	1.690257	0.841077
processed_	-	0	2	1	4	3	1	0	0.027399	0.015319	0.040227	0.03918	0.011553
pseudogen	peptidylpr	0	0	0	3	3	5	0	0	0	0.27701	0.359733	0.530384
pseudogen	-	1	0	0	0	0	0	0.03274	0	0	0	0	0
antisense	microRNA_	0	0	6	14	4	2	0	0	0.549317	0.84145	0.31221	0.138095
sense_intrc	-	1	0	3	0	3	1	0.077854	0	0.307779	0	0.262394	0.077374
antisense	-	7	8	4	1	4	1	1.052804	1.417903	0.792765	0.130111	0.675863	0.149472
pseudogen	-	1	0	0	0	0	0	0.152568	0	0	0	0	0
sense_intrc	-	0	0	1	0	4	5	0	0	0.025005	0	0.08527	0.09429
antisense	-	10	0	4	2	11	9	0.261566	0	0.137872	0.045256	0.323239	0.233956
processed_	-	2	1	0	3	1	0	0.180071	0.106102	0	0.233668	0.10115	0
lincRNA	-	4	4	0	0	0	0	0.074069	0.087286	0	0	0	0
lincRNA	-	5	0	0	0	0	0	0.285242	0	0	0	0	0
sense_intrc	-	144	142	127	171	156	119	4.159031	4.833092	4.833572	4.272566	5.06178	3.415751
sense_intrc	-	8	5	4	7	12	8	0.195174	0.143751	0.128596	0.147738	0.328899	0.193969
antisense	-	3	5	10	6	1	3	0.474098	0.93116	2.082486	0.820279	0.17754	0.471171
processed_	-	79	64	42	31	37	88	1.061777	1.013662	0.743858	0.360438	0.558672	1.175434
antisense	-	8	2	0	1	2	1	0.835361	0.246105	0	0.090333	0.234619	0.103775
antisense	-	2	5	2	1	0	4	0.188067	0.554065	0.247827	0.081348	0	0.373812
antisense	-	13	11	2	9	1	8	2.867637	2.859438	0.581361	1.717459	0.247816	1.753802

lincRNA	-	0	0	1	0	0	0	0	0	0.120074	0	0	0
pseudogen	SH3-domai	11	15	4	12	5	9	0.538217	0.864895	0.257905	0.507936	0.274843	0.43764
pseudogen	arachidona	2	0	0	0	0	0	0.086153	0	0	0	0	0
lincRNA	-	20	32	16	21	20	26	2.272146	4.284136	2.395306	2.063899	2.552614	2.935548
lincRNA	-	0	0	1	1	3	3	0	0	0.110385	0.072467	0.282322	0.24975
pseudogen	-	0	2	0	0	0	0	0	0.296379	0	0	0	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.077041	0
antisense	-	0	1	4	0	3	0	0	0.131898	0.589964	0	0.377226	0
sense_intrc	-	4	3	6	7	4	5	0.659701	0.583063	1.303987	0.99873	0.741133	0.819533
lincRNA	-	0	1	0	0	5	4	0	0.095981	0	0	0.457507	0.323779
antisense	-	0	2	0	0	0	0	0	0.054368	0	0	0	0
lincRNA	-	0	1	0	0	0	0	0	0.063856	0	0	0	0
sense_intrc	-	0	0	0	0	0	1	0	0	0	0	0	0.187239
pseudogen	ferritin_ligl	0	0	0	4	5	4	0	0	0	0.408008	0.662315	0.468722
antisense	-	4	2	4	1	0	6	0.161652	0.095248	0.213018	0.034961	0	0.24098
protein_co	-	0	3	0	2	0	0	0	0.185678	0	0.090871	0	0
lincRNA	-	0	0	0	3	0	0	0	0	0	0.230145	0	0
antisense	-	1	1	0	0	1	1	0.10546	0.124278	0	0	0.118478	0.104809
antisense	-	0	0	0	0	1	8	0	0	0	0	0.104161	0.73715
pseudogen	-	5	10	9	4	4	4	0.580493	1.368152	1.376907	0.401745	0.521719	0.461527
lincRNA	-	11	8	2	15	14	11	2.148896	1.841704	0.514858	2.534995	3.072557	2.135626
antisense	hsa-mir-13	7	1	4	0	2	4	0.087692	0.014763	0.066032	0	0.028148	0.0498
antisense	BZRAP1_an	0	0	0	8	13	15	0	0	0	0.156778	0.330846	0.337703
lincRNA	-	0	3	0	0	0	0	0	0.400778	0	0	0	0
sense_intrc	-	0	0	0	32	37	35	0	0	0	2.227302	3.34439	2.79862
processed_	-	0	0	0	5	0	1	0	0	0	0.064981	0	0.01493
lincRNA	-	0	1	3	7	7	7	0	0.107012	0.358988	0.549901	0.714119	0.63173
antisense	-	7	14	24	51	46	39	0.122833	0.289502	0.554961	0.774194	0.906825	0.680129
antisense	-	1	5	5	1	4	0	0.093867	0.553083	0.618469	0.081204	0.421815	0
antisense	-	13	2	8	4	8	8	1.379224	0.250051	1.118449	0.367125	0.953522	0.843512
antisense	-	3	14	1	6	3	3	0.2517	1.384197	0.11056	0.435489	0.28277	0.250146
sense_intrc	-	0	0	1	3	5	1	0	0	0.075257	0.148217	0.320798	0.056757
lincRNA	-	42	31	22	90	60	72	1.336251	1.162271	0.922351	2.477104	2.144564	2.276569
lincRNA	-	0	0	0	3	10	6	0	0	0	0.223773	0.968663	0.514144
pseudogen	-	2	1	3	0	3	7	0.038545	0.022711	0.076189	0	0.064954	0.134073
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.293933
pseudogen	phosphogl	0	1	0	0	1	0	0	0.043295	0	0	0.041274	0
lincRNA	-	1	0	2	0	1	0	0.095908	0	0.252766	0	0.107746	0
pseudogen	arginine-fif	9	7	6	5	2	15	0.502075	0.460183	0.441074	0.241301	0.125344	0.831624
pseudogen	-	9	13	10	9	4	25	0.534158	0.909238	0.7821	0.462097	0.266708	1.474609
antisense	-	2	2	0	1	5	0	0.153009	0.180311	0	0.066183	0.429739	0
antisense	-	1	0	0	0	0	0	0.091593	0	0	0	0	0
antisense	-	4	1	0	0	2	2	0.331918	0.097786	0	0	0.186445	0.164934
antisense	-	1	0	0	3	0	3	0.142314	0	0	0.369346	0	0.424307

antisense	-	1	0	1	1	2	0	0.137509	0	0.181203	0.118958	0.308966	0
processed_	-	38	8	8	10	15	20	1.135945	0.281819	0.315136	0.258605	0.503749	0.594173
lincRNA	-	0	0	0	0	3	1	0	0	0	0	0.248507	0.073279
sense_intrc	-	1	7	9	2	4	4	0.022869	0.188645	0.271218	0.039567	0.102766	0.09091
antisense	-	41	37	46	250	162	150	6.761934	7.191109	9.99723	35.66893	30.01588	24.586
lincRNA	-	26	8	7	7	0	10	2.992317	1.085004	1.061615	0.69694	0	1.143784
antisense	-	0	5	3	0	0	2	0	0.836297	0.561099	0	0	0.282113
antisense	-	0	4	1	0	2	1	0	0.36591	0.102292	0	0.174416	0.077147
antisense	-	9	7	5	11	13	7	1.334647	1.223289	0.977077	1.411171	2.16579	1.031648
pseudogen	-	0	1	0	0	0	0	0	0.063987	0	0	0	0
antisense	-	4	10	2	9	19	15	0.406457	1.197461	0.267805	0.791152	2.168987	1.5148
sense_intrc	-	7	12	12	0	0	3	0.816271	1.649015	1.843963	0	0	0.34767
lincRNA	-	11	2	4	1	0	3	0.591219	0.126676	0.283303	0.046496	0	0.160246
antisense	-	7	9	3	2	2	4	1.13677	1.722361	0.641993	0.280975	0.364883	0.645571
lincRNA	-	0	1	0	0	5	2	0	0.031477	0	0	0.15004	0.053092
antisense	hsa-mir-15	1	0	3	9	0	3	0.090964	0	0.359605	0.70823	0	0.271206
processed_	-	2	0	5	0	8	11	0.03008	0	0.099096	0	0.135173	0.164419
antisense	-	2	6	6	17	4	6	0.133185	0.470851	0.526515	0.979348	0.29925	0.397087
lincRNA	-	1	0	0	0	0	1	0.152568	0	0	0	0	0.151626
lincRNA	-	1	1	1	3	1	0	0.104834	0.12354	0.138145	0.272073	0.117774	0
lincRNA	-	1	2	0	0	0	0	0.079851	0.188198	0	0	0	0
lincRNA	-	3	5	3	0	0	0	0.385493	0.757133	0.507985	0	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.197594	0
sense_intrc	-	73	49	37	171	131	96	1.751901	1.385766	1.1701	3.550142	3.531888	2.289641
protein_co	Uncharacte	0	1	0	0	0	0	0	0.067156	0	0	0	0
sense_intrc	-	0	0	0	3	3	6	0	0	0	0.130605	0.169608	0.30008
antisense	-	0	0	2	0	1	1	0	0	0.322978	0	0.137676	0.121792
antisense	-	1	4	2	3	2	2	0.118436	0.558279	0.31214	0.307375	0.266111	0.23541
antisense	-	18	14	5	1	3	8	0.532368	0.487949	0.19487	0.025586	0.09968	0.235147
antisense	-	7	2	7	10	14	9	0.667724	0.224821	0.879897	0.825206	1.500293	0.853201
protein_co	ribosomal_	42	33	22	95	77	89	2.432737	2.252511	1.679204	4.76028	5.010553	5.12325
pseudogen	-	1	0	0	14	5	13	0.072821	0	0	0.88196	0.40905	0.940829
antisense	MAFG_anti	130	69	71	110	94	72	3.631836	2.271638	2.613822	2.658512	2.950257	1.999056
lincRNA	-	1	0	0	4	3	3	0.029249	0	0	0.101213	0.098579	0.087206
antisense	-	0	2	2	1	1	5	0	0.039674	0.044365	0.014562	0.018911	0.083647
pseudogen	-	0	7	5	5	5	3	0	0.457292	0.365253	0.239785	0.311392	0.16528
lincRNA	-	1	0	0	0	0	0	0.08853	0	0	0	0	0
lincRNA	-	1	3	1	2	8	9	0.061919	0.218904	0.081594	0.107132	0.5565	0.553832
antisense	-	3	5	1	0	5	4	0.290885	0.571316	0.127772	0	0.544651	0.385451
processed_	-	18	40	18	18	41	43	1.645834	4.310033	2.168807	1.4238	4.211593	3.907434
lincRNA	-	17	2	8	17	8	19	1.224486	0.169763	0.759328	1.059294	0.647357	1.360091
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.154975
antisense	-	28	16	20	16	17	4	1.823306	1.227803	1.716194	0.901331	1.243654	0.258864
antisense	-	0	0	0	3	0	0	0	0	0	0.087962	0	0

lincRNA	cytochrom	0	0	0	13	8	14	0	0	0	0.207019	0.165441	0.256118
pseudogen	ribonuclea	0	0	0	4	5	10	0	0	0	0.246894	0.400781	0.709084
sense_intrc	-	10	9	18	31	24	16	1.718863	1.823018	4.077075	4.60963	4.634487	2.733197
pseudogen	-	5	0	0	1	4	1	0.134573	0	0	0.023284	0.120947	0.026748
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.075862	0
sense_intrc	-	41	35	18	50	41	69	5.426452	5.458926	3.139348	5.724863	6.096282	9.075924
sense_intrc	-	2	10	1	0	1	3	0.246237	1.450877	0.16224	0	0.138316	0.367075
protein_co	fibrinogen_	2	4	1	1	7	2	0.042833	0.100951	0.028221	0.018527	0.168419	0.042568
antisense	-	3	5	2	0	2	2	0.232537	0.456718	0.204285	0	0.174161	0.154067
antisense	-	3	0	0	0	2	0	0.287202	0	0	0	0.215103	0
antisense	-	0	0	0	0	0	4	0	0	0	0	0	0.312714
antisense	-	2	5	0	9	4	12	0.176765	0.520766	0	0.68813	0.397168	1.054038
processed_	-	0	4	0	6	5	0	0	0.100869	0	0.111073	0.120202	0
pseudogen	-	0	1	0	4	5	6	0	0.098403	0	0.288952	0.469053	0.497925
lincRNA	long_interg	1	0	3	0	2	5	0.022595	0	0.089326	0	0.050769	0.112279
pseudogen	ubiquitin-c	0	1	4	4	6	2	0	0.122329	0.547163	0.359207	0.699717	0.20633
antisense	-	0	0	1	9	0	0	0	0	0.122392	0.723141	0	0
protein_co	uncharacte	0	0	0	13	24	12	0	0	0	0.987373	2.367201	1.047046
sense_intrc	-	0	0	0	0	4	3	0	0	0	0	0.659013	0.437236
antisense	-	7	14	4	12	6	7	0.45304	1.067761	0.341141	0.671867	0.436254	0.450242
lincRNA	-	1	0	0	0	0	2	0.14913	0	0	0	0	0.296417
lincRNA	-	0	2	0	0	0	0	0	0.264916	0	0	0	0
pseudogen	-	2	2	3	48	16	22	1.102937	1.299744	2.180103	22.89945	9.912653	12.05739
processed_	-	0	0	0	7	3	5	0	0	0	0.749048	0.416887	0.61465
sense_intrc	embryonic_	0	0	0	39	31	45	0	0	0	0.56884	0.587183	0.754023
lincRNA	-	2	0	1	2	0	3	0.059218	0	0.039017	0.051229	0	0.088279
antisense	microRNA_	1	0	0	0	0	0	0.093701	0	0	0	0	0
antisense	-	5	4	3	4	12	8	0.54466	0.513479	0.430638	0.376946	1.468541	0.866075
lincRNA	-	0	0	0	27	29	20	0	0	0	0.583288	0.813586	0.496359
processed_	-	1	2	1	0	0	0	0.076726	0.180834	0.101106	0	0	0
antisense	-	21	20	4	19	25	14	1.443845	1.620461	0.362407	1.130103	1.931036	0.956619
pseudogen	polymerase	0	0	2	3	0	3	0	0	0.038039	0.037458	0	0.043032
protein_co	-	6	6	0	0	0	0	0.196563	0.231638	0	0	0	0
lincRNA	-	1	4	3	6	1	0	0.05221	0.246105	0.2064	0.270999	0.058655	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.105641	0
lincRNA	-	0	4	0	0	0	0	0	0.52871	0	0	0	0
lincRNA	-	0	0	0	2	4	2	0	0	0	0.221251	0.574647	0.254174
antisense	-	2	2	1	3	0	0	0.472687	0.557033	0.311443	0.613378	0	0
sense_intrc	-	1	2	4	6	0	5	0.144648	0.340917	0.76244	0.750802	0	0.718771
pseudogen	-	0	0	1	0	1	0	0	0	0.059831	0	0.051009	0
antisense	-	2	3	0	0	1	1	0.171886	0.303836	0	0	0.096552	0.085412
pseudogen	-	3	0	0	0	0	0	0.622835	0	0	0	0	0
antisense	-	5	7	4	1	11	7	0.154437	0.254792	0.162808	0.02672	0.381701	0.214877
protein_co	STE20-relat	53	59	36	43	41	32	0.761431	0.998881	0.681541	0.534424	0.66174	0.456893

lincRNA	-	0	0	0	0	1	10	0	0	0	0	0.143662	1.270871
protein_co	Uncharacte	32	21	13	146	94	151	0.809031	0.625665	0.433105	3.193238	2.669884	3.794041
sense_intrc	NARF_intrc	5	14	7	0	7	4	0.34422	1.135797	0.635036	0	0.541393	0.273675
sense_intrc	-	0	0	2	0	0	0	0	0	0.166301	0	0	0
antisense	-	0	0	0	1	1	0	0	0	0	0.084344	0.109532	0
lincRNA	long_interg	2	0	0	1	0	0	0.030166	0	0	0.013048	0	0
protein_co	Uncharacte	5	4	3	3	3	8	0.324791	0.306197	0.256797	0.168585	0.21893	0.516457
antisense	-	0	2	1	3	0	7	0	0.218521	0.122177	0.240625	0	0.645006
lincRNA	-	0	0	0	1	0	0	0	0	0	0.081638	0	0
lincRNA	-	0	0	0	0	0	3	0	0	0	0	0	0.059857
pseudogen	ubiquitin-li	1	1	0	2	0	0	0.24174	0.284875	0	0.418255	0	0
lincRNA	-	3	0	0	2	1	5	0.34303	0	0	0.197835	0.128458	0.568186
lincRNA	-	11	10	5	6	0	0	0.749486	0.802931	0.448927	0.35366	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.009729	0
sense_intrc	hsa-mir-74	0	0	0	2	0	1	0	0	0	0.934672	0	0.536878
lincRNA	-	1	3	0	0	0	1	0.137867	0.487404	0	0	0	0.137016
lincRNA	-	0	0	0	4	0	1	0	0	0	0.403515	0	0.11589
lincRNA	-	0	1	2	0	0	1	0	0.087378	0.195415	0	0	0.073689
antisense	-	3	6	3	6	3	0	0.237759	0.560369	0.313308	0.411367	0.267107	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.070553	0
antisense	-	0	0	2	0	0	0	0	0	0.301353	0	0	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.038348
sense_intrc	-	3	4	7	11	6	4	0.057131	0.089767	0.175663	0.181219	0.128365	0.075704
lincRNA	-	23	32	16	5	2	6	0.568992	0.932901	0.521595	0.107007	0.055585	0.147516
lincRNA	-	3	5	7	0	0	0	0.287723	0.565106	0.884679	0	0	0
lincRNA	-	0	0	0	0	3	0	0	0	0	0	0.44385	0
antisense	-	2	0	2	0	2	1	0.186412	0	0.245645	0	0.209422	0.09263
antisense	-	0	0	0	5	7	5	0	0	0	0.157385	0.286138	0.180804
lincRNA	-	11	34	15	18	33	90	2.094788	7.630154	3.764206	2.965397	7.060091	17.03333
pseudogen	chromobo	13	10	10	8	4	10	0.481619	0.436583	0.488197	0.256397	0.166483	0.368188
lincRNA	-	0	0	4	0	0	9	0	0	0.305979	0	0	0.519218
antisense	-	0	5	0	0	2	0	0	0.635313	0	0	0.242264	0
antisense	-	3	11	2	5	3	13	0.189526	0.818932	0.166499	0.273263	0.212921	0.816208
sense_intrc	-	7	1	3	0	2	1	0.851924	0.14342	0.481126	0	0.273452	0.120952
antisense	-	5	13	6	34	17	16	0.125691	0.385109	0.198756	0.739394	0.4801	0.399727
antisense	-	2	0	4	0	0	0	0.109722	0	0.289174	0	0	0
antisense	-	203	177	173	372	233	273	12.49654	12.84027	14.03378	19.81069	16.11382	16.7019
antisense	-	32	11	11	7	11	1	2.458798	0.996031	1.113782	0.465301	0.949543	0.076363
lincRNA	-	22	8	7	32	6	17	2.521	1.080307	1.057019	3.172219	0.772415	1.936015
lincRNA	-	8	1	4	5	2	2	0.617388	0.090944	0.406783	0.333811	0.173399	0.153394
pseudogen	-	1	1	0	0	3	0	0.126351	0.148897	0	0	0.425842	0
lincRNA	-	0	1	0	0	0	0	0	0.035049	0	0	0	0
sense_intrc	-	0	0	0	0	1	3	0	0	0	0	0.106779	0.283379
antisense	-	0	0	0	1	0	0	0	0	0	0.020211	0	0

pseudogen	-	2	0	0	7	0	0	0.132684	0	0	0.401745	0	0
lincRNA	-	16	29	21	12	11	16	2.672101	5.707395	4.621542	1.733713	2.063833	2.655599
antisense	-	6	0	3	6	4	5	0.594843	0	0.391929	0.514594	0.445512	0.492641
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.028379
lincRNA	-	3	2	3	1	0	1	0.268282	0.210769	0.35353	0.077363	0	0.088875
lincRNA	-	0	0	0	3	2	1	0	0	0	0.159024	0.137676	0.060896
lincRNA	-	0	0	1	0	0	0	0	0	0.202212	0	0	0
lincRNA	-	0	0	0	1	0	0	0	0	0	0.072011	0	0
processed_	-	0	0	0	2	2	2	0	0	0	0.170573	0.221512	0.195955
antisense	-	0	0	1	0	3	6	0	0	0.170988	0	0.437323	0.773736
antisense	-	0	3	1	11	7	4	0	0.558696	0.208249	1.503845	1.24278	0.628227
lincRNA	-	0	1	0	0	0	0	0	0.072544	0	0	0	0
processed_	-	4	6	3	4	9	2	0.37815	0.66844	0.373732	0.327135	0.955863	0.187907
pseudogen	-	0	0	0	2	0	0	0	0	0	0.112666	0	0
lincRNA	-	9	18	7	57	53	86	1.567332	3.69401	1.606391	8.587295	10.36916	14.88424
antisense	-	2	0	1	0	0	3	0.306904	0	0.202212	0	0	0.457513
lincRNA	-	0	0	2	0	3	0	0	0	0.259343	0	0.33165	0
antisense	-	1	7	1	2	1	1	0.024532	0.20237	0.032328	0.042446	0.027561	0.024381
antisense	-	2	2	2	19	18	7	0.075415	0.088871	0.099378	0.619786	0.762512	0.262321
antisense	-	5	0	1	0	1	4	0.560816	0	0.147804	0	0.126008	0.445882
antisense	-	1	0	1	0	0	1	0.067873	0	0.08944	0	0	0.067454
lincRNA	-	78	59	81	39	36	43	2.499635	2.228133	3.420597	1.081209	1.296085	1.369494
protein_co	Putative_u	7	9	3	0	2	1	0.039395	0.059688	0.022248	0	0.012645	0.005593
antisense	-	4	4	0	3	0	0	0.29868	0.351976	0	0.193789	0	0
antisense	-	0	1	0	2	5	3	0	0.025156	0	0.036935	0.119911	0.063646
protein_co	TBC1_dom	0	0	0	13	0	2	0	0	0	0.197278	0	0.034867
lincRNA	-	3	1	0	0	0	0	0.342291	0.134456	0	0	0	0
lincRNA	-	0	0	1	0	0	0	0	0	0.136523	0	0	0
lincRNA	-	31	57	18	62	35	42	0.992244	2.15	0.759213	1.716767	1.258559	1.336028
antisense	-	1	1	2	0	0	0	0.050086	0.059023	0.132002	0	0	0
lincRNA	-	4	1	0	0	0	0	0.283107	0.083406	0	0	0	0
pseudogen	SH3-domai	27	21	22	18	20	17	0.734914	0.673595	0.789096	0.423846	0.611578	0.459866
sense_intrc	-	7	1	5	9	14	6	0.353276	0.059474	0.332523	0.392936	0.793768	0.300938
pseudogen	-	1	0	0	0	0	0	0.069294	0	0	0	0	0
sense_intrc	-	0	0	4	3	1	6	0	0	0.43534	0.214347	0.092786	0.492487
sense_intrc	-	8	1	6	0	0	0	0.614699	0.090548	0.607518	0	0	0
sense_intrc	-	1	2	4	1	1	0	0.015191	0.035804	0.080073	0.013142	0.017066	0
lincRNA	-	0	1	2	1	0	0	0	0.021315	0.047669	0.015647	0	0
lincRNA	-	3	0	0	0	0	0	0.341555	0	0	0	0	0
lincRNA	-	31	31	15	1	1	0	2.552365	3.007807	1.627448	0.071227	0.092498	0
sense_intrc	-	0	0	0	0	1	0	0	0	0	0	0.212414	0
antisense	-	0	2	0	0	0	0	0	0.258334	0	0	0	0
antisense	-	0	0	0	0	1	2	0	0	0	0	0.073246	0.129591
antisense	-	0	0	0	0	1	2	0	0	0	0	0.109331	0.193434

pseudogen	integral_m	0	8	0	0	0	0	0	0.751659	0	0	0	0
pseudogen	-	10	8	11	42	41	52	0.716387	0.675375	1.038425	2.602915	3.299746	3.702207
lincRNA	-	0	0	0	0	3	1	0	0	0	0	0.44944	0.132529
lincRNA	-	3	14	8	0	0	0	0.279618	1.537726	0.982581	0	0	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.011312	0
pseudogen	-	4	0	3	4	3	2	0.575446	0	0.568722	0.497814	0.484858	0.285946
antisense	-	3	3	0	2	2	1	0.221202	0.260673	0	0.127574	0.165671	0.073279
sense_intrc	-	16	10	10	22	37	17	0.519666	0.382747	0.427996	0.618145	1.350067	0.548735
lincRNA	-	18	3	9	8	18	23	2.437181	0.478678	1.605804	0.937062	2.738022	3.094944
sense_intrc	-	1	1	1	0	0	4	0.033026	0.038919	0.04352	0	0	0.131289
antisense	-	0	0	1	1	3	4	0	0	0.14718	0.096622	0.37643	0.444
antisense	-	5	0	5	0	3	0	0.319306	0	0.420768	0	0.215233	0
lincRNA	long_interg	69	28	26	48	34	37	1.434772	0.686118	0.712429	0.863451	0.794258	0.764619
pseudogen	-	2	0	1	0	2	1	0.048771	0	0.032134	0	0.054791	0.024235
pseudogen	solute_carr	0	2	1	3	0	2	0	0.225634	0.126154	0.248457	0	0.190286
pseudogen	-	10	15	12	16	14	9	0.721267	1.274954	1.140544	0.998341	1.134418	0.645131
lincRNA	-	1	14	7	11	5	2	0.047481	0.783344	0.437976	0.451828	0.266708	0.094375
lincRNA	-	0	0	0	4	0	4	0	0	0	0.319713	0	0.367288
antisense	-	3	7	1	35	20	28	0.237049	0.651812	0.104124	2.39248	1.775401	2.198796
lincRNA	-	1	5	2	2	2	0	0.023405	0.137904	0.061683	0.040494	0.052587	0
antisense	-	2	5	3	10	2	7	0.041522	0.122329	0.082074	0.179604	0.046648	0.144431
sense_intrc	-	0	0	0	1	1	1	0	0	0	0.093277	0.121132	0.107157
processed_	-	4	2	2	8	6	9	0.396562	0.233662	0.261286	0.686126	0.668269	0.886754
lincRNA	-	4	0	0	1	2	1	0.545783	0	0	0.118038	0.306577	0.135603
lincRNA	-	1	0	0	0	0	0	0.092071	0	0	0	0	0
lincRNA	-	120	121	71	114	67	155	12.83418	15.25033	10.00645	10.54763	8.050276	16.47511
pseudogen	-	1	0	3	1	2	6	0.053584	0	0.211832	0.046355	0.120397	0.319519
antisense	-	1	1	4	0	4	4	0.063784	0.075166	0.336209	0	0.286631	0.253562
sense_intrc	-	9	10	5	2	7	0	0.665459	0.871337	0.487174	0.12793	0.581468	0
lincRNA	-	15	8	6	13	8	6	1.443845	0.907458	0.761054	1.08252	0.865104	0.573971
antisense	-	5	3	5	0	3	8	0.723238	0.511375	0.95305	0	0.487508	1.150034
3prime_ov	-	31	20	24	87	48	73	0.629283	0.478434	0.641993	1.527801	1.094649	1.472709
pseudogen	-	0	1	0	0	0	0	0	0.104327	0	0	0	0
antisense	-	0	0	1	8	0	0	0	0	0.204584	1.074461	0	0
sense_intrc	-	4	4	1	7	5	4	0.288114	0.339525	0.094916	0.43618	0.404598	0.286335
pseudogen	-	1	2	0	0	0	0	0.146246	0.344684	0	0	0	0
pseudogen	mitochond	2	2	2	16	20	10	0.079194	0.093325	0.104358	0.54808	0.889692	0.393523
antisense	-	28	11	10	24	22	24	0.557693	0.258188	0.262465	0.413534	0.492276	0.47507
lincRNA	-	0	2	1	0	1	1	0	0.305822	0.170988	0	0.145774	0.128956
antisense	-	0	0	7	9	0	0	0	0	0.924892	0.780663	0	0
antisense	-	0	1	1	3	3	0	0	0.311939	0.348816	0.686984	0.892139	0
protein_co	Uncharacte	1	0	0	0	0	0	0.098039	0	0	0	0	0
pseudogen	-	2	0	0	0	0	0	0.687545	0	0	0	0	0
pseudogen	family_witl	0	0	3	1	0	0	0	0	0.417744	0.091415	0	0

sense_intrc	-	8	5	3	3	12	15	0.249281	0.183601	0.123184	0.080869	0.420077	0.464515
protein_co	alanyl-tRNA	17	25	15	30	32	34	0.680784	1.179798	0.791565	1.03931	1.439659	1.35316
sense_intrc	-	0	4	0	0	0	0	0	0.140355	0	0	0	0
antisense	-	1	2	1	3	7	5	0.11169	0.263239	0.14718	0.289866	0.878336	0.555001
lincRNA	-	21	24	16	11	4	13	1.430838	1.927034	1.436567	0.648376	0.306182	0.880287
pseudogen	-	0	0	0	4	4	6	0	0	0	0.034077	0.044253	0.058721
antisense	-	0	0	0	0	0	3	0	0	0	0	0	0.278873
antisense	-	5	3	5	3	11	5	1.098361	0.776611	1.447371	0.570111	2.714668	1.091578
lincRNA	-	1	1	0	10	21	18	0.011889	0.01401	0	0.10285	0.280484	0.212677
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.12986	0
antisense	-	5	3	1	0	1	2	0.297421	0.210296	0.078386	0	0.066827	0.118234
antisense	-	1	2	9	9	5	10	0.08285	0.195267	0.982581	0.645055	0.465383	0.823381
antisense	-	6	3	10	5	1	8	0.88235	0.519898	1.937869	0.636096	0.165211	1.169201
antisense	-	1	0	0	0	0	0	0.082591	0	0	0	0	0
antisense	-	14	10	14	4	15	21	0.575446	0.484377	0.758297	0.142233	0.692654	0.857838
processed_	-	1	1	2	4	0	2	0.095218	0.112208	0.250947	0.329489	0	0.189259
pseudogen	-	4	0	1	0	0	0	1.05882	0	0.348816	0	0	0
antisense	-	20	19	5	0	1	2	0.309687	0.3467	0.102023	0	0.017396	0.030777
lincRNA	-	0	0	1	6	18	5	0	0	0.012747	0.050209	0.195609	0.048067
antisense	-	1	1	2	4	0	0	0.108708	0.128106	0.286502	0.376172	0	0
lincRNA	-	22	8	19	10	24	22	0.977919	0.419061	1.112932	0.384542	1.198507	0.97188
antisense	-	11	14	4	7	1	7	0.174933	0.26237	0.083825	0.096303	0.017866	0.110633
lincRNA	-	0	0	0	10	0	0	0	0	0	4.721537	0	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.265517	0
lincRNA	-	2	3	3	1	0	0	0.090036	0.159152	0.177968	0.038945	0	0
processed_	-	5	0	9	0	0	5	0.342439	0	0.81225	0	0	0.340324
lincRNA	-	34	37	22	395	181	231	0.77253	0.990706	0.658709	7.764192	4.620232	5.216243
lincRNA	-	4	0	2	5	3	8	0.443021	0	0.291897	0.479068	0.37328	0.88057
lincRNA	-	62	40	47	0	2	1	1.070212	0.813665	1.069082	0	0.038784	0.017155
antisense	-	0	0	1	0	0	0	0	0	0.138971	0	0	0
antisense	-	27	18	15	1	6	3	1.262727	0.992031	0.924425	0.040458	0.315243	0.139437
lincRNA	-	1	0	0	0	5	1	0.047481	0	0	0	0.266708	0.047187
pseudogen	leucine_ric	165	174	136	295	288	236	2.345037	2.914219	2.547062	3.627027	4.598406	3.3334
antisense	-	1	0	0	2	0	2	0.119776	0	0	0.207235	0	0.238073
antisense	-	25	26	25	31	50	44	2.712141	3.323936	3.573939	2.909357	6.093844	4.74389
antisense	-	0	2	2	0	0	3	0	0.31509	0.35234	0	0	0.398591
pseudogen	-	0	1	0	0	1	5	0	0.163747	0	0	0.156105	0.690473
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.056482	0
antisense	-	2	2	3	0	0	3	0.183187	0.215874	0.362093	0	0	0.273083
lincRNA	-	2	6	0	12	18	10	0.074987	0.265104	0	0.389226	0.758192	0.372621
pseudogen	-	0	1	1	0	0	0	0	0.047014	0.052572	0	0	0
antisense	-	0	0	0	0	5	2	0	0	0	0	0.432238	0.152948
antisense	-	26	28	15	38	22	40	0.696592	0.884037	0.52958	0.880748	0.662181	1.065062
protein_co	zinc_finger	70	67	46	327	284	273	0.480408	0.541869	0.416011	1.941437	2.189676	1.862022

antisense	-	5	7	2	0	0	1	0.488386	0.805746	0.257429	0	0	0.097074
antisense	-	1	11	0	0	0	11	0.112163	1.453951	0	0	0	1.226175
lincRNA	-	4	0	0	2	3	2	0.460356	0	0	0.199126	0.387886	0.228757
processed_	-	2	6	0	0	0	0	0.189413	0.669636	0	0	0	0
antisense	-	7	4	1	34	14	41	0.867885	0.584428	0.16338	3.646751	1.95003	5.051935
lincRNA	-	0	0	1	1	1	0	0	0	0.126842	0.083271	0.108138	0
lincRNA	-	6	12	2	6	6	11	0.137807	0.324795	0.060532	0.119216	0.154818	0.251087
lincRNA	-	0	5	0	0	0	4	0	0.46558	0	0	0	0.314114
lincRNA	-	51	23	16	12	2	19	1.231186	0.654317	0.508989	0.25061	0.054242	0.455844
protein_co	cytochrom	3	3	1	17	9	9	0.118969	0.140197	0.052257	0.583207	0.400961	0.354701
protein_co	prostaglan	1	1	2	52	24	25	0.027791	0.032749	0.073242	1.250154	0.749303	0.690473
antisense	-	0	0	1	0	4	0	0	0	0.127772	0	0.435721	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.107164	0
antisense	-	2	0	1	1	1	1	0.069431	0	0.045746	0.030032	0.039001	0.034501
lincRNA	-	2	0	1	3	0	0	0.046644	0	0.030733	0.060527	0	0
lincRNA	-	0	3	3	3	0	0	0	0.297084	0.332206	0.21809	0	0
lincRNA	-	2	0	0	1	0	0	0.14445	0	0	0.062481	0	0
processed_	-	0	0	0	0	2	0	0	0	0	0	0.224015	0
lincRNA	-	0	1	1	0	0	1	0	0.150332	0.168104	0	0	0.126781
lincRNA	-	3	0	0	2	0	0	0.419058	0	0	0.241683	0	0
antisense	ASB16_anti	79	62	78	301	224	243	1.889895	1.747871	2.458896	6.229313	6.020156	5.777322
antisense	-	2	1	3	1	2	4	0.186084	0.109645	0.36782	0.08049	0.209054	0.36987
pseudogen	-	0	0	0	2	0	1	0	0	0	0.070568	0	0.040535
pseudogen	-	0	1	0	0	0	0	0	0.243702	0	0	0	0
pseudogen	-	1	1	1	3	0	0	0.120048	0.141469	0.158193	0.311557	0	0
lincRNA	-	3	0	0	0	0	2	0.359328	0	0	0	0	0.238073
pseudogen	C-terminal_	4	5	1	0	3	0	0.170228	0.250755	0.05608	0	0.143431	0
antisense	-	0	0	1	0	0	0	0	0	0.15503	0	0	0
lincRNA	-	7	2	1	0	7	2	0.549018	0.184853	0.103353	0	0.616787	0.155893
lincRNA	-	1	0	0	0	3	1	0.097677	0	0	0	0.329202	0.097074
sense_intro	-	8	1	3	7	4	20	0.52809	0.07779	0.26096	0.399741	0.296638	1.312071
lincRNA	ILF3_antise	165	155	128	442	243	366	4.405075	4.876499	4.503127	10.20833	7.288274	9.710914
pseudogen	-	2	3	2	66	28	35	0.168871	0.298506	0.22253	4.820937	2.656022	2.936988
protein_co	uncharacte	125	127	109	159	127	129	2.688998	3.219521	3.089881	2.95897	3.069257	2.757908
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.015154
lincRNA	-	0	1	0	3	0	2	0	0.371356	0	0.817838	0	0.626358
lincRNA	-	0	1	1	0	0	0	0	0.083854	0.093768	0	0	0
antisense	-	0	0	1	0	0	1	0	0	0.123039	0	0	0.092794
protein_co	Uncharacte	7	7	3	2	10	17	1.026557	1.209734	0.57975	0.253734	1.647532	2.47767
lincRNA	-	0	0	1	0	0	0	0	0	0.124577	0	0	0
antisense	-	1	9	0	1	1	6	0.120048	1.273219	0	0.103852	0.134866	0.715837
pseudogen	-	2	1	1	2	6	10	0.336133	0.198056	0.221471	0.290787	1.132875	1.670287
antisense	-	3	0	0	0	0	0	0.070966	0	0	0	0	0
antisense	-	1	6	3	0	5	1	0.019336	0.136715	0.076439	0	0.108612	0.019216

protein_co	Protein_LO	33	45	38	33	21	21	0.78767	1.265756	1.195223	0.681408	0.563117	0.498149
antisense	RNF157_an	0	0	0	4	3	2	0	0	0	0.101101	0.09847	0.058073
antisense	-	3	2	3	2	0	2	0.337921	0.26548	0.445298	0.194889	0	0.22389
lincRNA	-	0	0	0	2	0	0	0	0	0	0.053193	0	0
antisense	-	1	0	0	0	0	3	0.011157	0	0	0	0	0.033265
antisense	-	0	2	0	0	0	3	0	0.226042	0	0	0	0.285946
sense_intrc	-	2	0	1	3	0	2	0.31419	0	0.207013	0.407705	0	0.31225
antisense	-	11	23	11	3	12	18	0.959392	2.36395	1.264244	0.226354	1.175801	1.560219
pseudogen	-	3	0	0	2	0	3	0.158982	0	0	0.09169	0	0.158
lincRNA	-	0	0	0	2	0	1	0	0	0	0.161834	0	0.092958
lincRNA	-	0	0	0	0	2	1	0	0	0	0	0.155493	0.068777
processed_	-	3	9	1	0	2	2	0.124959	0.44177	0.054888	0	0.093589	0.082792
antisense	-	1	5	0	36	31	17	0.048794	0.287501	0	1.519595	1.699312	0.824368
lincRNA	hsa-mir-21	0	0	4	0	2	0	0	0	0.551488	0	0.235083	0
lincRNA	-	44	40	24	97	62	47	1.712797	1.834933	1.231117	3.26654	2.711402	1.81828
antisense	-	3	0	5	3	11	7	0.481282	0	1.057019	0.416354	1.982531	1.116056
antisense	-	4	6	3	2	5	5	0.082431	0.145709	0.081467	0.035655	0.115757	0.102402
lincRNA	-	123	68	99	182	108	188	3.463693	2.256577	3.673705	4.433724	3.416702	5.261405
antisense	-	10	5	5	0	2	4	0.247503	0.145834	0.163075	0	0.055611	0.09839
lincRNA	-	3	6	4	0	3	7	0.236696	0.557863	0.415876	0	0.265913	0.54888
antisense	-	69	47	62	36	57	53	1.276801	1.024895	1.511822	0.576288	1.184945	0.974675
sense_intrc	-	0	2	0	1	3	2	0	0.330969	0	0.121483	0.473283	0.27912
3prime_ov	-	0	0	0	2	0	0	0	0	0	0.139844	0	0
lincRNA	-	1	0	0	1	0	0	0.093535	0	0	0.080917	0	0
antisense	-	9	5	8	13	5	5	0.770985	0.504755	0.903085	0.963407	0.481197	0.42568
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.161889
lincRNA	-	11	14	7	3	8	2	1.084452	1.626496	0.909391	0.25586	0.886047	0.195955
pseudogen	protein_tyr	1	0	0	2	1	0	0.110755	0	0	0.191627	0.124427	0
antisense	-	2	9	6	4	2	0	0.204801	1.086053	0.809632	0.354344	0.230081	0
antisense	-	0	9	1	2	1	3	0	1.242234	0.154344	0.20265	0.131584	0.349208
antisense	-	1	0	6	0	0	0	0.096784	0	0.765228	0	0	0
lincRNA	-	43	27	24	78	45	41	0.90913	0.672711	0.668658	1.426643	1.068856	0.861492
lincRNA	hsa-mir-21	0	1	0	0	0	0	0	0.567161	0	0	0	0
sense_intrc	-	0	0	0	3	1	0	0	0	0	0.366391	0.158602	0
sense_intrc	-	0	3	4	1	6	3	0	0.524267	0.781661	0.128288	0.999595	0.442135
lincRNA	-	1	0	0	3	2	0	0.084033	0	0	0.21809	0.188812	0
antisense	-	6	5	7	12	8	4	0.064694	0.063531	0.099459	0.111932	0.096906	0.042863
lincRNA	hsa-mir-13	3	0	0	0	0	1	1.572505	0	0	0	0	0.520931
lincRNA	-	6	5	4	3	11	12	0.856189	0.840805	0.752165	0.370342	1.763437	1.701802
pseudogen	small_nucl	0	0	2	0	2	3	0	0	0.609286	0	0.51944	0.689267
antisense	-	0	0	0	0	0	2	0	0	0	0	0	0.245287
lincRNA	-	1	0	0	0	0	1	0.136446	0	0	0	0	0.135603
lincRNA	-	6	4	5	2	1	3	0.334013	0.262409	0.366789	0.096317	0.06254	0.165975
protein_co	Uncharacte	8	13	19	3	12	16	0.100196	0.191871	0.31358	0.032505	0.168846	0.199154

antisense	-	7	8	1	6	6	2	0.633482	0.853166	0.119253	0.469732	0.610009	0.179877
pseudogen	-	0	0	0	5	0	3	0	0	0	0.809168	0	0.557746
sense_intrc	-	0	6	1	9	6	9	0	0.491887	0.091673	0.541643	0.46893	0.622242
sense_intrc	-	1	0	1	3	2	0	0.077399	0	0.101993	0.200872	0.173906	0
antisense	-	1	2	6	23	8	11	0.071736	0.169072	0.567181	1.427337	0.644725	0.78422
protein_co	-	3	0	1	1	0	2	0.283107	0	0.124355	0.081638	0	0.187572
sense_intrc	-	0	2	0	2	5	3	0	0.078623	0	0.057718	0.187385	0.099459
lincRNA	-	0	0	1	0	0	0	0	0	0.18906	0	0	0
antisense	-	0	2	0	0	0	0	0	0.255687	0	0	0	0
processed_	-	18	20	21	5	2	6	2.242207	2.935893	3.447127	0.538811	0.279887	0.742787
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.106971	0
lincRNA	-	28	8	13	32	13	32	1.953027	0.657578	1.194892	1.930916	1.018692	2.218247
processed_	-	5	3	1	81	67	70	0.085032	0.060123	0.02241	1.191684	1.280079	1.183098
processed_	-	22	31	18	28	27	57	0.485292	0.805842	0.523225	0.534321	0.669104	1.249584
lincRNA	-	0	1	0	0	1	3	0	0.07553	0	0	0.072005	0.191092
lincRNA	-	0	1	0	3	0	1	0	0.128634	0	0.283292	0	0.108483
processed_	-	21	13	13	21	10	18	1.086765	0.792806	0.886532	0.940153	0.581387	0.92576
sense_intrc	-	1	7	4	38	25	21	0.073529	0.606547	0.387574	2.417164	2.065136	1.534576
lincRNA	-	0	0	0	3	0	0	0	0	0	0.265245	0	0
antisense	-	25	15	14	5	18	7	0.650381	0.45986	0.479944	0.112528	0.526077	0.180982
antisense	-	6	19	9	20	6	7	0.373701	1.394549	0.73867	1.077621	0.41983	0.433292
antisense	-	0	0	0	2	0	3	0	0	0	0.16098	0	0.277403
antisense	-	0	0	2	0	3	0	0	0	0.054652	0	0.069889	0
lincRNA	-	0	0	0	4	10	1	0	0	0	0.068052	0.220936	0.019545
protein_co	Uncharacte	0	0	1	10	11	4	0	0	0.03771	0.247562	0.353641	0.11376
antisense	-	1	0	1	0	1	0	0.09337	0	0.123039	0	0.104896	0
sense_intrc	-	0	4	3	0	3	0	0	0.324936	0.272513	0	0.232328	0
pseudogen	-	2	0	2	8	4	4	0.202451	0	0.266781	0.700557	0.454883	0.402402
antisense	-	19	7	16	48	23	42	1.279744	0.555616	1.420118	2.79688	1.740389	2.811438
lincRNA	-	0	0	1	6	4	1	0	0	0.091433	0.360149	0.3118	0.068957
antisense	-	0	0	0	1	0	3	0	0	0	0.0845	0	0.291222
protein_co	Uncharacte	52	38	53	32	45	43	0.825962	0.711291	1.109347	0.439713	0.803005	0.678789
lincRNA	-	2	0	3	3	0	1	0.031438	0	0.062141	0.040795	0	0.015622
lincRNA	-	1	1	0	0	2	0	0.080703	0.095103	0	0	0.181329	0
sense_over	-	6	10	8	7	12	16	0.678731	1.333071	1.192535	0.685026	1.525024	1.798771
antisense	-	1	4	0	7	2	2	0.077626	0.36591	0	0.470077	0.174416	0.154293
antisense	MAP3K14_	29	24	21	22	15	23	0.620319	0.604972	0.591931	0.407101	0.36046	0.488939
lincRNA	-	19	17	22	57	29	20	1.368543	1.442981	2.088153	3.551752	2.346669	1.431675
antisense	-	208	207	168	7	6	22	12.78946	14.99914	13.61235	0.372349	0.414466	1.344378
antisense	-	3	7	2	3	0	2	0.372824	1.02515	0.327527	0.322528	0	0.247014
antisense	-	8	6	3	14	7	17	0.640738	0.566303	0.316626	0.970022	0.629851	1.35316
lincRNA	-	0	0	0	4	3	1	0	0	0	0.32424	0.315801	0.093122
processed_	-	0	0	0	2	0	0	0	0	0	0.159578	0	0
processed_	-	0	0	0	0	3	0	0	0	0	0	0.042819	0

antisense	-	0	3	0	0	2	0	0	0.091388	0	0	0.058082	0
lincRNA	-	0	3	0	1	0	0	0	0.249551	0	0.061065	0	0
pseudogen	-	0	0	0	8	3	6	0	0	0	0.240414	0.117079	0.207142
pseudogen	-	1	0	1	0	0	0	0.093042	0	0.122607	0	0	0
antisense	-	2	0	0	3	0	4	0.048172	0	0	0.06251	0	0.095749
sense_intrc	-	6	9	1	0	0	2	0.56824	1.004454	0.1248	0	0	0.188243
lincRNA	-	2	1	0	0	2	1	0.066052	0.038919	0	0	0.074206	0.032822
antisense	-	4	17	9	10	3	3	0.439344	2.200397	1.302634	0.950185	0.370182	0.327473
sense_intrc	-	0	0	0	1	0	0	0	0	0	0.178902	0	0
antisense	-	6	14	21	21	27	22	0.228194	0.627463	1.052463	0.690932	1.153628	0.831544
lincRNA	-	1	3	4	0	2	0	0.048128	0.170148	0.253685	0	0.108138	0
pseudogen	-	0	0	0	2	0	0	0	0	0	0.085605	0	0
lincRNA	-	81	80	88	22	7	16	2.507731	2.918724	3.590157	0.589226	0.243469	0.492295
pseudogen	-	0	3	0	0	0	0	0	0.711647	0	0	0	0
lincRNA	-	2	0	0	1	0	2	0.175301	0	0	0.075826	0	0.174219
processed_	-	72	92	46	95	40	64	4.111922	6.191662	3.461824	4.693523	2.566383	3.632469
pseudogen	-	2	1	3	1	1	12	0.371516	0.218904	0.73435	0.160698	0.208687	2.215328
lincRNA	-	65	65	59	275	151	275	2.651128	3.124193	3.171058	9.703158	6.919001	11.14704
antisense	-	92	116	107	16	72	53	3.015834	4.4811	4.622087	0.453735	2.651558	1.726653
pseudogen	solute_carr	0	0	0	2	3	0	0	0	0	0.116983	0.227877	0
lincRNA	-	0	0	10	11	6	7	0	0	0.171366	0.12375	0.087658	0.090469
lincRNA	-	2	0	2	1	1	0	0.204405	0	0.269356	0.088415	0.114818	0
lincRNA	-	1	0	0	0	0	0	0.214336	0	0	0	0	0
antisense	-	0	4	6	3	18	30	0	0.420828	0.705868	0.231698	1.80534	2.661756
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.036759	0
lincRNA	-	0	4	0	0	0	0	0	0.120673	0	0	0	0
pseudogen	-	1	4	1	6	2	7	0.267379	1.260358	0.35234	1.387846	0.600767	1.860093
antisense	-	1	2	3	8	3	6	0.037309	0.087932	0.147491	0.258204	0.125742	0.22247
antisense	-	0	0	0	0	1	0	0	0	0	0	0.130144	0
antisense	-	2	1	1	4	1	0	0.185108	0.109069	0.121964	0.320272	0.103979	0
pseudogen	eukaryotic_	2	0	4	0	10	7	0.229182	0	0.604011	0	1.287358	0.797183
sense_overl	-	7	4	2	3	2	10	0.880254	0.592758	0.331417	0.326358	0.282546	1.24974
processed_	-	1	0	1	0	0	0	0.076726	0	0.101106	0	0	0
processed_	-	523	428	337	688	614	758	11.16457	10.76691	9.47993	12.7055	14.72509	16.08123
pseudogen	SH3-domai	26	21	17	39	28	40	1.480071	1.408755	1.275243	1.920599	1.790673	2.26297
pseudogen	ribosomal_	2	7	0	8	2	3	0.178553	0.736449	0	0.61786	0.200593	0.266176
lincRNA	RNA_U6_sn	2	8	2	0	3	0	0.989551	4.664503	1.303987	0	1.667549	0
antisense	KCNJ2_anti	6	2	0	10	7	5	0.130076	0.051096	0	0.187547	0.170488	0.107727
antisense	-	0	0	1	0	0	0	0	0	0.143251	0	0	0
pseudogen	-	12	6	11	10	3	9	0.892264	0.525739	1.077804	0.643243	0.250601	0.665065
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.094707	0
lincRNA	-	2	0	5	0	2	5	0.288507	0	0.950453	0	0.324119	0.716813
lincRNA	long_interg	6	0	0	55	38	55	0.137748	0	0	1.092342	0.980089	1.254888
antisense	-	4	11	4	1	5	3	0.875058	2.835806	1.153112	0.189252	1.228841	0.65224

lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.086679
lincRNA	-	25	31	10	63	21	20	2.023738	2.957217	1.066717	4.411821	1.909777	1.608992
antisense	-	7	6	2	143	140	156	0.292261	0.29521	0.110037	5.165019	6.566742	6.473022
antisense	-	0	2	0	0	0	0	0	0.092701	0	0	0	0
lincRNA	-	1	2	0	1	0	0	0.088235	0.207959	0	0.076332	0	0
pseudogen	-	2	0	0	0	5	0	0.129282	0	0	0	0.363101	0
antisense	-	6	12	3	13	3	1	0.404645	0.953698	0.266611	0.758453	0.227296	0.067024
antisense	-	9	14	8	3	8	9	0.902403	1.65422	1.057019	0.260221	0.90115	0.89683
antisense	-	10	11	12	5	9	18	0.644051	0.834872	1.018442	0.278582	0.651196	1.152132
lincRNA	-	18	19	18	6	7	5	0.592255	0.73671	0.780447	0.170785	0.258752	0.163499
lincRNA	-	2	0	1	0	0	0	0.191815	0	0.126383	0	0	0
antisense	-	4	0	1	0	1	1	0.475874	0	0.156771	0	0.133654	0.118234
lincRNA	-	3	3	5	15	14	5	0.270567	0.318847	0.594236	1.17033	1.418506	0.448161
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.216519
processed_	-	3	2	0	14	3	2	0.157095	0.123418	0	0.634208	0.176486	0.104083
sense_intrc	-	0	1	1	0	0	0	0	0.036527	0.040845	0	0	0
lincRNA	-	0	0	0	7	7	4	0	0	0	0.287527	0.373391	0.18875
lincRNA	-	40	36	64	57	23	36	1.025491	1.087631	2.162155	1.264183	0.662444	0.917243
lincRNA	-	5	3	2	0	3	0	0.378691	0.267758	0.199609	0	0.255261	0
antisense	-	4	0	3	0	0	0	0.404902	0	0.400172	0	0	0
processed_	-	15	19	13	28	9	23	0.988935	1.476173	1.129418	1.596973	0.666604	1.507003
lincRNA	-	3	0	0	3	2	2	0.20258	0	0	0.175251	0.151724	0.13422
pseudogen	-	2	1	0	5	4	4	0.096784	0.057027	0	0.209319	0.217462	0.192373
antisense	-	0	0	0	3	0	0	0	0	0	0.185922	0	0
lincRNA	-	1231	1040	871	1395	1191	1432	30.98924	30.8527	28.89387	30.38016	33.68322	35.82659
sense_intrc	-	0	0	4	1	1	2	0	0	0.252995	0.041522	0.053922	0.095402
pseudogen	-	2	3	3	1	3	2	0.091832	0.162327	0.181518	0.039722	0.154751	0.091265
processed_	-	0	0	0	3	0	0	0	0	0	0.147421	0	0
antisense	-	17	17	12	13	25	11	0.525699	0.619504	0.488995	0.347772	0.868515	0.338058
lincRNA	-	0	0	0	0	1	1	0	0	0	0	0.108335	0.095836
sense_intrc	-	2	4	6	12	7	26	0.17706	0.417309	0.699966	0.919042	0.696206	2.287567
lincRNA	-	0	0	0	0	0	6	0	0	0	0	0	0.110961
lincRNA	-	0	0	0	3	2	3	0	0	0	0.323286	0.279887	0.371393
processed_	ZNF582_an	8	2	5	10	12	18	0.263716	0.077693	0.217196	0.285174	0.444403	0.589697
lincRNA	-	3	4	0	1	0	2	0.291954	0.458733	0	0.084189	0	0.193434
lincRNA	-	9	21	9	7	3	4	1.240805	3.411829	1.635077	0.834876	0.464656	0.548063
lincRNA	-	2	0	0	0	0	0	0.060092	0	0	0	0	0
pseudogen	ubiquitin-c	0	0	0	0	5	0	0	0	0	0	0.590039	0
lincRNA	-	0	0	1	1	7	0	0	0	0.039481	0.025919	0.235615	0
antisense	-	12	5	7	1	5	5	0.228769	0.112329	0.175853	0.016492	0.107087	0.094732
pseudogen	-	0	0	0	3	5	3	0	0	0	0.20325	0.439911	0.233494
lincRNA	-	82	75	65	28	18	39	2.552123	2.750782	2.665851	0.753891	0.629375	1.206319
sense_intrc	-	1	1	1	0	0	1	0.059551	0.070177	0.078474	0	0	0.059183
lincRNA	-	4	5	6	15	13	4	0.372824	0.549188	0.736936	1.209478	1.361245	0.370521

antisense	-	3	0	2	7	15	9	0.399053	0	0.350569	0.805508	2.241555	1.189765
sense_intrc	-	0	1	1	3	6	4	0	0.151795	0.16974	0.334299	0.868262	0.512059
antisense	-	7	5	11	11	6	18	0.703201	0.591914	1.45616	0.955954	0.677145	1.797064
sense_intrc	-	6	10	5	6	11	16	0.344892	0.677391	0.378737	0.298364	0.710353	0.914033
antisense	-	12	8	11	7	2	3	0.672267	0.52815	0.812059	0.339251	0.125875	0.167029
antisense	CIRBP_anti	14	13	5	3	8	15	1.154477	1.263303	0.543328	0.214014	0.741133	1.2293
protein_co	family_with	0	0	1	0	0	0	0	0	0.092894	0	0	0
lincRNA	-	0	0	0	0	0	2	0	0	0	0	0	0.148418
pseudogen	-	5	2	6	21	21	19	0.188134	0.088682	0.297498	0.683566	0.8877	0.710495
lincRNA	-	0	4	0	19	29	19	0	0.337231	0	1.175918	2.330813	1.350901
sense_intrc	-	1	1	0	0	1	0	0.048084	0.056665	0	0	0.05402	0
lincRNA	-	1	2	0	20	4	8	0.094201	0.22202	0	1.629854	0.423316	0.748954
lincRNA	-	0	0	0	0	7	1	0	0	0	0	0.084931	0.010733
pseudogen	-	2	0	0	0	0	0	0.216971	0	0	0	0	0
protein_co	zinc_finger_	107	49	69	43	40	54	0.942073	0.508398	0.800543	0.327516	0.395649	0.472503
lincRNA	-	3	0	0	9	1	18	0.277178	0	0	0.719355	0.103797	1.652797
antisense	-	10	5	7	14	12	14	1.307185	0.770219	1.205785	1.583172	1.762249	1.818757
pseudogen	-	1	0	0	2	0	2	0.088827	0	0	0.153688	0	0.176557
lincRNA	-	144	94	77	94	59	100	4.297352	3.305776	3.028057	2.426774	1.97806	2.965843
lincRNA	-	40	20	22	10	31	9	0.94369	0.55604	0.683954	0.204095	0.821637	0.211019
lincRNA	-	0	0	3	1	0	0	0	0	0.126002	0.027573	0	0
antisense	-	28	13	11	41	37	65	2.700087	1.477305	1.397807	3.420319	4.008395	6.22935
pseudogen	ribosomal_	1	0	1	0	0	0	0.063631	0	0.08385	0	0	0
pseudogen	-	0	4	0	0	0	0	0	0.172461	0	0	0	0
processed_	-	1	0	1	0	0	0	0.031178	0	0.041086	0	0	0
lincRNA	-	3	0	0	15	0	21	0.191584	0	0	0.828689	0	1.332805
pseudogen	-	0	0	2	0	0	1	0	0	0.121539	0	0	0.045831
protein_co	sphingosin	384	327	249	41	49	38	17.33107	17.39198	14.80909	1.600814	2.484501	1.704462
lincRNA	long_interg	0	0	0	0	0	2	0	0	0	0	0	0.123362
lincRNA	-	0	0	0	6	5	11	0	0	0	1.48537	1.607457	3.128403
pseudogen	-	1	0	0	6	3	0	0.235293	0	0	1.221304	0.793012	0
sense_intrc	-	3	5	13	3	9	4	0.278637	0.547261	1.591092	0.241047	0.939093	0.369221
antisense	-	6	13	4	3	6	9	0.54956	1.403184	0.482791	0.237711	0.617397	0.81925
lincRNA	-	1	2	1	82	26	40	0.098587	0.232357	0.129913	6.993501	2.879653	3.91911
3prime_ov	-	41	55	31	34	23	32	0.845242	1.336186	0.842158	0.606372	0.532689	0.655627
processed_	-	5	5	1	7	3	4	0.170777	0.201251	0.045009	0.206834	0.115115	0.135778
protein_co	Uncharacte	0	0	0	0	0	2	0	0	0	0	0	0.149472
lincRNA	-	3	0	0	0	0	0	0.289295	0	0	0	0	0
antisense	-	2	0	0	1	0	1	0.184785	0	0	0.079928	0	0.091822
antisense	-	1	0	0	1	2	0	0.08311	0	0	0.071898	0.186738	0
pseudogen	-	0	2	0	4	4	4	0	0.28166	0	0.413534	0.537029	0.47507
antisense	-	0	0	0	3	1	0	0	0	0	0.262709	0.113721	0
antisense	-	12	5	8	25	11	18	1.576407	0.774041	1.384879	2.841123	1.623412	2.350007
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.230527	0

processed_	-	1	0	1	4	0	0	0.084978	0	0.11198	0.294054	0	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.054653	0	0
processed_	-	2	3	4	5	4	15	0.179766	0.317764	0.473774	0.388785	0.403911	1.339916
pseudogen	keratin_8_p	1	1	0	0	0	0	0.036311	0.04279	0	0	0	0
processed_	-	52	46	38	76	82	75	1.146577	1.195267	1.104125	1.449695	2.031247	1.643504
antisense	-	0	0	4	0	0	0	0	0	0.169844	0	0	0
antisense	-	0	0	0	0	9	0	0	0	0	0	1.59786	0
lincRNA	-	0	2	0	0	0	0	0	0.204886	0	0	0	0
antisense	-	0	0	0	1	0	2	0	0	0	0.127219	0	0.2923
lincRNA	-	0	1	3	0	0	0	0	0.089509	0.300272	0	0	0
lincRNA	-	3	8	2	0	2	2	0.047045	0.147838	0.041329	0	0.035235	0.031169
pseudogen	-	2	2	3	1	0	0	0.170502	0.200927	0.337021	0.07375	0	0
lincRNA	microRNA_	0	0	0	0	3	0	0	0	0	0	0.250601	0
pseudogen	NADH_deh	3	5	1	8	0	3	0.63025	1.237852	0.276838	1.453934	0	0.626358
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.141273	0
pseudogen	-	4	0	0	0	0	0	0.941173	0	0	0	0	0
pseudogen	-	2	0	1	2	4	8	1.323525	0	0.872041	1.144973	2.973796	5.261405
pseudogen	ribose_5-ph	1	0	1	0	2	1	0.071349	0	0.094021	0	0.160312	0.070908
antisense	-	2	0	0	0	0	0	0.214336	0	0	0	0	0
lincRNA	-	3	0	0	2	0	2	0.195354	0	0	0.112666	0	0.129432
processed_	-	1	3	2	3	1	0	0.081573	0.288387	0.214987	0.211705	0.091642	0
antisense	-	2	3	3	0	0	0	0.067056	0.118533	0.132546	0	0	0
lincRNA	-	0	1	1	3	0	4	0	0.10398	0.116272	0.228995	0	0.35076
antisense	-	0	2	0	1	3	2	0	0.425855	0	0.15631	0.608968	0.35914
pseudogen	-	24	40	17	20	44	68	1.562834	3.069507	1.458765	1.126664	3.218869	4.400683
lincRNA	-	0	0	0	0	3	0	0	0	0	0	0.314133	0
processed_	-	1	0	0	0	0	0	0.009788	0	0	0	0	0
sense_intrc	-	15	18	19	4	23	15	0.457439	0.646877	0.763538	0.105527	0.787987	0.454614
sense_intrc	-	2	0	0	0	8	0	0.474807	0	0	0	2.133665	0
processed_	-	2	4	0	0	1	0	0.294936	0.695128	0	0	0.165671	0
lincRNA	-	0	0	0	2	0	7	0	0	0	0.086576	0	0.348108
pseudogen	-	2	1	1	5	8	1	0.198281	0.116831	0.130643	0.428829	0.891025	0.098528
lincRNA	-	0	0	0	1	0	0	0	0	0	0.018378	0	0
lincRNA	-	1	0	0	0	1	0	0.073427	0	0	0	0.082491	0
antisense	-	1	0	0	0	0	0	0.02105	0	0	0	0	0
pseudogen	-	0	0	0	7	7	7	0	0	0	0.368074	0.477992	0.422845
lincRNA	-	0	4	2	1	5	2	0	0.291191	0.162808	0.053441	0.347001	0.122787
antisense	-	0	1	1	0	0	0	0	0.05346	0.05978	0	0	0
lincRNA	-	5	5	0	1	4	1	0.124626	0.146864	0	0.021563	0.112007	0.024771
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.104527	0
sense_intrc	-	3	13	2	17	4	12	0.222441	1.135911	0.195415	1.09045	0.333198	0.88427
pseudogen	-	0	0	0	2	0	3	0	0	0	0.129011	0	0.222313
pseudogen	-	1	0	0	0	0	0	0.130076	0	0	0	0	0
lincRNA	-	6	4	5	5	0	2	0.747402	0.587179	0.820744	0.538811	0	0.247596

lincRNA	-	24	22	17	2	10	16	0.485697	0.524667	0.453355	0.035014	0.227354	0.321798
lincRNA	-	4	2	2	0	0	0	0.37815	0.222813	0.249155	0	0	0
lincRNA	-	1	3	1	6	0	0	0.02813	0.099449	0.037069	0.146011	0	0
antisense	-	0	0	0	3	1	0	0	0	0	0.480408	0.207958	0
antisense	-	0	1	0	0	1	2	0	0.099344	0	0	0.094707	0.167561
pseudogen	-	35	23	28	0	0	0	1.932153	1.496265	2.036884	0	0	0
sense_intrc	-	0	0	1	2	2	1	0	0	0.056996	0.074835	0.097183	0.042985
protein_co	ferredoxin_	0	0	0	0	0	4	0	0	0	0	0	0.107595
lincRNA	-	0	2	0	0	3	0	0	0.193151	0	0	0.276204	0
pseudogen	threonine_	8	4	1	2	5	11	0.369893	0.217948	0.060929	0.079998	0.25972	0.505462
lincRNA	-	0	0	0	2	0	2	0	0	0	0.219659	0	0.252346
protein_co	zinc_finger_	6	19	12	12	16	5	0.106094	0.395914	0.279612	0.183563	0.317841	0.087866
pseudogen	-	7	4	5	9	3	3	1.23529	0.831836	1.162721	1.373967	0.594759	0.526141
sense_intrc	-	7	7	3	4	2	11	0.988232	1.164571	0.558106	0.488522	0.317205	1.543345
pseudogen	-	2	2	0	2	4	0	0.542985	0.639874	0	0.469732	1.220019	0
pseudogen	SHC_(Src_h	0	0	3	0	0	0	0	0	0.142471	0	0	0
pseudogen	TAF9_RNA_	0	1	0	2	2	0	0	0.491242	0	0.721243	0.936629	0
lincRNA	-	1	0	0	0	0	0	0.115845	0	0	0	0	0
antisense	-	1	0	0	4	7	9	0.082334	0	0	0.284908	0.647483	0.736433
sense_intrc	-	2	5	1	0	0	0	0.02512	0.074007	0.016551	0	0	0
antisense	-	0	0	0	0	1	0	0	0	0	0	0.148319	0
antisense	-	1	1	1	1	0	3	0.12881	0.151795	0.16974	0.111433	0	0.384044
pseudogen	-	0	0	0	0	0	5	0	0	0	0	0	0.454353
protein_co	Uncharacte	52	37	34	30	24	26	4.355905	3.652446	3.753088	2.173999	2.258579	2.164502
lincRNA	-	0	0	0	10	8	3	0	0	0	1.162409	1.207633	0.400615
lincRNA	-	0	2	0	0	0	0	0	0.060336	0	0	0	0
antisense	-	1	7	0	3	0	1	0.128498	1.059986	0	0.333487	0	0.127704
pseudogen	serine/argi	0	1	1	3	4	0	0	0.081659	0.091313	0.179839	0.311392	0
lincRNA	-	0	0	0	4	6	0	0	0	0	0.292178	0.569148	0
antisense	-	3	2	0	0	0	3	0.075023	0.05894	0	0	0	0.074559
antisense	-	3	0	1	3	1	3	0.806208	0	0.354128	0.697445	0.301908	0.801229
lincRNA	-	2	0	0	7	2	2	0.164158	0	0	0.497042	0.184421	0.163144
lincRNA	-	5	4	1	0	4	7	0.354832	0.334519	0.093516	0	0.318906	0.493698
pseudogen	high_mobil	1	0	1	0	1	5	0.086364	0	0.113806	0	0.097024	0.429152
lincRNA	-	7	4	1	3	0	0	0.463813	0.312329	0.087313	0.171961	0	0
pseudogen	ubiquitin-c	3	5	3	1	5	4	0.342291	0.672282	0.451056	0.098705	0.640904	0.453569
pseudogen	family_with	0	0	0	1	2	4	0	0	0	0.068974	0.179144	0.316952
processed_	-	6	7	2	20	17	18	0.262084	0.360325	0.115121	0.755758	0.834233	0.781397
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.103775
antisense	-	0	0	0	0	4	3	0	0	0	0	0.424071	0.281359
processed_	-	4	16	1	5	6	4	0.0407	0.191852	0.013408	0.044012	0.068586	0.040449
antisense	-	7	7	6	11	12	13	0.51542	0.607391	0.582169	0.700679	0.992644	0.951297
sense_intrc	-	17	10	10	0	2	10	0.467046	0.323756	0.362031	0	0.061729	0.273036
pseudogen	-	5	0	4	0	6	9	0.318922	0	0.336209	0	0.429946	0.570514

antisense	-	0	3	1	0	0	0	0	0.377345	0.140652	0	0	0
sense_intrc	-	15	12	15	11	37	30	3.452674	3.255012	4.549779	2.190382	9.567865	6.862702
lincRNA	-	0	0	1	0	0	0	0	0	0.099096	0	0	0
antisense	-	7	0	3	0	1	0	0.796961	0	0.450086	0	0.127905	0
antisense	-	18	5	21	0	1	1	1.086588	0.355688	1.6705	0	0.067817	0.059993
antisense	-	11	3	4	0	2	1	0.809946	0.26031	0.388113	0	0.165441	0.073177
lincRNA	-	0	0	0	2	5	0	0	0	0	0.044101	0.143177	0
antisense	-	8	3	10	16	14	12	0.830447	0.366987	1.367907	1.436828	1.632672	1.237978
pseudogen	-	0	0	0	4	0	3	0	0	0	1.650411	0	1.422001
protein_co	Uncharacte	0	0	0	0	0	1	0	0	0	0	0	0.081446
antisense	-	0	0	0	0	1	0	0	0	0	0	0.155696	0
sense_intrc	-	0	1	1	7	0	0	0	0.10738	0.120074	0.551794	0	0
lincRNA	-	1	0	0	0	0	0	0.078199	0	0	0	0	0
lincRNA	-	4	7	1	2	0	0	0.250905	0.517434	0.082658	0.108528	0	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.144942
pseudogen	-	2	1	1	2	2	0	0.227703	0.134167	0.150029	0.196985	0.25581	0
antisense	-	0	0	0	4	0	0	0	0	0	0.581573	0	0
processed_	-	8	6	9	1	5	1	0.847056	0.748653	1.255739	0.091598	0.594759	0.105228
antisense	-	0	0	4	3	1	0	0	0	0.141221	0.069533	0.030099	0
pseudogen	-	5	3	3	7	3	4	0.464395	0.328356	0.367175	0.562443	0.313031	0.369221
protein_co	Homo_sapi	0	0	0	2	0	3	0	0	0	0.106262	0	0.183112
protein_co	lin-37_hom	18	20	17	15	11	32	0.582837	0.763153	0.725367	0.420173	0.400144	1.029755
sense_intrc	-	5	0	4	0	3	3	0.372824	0	0.393033	0	0.251307	0.222313
pseudogen	-	1	0	0	6	4	3	0.037815	0	0	0.196281	0.169931	0.112744
pseudogen	-	6	1	4	1	2	0	1.163538	0.228526	1.022173	0.167762	0.435721	0
antisense	-	2	0	0	0	0	0	0.033349	0	0	0	0	0
lincRNA	-	0	0	0	0	3	3	0	0	0	0	0.457507	0.404723
lincRNA	-	1	0	0	0	0	0	0.044789	0	0	0	0	0
pseudogen	NADH_deh	55	48	30	76	65	81	3.210314	3.301666	2.307496	3.837615	4.262331	4.698719
lincRNA	-	0	0	1	8	2	0	0	0	0.140369	0.737206	0.23934	0
lincRNA	-	13	12	12	5	1	9	1.333785	1.450877	1.622402	0.443788	0.115263	0.917687
protein_co	HCG20223	2	0	3	0	0	0	0.191815	0	0.379148	0	0	0
protein_co	Uncharacte	15	12	16	3	22	23	1.623957	1.530987	2.282643	0.280975	2.675808	2.474689
protein_co	-	0	0	3	0	5	0	0	0	0.840521	0	1.194296	0
antisense	-	1	1	3	0	1	1	0.145843	0.171867	0.576556	0	0.163846	0.144942
protein_co	NADH_deh	16	15	9	13	24	16	1.409411	1.557098	1.044708	0.990659	2.375078	1.400707
protein_co	-	1	1	5	0	0	5	0.072029	0.084881	0.47458	0	0	0.357919
antisense	-	58	59	33	26	35	54	1.196174	1.433921	0.89684	0.463877	0.81093	1.106801
lincRNA	-	1	0	0	5	7	13	0.040818	0	0	0.176557	0.320996	0.527357
antisense	-	3	9	4	21	24	16	0.223066	0.788609	0.391929	1.35081	2.004806	1.182338
sense_intrc	-	1	0	1	0	0	0	0.130719	0	0.172255	0	0	0
protein_co	HCG20187	3	21	8	4	4	4	0.071477	0.589623	0.251173	0.082446	0.107067	0.094715
protein_co	-	7	2	1	0	0	0	1.046856	0.352473	0.197071	0	0	0
protein_co	-	3	1	0	0	0	0	0.423528	0.166367	0	0	0	0

lincRNA	-	14	4	8	59	62	48	1.275687	0.42952	0.960596	4.650835	6.346828	4.346772
protein_co	Uncharacte	0	0	1	0	0	0	0	0	0.484467	0	0	0
antisense	-	0	3	0	1	3	2	0	0.118458	0	0.028987	0.112929	0.0666
protein_co	Uncharacte	0	0	0	0	0	4	0	0	0	0	0	0.296835
antisense	-	5	3	2	7	4	14	0.483038	0.341539	0.254611	0.585023	0.434131	1.344155
lincRNA	-	2	7	1	3	0	5	0.129282	0.533228	0.085181	0.167762	0	0.321209
sense_intrc	-	154	123	86	95	78	126	14.93208	14.05438	10.98836	7.968674	8.49656	12.1417
antisense	-	0	0	0	2	5	0	0	0	0	0.209606	0.680502	0
protein_co	zinc_finger	3	0	3	5	0	2	0.106521	0	0.140369	0.153585	0	0.070576
protein_co	-	4	3	3	1	3	0	0.341005	0.30139	0.337021	0.07375	0.287323	0
lincRNA	-	1	4	3	9	6	6	0.097677	0.460426	0.386144	0.760498	0.658405	0.582443
pseudogen	sorting_ne	0	0	1	0	2	0	0	0	0.056996	0	0.097183	0
lincRNA	-	0	0	0	8	5	4	0	0	0	1.103588	0.895722	0.633904
lincRNA	-	0	0	0	0	4	6	0	0	0	0	0.103843	0.137793
antisense	-	7	0	0	4	5	3	0.641154	0	0	0.316947	0.514498	0.273083
antisense	-	13	7	8	16	13	8	0.134054	0.085063	0.108708	0.142731	0.150601	0.081985
protein_co	Uncharacte	4	0	2	3	0	6	0.904974	0	0.596267	0.587165	0	1.349078
pseudogen	-	2	5	0	1	3	5	0.317012	0.933948	0	0.137122	0.534215	0.787635
lincRNA	-	2	10	9	11	4	6	0.251501	1.481894	1.491377	1.196646	0.565092	0.749844
lincRNA	-	12	8	5	22	9	12	0.469543	0.368885	0.25781	0.744698	0.395627	0.466643
protein_co	HCG19838	0	0	3	1	5	0	0	0	0.17934	0.039245	0.254824	0
protein_co	Uncharacte	42	27	26	17	19	17	10.89962	8.257199	8.891399	3.816575	5.539424	4.384504
lincRNA	-	0	0	2	3	18	11	0	0	0.034366	0.033842	0.263686	0.14255
lincRNA	-	33	21	24	76	67	72	2.868724	2.151301	2.749292	5.715463	6.543328	6.22038
lincRNA	microRNA_	7	9	2	2	3	3	0.41085	0.622494	0.154686	0.10155	0.197813	0.174991
pseudogen	olfactory_r	0	0	1	0	0	0	0	0	0.076917	0	0	0
protein_co	-	0	1	0	0	0	0	0	1.223289	0	0	0	0
protein_co	Uncharacte	0	0	3	3	0	2	0	0	0.840521	0.551794	0	0.422603
antisense	-	5	1	1	9	4	12	0.354832	0.08363	0.093516	0.552534	0.318906	0.846339
protein_co	Uncharacte	4	0	0	4	2	0	0.608517	0	0	0.526424	0.341816	0
protein_co	Uncharacte	7	1	4	3	8	12	4.751115	0.799843	3.577604	1.761496	6.100094	8.094469
antisense	-	0	1	1	0	0	1	0	0.160793	0.179802	0	0	0.135603
protein_co	Uncharacte	0	0	0	0	5	6	0	0	0	0	0.597148	0.633904
protein_co	hsa-mir-15	0	2	2	0	0	2	0	0.149611	0.167298	0	0	0.126173
antisense	-	16	8	15	66	28	27	0.430196	0.25348	0.531462	1.535159	0.845772	0.721473
antisense	PTOV1_ant	212	188	177	336	224	255	3.52829	3.687172	3.88183	4.837608	4.188182	4.217725
protein_co	Uncharacte	0	0	0	0	0	1	0	0	0	0	0	0.265728
antisense	-	5	8	8	5	11	16	0.444882	0.838827	0.937994	0.384865	1.099555	1.414832
lincRNA	-	0	0	0	17	17	17	0	0	0	1.177884	1.529638	1.35316
antisense	-	42	16	13	14	21	29	1.111205	0.498852	0.453235	0.320432	0.624185	0.762522
pseudogen	-	1	0	0	1	1	3	0.037761	0	0	0.032667	0.042422	0.112584
pseudogen	-	2	0	3	0	6	8	0.141743	0	0.280174	0	0.477718	0.56347
protein_co	Uncharacte	59	37	39	0	3	1	8.898914	6.576484	7.751476	0	0.508341	0.149898
pseudogen	-	6	7	9	1	7	0	0.470587	0.646984	0.930177	0.06785	0.616787	0

protein_co	Uncharacte	3	5	0	0	0	0	0.912776	1.792751	0	0	0	0
antisense	-	3	15	2	3	0	11	0.328147	1.933504	0.288278	0.283878	0	1.195774
antisense	-	38	33	28	11	10	19	1.743291	1.784051	1.692697	0.436558	0.515389	0.866263
sense_intrc	-	0	0	0	0	0	1	0	0	0	0	0	0.086679
antisense	-	0	0	2	0	0	1	0	0	0.298772	0	0	0.112664
pseudogen	-	0	0	0	4	1	3	0	0	0	0.329489	0.106971	0.283889
protein_co	Uncharacte	3	0	0	0	0	0	0.225601	0	0	0	0	0
antisense	NAPA_antis	10	15	9	6	4	7	0.302002	0.533837	0.358169	0.156756	0.135712	0.210096
protein_co	Uncharacte	0	2	0	4	0	1	0	0.115319	0	0.169312	0	0.048627
pseudogen	-	3	2	0	11	5	9	0.277663	0.218139	0	0.880748	0.519894	0.827843
protein_co	Uncharacte	1	4	0	2	0	2	0.476946	2.248206	0	0.825206	0	0.948001
protein_co	Uncharacte	4	0	0	0	0	5	0.449605	0	0	0	0	0.558536
antisense	-	0	0	0	0	0	4	0	0	0	0	0	0.470819
protein_co	-	2	0	0	0	0	5	2.352933	0	0	0	0	5.846006
lincRNA	-	66	51	63	55	64	61	9.292834	8.462165	11.68906	6.699308	10.12356	8.53579
processed_	-	13	2	10	8	4	5	0.898476	0.162892	0.910748	0.478318	0.310579	0.343434
antisense	-	1	3	0	3	1	1	0.091435	0.323252	0	0.2373	0.102722	0.090871
protein_co	Uncharacte	1	0	1	0	0	0	0.464395	0	0.611959	0	0	0
pseudogen	-	4	0	0	3	5	1	0.236344	0	0	0.153345	0.331897	0.058721
antisense	-	0	2	0	0	1	2	0	0.239953	0	0	0.114377	0.202362
protein_co	Uncharacte	0	0	0	0	3	7	0	0	0	0	2.973796	6.138306
pseudogen	vomeronas	8	0	0	6	2	3	1.802247	0	0	1.169334	0.506178	0.671669
processed_	-	8	2	2	257	181	236	0.090304	0.026605	0.02975	2.509663	2.295339	2.64753
protein_co	Uncharacte	0	0	0	0	0	1	0	0	0	0	0	0.427757
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.106018	0
protein_co	-	0	0	0	1	5	1	0	0	0	2.1809	14.16093	2.505431
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.05747
protein_co	-	4	3	2	0	3	0	0.564704	0.499102	0.372071	0	0.475807	0
antisense	-	10	7	13	0	1	6	1.07168	0.884037	1.835876	0	0.120397	0.639037
protein_co	HBcAg-binc	1	0	0	3	1	0	0.089579	0	0	0.232482	0.100636	0
protein_co	Uncharacte	0	0	1	2	0	1	0	0	0.105065	0.137949	0	0.079238
lincRNA	-	9	19	9	1	2	12	0.725219	1.804211	0.955661	0.069709	0.181053	0.960987
protein_co	Uncharacte	2	0	1	0	0	0	0.235293	0	0.15503	0	0	0
protein_co	Uncharacte	30	16	27	5	7	8	0.77211	0.485272	0.915707	0.111325	0.202397	0.204624
pseudogen	-	0	0	3	4	7	0	0	0	0.376421	0.329489	0.748798	0
protein_co	LOC64690	58	43	37	225	239	273	2.088828	1.824947	1.755947	7.010037	9.669894	9.771181
protein_co	Uncharacte	0	1	2	0	0	12	0	0.185678	0.415258	0	0	1.879073
protein_co	small_integ	4	4	4	6	2	2	0.196807	0.231925	0.259343	0.255384	0.11055	0.097796
lincRNA	-	0	0	0	3	0	1	0	0	0	0.314409	0	0.120398
processed_	-	20	15	7	28	18	21	0.597866	0.528411	0.275744	0.724093	0.604498	0.623882
antisense	-	2	6	0	0	1	9	0.060747	0.21476	0	0	0.034123	0.271673
sense_intrc	-	14	28	10	14	18	7	1.347589	3.176103	1.268423	1.16579	1.946485	0.669633
antisense	-	1	0	2	5	0	2	0.062801	0	0.165512	0.271642	0	0.124826
lincRNA	-	702	647	352	1119	645	814	8.728177	9.47977	5.767185	12.03593	9.009386	10.0582

protein_co	Uncharacte	1	0	0	0	0	0	0.375468	0	0	0	0	0
protein_co	-	4	1	2	2	0	4	6.41709	1.890537	4.228078	2.775691	0	6.377461
protein_co	CDNA:_FLJ	11	13	8	9	5	6	0.315466	0.43935	0.302333	0.223288	0.161094	0.17101
protein_co	-	30	38	21	40	20	44	0.433943	0.647741	0.400281	0.500534	0.325005	0.632519
antisense	-	74	83	78	84	63	55	2.199682	2.907457	3.055326	2.160083	2.103865	1.624802
pseudogen	eukaryotic_	0	0	2	0	0	0	0	0	0.100091	0	0	0
pseudogen	-	14	6	10	36	17	21	0.699221	0.353138	0.658144	1.555435	0.953859	1.042354
processed_	-	32	49	25	15	20	26	0.509967	0.920228	0.52501	0.206798	0.358073	0.41179
protein_co	Uncharacte	0	0	0	3	0	0	0	0	0	0.088586	0	0
antisense	antisense_c	4	1	1	5	3	0	0.048414	0.014263	0.01595	0.052354	0.040793	0
sense_over	-	1	0	3	0	0	0	0.060366	0	0.238643	0	0	0
protein_co	-	2	1	3	5	10	10	2.941166	1.732992	5.813607	6.360959	16.52109	14.61501
lincRNA	-	1	1	0	1	1	0	0.098221	0.115747	0	0.08497	0.110345	0
protein_co	-	0	0	0	0	1	0	0	0	0	0	1.652109	0
pseudogen	-	0	0	0	0	0	4	0	0	0	0	0	0.153955
lincRNA	-	14	8	14	14	14	9	0.941771	0.634183	1.241024	0.81472	1.058021	0.601685
pseudogen	-	0	0	0	0	1	2	0	0	0	0	0.053534	0.094715
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.187907
pseudogen	-	0	4	3	7	0	0	0	0.729681	0.611959	0.937404	0	0
pseudogen	C-type_lect	0	0	0	13	8	39	0	0	0	0.684351	0.546905	2.358561
antisense	-	2	0	4	0	0	0	0.288507	0	0.760363	0	0	0
protein_co	Uncharacte	0	0	0	0	0	2	0	0	0	0	0	0.556762
lincRNA	-	2	2	4	2	0	0	0.23068	0.271842	0.607959	0.19956	0	0
protein_co	Uncharacte	0	0	0	2	1	2	0	0	0	0.090601	0.058829	0.104083
pseudogen	-	6	3	0	0	4	3	0.56824	0.334818	0	0	0.425588	0.282365
protein_co	-	0	0	4	3	1	3	0	0	1.788802	0.880748	0.381256	1.011809
protein_co	Uncharacte	2	0	2	3	2	5	0.551469	0	0.726701	0.715608	0.619541	1.370158
processed_	-	5	12	2	8	13	1	0.229579	0.649309	0.121012	0.317772	0.670587	0.045632
lincRNA	-	6	3	11	7	5	10	0.743902	0.438321	1.797181	0.750802	0.696439	1.232179
protein_co	Uncharacte	2	0	0	0	0	0	0.15548	0	0	0	0	0
lincRNA	-	0	0	0	0	2	1	0	0	0	0	0.200256	0.088576
pseudogen	vomeronas	7	3	7	47	24	27	0.996201	0.503127	1.31275	5.786421	3.837156	3.818762
protein_co	HCG16587	1	0	0	15	18	22	0.051349	0	0	0.666327	1.038377	1.122705
lincRNA	-	75	44	57	85	66	86	2.019621	1.396267	2.022638	1.980115	1.996648	2.30153
antisense	-	24	30	23	17	14	15	0.698891	1.0295	0.882594	0.428263	0.45801	0.434109
protein_co	Uncharacte	0	0	2	0	0	0	0	0	2.022124	0	0	0
antisense	-	8	5	5	3	8	20	0.759011	0.55903	0.625119	0.246231	0.852701	1.885808
protein_co	HCG18184	4	0	1	1	1	1	0.624672	0	0.205791	0.1351	0.175445	0.155204
antisense	-	0	0	2	0	0	0	0	0	0.536641	0	0	0
lincRNA	FOXF1_adj	6	6	7	0	0	0	0.102632	0.120946	0.157784	0	0	0
lincRNA	-	4	10	7	7	6	0	0.458364	1.350384	1.057019	0.693923	0.772415	0
protein_co	Uncharacte	0	0	0	2	0	0	0	0	0	1.221304	0	0
protein_co	Uncharacte	3	0	0	0	1	0	0.208429	0	0	0	0.078052	0
lincRNA	-	5	16	1	2	7	11	0.48659	1.834933	0.128241	0.168378	0.765315	1.063887

protein_co	-	14	12	8	9	7	6	15.44112	15.59693	11.62721	8.587295	8.673571	6.576756
protein_co	LOC64465(	2	2	2	2	2	3	0.401068	0.472634	0.52851	0.346961	0.450575	0.597887
protein_co	CDNA_FLJ2	18	12	7	5	10	6	0.517058	0.406214	0.264972	0.124251	0.322713	0.171288
protein_co	Uncharacte	3	1	2	1	1	2	0.389272	0.152911	0.341977	0.112252	0.145774	0.257912
protein_co	Uncharacte	0	0	0	0	1	0	0	0	0	0	0.092642	0
protein_co	Uncharacte	2	0	0	0	5	1	0.213903	0	0	0	0.600767	0.106291
pseudogen	-	0	0	6	22	11	11	0	0	1.01597	2.445573	1.587949	1.404744
pseudogen	hepatitis_A	14	5	7	25	5	10	0.701869	0.295396	0.462446	1.084254	0.281609	0.498239
pseudogen	-	0	0	0	2	0	0	0	0	0	0.057428	0	0
protein_co	-	2	1	1	3	6	0	2.076117	1.223289	1.367907	2.694053	6.997167	0
lincRNA	-	2	3	1	3	0	3	0.318922	0.563745	0.21013	0.413846	0	0.475428
processed_	-	2	1	0	2	0	1	0.031644	0.018645	0	0.027375	0	0.015724
protein_co	Uncharacte	3	1	0	17	0	3	0.670139	0.263239	0	3.285154	0	0.666001
protein_co	-	6	10	9	6	6	13	0.284884	0.559531	0.563112	0.246452	0.32005	0.613437
pseudogen	-	0	0	0	3	0	0	0	0	0	0.252567	0	0
lincRNA	microRNA_	43	45	42	93	49	84	0.758821	0.935816	0.976686	1.419766	0.97144	1.473193
protein_co	LOC100132	0	0	1	1	2	1	0	0	0.061737	0.04053	0.105267	0.046561
protein_co	Uncharacte	3	0	0	2	0	3	0.38363	0	0	0.221251	0	0.381261
sense_intrc	-	21	11	1	1	1	3	2.301782	1.420839	0.144437	0.094822	0.123139	0.326795
sense_intrc	-	2	4	0	0	1	2	0.245097	0.577664	0	0	0.137676	0.243584
protein_co	-	1	2	1	0	0	0	0.322811	0.760826	0.425386	0	0	0
antisense	-	105	56	64	106	82	103	2.055011	1.291576	1.650592	1.794708	1.802967	2.003419
lincRNA	-	6	12	4	1	2	11	0.507422	1.195931	0.445772	0.073161	0.190019	0.924528
sense_intrc	-	9	9	2	7	17	7	1.007334	1.187082	0.294982	0.677785	2.137612	0.778643
pseudogen	vomeronas	10	8	6	27	25	23	1.189685	1.121577	0.940629	2.77881	3.341344	2.719378
pseudogen	cytochrom	0	0	0	6	10	1	0	0	0	0.336344	0.727979	0.064399
protein_co	-	0	0	0	4	0	0	0	0	0	0.26901	0	0
protein_co	-	1	1	3	9	2	6	0.101614	0.119746	0.401708	0.791152	0.228314	0.60592
pseudogen	-	0	1	1	0	0	0	0	0.093116	0.104124	0	0	0
lincRNA	-	0	0	0	2	0	2	0	0	0	0.219134	0	0.251742
protein_co	Uncharacte	4	6	4	0	19	10	3.069043	5.42502	4.044248	0	16.37743	7.625225
protein_co	-	5	2	1	1	7	2	1.025988	0.483626	0.2704	0.177515	1.613688	0.407861
lincRNA	-	12	6	14	14	12	13	1.283418	0.756215	1.973103	1.295323	1.44184	1.381783
pseudogen	vomeronas	4	1	1	2	8	1	1.013225	0.298506	0.333796	0.438267	2.27659	0.251742
antisense	-	10	18	11	10	12	20	0.267649	0.567735	0.387966	0.231541	0.360825	0.531992
protein_co	Uncharacte	2	3	0	0	0	0	0.371516	0.656713	0	0	0	0
lincRNA	-	0	0	0	3	1	3	0	0	0	0.116636	0.050489	0.133992
lincRNA	-	0	1	0	0	0	0	0	0.099344	0	0	0	0
antisense	-	2	4	1	5	3	3	0.297421	0.700986	0.195964	0.643243	0.501202	0.443377
lincRNA	-	0	2	1	0	1	2	0	0.093957	0.052533	0	0.044786	0.079238
lincRNA	-	17	13	15	43	12	16	0.205385	0.185085	0.238806	0.449419	0.162873	0.19211
processed_	-	107	98	91	79	69	79	1.115315	1.20378	1.249943	0.712367	0.808001	0.818372
protein_co	Uncharacte	13	0	2	0	9	2	2.549011	0	0.516765	0	1.982531	0.389734
antisense	-	3	0	0	7	1	1	0.280606	0	0	0.566418	0.105081	0.092958

antisense	-	6	4	11	12	11	9	0.399555	0.313901	0.965278	0.691304	0.822937	0.595631
protein_co	Uncharacte	15	14	19	9	17	23	0.456388	0.50197	0.761783	0.236891	0.581087	0.695473
pseudogen	-	4	4	3	2	2	8	0.458364	0.540154	0.453008	0.198264	0.257472	0.911066
pseudogen	vomeronas	3	2	0	0	0	7	0.46989	0.369158	0	0	0	1.08964
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.09463
antisense	-	1	0	0	0	0	0	0.083241	0	0	0	0	0
lincRNA	-	5	1	6	14	10	23	0.685764	0.161626	1.084403	1.6611	1.540827	3.135034
lincRNA	-	0	0	0	0	2	2	0	0	0	0	0.114708	0.101474
protein_co	Uncharacte	17	3	5	1	4	3	4.918016	1.02275	1.906101	0.250267	1.30002	0.862525
lincRNA	hsa-mir-29	10	7	4	14	2	15	0.891263	0.735209	0.469786	1.079435	0.200256	1.328638
processed_	-	1	2	1	4	2	0	0.058113	0.136965	0.076579	0.201093	0.130573	0
lincRNA	-	0	0	0	3	1	1	0	0	0	0.278695	0.120641	0.106722
protein_co	-	7	8	3	5	3	9	5.882333	7.922251	3.322061	3.634834	2.832187	7.516293
protein_co	Uncharacte	0	0	0	0	0	1	0	0	0	0	0	0.020267
lincRNA	-	0	0	0	40	45	26	0	0	0	0.487222	0.711813	0.363821
protein_co	Uncharacte	1	0	0	0	0	0	0.392156	0	0	0	0	0
pseudogen	WW_doma	2	0	0	0	0	0	0.249722	0	0	0	0	0
sense_intrc	-	24	12	22	3	15	15	1.857579	1.094522	2.243848	0.200872	1.304296	1.153817
antisense	-	3	1	0	0	1	0	0.151984	0.059701	0	0	0.056915	0
sense_intrc	-	1	1	0	0	1	0	0.128186	0.15106	0	0	0.144009	0
antisense	-	1	0	1	6	0	1	0.016225	0	0.02138	0.084215	0	0.016124
protein_co	Uncharacte	1	4	3	0	1	0	0.259515	1.223289	1.025931	0	0.291549	0
pseudogen	-	1	0	1	7	0	0	0.095561	0	0.125927	0.578687	0	0
lincRNA	-	1	0	0	4	0	3	0.10442	0	0	0.361333	0	0.311326
lincRNA	-	66	44	28	79	49	78	2.52282	1.981993	1.410377	2.612356	2.104202	2.963102
pseudogen	-	0	1	0	0	0	0	0	0.055407	0	0	0	0
protein_co	Uncharacte	0	1	1	0	0	2	0	0.770219	0.861275	0	0	1.299112
pseudogen	-	0	1	0	3	5	1	0	0.158344	0	0.348723	0.754771	0.133538
protein_co	Uncharacte	1	4	0	0	0	1	0.551469	2.599489	0	0	0	0.548063
sense_intrc	-	19	15	11	5	5	7	2.711264	2.522415	2.068453	0.617236	0.801562	0.992718
protein_co	Uncharacte	0	0	1	0	0	0	0	0	0.026904	0	0	0
lincRNA	-	16	12	5	5	0	1	2.462372	2.176316	1.014001	0.665682	0	0.152948
pseudogen	-	6	0	0	3	0	0	1.024664	0	0	0.443215	0	0
lincRNA	secretoglob	2	1	1	10	6	1	0.17301	0.101941	0.113992	0.748348	0.583097	0.085971
antisense	-	8	5	10	6	10	6	0.748283	0.551128	1.232567	0.485501	1.050811	0.557746
protein_co	Protein_LO	1	0	0	8	0	0	0.009686	0	0	0.067031	0	0
antisense	-	6	2	0	4	0	2	0.968433	0.380413	0	0.558523	0	0.320817
pseudogen	ribosomal_	1	0	3	0	0	0	0.072821	0	0.287881	0	0	0
protein_co	Small_inte	0	0	0	1	0	0	0	0	0	0.047907	0	0
protein_co	Uncharacte	0	2	0	0	0	0	0	0.305822	0	0	0	0
protein_co	Uncharacte	45	40	37	17	12	19	2.165768	2.268645	2.346583	0.707801	0.648828	0.908788
pseudogen	-	3	0	0	0	0	0	0.38832	0	0	0	0	0
protein_co	Uncharacte	5	2	8	1	2	4	2.673788	1.260358	5.637437	0.462615	1.201534	2.12582
protein_co	HCG40128	0	1	0	0	0	0	0	0.180834	0	0	0	0

protein_co	Uncharacte	30	8	22	1	2	8	2.196722	0.690321	2.122811	0.063346	0.164525	0.582175
lincRNA	-	11	21	11	63	37	42	0.877035	1.973106	1.155717	4.345378	3.31417	3.327997
protein_co	Uncharacte	3	1	4	0	1	3	2.406409	0.945269	4.228078	0	0.90115	2.391548
lincRNA	-	0	1	0	0	8	3	0	0.114054	0	0	0.869849	0.28856
protein_co	HCG20053	2	0	0	2	0	1	0.083635	0	0	0.072352	0	0.041559
antisense	-	0	0	0	12	14	23	0	0	0	1.530883	2.319395	3.370817
protein_co	-	0	0	0	5	1	0	0	0	0	1.659381	0.430985	0
pseudogen	sialic_acid_	1	0	1	0	0	0	0.096082	0	0.126612	0	0	0
protein_co	CDNA_FLJ2	13	22	24	13	20	12	0.35294	0.703862	0.858625	0.305326	0.610009	0.323779
protein_co	Uncharacte	5	2	4	1	6	1	2.005341	0.945269	2.114039	0.346961	2.703451	0.398591
protein_co	Protein_LO	4	4	6	4	5	10	0.089239	0.105163	0.176393	0.0772	0.125318	0.22172
pseudogen	-	0	0	0	1	4	0	0	0	0	0.047509	0.246788	0
pseudogen	espin_pseu	0	0	0	5	3	1	0	0	0	0.113645	0.08855	0.026111
pseudogen	IGF-like_far	0	0	0	0	0	2	0	0	0	0	0	0.2923
pseudogen	-	1	2	2	0	0	0	0.089126	0.21006	0.234893	0	0	0
protein_co	Uncharacte	16	14	16	15	34	51	1.138516	1.173963	1.500286	0.923365	2.717985	3.606608
lincRNA	-	0	0	0	2	0	0	0	0	0	0.16386	0	0
protein_co	Uncharacte	11	11	8	8	5	22	7.466038	8.79827	7.155208	4.697324	3.812559	14.83986
pseudogen	-	0	0	0	1	0	1	0	0	0	0.04156	0	0.047744
antisense	PLCE1_anti	2	1	1	2	3	0	0.062913	0.037069	0.041452	0.054425	0.106018	0
antisense	A1BG_antis	43	46	46	14	7	33	1.068762	1.347341	1.506625	0.301026	0.195461	0.815147
antisense	-	6	10	0	0	0	0	0.709031	1.392583	0	0	0	0
pseudogen	-	0	1	0	0	1	4	0	0.082633	0	0	0.078776	0.27875
lincRNA	-	17	31	28	4	13	2	0.357567	0.768383	0.776071	0.072783	0.307186	0.041807
lincRNA	-	10	4	5	18	15	13	1.195056	0.56332	0.787396	1.860904	2.013857	1.543979
protein_co	Protein_LO	2	0	0	0	0	0	0.043953	0	0	0	0	0
protein_co	-	19	15	7	24	10	33	0.241218	0.224416	0.117109	0.263591	0.142628	0.41637
antisense	-	0	0	0	2	0	0	0	0	0	0.179252	0	0
antisense	-	0	4	3	2	2	5	0	0.592758	0.497126	0.217572	0.282546	0.62487
protein_co	HCG17855	0	2	4	1	1	0	0	0.132038	0.295294	0.048464	0.062937	0
protein_co	CDC28_prc	0	5	0	15	9	19	0	1.299744	0	2.862432	2.230347	4.165279
lincRNA	-	9	1	3	3	5	13	0.750345	0.098248	0.32959	0.216373	0.468314	1.077138
sense_intrc	-	2	2	1	15	9	10	0.104215	0.12281	0.068665	0.676165	0.526854	0.517855
protein_co	Uncharacte	36	22	14	14	17	19	7.302206	5.258736	3.742092	2.456646	3.87391	3.830142
protein_co	HCG17876	0	1	0	2	0	1	0	0.147489	0	0.216543	0	0.124383
protein_co	Liver-relate	0	0	0	0	0	1	0	0	0	0	0	0.30238
protein_co	endogenou	0	0	0	13	0	6	0	0	0	0.244914	0	0.129858
protein_co	Uncharacte	0	0	0	0	4	0	0	0	0	0	0.558459	0
sense_intrc	-	22	31	15	30	28	74	1.808543	3.003136	1.624921	2.133489	2.585909	6.045714
protein_co	HCG19799	1	0	0	0	0	0	0.569258	0	0	0	0	0
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.129911
sense_intrc	-	0	0	0	0	4	0	0	0	0	0	0.440562	0
pseudogen	-	3	0	1	4	2	0	0.207883	0	0.091313	0.239785	0.155696	0
pseudogen	vomeronas	10	8	10	79	30	34	1.487107	1.401971	1.959643	10.16324	5.012015	5.024937

protein_co	Uncharacte	18	18	11	5	7	17	3.0252	3.565013	2.436178	0.726967	1.321687	2.839488
pseudogen	zinc_finger_	0	1	0	7	11	6	0	0.152537	0	0.783844	1.599597	0.771844
antisense	-	1	0	3	3	0	0	0.05532	0	0.218694	0.14357	0	0
protein_co	Uncharacte	1	0	0	0	0	1	0.086505	0	0	0	0	0.085971
protein_co	MT-RNR2-li	6	3	3	7	5	7	0.311418	0.183493	0.205186	0.314306	0.291549	0.361077
lincRNA	-	5	4	3	17	8	8	0.58563	0.552104	0.463031	1.722525	1.052671	0.931222
pseudogen	-	0	0	0	4	2	0	0	0	0	0.328897	0.213558	0
protein_co	-	4	0	0	0	0	0	4.152235	0	0	0	0	0
sense_intro	-	163	149	121	204	134	206	5.882333	6.336586	5.754163	6.368764	5.432701	7.388203
protein_co	CDNA_FLJ2	6	13	5	0	0	0	0.135688	0.34645	0.149003	0	0	0
protein_co	-	0	1	0	1	2	0	0	0.2929	0	0.215018	0.558459	0
antisense	-	0	0	0	3	0	0	0	0	0	0.272613	0	0
lincRNA	-	1	0	0	5	0	3	0.097139	0	0	0.420173	0	0.289619
antisense	-	3	1	1	6	2	6	0.201042	0.078972	0.088308	0.34784	0.150572	0.3996
protein_co	calreticulin	0	0	0	0	1	2	0	0	0	0	0.046034	0.081446
antisense	-	7	5	4	1	2	9	0.60752	0.511375	0.457464	0.07508	0.195003	0.776273
antisense	-	2	7	0	7	13	10	0.194636	0.802783	0	0.589324	1.421299	0.96717
pseudogen	-	19	28	24	8	5	6	0.49332	0.856722	0.821147	0.179692	0.145846	0.154823
protein_co	-	0	0	0	0	1	1	0	0	0	0	1.652109	1.461501
protein_co	Uncharacte	3	2	1	0	5	1	1.604273	1.260358	0.70468	0	3.003834	0.531455
lincRNA	-	0	0	0	2	3	4	0	0	0	0.017276	0.033653	0.039694
protein_co	Uncharacte	5	0	8	2	8	15	0.20315	0	0.428324	0.070298	0.365163	0.605687
antisense	-	1	1	1	2	1	1	0.092879	0.109452	0.122392	0.160698	0.104344	0.092305
pseudogen	-	0	0	0	0	8	0	0	0	0	0	0.626062	0
antisense	-	3	8	4	3	7	7	0.355309	1.116559	0.62428	0.307375	0.93139	0.823934
protein_co	Uncharacte	6	0	6	9	0	12	1.654406	0	2.180103	2.146824	0	3.288378
protein_co	-	1	0	0	0	0	2	1.357461	0	0	0	0	2.698156
protein_co	-	0	0	1	2	0	1	0	0	0.2236	0.293583	0	0.168635
antisense	-	3	12	2	0	0	2	0.336489	1.586129	0.295607	0	0	0.222941
antisense	-	0	3	0	6	0	5	0	1.028369	0	1.509854	0	1.445441
antisense	-	91	96	60	116	72	130	1.994052	2.478983	1.732532	2.198954	1.772461	2.831054
pseudogen	-	0	0	0	1	0	0	0	0	0	0.058194	0	0
antisense	-	1	0	2	0	1	1	0.167006	0	0.440147	0	0.187621	0.165975
antisense	-	4	4	4	3	14	12	0.277178	0.326637	0.365253	0.179839	1.089873	0.826399
pseudogen	-	1	0	1	0	0	1	0.078315	0	0.1032	0	0	0.077831
antisense	-	13	6	4	19	9	22	1.496159	0.813753	0.606637	1.891694	1.163659	2.516324
protein_co	HCG17453	6	2	7	6	2	1	0.201169	0.079022	0.309274	0.17403	0.075334	0.033321
antisense	-	3	5	5	3	2	5	0.435131	0.854626	0.955661	0.376429	0.325895	0.72074
protein_co	Uncharacte	13	7	5	19	10	19	0.363567	0.230699	0.184266	0.459683	0.314189	0.528086
antisense	-	0	4	0	0	0	0	0	0.328356	0	0	0	0
antisense	-	1	0	0	0	0	0	0.094369	0	0	0	0	0
protein_co	-	0	0	0	0	2	0	0	0	0	0	3.604601	0
sense_intro	-	0	0	4	0	0	1	0	0	0.265512	0	0	0.050061
protein_co	F-box_prot	460	376	249	154	104	115	10.21941	9.843805	7.289575	2.959728	2.595676	2.539075

antisense	-	3	5	2	6	2	7	0.360961	0.708951	0.317106	0.624531	0.270345	0.837042
lincRNA	-	5	19	5	2	3	7	0.171663	0.76872	0.22621	0.059402	0.115712	0.238845
protein_co	Uncharacte	0	0	0	0	0	2	0	0	0	0	0	0.14615
pseudogen	-	6	15	11	7	9	7	0.632761	1.864175	1.528677	0.63863	1.066301	0.733662
antisense	-	2	2	5	9	11	6	0.151693	0.178761	0.499737	0.59053	0.9373	0.45227
pseudogen	-	0	0	0	1	0	0	0	0	0	0.046734	0	0
antisense	-	12	6	6	8	13	7	0.212686	0.125319	0.140134	0.122662	0.258851	0.1233
lincRNA	-	4	0	0	0	3	0	1.224069	0	0	0	1.031374	0
protein_co	-	0	0	1	0	0	0	0	0	0.310059	0	0	0
antisense	-	0	0	2	4	0	7	0	0	0.088029	0.115581	0	0.232365
lincRNA	-	11	5	4	5	5	4	0.83193	0.445627	0.398647	0.327135	0.424828	0.300652
protein_co	Uncharacte	3	1	1	1	2	4	0.594843	0.233662	0.261286	0.171531	0.445512	0.788225
antisense	-	91	53	54	36	40	52	2.227291	1.528687	1.741663	0.762256	1.099878	1.264878
antisense	-	0	0	3	0	0	4	0	0	0.057293	0	0	0.057612
antisense	-	0	0	0	0	1	0	0	0	0	0	0.110756	0
protein_co	Uncharacte	0	1	0	4	1	0	0	0.087378	0	0.256577	0.0833	0
antisense	-	3	0	2	0	3	1	0.281103	0	0.24695	0	0.315801	0.093122
pseudogen	-	5	6	10	1	0	3	0.832406	1.177127	2.193814	0.144022	0	0.496359
protein_co	HCG20114	3	1	2	4	5	2	1.126404	0.442466	0.98955	1.29926	2.109075	0.746299
antisense	-	10	14	9	16	21	14	0.292169	0.482024	0.346506	0.404405	0.68929	0.40651
antisense	-	1	2	0	1	3	1	0.147468	0.347564	0	0.127574	0.497013	0.146557
protein_co	Uncharacte	6	10	12	2	18	16	0.134141	0.263462	0.35353	0.038682	0.452097	0.3555
protein_co	Uncharacte	0	1	0	0	0	0	0	1.094522	0	0	0	0
protein_co	zinc_finger	169	161	127	1000	612	735	2.679553	3.008213	2.65347	13.71635	10.90125	11.58171
antisense	-	0	0	0	0	0	1	0	0	0	0	0	0.059789
antisense	-	22	31	19	20	25	53	1.619891	2.689874	1.843536	1.273961	2.068008	3.878365
protein_co	Uncharacte	3	8	2	1	0	0	1.176467	3.697051	1.03353	0.339251	0	0
sense_intrc	-	5	1	4	9	6	5	0.93867	0.221233	0.98955	1.461667	1.265445	0.932873
protein_co	Uncharacte	1	0	0	0	0	0	0.392156	0	0	0	0	0
pseudogen	-	0	0	0	5	9	2	0	0	0	1.293754	3.024199	0.594509
pseudogen	-	0	0	0	3	0	1	0	0	0	0.433428	0	0.165975
pseudogen	-	0	0	1	0	0	0	0	0	0.109176	0	0	0
sense_intrc	-	0	0	0	3	0	1	0	0	0	0.211705	0	0.081069
pseudogen	integrin_be	30	45	43	55	51	68	2.607931	4.609931	4.925815	4.13619	4.980742	5.874804
antisense	RAB11B_an	13	3	13	7	7	10	0.679401	0.184761	0.895284	0.316478	0.410989	0.519388
lincRNA	-	0	0	2	0	0	0	0	0	0.825601	0	0	0
pseudogen	-	52	61	16	17	21	17	2.963328	4.096503	1.20152	0.838085	1.34445	0.962797
antisense	-	0	0	0	0	4	0	0	0	0	0	0.782578	0
protein_co	Protein_LO	10	0	1	0	2	0	1.056706	0	0.139248	0	0.237429	0
sense_intrc	-	0	3	2	54	46	38	0	0.124775	0.093018	1.648761	1.823928	1.332889
lincRNA	-	27	14	14	72	38	54	0.740242	0.452319	0.505793	1.707675	1.170422	1.471341
protein_co	Uncharacte	2	0	3	7	5	2	0.20884	0	0.4128	0.632332	0.586548	0.20755
protein_co	Uncharacte	0	0	1	0	0	0	0	0	0.126612	0	0	0
protein_co	Spi-B_trans	0	0	5	0	0	6	0	0	0.092012	0	0	0.083272

protein_co	-	2	0	4	1	3	2	1.857579	0	4.895669	0.80349	3.130311	1.846107
lincRNA	-	0	0	0	202	133	147	0	0	0	3.344678	2.859833	2.796191
antisense	-	0	4	0	0	0	0	0	0.43935	0	0	0	0
pseudogen	zinc_finger_	0	0	2	4	1	3	0	0	0.146254	0.192029	0.062344	0.165453
protein_co	-	2	3	1	0	2	1	2.205875	3.899233	1.453402	0	2.478163	1.096126
lincRNA	-	5	3	0	2	0	2	0.430415	0.30433	0	0.14894	0	0.171103
antisense	-	0	0	0	8	2	8	0	0	0	1.31323	0.426351	1.508647
antisense	-	73	73	48	87	61	108	8.53133	10.05365	7.392136	8.795816	8.008898	12.54375
protein_co	LRRC3_dov	164	140	101	88	74	107	3.833255	3.856195	3.110857	1.779384	1.943143	2.48552
pseudogen	-	0	1	0	1	0	0	0	0.111407	0	0.081784	0	0
lincRNA	-	66	48	33	27	10	24	4.508523	3.864014	2.970566	1.595575	0.767431	1.629338
sense_overl	-	4	6	0	7	3	8	0.473745	0.837419	0	0.717209	0.399167	0.941638
protein_co	Protein_LO	0	0	0	0	1	0	0	0	0	0	0.024802	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.695625	0
sense_intrc	-	1	7	6	1	5	2	0.138589	1.143231	1.095758	0.119892	0.778481	0.275466
pseudogen	-	0	0	1	6	10	16	0	0	0.16974	0.668597	1.447103	2.048236
pseudogen	-	1	0	0	1	0	0	0.096784	0	0	0.083727	0	0
lincRNA	-	23	11	11	9	13	12	0.225406	0.127039	0.142058	0.076303	0.14313	0.116877
antisense	-	0	0	1	0	0	0	0	0	0.110911	0	0	0
antisense	-	4	7	7	2	6	9	0.30646	0.632003	0.706719	0.132558	0.516433	0.685277
lincRNA	-	3	0	0	0	3	2	0.375468	0	0	0	0.421815	0.248766
lincRNA	-	7	8	5	16	12	8	0.112401	0.151381	0.105798	0.222257	0.216473	0.127665
antisense	-	6	2	1	1	1	2	0.565206	0.22202	0.124134	0.081493	0.105829	0.187239
lincRNA	-	0	0	0	1	0	0	0	0	0	0.083422	0	0
protein_co	SBP1;_Uncl	3	10	10	21	3	9	0.569258	2.236119	2.500476	3.447229	0.639526	1.697227
pseudogen	-	5	2	10	1	2	3	0.127201	0.059959	0.335239	0.022008	0.057161	0.075849
protein_co	HCG20271	0	1	0	0	0	0	0	0.378107	0	0	0	0
protein_co	-	0	3	1	15	2	1	0	0.051348	0.019139	0.188473	0.032634	0.014435
lincRNA	-	2	1	3	4	1	5	0.294936	0.173782	0.58298	0.510294	0.165671	0.732786
protein_co	endogenou	0	0	0	6	4	1	0	0	0	0.124793	0.10804	0.023894
protein_co	Uncharacte	1	2	4	2	3	3	0.143472	0.338145	0.756242	0.248233	0.483544	0.427757
protein_co	Uncharacte	0	0	2	2	0	0	0	0	0.221471	0.145393	0	0
antisense	-	12	2	3	4	11	18	0.745648	0.14645	0.245645	0.215018	0.767882	1.111564
antisense	-	1	5	6	7	3	0	0.027791	0.163747	0.219727	0.16829	0.093663	0
pseudogen	-	1	0	0	0	0	0	0.039187	0	0	0	0	0
protein_co	Uncharacte	0	0	0	3	0	0	0	0	0	0.093914	0	0
protein_co	CDNA_FLJ2	1	0	0	7	6	13	0.016807	0	0	0.101775	0.113287	0.217137
protein_co	Uncharacte	82	60	28	95	69	68	2.234257	1.926538	1.005338	2.239267	2.112114	1.841356
protein_co	Protein_LO	0	0	0	1	0	0	0	0	0	0.050551	0	0
protein_co	Uncharacte	0	0	1	0	0	0	0	0	0.091915	0	0	0
sense_intrc	-	2	0	0	5	1	1	0.198653	0	0	0.429633	0.111587	0.098713
protein_co	CDNA:_FLJ2	0	0	0	0	0	1	0	0	0	0	0	0.021941
protein_co	Uncharacte	0	0	1	3	0	3	0	0	0.407972	0.80349	0	0.923054
sense_intrc	-	0	0	0	0	0	1	0	0	0	0	0	0.141817

sense_intrc	-	5	2	3	0	1	5	0.24487	0.115426	0.193608	0	0.055019	0.243358
pseudogen	teratocarci	0	0	0	2	6	0	0	0	0	0.16386	0.638382	0
antisense	-	19	21	11	12	4	7	0.605586	0.788767	0.462008	0.330877	0.143229	0.221733
protein_co	-	7	7	2	3	3	6	0.533987	0.629271	0.201047	0.197978	0.257101	0.454877
antisense	-	3	4	1	7	1	0	0.178453	0.280394	0.078386	0.360216	0.066827	0
protein_co	Uncharacte	0	0	0	0	3	1	0	0	0	0	2.478163	0.730751
processed_	-	21	6	6	154	106	152	0.453225	0.152599	0.17064	2.875268	2.570097	3.260227
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.122127	0
protein_co	HCG19953	0	0	0	0	3	0	0	0	0	0	0.646477	0
antisense	-	0	0	1	0	0	1	0	0	0.110911	0	0	0.083647
protein_co	CDNA_FLJ2	2	2	4	4	4	3	0.058402	0.068823	0.153918	0.101046	0.131221	0.087061
lincRNA	-	0	0	1	0	0	0	0	0	0.251853	0	0	0
pseudogen	ribosomal_	0	0	0	0	0	1	0	0	0	0	0	0.105651
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.032932	0
pseudogen	-	0	0	0	1	3	0	0	0	0	0.05979	0.232934	0
lincRNA	-	4	4	0	5	8	6	0.435728	0.513479	0	0.471182	0.979027	0.649556
antisense	-	0	2	1	0	5	5	0	0.436278	0.243928	0	1.039789	0.919826
sense_intrc	-	5	6	3	0	2	0	0.140056	0.198056	0.110735	0	0.062937	0
antisense	-	0	10	9	12	3	3	0	1.155328	1.162721	1.017753	0.330422	0.2923
protein_co	Uncharacte	100	114	70	8	11	15	1.469767	1.974514	1.355755	0.101719	0.181631	0.219103
pseudogen	-	0	0	0	1	3	2	0	0	0	0.08267	0.322072	0.189942
antisense	-	1	7	4	9	10	15	0.077173	0.636609	0.406783	0.60086	0.866996	1.150453
protein_co	HCG20067	1	2	0	0	8	1	0.025837	0.060896	0	0	0.232214	0.025678
sense_intrc	-	7	14	6	12	17	16	0.751698	1.77166	0.849046	1.114781	2.050894	1.707555
protein_co	Uncharacte	37	21	24	7	35	23	2.698095	1.804604	2.306224	0.441587	2.867296	1.666836
protein_co	-	27	19	9	9	10	14	0.244051	0.202385	0.1072	0.070376	0.101547	0.125763
antisense	-	2	1	0	3	0	4	0.155025	0.091344	0	0.201166	0	0.308135
antisense	-	21	9	19	8	14	14	0.543648	0.274567	0.648167	0.179164	0.40717	0.360194
sense_over	-	6	2	0	0	0	0	0.717034	0.28166	0	0	0	0
lincRNA	-	208	171	151	382	183	271	5.271291	5.106894	5.042726	8.374908	5.210193	6.82547
lincRNA	-	2	4	3	0	2	0	0.17301	0.407763	0.341977	0	0.194366	0
antisense	-	22	20	25	11	25	11	0.819059	0.877465	1.226499	0.354281	1.045638	0.407
protein_co	Uncharacte	0	2	0	1	0	0	0	0.327495	0	0.120207	0	0
protein_co	Uncharacte	1	0	0	1	0	1	0.114591	0	0	0.099132	0	0.113883
protein_co	Uncharacte	2	0	0	0	1	1	0.180071	0	0	0	0.10115	0.08948
pseudogen	exosome_c	0	0	0	0	0	2	0	0	0	0	0	0.211727
lincRNA	-	25	25	16	60	41	53	4.110326	4.843768	3.466498	8.533958	7.573021	8.660077
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.038447
protein_co	CDNA_FLJ2	17	13	11	8	4	18	0.461064	0.415492	0.393133	0.1877	0.121877	0.485171
protein_co	Golgin_sub	1	0	0	0	0	0	0.015543	0	0	0	0	0
pseudogen	-	7	4	1	8	1	3	0.305513	0.20573	0.057513	0.302054	0.049032	0.130125
protein_co	Uncharacte	0	0	0	4	1	2	0	0	0	2.907867	0.944062	1.670287
pseudogen	-	0	0	0	2	0	0	0	0	0	0.102458	0	0
antisense	-	2	1	1	4	0	4	0.193569	0.114054	0.127538	0.33491	0	0.384746

pseudogen	secretoglob	0	0	0	0	3	0	0	0	0	0	0.436254	0
lincRNA	-	0	0	0	0	1	0	0	0	0	0	0.131004	0
sense_intrc	-	4	5	4	4	14	14	0.423528	0.623877	0.558106	0.366391	1.665326	1.473193
antisense	KCNQ1_op	495	548	560	84	220	138	0.28588	0.372964	0.426189	0.041968	0.142742	0.079208
sense_intrc	-	90	73	50	1019	892	1145	1.672995	1.599124	1.224777	16.38662	18.62799	21.15277
protein_co	Uncharacte	2	1	0	0	2	0	0.820791	0.483626	0	0	0.922107	0
protein_co	HCG17868	3	3	1	1	6	0	0.125453	0.147838	0.055105	0.036176	0.281876	0
processed_	-	8	4	1	21	17	27	0.155025	0.091344	0.025536	0.352041	0.370092	0.519978
antisense	-	3	9	4	0	3	5	1.270584	4.491917	2.232425	0	1.427422	2.104562
pseudogen	-	58	32	24	322	228	257	1.063588	0.691516	0.579951	5.108156	4.697094	4.683689
lincRNA	-	37	32	14	9	3	9	4.063935	4.141924	2.026319	0.855166	0.370182	0.98242
pseudogen	-	8	4	6	9	13	9	0.157328	0.092701	0.15549	0.153117	0.287217	0.175901
protein_co	RBL1_prote	0	0	0	12	2	1	0	0	0	0.394252	0.085331	0.037743
protein_co	uncharacte	3	0	0	5	1	1	0.167006	0	0	0.240793	0.06254	0.055325
protein_co	egl_nine_h	174	169	164	131	199	236	2.365622	2.707634	2.938156	1.540744	3.039473	3.18873
protein_co	-	0	0	0	2	0	0	0	0	0	0.240414	0	0
sense_intrc	-	92	96	56	121	85	139	7.173154	8.820651	5.753673	8.161513	7.445439	10.77077
lincRNA	-	8	7	0	3	5	2	1.25676	1.295888	0	0.407705	0.882432	0.31225
protein_co	-	3	6	0	0	5	0	0.441175	1.039795	0	0	0.826054	0
antisense	-	1	0	0	1	0	0	0.157562	0	0	0.136306	0	0
sense_intrc	-	1	3	0	5	2	5	0.074043	0.261767	0	0.320272	0.166366	0.36793
antisense	-	8	11	7	2	10	14	0.107087	0.173518	0.123475	0.02316	0.150382	0.186244
protein_co	Rho_GTPas	1	0	1	0	0	2	0.005911	0	0.00779	0	0	0.011749
lincRNA	-	8	6	5	5	4	0	0.644639	0.569751	0.530923	0.348546	0.362106	0
lincRNA	small_nucl	795	764	428	901	633	940	62.63109	70.92891	44.43257	61.40597	56.02419	73.59703
sense_intrc	-	1	2	7	5	9	7	0.095734	0.225634	0.88308	0.414095	0.967962	0.666001
lincRNA	-	0	0	2	15	17	20	0	0	0.117052	0.576329	0.84823	0.882786
processed_	-	20	8	7	38	27	14	0.439892	0.207354	0.202884	0.72304	0.667158	0.306023
antisense	-	0	1	0	0	1	0	0	0.125277	0	0	0.11943	0
sense_intrc	-	30	23	33	13	1	8	6.673235	6.029066	9.67306	2.501621	0.249899	1.76854
lincRNA	-	419	476	686	2	276	314	82.76969	110.8081	178.5732	0.341783	61.25132	61.64482
antisense	-	9	2	2	4	0	2	1.05882	0.277279	0.310059	0.407101	0	0.23384
lincRNA	-	14	4	7	3	4	6	1.403738	0.472634	0.924892	0.260221	0.450575	0.597887
lincRNA	-	5	7	2	7	4	7	0.611328	1.008578	0.322232	0.740398	0.549431	0.850574
pseudogen	mitogen-ac	1	0	2	0	1	1	0.020851	0	0.054953	0	0.023425	0.020722
sense_intrc	-	16	14	7	36	21	29	1.268048	1.307527	0.731052	2.468204	1.869752	2.284143
pseudogen	-	2	9	5	4	5	1	0.320855	1.701484	1.057019	0.555138	0.90115	0.159437
antisense	-	5	10	4	10	19	16	0.494776	1.166126	0.521595	0.856054	2.112229	1.573504
sense_intrc	family_with	0	0	0	4	0	3	0	0	0	0.12295	0	0.105934
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.117969
antisense	-	0	0	0	1	4	5	0	0	0	0.086088	0.447187	0.494493
lincRNA	-	0	3	0	0	1	0	0	0.204774	0	0	0.065072	0
sense_intrc	-	126	102	65	241	111	251	3.312098	3.159657	2.251546	5.480405	3.277968	6.557163
sense_intrc	-	0	0	0	0	0	1	0	0	0	0	0	0.11589

lincRNA	-	0	0	0	0	6	1	0	0	0	0	0.674585	0.099459
lincRNA	-	10	4	4	6	1	1	0.186741	0.088025	0.098431	0.096929	0.020979	0.018559
sense_intrc	-	6	8	4	2	8	5	0.422402	0.663699	0.371081	0.121806	0.632723	0.349827
sense_intrc	-	13	10	4	10	15	13	1.751229	1.587474	0.710059	1.165367	2.270073	1.740414
lincRNA	-	2	4	5	14	5	10	0.160427	0.378107	0.52851	0.971492	0.450575	0.797183
lincRNA	-	7	2	1	10	4	5	0.258249	0.086952	0.048616	0.319156	0.165787	0.183324
lincRNA	-	0	3	0	0	0	2	0	0.236317	0	0	0	0.132864
lincRNA	-	45	32	29	175	133	192	0.650558	0.545169	0.552467	2.188642	2.160103	2.758574
sense_intrc	-	0	0	0	2	3	5	0	0	0	0.141137	0.274927	0.405347
antisense	-	0	4	2	2	0	0	0	0.168274	0.094084	0.061765	0	0
antisense	-	0	0	0	6	2	1	0	0	0	0.165041	0.071443	0.0316
lincRNA	hsa-mir-14	174	168	114	18	14	14	3.613861	4.111863	3.120053	0.323413	0.326663	0.288975
antisense	-	17	12	13	7	10	3	0.248207	0.206468	0.250117	0.088415	0.164026	0.043531
sense_intrc	-	4	5	14	0	1	2	0.380187	0.560033	1.753476	0	0.106779	0.188919
sense_intrc	-	9	12	8	19	14	19	0.779818	1.225291	0.913431	1.424189	1.362787	1.636116
lincRNA	-	1	1	0	3	3	5	0.099326	0.11705	0	0.25778	0.334761	0.493565
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.014514
lincRNA	-	15	14	7	2	2	10	3.379212	3.716716	2.078055	0.389778	0.506178	2.238896
lincRNA	-	17	7	9	24	12	19	1.335307	0.647944	0.931557	1.630822	1.058918	1.483185
protein_co	-	0	0	0	1	0	0	0	0	0	0.021472	0	0
lincRNA	-	4	3	2	10	3	5	0.473745	0.41871	0.31214	1.024584	0.399167	0.588524
lincRNA	-	0	8	1	0	0	0	0	0.684639	0.095697	0	0	0
sense_intrc	-	3	9	7	16	12	15	0.236344	0.83555	0.726701	1.09045	1.06207	1.174421
sense_intrc	-	2	3	5	10	2	1	0.316066	0.558696	1.041243	1.367132	0.35508	0.157057
lincRNA	-	0	0	0	1	0	0	0	0	0	0.090871	0	0
antisense	MKNK1_an	13	3	8	8	12	4	0.281486	0.076549	0.228264	0.149853	0.291906	0.086076
sense_intrc	-	224	164	144	411	343	569	14.62242	12.61601	12.38707	23.21005	25.15443	36.91417
antisense	hsa-mir-12	20	15	10	4	10	18	0.267244	0.236198	0.176081	0.046238	0.150116	0.239034
lincRNA	-	2	0	1	4	0	3	0.20884	0	0.1376	0.361333	0	0.311326
lincRNA	-	0	0	0	14	13	21	0	0	0	1.194012	1.439827	2.057533
lincRNA	-	14	17	12	81	68	61	1.085174	1.552842	1.225709	5.431495	5.921468	4.699059
protein_co	-	0	0	2	0	2	0	0	0	0.029068	0	0.024782	0
sense_intrc	-	5	0	0	1	0	0	0.394493	0	0	0.068255	0	0
lincRNA	-	2	4	7	6	4	2	0.180378	0.425129	0.83193	0.468132	0.405287	0.179264
sense_intrc	-	0	0	3	0	0	0	0	0	1.137445	0	0	0
lincRNA	-	59	74	52	121	99	97	0.966734	1.428874	1.122776	1.715156	1.822382	1.579561
lincRNA	-	19	8	8	34	17	67	1.372277	0.680903	0.7614	2.124369	1.379387	4.809197
lincRNA	-	0	0	1	0	0	0	0	0	0.057703	0	0	0
lincRNA	-	0	0	1	1	0	1	0	0	0.158914	0.104326	0	0.11985
lincRNA	-	0	0	0	3	1	3	0	0	0	0.514594	0.222756	0.591169
lincRNA	-	27	19	31	39	38	41	2.018936	1.674247	3.054607	2.522821	3.19221	3.046859
antisense	-	7	7	2	1	2	0	1.080428	1.273219	0.406783	0.133525	0.346798	0
antisense	-	50	40	36	35	38	49	0.692401	0.652762	0.656939	0.419294	0.591181	0.674363
lincRNA	-	0	4	0	0	0	2	0	0.347564	0	0	0	0.146557

antisense	-	16	12	12	21	23	23	0.269506	0.238197	0.266357	0.306006	0.435236	0.385022
antisense	-	6	1	2	3	2	0	0.246046	0.048325	0.108076	0.106427	0.092139	0
lincRNA	-	159	122	113	108	83	91	4.128307	3.732861	3.866234	2.425837	2.42104	2.34815
sense_intrc	-	0	0	4	1	0	2	0	0	0.775148	0.127219	0	0.2923
lincRNA	-	0	0	0	0	3	4	0	0	0	0	0.379634	0.447779
lincRNA	-	6	15	12	28	23	18	0.157876	0.465117	0.416083	0.637361	0.679894	0.470702
lincRNA	-	214	202	171	608	352	385	8.544022	9.504013	8.996622	20.9998	15.78848	15.27633
sense_intrc	-	5	2	8	4	5	3	0.478671	0.225634	1.009234	0.331276	0.537757	0.285429
lincRNA	-	0	1	0	0	0	1	0	0.07171	0	0	0	0.060476
antisense	-	3	5	4	11	6	1	0.367646	0.72208	0.645956	1.166176	0.826054	0.121792
lincRNA	-	7	0	3	7	3	10	0.859831	0	0.485591	0.743834	0.413986	1.220744
lincRNA	-	6	11	4	0	5	5	0.646937	1.397688	0.568336	0	0.605661	0.535785
processed_	-	0	0	0	22	15	12	0	0	0	0.384718	0.340641	0.241072
antisense	-	9	9	1	11	1	12	1.20625	1.421493	0.176616	1.275413	0.150572	1.598402
lincRNA	-	2	1	0	0	6	2	0.163904	0.096575	0	0	0.552408	0.162892
sense_intrc	-	0	1	0	1	6	4	0	0.124031	0	0.091052	0.709454	0.418402
protein_co	Zinc_finger	0	1	1	0	1	4	0	0.025258	0.028244	0	0.024079	0.085205
lincRNA	-	24	29	14	27	37	71	0.467987	0.666388	0.359737	0.455459	0.810537	1.375911
sense_intrc	-	60	69	61	68	80	51	1.677117	2.272837	2.246864	1.644311	2.512182	1.416746
antisense	-	0	0	1	1	0	0	0	0	0.139806	0.091781	0	0
lincRNA	-	15	23	11	42	32	24	1.390744	2.512991	1.343951	3.368746	3.333151	2.211449
lincRNA	-	13	9	12	4	12	19	0.444595	0.362719	0.540801	0.118343	0.461054	0.64578
lincRNA	-	9	12	6	14	3	1	0.135553	0.212988	0.119084	0.182414	0.050762	0.014968
antisense	-	4	3	1	3	1	0	0.10499	0.092793	0.034588	0.068119	0.029487	0
lincRNA	-	2	2	0	1	2	3	0.159461	0.187915	0	0.068974	0.179144	0.237714
protein_co	Serine/thre	0	2	1	0	0	0	0	0.042311	0.023657	0	0	0
antisense	-	36	25	15	18	6	10	3.059191	2.50352	1.679694	1.323243	0.572802	0.844527
lincRNA	-	3	4	0	0	1	0	0.268282	0.421539	0	0	0.100466	0
sense_intrc	-	2	0	1	0	0	2	0.294936	0	0.194327	0	0	0.293114
protein_co	Uncharacte	4	4	3	0	0	0	0.041555	0.04897	0.041069	0	0	0
lincRNA	-	0	0	0	0	3	0	0	0	0	0	0.313031	0
lincRNA	-	0	0	0	0	1	5	0	0	0	0	0.082149	0.363357
lincRNA	-	11	19	11	17	16	16	1.007528	2.050808	1.327675	1.347027	1.646392	1.456444
sense_intrc	-	1	0	1	2	0	0	0.118702	0	0.15642	0.205376	0	0
lincRNA	-	86	62	33	44	29	46	7.439421	6.320326	3.761746	3.292732	2.818303	3.954651
sense_intrc	-	5	3	6	0	2	1	1.006483	0.711647	1.591558	0	0.452288	0.200053
processed_	-	5	9	5	5	16	21	0.380323	0.806738	0.501173	0.329015	1.367262	1.587493
lincRNA	-	2	0	0	3	0	0	0.243407	0	0	0.315855	0	0
sense_intrc	-	96	90	52	60	49	62	2.161776	2.388301	1.543042	1.168836	1.239609	1.387525
sense_intrc	-	0	0	1	0	0	0	0	0	0.15503	0	0	0
sense_intrc	-	12	8	4	13	12	11	1.10678	0.869515	0.486155	1.037257	1.243399	1.008283
sense_intrc	-	4	13	7	14	2	7	0.596518	2.284621	1.375614	1.806154	0.335076	1.03746
sense_intrc	-	8	6	3	14	14	15	0.853887	0.75469	0.421955	1.292711	1.678756	1.591151
lincRNA	-	20	19	69	5	31	18	2.479672	2.776035	11.27322	0.536287	4.317924	2.217922

antisense	-	12	20	16	36	12	19	0.949614	1.865104	1.668479	2.464515	1.066833	1.49427
antisense	-	0	0	0	4	0	3	0	0	0	0.402628	0	0.346906
lincRNA	-	76	77	84	180	74	122	2.288689	2.732568	3.333399	4.689308	2.503537	3.651259
lincRNA	-	0	7	2	0	0	0	0	0.751659	0.240149	0	0	0
sense_intrc	-	2	2	10	2	2	2	0.246237	0.290175	1.622402	0.213018	0.276632	0.244717
lincRNA	-	8	3	0	38	18	23	0.599049	0.264729	0	2.46161	1.514238	1.711631
sense_intrc	-	2	0	0	3	0	1	0.191123	0	0	0.248009	0	0.094971
lincRNA	-	0	0	1	0	0	0	0	0	0.08944	0	0	0
lincRNA	-	344	332	235	1248	784	1077	8.530071	9.701511	7.678862	26.77144	21.84034	26.54114
sense_intrc	-	14	3	8	10	4	16	1.857579	0.469081	1.398763	1.147842	0.59625	2.109837
antisense	GAS5_antis	21	13	13	24	19	34	1.601961	1.168646	1.306805	1.583824	1.628303	2.577634
lincRNA	-	11	1	9	26	12	20	0.855141	0.091612	0.921982	1.748563	1.048034	1.5452
pseudogen	-	0	0	2	0	0	0	0	0	1.073281	0	0	0
lincRNA	-	4	2	10	0	0	0	0.137777	0.081181	0.453893	0	0	0
sense_intrc	-	0	1	0	1	4	4	0	0.241813	0	0.177515	0.922107	0.815722
lincRNA	-	0	4	0	4	2	0	0	0.721245	0	0.529467	0.343791	0
sense_intrc	-	23	18	13	52	18	40	1.551137	1.430547	1.155315	3.033813	1.363779	2.680971
lincRNA	-	8	5	0	14	20	8	0.887899	0.653959	0	1.344203	2.493749	0.882416
lincRNA	-	0	0	1	0	2	2	0	0	0.532544	0	0.908029	0.803268
lincRNA	-	1	4	0	0	0	0	0.092232	0.434758	0	0	0	0
lincRNA	-	0	2	0	0	0	0	0	0.323252	0	0	0	0
protein_co	Disrupted_	0	0	2	0	0	0	0	0	0.039226	0	0	0
sense_intrc	-	43	29	24	24	37	45	4.124027	3.277616	3.033186	1.991257	3.98661	4.289189
lincRNA	-	8	4	5	29	12	18	1.003621	0.591353	0.826579	3.147318	1.691258	2.244201
antisense	-	6	11	17	0	12	9	0.415767	0.898253	1.552324	0	0.934177	0.619799
processed_	-	5	0	0	1	3	0	0.056501	0	0	0.009776	0.038085	0
lincRNA	-	1	5	1	1	8	4	0.112881	0.665114	0.148749	0.097652	1.014515	0.448734
sense_intrc	-	7	4	15	11	3	5	0.699221	0.470851	1.974433	0.950543	0.336656	0.496359
lincRNA	-	10	6	6	2	1	3	0.880882	0.622839	0.696472	0.152409	0.098962	0.262633
antisense	-	0	0	1	0	2	5	0	0	0.436021	0	0.743449	1.644189
lincRNA	-	12	22	5	20	19	12	0.266147	0.575002	0.146132	0.383736	0.473415	0.264503
sense_intrc	-	7	9	6	0	9	2	0.701869	1.063427	0.792765	0	1.013794	0.199296
lincRNA	-	0	0	2	12	3	0	0	0	0.374066	1.473423	0.478359	0
sense_intrc	-	0	2	2	1	4	1	0	0.305074	0.341141	0.111978	0.581672	0.128641
sense_intrc	-	1	0	0	4	0	4	0.073022	0	0	0.252684	0	0.290284
lincRNA	-	0	0	1	0	0	0	0	0	0.149386	0	0	0
sense_intrc	-	0	6	1	0	3	2	0	1.011693	0.188549	0	0.482237	0.2844
lincRNA	-	22	22	47	6	14	18	2.152869	2.537024	6.060766	0.507936	1.539118	1.75056
lincRNA	-	52	36	36	108	81	97	5.618228	4.583588	5.125466	10.09445	9.831733	10.41543
lincRNA	-	4	9	6	123	69	103	0.145743	0.386435	0.28808	3.876989	2.82439	3.729695
lincRNA	-	4	0	0	0	1	1	0.37815	0	0	0	0.106207	0.093954
protein_co	Junctional_	0	0	0	2	5	5	0	0	0	0.043701	0.14188	0.125511
lincRNA	-	9	0	4	5	8	7	0.72083	0	0.422168	0.346437	0.71983	0.557184
lincRNA	-	27	12	9	35	14	26	1.974319	1.034051	0.867223	2.214035	1.150087	1.889455

sense_intrc	-	10	5	5	12	2	2	0.572335	0.337231	0.377099	0.594148	0.128597	0.11376
antisense	-	0	0	0	0	4	0	0	0	0	0	0.583097	0
lincRNA	-	0	2	0	35	24	49	0	0.072628	0	0.933039	0.830863	1.500634
sense_intrc	-	4	13	9	4	1	3	0.372169	1.425379	1.103461	0.321961	0.104527	0.277403
lincRNA	-	1	4	2	0	2	8	0.107823	0.50825	0.284168	0	0.242264	0.857255
lincRNA	-	0	2	4	0	0	2	0	0.204215	0.456715	0	0	0.172223
lincRNA	-	382	308	200	769	476	653	22.02991	20.93183	15.19897	38.36531	30.83936	37.4259
lincRNA	-	34	21	33	88	73	81	0.826823	0.601811	1.057505	1.851311	1.994369	1.95762
lincRNA	-	1	0	2	2	0	4	0.052521	0	0.138419	0.090871	0	0.208786
antisense	-	3	0	2	0	2	0	0.197051	0	0.17311	0	0.147583	0
antisense	-	0	9	5	31	8	13	0	0.724503	0.450086	1.831956	0.613945	0.882558
lincRNA	-	7	8	2	10	4	6	0.261345	0.351976	0.098397	0.322982	0.167774	0.222626
lincRNA	-	3	0	2	3	0	5	0.522444	0	0.458969	0.451963	0	0.865363
sense_intrc	-	14	2	0	2	7	5	1.158084	0.194962	0	0.143122	0.650518	0.411047
antisense	-	11	5	3	9	17	16	0.845212	0.452741	0.303759	0.598244	1.467475	1.221807
lincRNA	-	109	117	86	72	62	95	3.17413	4.015052	3.300133	1.813818	2.028332	2.749359
lincRNA	-	2	2	0	1	9	2	0.174723	0.2059	0	0.075576	0.883306	0.173644
lincRNA	-	12	14	10	29	21	27	0.792135	1.089063	0.869866	1.65607	1.557349	1.771296
pseudogen	-	0	0	0	3	2	1	0	0	0	0.217744	0.188513	0.083382
pseudogen	-	2	0	1	0	0	0	0.208429	0	0.137329	0	0	0
antisense	-	0	0	0	2	0	0	0	0	0	0.090871	0	0
lincRNA	-	12	13	2	10	0	5	0.819732	1.046504	0.180034	0.590954	0	0.339445
pseudogen	-	0	0	0	0	2	1	0	0	0	0	0.201956	0.089328
sense_intrc	-	31	31	19	36	33	17	1.813448	2.137038	1.464643	1.821835	2.168735	0.98833
pseudogen	-	10	11	3	22	17	24	0.258754	0.335418	0.102292	0.492461	0.494179	0.617174
pseudogen	-	5	2	0	0	0	4	0.906524	0.427313	0	0	0	0.72074
lincRNA	-	0	0	0	0	4	0	0	0	0	0	0.474858	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.133915	0	0
sense_intrc	-	30	14	28	13	49	36	3.108082	1.709253	3.822646	1.165138	5.70317	3.706665
pseudogen	-	9	5	3	3	5	2	1.164961	0.762686	0.511711	0.335933	0.727089	0.257281
pseudogen	-	3	0	0	2	0	0	0.490194	0	0	0.282709	0	0
pseudogen	-	0	4	2	0	3	9	0	1.363666	0.76244	0	0.975015	2.587576
pseudogen	double_ho	0	0	3	0	0	0	0	0	0.341419	0	0	0
pseudogen	NADH_deh	0	1	3	4	4	11	0	0.115962	0.389015	0.340512	0.4422	1.075752
lincRNA	-	0	0	0	0	2	0	0	0	0	0	0.220281	0
pseudogen	-	3	4	2	4	0	0	0.325457	0.511375	0.285915	0.375401	0	0
pseudogen	-	1	1	0	2	6	6	0.091752	0.108124	0	0.158748	0.618467	0.547113
antisense	-	4	8	2	6	2	9	0.117778	0.277587	0.077601	0.152833	0.066158	0.263363
pseudogen	-	0	2	0	0	0	0	0	0.338145	0	0	0	0
pseudogen	-	2	2	2	0	0	0	0.472687	0.557033	0.622886	0	0	0
pseudogen	-	0	0	2	0	0	0	0	0	0.115026	0	0	0
pseudogen	-	0	0	0	0	1	1	0	0	0	0	0.167538	0.148209
lincRNA	-	0	0	2	0	0	0	0	0	0.225771	0	0	0
protein_co	-	0	0	2	2	0	0	0	0	0.05141	0.03375	0	0

pseudogen	-	0	3	3	3	3	6	0	0.132364	0.148013	0.097169	0.126187	0.223256
lincRNA	-	0	0	0	4	0	0	0	0	0	0.446819	0	0
pseudogen	-	1	1	0	2	0	0	0.245097	0.288832	0	0.424064	0	0
pseudogen	-	0	0	0	0	3	0	0	0	0	0	0.160891	0
pseudogen	-	0	4	0	1	0	0	0	1.356255	0	0.248907	0	0
pseudogen	-	0	0	0	0	2	1	0	0	0	0	0.341816	0.15119
pseudogen	-	0	0	0	3	0	0	0	0	0	0.248457	0	0
pseudogen	-	0	0	2	0	0	0	0	0	0.722936	0	0	0
lincRNA	-	0	0	6	5	1	4	0	0	0.059627	0.03262	0.008472	0.02998
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.165453
pseudogen	-	3	7	1	12	7	9	0.235293	0.646984	0.103353	0.814203	0.616787	0.701521
antisense	-	0	0	5	10	1	1	0	0	1.032001	1.354997	0.175964	0.155663
lincRNA	-	35	31	28	38	11	22	0.71349	0.744713	0.752165	0.670142	0.25192	0.44571
lincRNA	-	0	0	0	10	4	6	0	0	0	0.29701	0.154283	0.204724
pseudogen	-	0	0	0	1	0	1	0	0	0	0.209127	0	0.240247
IG_V_pseu	immunoglo	0	0	1	0	0	0	0	0	0.200469	0	0	0
lincRNA	-	0	0	0	0	0	1	0	0	0	0	0	0.076252
antisense	-	17	13	8	23	37	25	0.305498	0.275302	0.189445	0.357561	0.746982	0.446487
pseudogen	-	1	0	0	0	0	0	0.307796	0	0	0	0	0
pseudogen	-	2	1	1	3	3	0	0.123406	0.072713	0.081309	0.160136	0.207958	0
pseudogen	-	0	0	3	0	0	1	0	0	0.239462	0	0	0.060199
pseudogen	-	0	0	0	0	1	1	0	0	0	0	0.430985	0.381261
pseudogen	-	0	0	0	0	4	0	0	0	0	0	0.385581	0
pseudogen	-	0	0	1	0	0	0	0	0	0.275744	0	0	0
processed_	-	4	0	2	4	1	0	0.372824	0	0.245645	0.322528	0.104711	0
pseudogen	-	4	0	3	1	1	4	0.255137	0	0.252156	0.055179	0.071658	0.253562
lincRNA	colon_ader	19	15	13	15	12	22	1.122633	1.044437	1.01219	0.766723	0.796552	1.291863
pseudogen	-	0	0	2	8	1	0	0	0	0.387574	1.017753	0.165211	0
pseudogen	-	0	0	3	1	4	2	0	0	0.328555	0.071898	0.373475	0.165193
sense_intrc	-	1	0	1	2	5	6	0.077173	0	0.101696	0.133525	0.433498	0.460181
pseudogen	nuclear_re	21	14	5	11	12	12	1.410864	1.108411	0.44266	0.639325	0.905725	0.801229
pseudogen	-	0	1	1	0	1	3	0	0.047371	0.052971	0	0.04516	0.11985
pseudogen	-	1	12	2	1	3	1	0.028235	0.399281	0.074414	0.024426	0.095161	0.028061
pseudogen	-	6	21	11	10	13	8	0.176568	0.728261	0.426568	0.25458	0.429787	0.23397
lincRNA	-	0	3	0	1	0	0	0	0.553737	0	0.1355	0	0
lincRNA	-	0	0	0	6	2	8	0	0	0	0.866856	0.375242	1.327799
antisense	-	3	2	2	13	1	0	0.38363	0.30139	0.337021	1.43813	0.143662	0
pseudogen	-	0	2	0	0	0	6	0	0.153854	0	0	0	0.389253
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.055481	0
pseudogen	-	0	0	0	1	13	5	0	0	0	0.050831	0.858143	0.291976
pseudogen	-	0	0	1	14	3	3	0	0	0.095305	0.875935	0.243754	0.215631
lincRNA	-	3	1	8	3	3	9	0.259939	0.102108	0.913431	0.224872	0.292026	0.775002
antisense	-	0	1	1	1	0	1	0	0.483626	0.540801	0.35503	0	0.407861
pseudogen	-	0	0	0	0	3	3	0	0	0	0	0.08272	0.073177

pseudogen	-	2	1	1	0	0	0	0.360143	0.212203	0.23729	0	0	0
pseudogen	-	0	1	0	0	3	0	0	0.127582	0	0	0.364883	0
pseudogen	-	3	8	5	0	1	3	0.320208	1.006254	0.703259	0	0.119911	0.31823
pseudogen	-	0	1	0	4	1	0	0	0.042731	0	0.125476	0.040737	0
antisense	-	122	87	80	25	21	30	2.339298	1.965857	2.021392	0.414695	0.45237	0.571685
pseudogen	-	0	3	2	3	5	4	0	0.287501	0.214327	0.211055	0.456804	0.323281
sense_intrc	-	0	0	1	8	0	0	0	0	0.193787	1.017753	0	0
pseudogen	-	3	6	0	0	0	0	0.592623	1.39674	0	0	0	0
pseudogen	phosphatid	0	0	0	3	2	0	0	0	0	0.246231	0.213175	0
antisense	-	0	0	0	0	3	2	0	0	0	0	0.115637	0.068197
pseudogen	-	2	0	0	0	0	0	0.444882	0	0	0	0	0
pseudogen	-	4	1	0	1	3	3	0.586604	0.172819	0	0.126867	0.49426	0.437236
pseudogen	-	1	0	4	0	0	0	0.048172	0	0.253915	0	0	0
lincRNA	-	0	0	0	10	1	16	0	0	0	0.518674	0.067357	0.953369
pseudogen	-	20	24	6	66	22	42	2.00155	2.830445	0.791266	5.714041	2.473479	4.177297
lincRNA	-	9	11	13	0	0	0	0.193137	0.278178	0.367622	0	0	0
sense_intrc	-	0	3	1	3	1	1	0	0.147722	0.055062	0.108443	0.046942	0.041526
antisense	-	1	2	2	8	6	9	0.015507	0.036548	0.040869	0.10732	0.104527	0.138701
antisense	-	0	2	0	0	0	0	0	0.05894	0	0	0	0
pseudogen	-	1	2	0	9	7	14	0.588233	1.386394	0	4.579891	4.625905	8.184408
pseudogen	-	0	2	0	1	0	0	0	0.481759	0	0.17683	0	0
pseudogen	-	23	7	6	1	1	10	2.143737	0.768863	0.736936	0.080632	0.104711	0.926304
processed_	-	22	15	6	13	13	15	0.401345	0.322473	0.144238	0.205164	0.266432	0.271954
processed_	-	0	1	2	0	0	0	0	0.135921	0.303979	0	0	0
pseudogen	-	0	7	4	0	0	2	0	0.656713	0.419629	0	0	0.158238
pseudogen	-	2	7	12	23	17	10	0.256373	1.057419	2.02702	2.550544	2.448161	1.273948
antisense	-	25	14	16	1	4	6	0.802623	0.529671	0.676903	0.027774	0.144271	0.19144
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.152504
antisense	-	2	9	0	2	1	1	0.192163	1.019037	0	0.166239	0.107942	0.095488
processed_	HLA_compl	0	1	4	0	0	10	0	0.085229	0.38122	0	0	0.718771
antisense	-	53	51	35	87	35	82	1.442608	1.635874	1.25538	2.048589	1.070261	2.218176
pseudogen	-	0	0	1	4	1	5	0	0	0.141795	0.372349	0.120886	0.534696
lincRNA	-	0	1	0	12	7	7	0	0.037003	0	0.325971	0.246934	0.218445
pseudogen	-	1	4	2	1	2	1	0.08853	0.417309	0.233322	0.076587	0.198916	0.087983
pseudogen	-	0	0	0	1	0	0	0	0	0	0.075327	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.104711	0
pseudogen	-	1	0	0	0	0	0	0.187071	0	0	0	0	0
lincRNA	-	0	0	0	0	3	3	0	0	0	0	0.108204	0.09572
sense_intrc	-	25	17	17	1	4	22	4.471368	3.583079	4.006675	0.154726	0.803729	3.910504
pseudogen	divergent-p	0	1	0	0	0	0	0	0.115747	0	0	0	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.294757
lincRNA	-	1	5	1	12	8	8	0.076726	0.452085	0.101106	0.796503	0.689576	0.610018
pseudogen	-	3	0	0	0	0	0	0.7563	0	0	0	0	0
pseudogen	-	0	0	1	0	1	0	0	0	0.295607	0	0.252017	0

pseudogen	-	0	0	2	0	0	0	0	0	0.301353	0	0	0
lincRNA	-	8	6	9	15	17	21	0.589872	0.521346	0.87447	0.956802	1.408204	1.538851
lincRNA	-	32	45	40	390	346	320	0.700336	1.160582	1.153589	7.383867	8.507097	6.960106
pseudogen	-	2	0	1	4	0	2	0.201297	0	0.13263	0.348281	0	0.200053
antisense	-	15	22	12	9	2	7	0.71349	1.233181	0.752165	0.370342	0.106875	0.330906
pseudogen	-	1	2	0	0	0	0	0.31326	0.738316	0	0	0	0
pseudogen	-	17	2	15	0	3	4	0.60443	0.083798	0.702787	0	0.119831	0.141341
pseudogen	-	0	0	2	0	0	1	0	0	0.287684	0	0	0.108483
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.094707	0
pseudogen	-	0	1	0	0	0	0	0	0.1289	0	0	0	0
antisense	-	136	120	124	300	161	175	4.121337	4.285362	4.951715	7.864723	5.481181	5.27044
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.19629	0
sense_intrc	-	69	20	65	84	106	122	11.78364	4.025015	14.62778	12.41003	20.33693	20.70617
pseudogen	-	0	0	0	5	0	0	0	0	0	5.452251	0	0
pseudogen	-	0	0	0	0	3	0	0	0	0	0	0.176836	0
pseudogen	-	1	0	0	0	0	0	0.174723	0	0	0	0	0
pseudogen	-	2	2	0	4	3	1	0.25762	0.30359	0	0.445731	0.434131	0.128015
pseudogen	-	0	0	0	7	7	3	0	0	0	1.065091	1.383161	0.524393
lincRNA	-	1	0	5	4	2	2	0.090036	0	0.593225	0.311557	0.202299	0.178959
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.20633
lincRNA	-	2	0	0	0	0	0	0.665924	0	0	0	0	0
pseudogen	-	21	27	27	42	21	44	2.11764	3.208512	3.587826	3.663912	2.379037	4.409558
pseudogen	-	3	0	0	4	6	0	0.44364	0	0	0.51172	0.996803	0
pseudogen	-	0	0	0	0	2	1	0	0	0	0	0.321491	0.1422
pseudogen	-	2	0	2	1	3	0	0.096962	0	0.127772	0.04194	0.163395	0
lincRNA	-	2	1	0	9	0	0	0.211341	0.124526	0	0.822735	0	0
antisense	-	0	2	3	0	0	0	0	0.335418	0.562607	0	0	0
lincRNA	-	3	3	2	1	0	2	0.430415	0.507217	0.378121	0.124116	0	0.285171
antisense	-	5	10	6	2	5	7	0.69843	1.646114	1.104432	0.241683	0.784643	0.971763
lincRNA	-	2	6	1	9	15	15	0.320855	1.134322	0.211404	1.249061	2.703451	2.391548
pseudogen	-	2	0	1	1	0	0	0.290088	0	0.191132	0.125476	0	0
pseudogen	-	0	4	0	1	0	1	0	0.233225	0	0.042803	0	0.049172
pseudogen	-	0	0	0	1	0	0	0	0	0	0.060741	0	0
pseudogen	-	0	1	1	0	0	0	0	0.270077	0.302006	0	0	0
pseudogen	-	0	5	0	0	0	0	0	0.552104	0	0	0	0
pseudogen	-	1	6	3	5	8	19	0.175884	1.243609	0.695315	0.760779	1.580755	3.321153
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.122757	0
pseudogen	-	6	0	0	0	0	0	0.939781	0	0	0	0	0
pseudogen	-	1	0	0	0	0	0	0.259515	0	0	0	0	0
pseudogen	-	0	5	3	0	1	0	0	0.373579	0.250647	0	0.071229	0
pseudogen	-	12	4	3	2	7	4	2.069355	0.812869	0.681726	0.298364	1.356128	0.685525
pseudogen	-	43	35	41	40	19	31	2.554953	2.450696	3.210207	2.056068	1.268286	1.830567
pseudogen	-	8	5	5	4	1	0	1.480867	1.090695	1.219638	0.640544	0.207958	0
pseudogen	-	0	0	2	0	0	0	0	0	0.30531	0	0	0

lincRNA	-	1	2	6	14	5	6	0.090497	0.213291	0.715521	1.096042	0.508341	0.539631
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.449693
pseudogen	NANOGNB_	1	4	1	11	3	2	0.108708	0.512425	0.143251	1.034472	0.366381	0.216074
antisense	-	22	22	35	42	19	21	2.046928	2.412179	4.291239	3.380587	1.986015	1.941819
pseudogen	-	2	1	3	0	1	3	0.641709	0.378107	1.268423	0	0.36046	0.956619
antisense	hsa-mir-33	10	12	8	4	4	0	0.200991	0.284227	0.211885	0.06955	0.09032	0
pseudogen	neurofibro	0	0	0	5	0	0	0	0	0	0.086576	0	0
pseudogen	-	5	1	0	0	2	2	0.46603	0.109838	0	0	0.209422	0.185261
pseudogen	-	7	1	2	1	0	0	0.619711	0.104327	0.233322	0.076587	0	0
pseudogen	-	2	6	2	0	1	0	0.294117	1.039795	0.387574	0	0.165211	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.097433
pseudogen	-	0	0	0	0	1	2	0	0	0	0	0.1361	0.240797
pseudogen	-	1	1	1	0	0	0	0.037441	0.044121	0.049338	0	0	0
pseudogen	-	3	0	0	0	0	0	0.329508	0	0	0	0	0
pseudogen	-	2	0	1	0	0	3	0.090652	0	0.059729	0	0	0.135139
lincRNA	-	0	0	3	0	0	0	0	0	0.334864	0	0	0
pseudogen	-	8	1	6	21	24	13	0.335867	0.049475	0.331943	0.76271	1.131976	0.542413
pseudogen	-	0	1	4	0	0	2	0	0.218139	0.97571	0	0	0.36793
lincRNA	-	4	0	0	0	0	0	0.457374	0	0	0	0	0
pseudogen	-	16	7	9	9	3	8	1.348815	0.695405	0.999792	0.656354	0.284121	0.670243
pseudogen	-	0	0	0	3	0	0	0	0	0	0.400574	0	0
pseudogen	-	0	3	0	0	0	0	0	0.234835	0	0	0	0
protein_co	Ankyrin_re	0	5	8	0	2	0	0	0.147628	0.26413	0	0.056295	0
pseudogen	nudix_(nuc	4	0	0	0	1	0	0.36199	0	0	0	0.101668	0
pseudogen	-	0	0	1	0	0	0	0	0	0.29068	0	0	0
pseudogen	-	7	2	5	5	6	9	0.378536	0.127452	0.356299	0.233907	0.36451	0.483684
lincRNA	-	0	0	0	68	47	45	0	0	0	0.600873	0.539334	0.456807
pseudogen	-	2	0	0	0	0	0	0.058531	0	0	0	0	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.316952
pseudogen	-	8	1	2	4	3	9	1.141585	0.168161	0.376082	0.493789	0.480937	1.276352
antisense	-	1	0	2	0	0	0	0.098403	0	0.259343	0	0	0
pseudogen	taste_recep	0	11	4	0	2	4	0	0.830829	0.337837	0	0.144009	0.25479
pseudogen	-	0	0	1	0	5	8	0	0	0.103353	0	0.440562	0.623574
lincRNA	-	0	0	0	10	2	9	0	0	0	0.613104	0.159239	0.633904
pseudogen	-	0	1	0	0	0	0	0	0.101774	0	0	0	0
pseudogen	-	0	2	0	0	1	0	0	0.18679	0	0	0.089036	0
pseudogen	-	0	1	0	0	1	0	0	0.097026	0	0	0.092498	0
pseudogen	-	2	0	3	3	3	1	0.379505	0	0.750143	0.492461	0.639526	0.188581
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.185283	0
pseudogen	-	4	1	0	6	1	3	0.270107	0.079576	0	0.350502	0.075862	0.201329
lincRNA	-	65	78	77	128	121	112	1.099062	1.554214	1.715673	1.872328	2.298494	1.882074
antisense	-	0	3	0	0	4	0	0	0.479906	0	0	0.610009	0
antisense	-	1	0	3	0	0	0	0.084978	0	0.335939	0	0	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.025078

antisense	-	2	1	1	7	0	3	0.156862	0.092426	0.103353	0.474952	0	0.23384
antisense	LPP_antise	50	52	32	45	36	27	0.928138	1.137504	0.782758	0.722633	0.750748	0.498099
pseudogen	-	1	0	0	0	0	0	0.178855	0	0	0	0	0
lincRNA	-	7	3	4	19	6	10	0.24174	0.122089	0.182031	0.567632	0.232782	0.34321
pseudogen	-	0	2	0	0	3	0	0	0.436278	0	0	0.623873	0
lincRNA	-	0	4	0	0	0	0	0	0.502115	0	0	0	0
pseudogen	-	0	1	1	3	0	1	0	0.13957	0.15607	0.307375	0	0.117705
pseudogen	-	1	0	0	0	0	0	0.059551	0	0	0	0	0
pseudogen	-	0	0	0	0	1	1	0	0	0	0	0.093222	0.082467
pseudogen	-	0	0	0	4	0	0	0	0	0	0.248907	0	0
lincRNA	-	0	0	1	0	3	0	0	0	0.140369	0	0.35901	0
pseudogen	-	0	0	0	2	1	0	0	0	0	0.704599	0.457507	0
pseudogen	-	0	0	0	0	0	4	0	0	0	0	0	0.224846
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.112906
lincRNA	-	0	2	0	6	0	4	0	0.138794	0	0.305666	0	0.2341
pseudogen	-	1	10	4	2	1	6	0.168067	1.980563	0.885883	0.290787	0.188812	1.002172
lincRNA	-	10	5	17	7	6	6	0.273314	0.161042	0.612275	0.16551	0.184231	0.162976
pseudogen	-	0	0	3	0	2	0	0	0	1.635077	0	0.929311	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.308165	0
lincRNA	-	17	9	8	27	20	34	1.68855	1.053451	1.047104	2.32002	2.231742	3.356243
pseudogen	-	0	0	0	0	1	3	0	0	0	0	0.128736	0.34165
pseudogen	-	2	0	0	3	0	6	0.446759	0	0	0.579733	0	1.332001
pseudogen	-	0	3	0	0	0	0	0	0.129256	0	0	0	0
antisense	-	17	21	8	4	8	9	1.711021	2.490765	1.061039	0.348281	0.904577	0.90024
lincRNA	-	8	3	1	6	5	8	0.823984	0.364131	0.135726	0.534618	0.57856	0.818896
protein_co	MT-RNR2-li	0	3	3	8	1	2	0	0.180485	0.201822	0.353318	0.057354	0.101474
pseudogen	-	2	0	1	0	3	4	0.121146	0	0.079821	0	0.204151	0.240797
lincRNA	-	0	0	0	848	655	832	0	0	0	52.27116	52.43166	58.91641
pseudogen	-	0	0	0	0	4	0	0	0	0	0	1.003813	0
pseudogen	-	12	14	5	4	1	2	2.64705	3.639284	1.453402	0.763315	0.247816	0.43845
antisense	-	0	0	0	0	2	2	0	0	0	0	0.342801	0.303251
pseudogen	-	1	0	2	0	0	0	0.064327	0	0.169534	0	0	0
pseudogen	-	1	0	0	0	0	4	0.06472	0	0	0	0	0.257281
pseudogen	-	10	6	2	1	3	2	0.696592	0.492535	0.183588	0.060262	0.234773	0.138458
pseudogen	-	0	0	2	0	1	2	0	0	0.067764	0	0.028886	0.051106
pseudogen	-	0	0	4	0	0	0	0	0	0.917938	0	0	0
lincRNA	-	0	4	0	5	2	0	0	0.116995	0	0.107358	0.055767	0
pseudogen	-	1	0	0	0	0	0	0.236344	0	0	0	0	0
pseudogen	-	0	2	0	0	1	0	0	0.738316	0	0	0.351929	0
pseudogen	sex_comb_	4	2	1	2	1	0	0.392156	0.231066	0.129191	0.169626	0.110141	0
lincRNA	-	0	0	0	21	4	8	0	0	0	1.687328	0.417375	0.738443
lincRNA	-	0	0	1	8	9	10	0	0	0.042001	0.220585	0.322266	0.316761
antisense	-	200	164	169	193	206	174	2.521	2.436092	2.807142	2.104569	2.917152	2.179725
sense_intrc	-	0	0	3	0	1	0	0	0	0.150785	0	0.04285	0

pseudogen	-	0	1	0	0	0	0	0	0.130246	0	0	0	0
antisense	-	3	2	2	3	4	12	0.215499	0.169302	0.189317	0.186427	0.3228	0.856674
pseudogen	-	0	2	0	1	1	3	0	0.141149	0	0.051809	0.06728	0.178554
IG_V_pseu	immunoglo	0	0	0	0	1	0	0	0	0	0	0.149813	0
pseudogen	-	4	4	1	0	0	0	0.533411	0.628592	0.175726	0	0	0
lincRNA	-	1	2	8	6	1	10	0.04957	0.116831	0.522571	0.257297	0.055689	0.492641
pseudogen	-	0	2	1	0	4	4	0	0.274836	0.153664	0	0.524017	0.46356
antisense	-	0	0	1	0	9	2	0	0	0.04976	0	0.3818	0.075056
lincRNA	-	0	1	1	1	4	0	0	0.105563	0.118043	0.077494	0.402544	0
pseudogen	-	18	11	10	17	13	19	1.680666	1.210344	1.230393	1.373159	1.363645	1.763081
lincRNA	-	0	6	0	0	0	1	0	0.732537	0	0	0	0.102963
pseudogen	-	2	0	0	0	3	0	0.430415	0	0	0	0.725316	0
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.306787
lincRNA	-	0	2	0	0	0	0	0	0.398644	0	0	0	0
lincRNA	-	0	0	3	0	0	0	0	0	0.381916	0	0	0
sense_over	-	4	2	4	7	5	7	0.610271	0.359583	0.804188	0.923897	0.857002	1.061379
lincRNA	-	1	0	0	0	0	1	0.123984	0	0	0	0	0.123218
lincRNA	-	0	2	5	0	0	0	0	0.06245	0.174583	0	0	0
pseudogen	-	0	1	0	0	0	0	0	0.415918	0	0	0	0
pseudogen	-	1	0	0	0	0	0	0.297421	0	0	0	0	0
pseudogen	-	0	0	0	0	1	2	0	0	0	0	0.150192	0.265728
lincRNA	-	23	14	17	1	0	0	1.602162	1.149248	1.560494	0.060262	0	0
antisense	-	1	0	1	6	1	1	0.116099	0	0.15299	0.602617	0.13043	0.115382
pseudogen	-	1	0	1	38	12	10	0.093701	0	0.123475	3.08028	1.263205	0.931222
pseudogen	-	0	0	0	4	0	0	0	0	0	0.541999	0	0
antisense	-	3	0	6	4	1	6	0.515659	0	1.359025	0.594791	0.193104	1.024949
lincRNA	-	0	0	2	1	0	2	0	0	0.279053	0.091598	0	0.210456
pseudogen	-	0	0	0	1	0	1	0	0	0	0.075451	0	0.086679
lincRNA	-	2	2	0	1	2	0	0.196078	0.231066	0	0.084813	0.220281	0
pseudogen	-	0	0	0	1	0	0	0	0	0	0.186174	0	0
lincRNA	-	5	2	0	1	8	2	0.593509	0.279766	0	0.102688	1.066833	0.235937
pseudogen	-	5	3	7	13	6	4	1.02998	0.728261	1.900167	2.316676	1.388543	0.818896
antisense	-	107	99	67	78	68	50	1.620334	1.766701	1.336997	1.021829	1.156854	0.752489
pseudogen	-	5	0	0	2	0	0	0.418837	0	0	0.144933	0	0
pseudogen	-	0	1	0	0	0	0	0	0.30139	0	0	0	0
protein_co	sulfiredoxi	5	6	13	6	3	17	0.098112	0.138742	0.336146	0.101851	0.066133	0.331519
pseudogen	divergent-p	0	0	0	0	1	0	0	0	0	0	0.106779	0
antisense	-	0	0	2	0	3	3	0	0	0.305979	0	0.391289	0.346145
pseudogen	-	0	0	0	0	3	7	0	0	0	0	0.304484	0.628495
lincRNA	-	3	0	0	0	0	0	0.240641	0	0	0	0	0
protein_co	CTAGE_fam	0	0	0	0	0	1	0	0	0	0	0	0.020174
lincRNA	-	2	0	4	12	6	2	0.21092	0	0.555883	1.094795	0.710868	0.209618
lincRNA	-	23	27	15	17	10	13	0.814477	1.126735	0.699966	0.52079	0.397832	0.457513
pseudogen	-	2	0	0	0	0	1	0.133018	0	0	0	0	0.066098

pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.391289	0
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.176557
lincRNA	-	30	12	16	6	1	1	2.651469	1.249838	1.86346	0.458754	0.099292	0.087836
antisense	-	38	25	15	78	30	90	1.817306	1.408937	0.945302	3.227023	1.611813	4.277565
sense_intrc	-	25	16	14	54	17	42	1.490456	1.124103	1.099872	2.785069	1.138616	2.488502
lincRNA	-	4	4	3	14	10	6	0.167138	0.196962	0.165185	0.506065	0.469423	0.249159
sense_intrc	-	14	12	27	16	24	19	2.765574	2.79348	7.02839	2.734263	5.326202	3.730101
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.142457	0
lincRNA	-	15	14	20	45	33	23	1.157602	1.273219	2.033915	3.004301	2.861086	1.764028
pseudogen	HIV-1_Tat_	17	12	15	12	1	0	1.426303	1.186454	1.658398	0.870978	0.094257	0
antisense	-	0	0	0	16	9	18	0	0	0	1.185732	0.866154	1.532448
lincRNA	-	0	7	0	9	1	4	0	0.796924	0	0.752172	0.108533	0.384044
pseudogen	-	78	62	59	35	30	52	7.347682	6.882632	7.323903	2.852245	3.174871	4.868204
pseudogen	-	0	0	2	0	0	0	0	0	0.368144	0	0	0
pseudogen	-	1	4	0	0	0	1	0.195354	0.920852	0	0	0	0.194148
pseudogen	-	0	0	0	0	1	1	0	0	0	0	0.086072	0.076142
lincRNA	-	1	0	1	0	0	0	0.019092	0	0.025158	0	0	0
lincRNA	-	0	0	2	0	0	4	0	0	0.20732	0	0	0.312714
pseudogen	-	0	2	0	0	0	0	0	0.952484	0	0	0	0
lincRNA	-	3	5	0	3	6	4	0.166831	0.327667	0	0.144324	0.374848	0.221067
lincRNA	-	0	0	0	4	0	0	0	0	0	0.367125	0	0
pseudogen	-	5	2	3	5	2	0	0.296091	0.13957	0.234105	0.256146	0.133056	0
lincRNA	-	3	0	2	0	0	5	0.373701	0	0.328298	0	0	0.618989
lincRNA	-	0	0	0	3	1	0	0	0	0	0.296753	0.128458	0
pseudogen	-	2	0	1	0	0	0	0.426943	0	0.281304	0	0	0
pseudogen	-	0	4	0	2	3	0	0	0.205223	0	0.075327	0.146733	0
pseudogen	-	6	1	4	0	3	2	0.844803	0.165925	0.742163	0	0.474542	0.279862
pseudogen	-	1	1	2	1	1	3	0.118969	0.140197	0.313543	0.102919	0.133654	0.354701
pseudogen	-	0	1	0	1	0	0	0	0.264355	0	0.194063	0	0
lincRNA	-	0	3	0	0	0	2	0	0.287943	0	0	0	0.161889
pseudogen	-	6	0	0	0	0	3	0.664531	0	0	0	0	0.330214
lincRNA	-	4	0	2	1	1	5	0.368285	0	0.242655	0.07965	0.103436	0.457513
pseudogen	-	1	0	1	7	0	2	0.108486	0	0.142958	0.656952	0	0.215631
sense_intrc	-	167	143	145	209	162	106	2.268706	2.289311	2.59576	2.456241	2.47244	1.431124
processed_	-	0	0	0	0	0	2	0	0	0	0	0	0.077431
pseudogen	-	0	0	1	1	2	2	0	0	0.129672	0.085128	0.2211	0.195591
pseudogen	-	0	0	0	0	7	0	0	0	0	0	0.730406	0
sense_intrc	-	5	10	5	7	9	3	0.568036	1.338792	0.748533	0.687966	1.148677	0.338717
pseudogen	-	0	0	8	2	0	0	0	0	0.446842	0.073337	0	0
processed_	-	0	0	2	0	0	3	0	0	0.137059	0	0	0.155051
antisense	-	0	1	2	51	54	65	0	0.018741	0.041912	0.701635	0.964764	1.027309
pseudogen	-	0	3	0	0	0	0	0	0.719858	0	0	0	0
pseudogen	-	0	2	0	0	1	0	0	0.765494	0	0	0.364883	0
pseudogen	-	1	4	1	3	1	0	0.047269	0.222813	0.062289	0.122676	0.053103	0

pseudogen	-	1	0	0	0	0	0	0.51399	0	0	0	0	0
pseudogen	-	0	0	0	0	1	0	0	0	0	0	0.030865	0
pseudogen	-	1	1	3	6	10	1	0.026751	0.031525	0.105755	0.138855	0.300535	0.026586
pseudogen	-	0	2	0	0	0	0	0	0.363777	0	0	0	0
pseudogen	-	0	1	1	0	2	0	0	0.253609	0.283591	0	0.483544	0
pseudogen	-	0	4	1	124	127	92	0	0.419413	0.117249	9.544646	12.69486	8.135282
pseudogen	-	473	432	350	231	357	387	9.165846	9.865117	8.937463	3.872455	7.771926	7.453015
pseudogen	-	0	1	1	3	7	1	0	0.223612	0.250048	0.492461	1.492227	0.188581
sense_intrc	-	97	136	128	127	116	103	1.393562	2.302505	2.423256	1.578415	1.872241	1.470623
pseudogen	-	2	0	1	11	1	6	0.180686	0	0.11905	0.859706	0.101495	0.53871
lincRNA	-	1	0	1	5	0	0	0.049991	0	0.065877	0.216237	0	0
pseudogen	-	2	1	1	0	1	1	0.50181	0.295676	0.330632	0	0.281876	0.249356
pseudogen	-	0	0	0	0	4	0	0	0	0	0	10.34364	0
pseudogen	-	2	0	2	1	0	5	0.207205	0	0.273046	0.089626	0	0.514815
pseudogen	-	5	11	5	36	46	37	0.470169	1.218943	0.619567	2.928527	4.859489	3.457762
lincRNA	-	0	2	2	8	10	9	0	0.173782	0.194327	0.510294	0.828355	0.659508
lincRNA	-	14	4	10	14	9	12	0.665327	0.224013	0.626241	0.57557	0.480506	0.566758
antisense	-	4	2	1	1	0	5	0.550036	0.324092	0.181203	0.118958	0	0.683299
sense_intrc	-	8	2	0	3	2	2	1.772083	0.522073	0	0.574882	0.497706	0.440285
pseudogen	-	1	2	2	1	1	3	0.147468	0.347564	0.388653	0.127574	0.165671	0.439672
lincRNA	-	17	36	18	60	20	15	0.562147	1.402847	0.784347	1.716386	0.742985	0.492949
pseudogen	-	3	7	5	3	3	7	0.20258	0.557033	0.444919	0.175251	0.227586	0.469768
lincRNA	-	0	0	0	6	3	0	0	0	0	0.540932	0.351236	0
pseudogen	-	0	0	1	0	0	0	0	0	0.15299	0	0	0
pseudogen	-	0	0	2	0	0	0	0	0	0.450086	0	0	0
lincRNA	-	0	3	4	1	2	5	0	0.126291	0.188295	0.030903	0.080264	0.17751
pseudogen	-	0	1	0	0	0	0	0	0.23279	0	0	0	0
pseudogen	-	1	0	0	0	0	0	0.096784	0	0	0	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.549317	0	0	0
protein_co	mast_cell_i	9	10	7	2	0	1	0.755101	0.988712	0.773919	0.145163	0	0.083382
pseudogen	-	3	3	4	1	1	1	0.510685	0.601811	0.897277	0.147263	0.191241	0.169177
pseudogen	-	0	0	0	0	0	1	0	0	0	0	0	0.276916
pseudogen	-	2	0	0	0	0	0	0.350603	0	0	0	0	0
lincRNA	-	36	26	20	44	31	54	0.524746	0.446608	0.384159	0.554833	0.507641	0.782257
pseudogen	-	2	3	0	0	0	0	0.167006	0.29521	0	0	0	0
pseudogen	-	0	0	1	0	0	0	0	0	0.082658	0	0	0
pseudogen	-	0	0	0	1	0	3	0	0	0	0.119892	0	0.413199
antisense	-	0	0	2	8	2	1	0	0	0.228732	0.600641	0.195003	0.086253
pseudogen	-	0	0	0	0	0	2	0	0	0	0	0	0.182371
pseudogen	-	0	0	3	0	1	0	0	0	0.134939	0	0.038347	0
pseudogen	-	0	1	1	0	0	0	0	0.097026	0.108497	0	0	0
lincRNA	-	17	11	12	50	42	42	0.712587	0.543361	0.662834	1.8131	1.977821	1.749636
pseudogen	-	3	1	1	1	7	4	1.430838	0.562052	0.628498	0.412603	3.750734	1.896002
lincRNA	-	21	26	10	3	2	19	0.444171	0.648055	0.278719	0.054893	0.047524	0.399388

pseudogen	-	1	0	0	0	0	0	0.134368	0	0	0	0	0
lincRNA	-	0	0	2	0	0	0	0	0	0.115311	0	0	0
pseudogen	-	0	1	0	2	1	0	0	0.157944	0	0.231893	0.150572	0
antisense	-	2	4	1	4	2	6	0.222441	0.524267	0.146562	0.384865	0.249899	0.663202
pseudogen	-	0	0	0	2	0	0	0	0	0	0.085605	0	0
pseudogen	-	6	6	10	2	3	11	0.290088	0.341851	0.637108	0.083651	0.162948	0.528543
pseudogen	-	2	0	0	0	0	0	0.109836	0	0	0	0	0
pseudogen	-	3	0	0	0	0	0	0.340822	0	0	0	0	0
pseudogen	-	0	0	0	0	0	4	0	0	0	0	0	0.444
pseudogen	-	0	7	0	0	0	0	0	2.799449	0	0	0	0
pseudogen	-	0	0	0	0	2	0	0	0	0	0	0.432552	0
pseudogen	-	0	0	0	1	1	0	0	0	0	0.079237	0.1029	0
pseudogen	-	1	0	0	0	0	0	0.10084	0	0	0	0	0
lincRNA	-	4	0	4	0	0	0	0.299102	0	0.394143	0	0	0
pseudogen	-	0	8	3	8	9	4	0	0.81023	0.339756	0.594791	0.868966	0.34165